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Global Responses and Interdisciplinary Research Towards Eliminating Tropical Diseases

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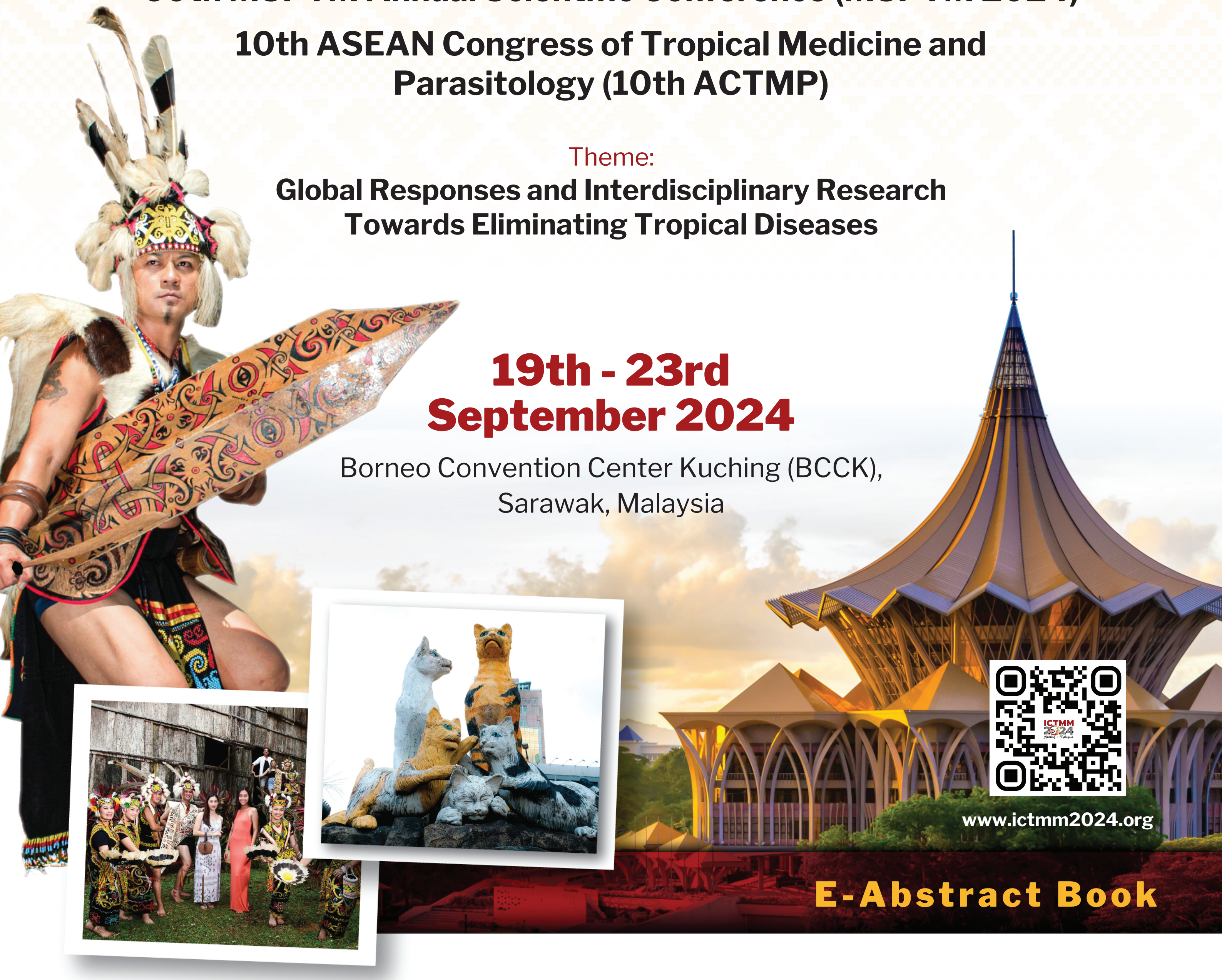

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ICTMM 2024 CONGRESS ABSTRACT BOOK

INVITED SPEAKERS – KEYNOTE & PLENARY

INVITED SPEAKERS – KEYNOTE & PLENARY

Keynote

Plenary

Abstract Reference: 20539
Mode of Presentation: Invited Speaker - Keynote
Topic: ICTMM 2024 Invited Speaker

The M&Ms: Malaria, man and monkeys

Balbir Singh*[1]

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Abstract Content

Long-tailed and pig-tailed macaques, the most common non-human primates in Southeast Asia, are natural hosts of *Plasmodium knowlesi*, *P. cynomolgi*, *P. inui*, *P. fieldi*, *P. coatneyi* and *P. simiovale*. Naturally-acquired human infections with these simian malaria parasites were thought to be extremely rare, until a large number of human infections with *P. knowlesi* was reported in 2004 in Sarawak, Malaysian Borneo. Subsequently, knowlesi malaria cases were described throughout Southeast Asia, together with a small number of human infections with *P. cynomolgi*, *P. inui*, *P. coatneyi*, *P. fieldi* and *P. simiovale*. Zoonotic malaria cases have continued to rise and in Malaysia alone, 22,759 knowlesi malaria cases have been reported from 2017-2023. The reasons for this rise will be discussed, together with the molecular, entomological and epidemiological data that indicates knowlesi malaria is primarily a zoonosis. Methods that are currently used to prevent and control human-to-human transmission of malaria, such as insecticide-treated bed nets and indoor residual spraying of houses, will be ineffective against zoonotic malaria since the vectors are exophilic and exophagic. In order to control zoonotic malaria, it is essential to develop novel methods of control directed mainly at the vectors and the non-human primate hosts. It remains to be seen whether *P. knowlesi* and other simian malaria parasites continue as zoonotic infections or whether ecological changes due to changes in land use, with an associated increase in the human population and alterations in mosquito biting behaviour, result in these parasites switching to humans as the preferred host.

Abstract Reference: 20988
Mode of Presentation: Invited Speaker - Keynote
Topic: ICTMM 2024 Invited Speaker

Antimalarial drugs: Past, present and future

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Abstract Content

It is 100 years since the first synthetic antimalarial drug (plasmoquine or pamaquine) joined the Cinchona alkaloids (mainly quinine) upon which malaria treatment had relied upon for the preceding three centuries. This was followed in 1932 by mepacrine (quinacrine) and in 1934 by chloroquine. Then, in the following 20 years, came proguanil, pyrimethamine, amodiaquine, and primaquine. Indirectly the Vietnam war led to mefloquine and, from China, the artemisinin derivatives, piperaquine, lumefantrine and pyronaridine. These are the main antimalarial drugs we rely upon today with artesunate the treatment of choice for severe malaria, and artemisinin-based combination treatments (ACTs) for uncomplicated malaria. Preventive chemotherapy with slowly eliminated compounds is also widely deployed in high transmission settings. Antimalarial drug resistance is the main threat, particularly the emergence and spread of artemisinin resistance in East Africa. It has proved harder than expected to develop new antimalarials, so for the foreseeable future we must rely on existing drugs. Triple ACTs comprising an artemisinin derivative with two slowly eliminated antimalarial compounds offers the best prospect for combatting resistance and preserving therapeutic efficacy.

Abstract Reference: 20139
Mode of Presentation: Invited Speaker - Plenary
Topic: ICTMM 2024 Invited Speaker

A naturally isolated symbiotic bacterium suppresses flavivirus transmission by *Aedes* mosquitoes

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Abstract Content

The commensal microbiota of the mosquito gut plays a complex role in determining the vector competence of arboviruses. Here, we identified a bacterium from the gut of field Aedes albopictus mosquitoes, named Rosenbergiella sp. YN46 (Rosenbergiella_YN46), that rendered mosquitoes refractory to infection with dengue and Zika viruses. Inoculation of Rosenbergiella_YN46 into Aedes mosquitoes effectively prevents viral infection. Mechanistically, this bacterium secretes glucose dehydrogenase (RyGDH), which acidifies the gut lumen of fed mosquitoes, causes an irreversible conformational changes in the flavivirus envelope protein thus prevents viral entry into cells. In semi-field conditions, Rosenbergiella_YN46 exhibits effective transstadial transmission in field mosquitoes, which blocks transmission of dengue virus by newly emerged adult mosquitoes. The prevalence of Rosenbergiella_YN46 is greater in mosquitoes from low-dengue areas than in those from dengue-endemic regions. Rosenbergiella_YN46 may offer an effective and safe lead for flavivirus biocontrol.

Abstract Reference: 20140
Mode of Presentation: Invited Speaker - Plenary
Topic: ICTMM 2024 Invited Speaker

Dengue is on the increase: New tools needed for surveillance

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Abstract Content

Dengue continues to be the number one arboviral disease on a global scale. Vector control is the hallmark of dengue control programme in most countries. However, the current program lacks sensitivity and proactivity. Fogging and ULV are being carried out when cases are reported. ULV is known to be ineffective since the insecticide droplets only reach the living rooms. Dengue cases have increased over the years perhaps since asymptomatic people are infectious to mosquitoes. Thus, new proactive tools are required. Novel techniques such as the release of genetically modified mosquitoes (RIDL), sterile males and use of *Wolbachia* to control the population of the *Ae. aegypti* are currently undergoing trials in many countries. However, it is imperative to carry out control measures based on positive adult mosquitoes. A randomised control trial was conducted to determine the efficacy of a combination of gravid oviposition sticky (GOS) traps and dengue non-structural 1 (NS1) antigen for early surveillance of dengue among *Aedes* mosquitoes. Detection of NS1 positive mosquitoes were significantly associated with occurrence of dengue cases. The result of this randomized control trial further supports the notion that dengue surveillance using GOS trap and dengue NS1 test can detect dengue-positive mosquitoes before dengue cases were reported. This is the first study that demonstrates a dengue surveillance system which can capture asymptomatic, dengue-viraemic individuals living in an area with infected mosquitoes. In conclusion infected *Aedes* mosquitoes can serve as an early warning and should be the way forward for proactive dengue surveillance and control measures.

Abstract Reference: 20147
Mode of Presentation: Invited Speaker - Plenary
Topic: ICTMM 2024 Invited Speaker

Gram-negative healthcare associated infections – Another tropical scourge?

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Abstract Content

As we succeed in eliminating many so-called tropical diseases such as malaria, lymphatic filariasis and other parasitic infections, we are becoming more aware of other infections that are more common in tropical than temperate countries. These include gram-negative bacterial infections. Unlike parasitic diseases, these tend to affect high income as well as low income countries in the region. Many of us are familiar with melioidosis which is well known as a tropical scourge which remains a challenge however, other gram negative community acquired bacterial infections including hypervirulent Klebsiella and also Acinetobacter are more common in the region that in the North. In addition, healthcare acquired infections in the tropics have a different epidemiology to what has been recognised in Europe and North America. This is not just an academic matter. It has implications for guideline development, the use of diagnostics and the development of therapeutics. There are plenty of opportunities for talented parasitologists and no danger of any of us losing our jobs in the near future!

Abstract Reference: 20964
Mode of Presentation: Invited Speaker - Planery
Topic: ICTMM 2024 Invited Speaker

Gut and skin microbiome of indigenous peninsular Malaysians (Orang Asli): Insights into urbanization and infections

Yvonne Ai-Lian Lim[*1], Soo Ching Lee[2], Mian Zi Tee[1], Yi Xian Er[1], Azdayanti Muslim[3, 4], Nan Jiun Yap[1], Leslie Thian Lung Than[5], Heidi H. Kong[6], Julia A. Segre[7], P'ng Loke[2]

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Abstract Content

As societies become more urbanized, there are significant changes in lifestyle, diet, and exposure to environmental factors. These changes can affect the composition of the human microbiome as well as the burden of diseases and infections. Currently, microbiome data is overrepresented by data available from industrialized countries and under-represented for indigenous communities worldwide, especially those in Southeast Asia. It is crucial to record the remote or traditional Orang Asli (Indigenous Peninsular Malaysians)'s microbiome before they blend in with the urban microbiome. Besides, it would be valuable to elucidate the disease profiles of these communities with different levels of urbanization. Hence, a comparative study of gut and skin microbiomes across different populations with various levels of urbanization, spanning a gradient of rural, remote communities to acculturated, market-integrated urban areas will be presented which would provide valuable insights into the effects of urbanization on microbial community structure and associated health implications, and expand the global repository of microbiome data. In addition, comparison between healthy samples and infected samples from these populations will grant us the opportunity to study the impact of infections on the host microbiome. Understanding these interactions holds promise for elucidating novel avenues of research in both infectious diseases and microbiome science, with potential implications for human health and disease.

Abstract Reference: 20995
Mode of Presentation: Invited Speaker - Plenary
Topic: ICTMM 2024 Invited Speaker

Diagnostics – The key to unlocking the advocacy of a One Health approach for controlling zoonotic ancylostomiasis

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Abstract Content

Over the last 15 years, the canine and feline hookworm, *Ancylostoma ceylanicum*, has emerged as the second most common hookworm infecting humans in the Asia Pacific. Despite growing case reports describing the ability of this hookworm to cause severe abdominal pain, weight loss, diarrhoea, vomiting, melena, anaemia and hyper-eosinophilia, no population-level morbidity data exists for humans. Initially presumed to be confined to the Asia Pacific, *A. ceylanicum* has now been detected in humans and animals in parts of Africa as well as Central America and the Caribbean. High-throughput species-specific quantitative real-time PCR, and next-generation sequencing assays have proved invaluable in informing the epidemiology, geographical distribution, infection dynamics and population genetics of this zoonotic hookworm in animals and humans living in shared environments. This data, in turn, has informed mathematical models that reveal One Health interventions, targeting both dogs and humans, could suppress the prevalence of *A. ceylanicum* in humans to ≤ 1% by the end of 2030, even with only modest coverage (25–50%) of the animal reservoirs. As the World Health Organisation's newly launched 2030 RoadMap to accelerate the end of morbidity associated with Neglected Tropical Diseases ensues, quantitation of the population-level morbidity associated with this zoonotic canine and feline hookworm becomes increasingly important to effectively advocate for a 'One Health' approach for its control.

Abstract Reference: 20998
Mode of Presentation: Invited Speaker - Plenary
Topic: ICTMM 2024 Invited Speaker

Can prior bacterial or parasitic infection promote host resistance to SARS-COV2?

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Abstract Content

Susceptibility to infectious disease is governed by both host intrinsic and environmental factors. Recently, evidence has accumulated for an important role of previous unrelated microbial exposure as one environmentally determined influence. During the COVID-19 pandemic this mechanism was proposed as an explanation for why different global regions and societies appeared to suffer less from SARS-CoV2 infection and disease. In particular, childhood vaccination with BCG (a live bacterial vaccine) and helminth infection were hypothesized as microbial stimuli that might be stimulating non-specific protection against COVID in resource limited countries/regions. Here I will discuss work in which we used SARS-COV2 murine infection models to test this concept. While not directly supporting a major protective role for conventional intradermal BCG vaccination, our findings revealed an influence of lung migrating helminth infection as well as novel immunologic pathways in the control of this important virus.

This work was supported by the Intramural Research Program of the National Institute of Allergy and Infection Diseases, NIH, USA

Abstract Reference: 20999
Mode of Presentation: Invited Speaker - Plenary
Topic: ICTMM 2024 Invited Speaker

Global elimination of infectious diseases - Where are we now

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Abstract Content

Throughout history, infectious diseases have had significant impact on human life and on culture, economy, and society with several devastating plagues, including the Plague of Athens in the 5th century BC, and the Black Death in the 14th century to modern day pandemics characterised by AIDS and more recently COVID-19. However, over the last four decades advances in modern medicine, in particular the development of vaccines has made it possible that diseases once feared, such as small pox to be eliminated with polio close to being eradicated. Advances in diagnostics and therapeutics have also made it possible that AIDS, a disease that has taken the lives of more than 40 million people can be successfully controlled. Despite these successes, a myriad of common infectious diseases including TB, malaria and dengue and a range of neglected tropical diseases continue to cause significant morbidity and mortality particularly in low and middle income countries. The rising threat of antimicrobial resistance and zoonotic infections capable of causing the next pandemic poses continue to pose ongoing challenges for control and elimination of infectious diseases. Ultimately the global control of infectious diseases will not only rely on traditional biomedical and public health tools such as improved surveillance, vaccines, diagnostics and therapeutics, but also on multiple other factors that increase the risk of infectious diseases including climate change, global trade and human behaviour.

Abstract Reference: 21000
Mode of Presentation: Invited Speaker - Plenary
Topic: ICTMM 2024 Invited Speaker

Application of One Health approach in schistosomiasis elimination in China

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Abstract Content

Schistosomiasis japonica is one of zoonoses prevalent in the tropical and sub-tropical regions where resources limited, of which the transmission features that cross-species transmission between human and animals, the parasite has to complete its life cycle in multi-hosts including definite animal hosts and intermediate snail hosts, high burden of the disease affected to the human health hampering the local economic and social development, have brought difficulties to control and eliminate the disease. Schistosomiasis japonica had affected local people's health about 2000 years ago, while it has been well controlled through One Health approach in China where the prevalence rate has been under 1% since 2016 in all epidemic counties, and 95% of the epidemic counties have been eliminated with zero infection. Due to the nature of zoonotic disease, it is essential to implement One Health approach in the control and elimination of schistosomiasis japonica in China. We took the system review on how to design and implement the One Health approach in the control and elimination of schistosomiasis in China. The major intervention of One Health approach to control schistosomiasis in China included five components, such as taking leadership by governments along with multi-sectoral cooperation among National Health Commission, Ministry of Agriculture and Countryside, Ministry of Water Conservation, National Forestry and Grassland Administration, etc., adapting control strategy to the local settings with the programme progress, mobilization of local community along with education, information and communication. The integrated control intervention has been gained cost-effective performed in the highpo-endemic areas, including engineering project on agriculture and water conservation, WASH project subsided by local government, and ecological protection projects, etc. One of case study to explored the comprehensive model to eliminate schistosomiasis was carried out in Eryuan County, Yunnan Province of China, through integration with the ecological protection programme of the Erhai Lake. System modelling was performed using system dynamics software to establish a simulation model in order to evaluate the effectiveness of intervention activities. Results showed that implementing precise interventions could stop schistosomiasis transmission by means of controlling the source of infection, blocking the biological transmission chains and cutting off the route of disease transmission, along with the improvement of the ecological environment, from 2012 to 2017. As a result, the number of schistosomiasis infections both in humans and cattle was reduced to zero after ecological management approaches were initiated in Eryuan County, and the area of snail habitats was also reduced by 16.90%. It is concluded that One Health approach is able to improve the cost-effectiveness of the schistosomiasis elimination programme, thanks to the application of precise One Health interventions.

Abstract Reference: 21001
Mode of Presentation: Invited Speaker - Plenary
Topic: ICTMM 2024 Invited Speaker

Worldwide upsurge of communicable diseases – Emphasis on monkeypox: Why the new Public Health Emergency of International Concern (PHEIC) and how to manage it

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Abstract Content

This presentation prvides a comprehensive overview of the evolving epidemiology of the Monkeypox (Mpox) virus, focusing on the recent global outbreak and its implications for public health. The study examines the historical context of Mpox, its genetic diversity, and the changing patterns of transmission across different clades. The presentation provides a comprehensive overview of the four main Mpox clades (Ia, Ib, IIa, and IIb), highlighting their distinct epidemiological and clinical characteristics. The presentation explains the rapidly changing epidemiology of Mpox, the unprecedented spread of Clade IIb, and the rise of Clade Ib, which are attributed to factors such as increased global connectivity, changes in human behavior, and viral adaptations. The presentation emphasizes that 2024 has seen the highest number of yearly confirmed Mpox cases ever recorded. Study Methods include analysis of genomic data, epidemiological trends, and clinical characteristics across different Mpox clades. The work also explores the One Health approach, examining Mpox susceptibility in various animal species. Anthropogenic changes, including deforestation, urbanization, and climate change, are identified as key drivers of emerging infectious diseases like Mpox. These changes alter ecosystems, bringing humans into closer contact with wildlife reservoirs and creating conditions conducive to zoonotic spillover events. The presentation discusses the wide range of animal species susceptible to Mpox and other orthopoxviruses, emphasizing the importance of a holistic approach to disease control. Results demonstrate significant differences in transmission patterns, clinical presentations, and geographical distribution among Mpox clades. Limitations of current knowledge are addressed, including gaps in understanding asymptomatic transmission, the full extent of the animal reservoir, and the long-term evolutionary trajectory of the virus. It emphasizes the need for continued research into viral evolution, vaccine efficacy, and novel therapeutics. The presentation concludes by discussing the practical implications for disease control, stressing the need for enhanced surveillance, improved diagnostics, targeted interventions, and health equity. It calls for enhancing tech transfer and further research into vaccine efficacy against emerging strains and the development of novel therapeutics. The presentation calls for a multifaceted approach to Mpox control and urges the global health community to adopt a proactive stance, leveraging the One Health framework to mitigate the risks posed by Mpox and other emerging infectious diseases in our increasingly interconnected world.

Abstract Reference: 21002
Mode of Presentation: Invited Speaker - Plenary
Topic: ICTMM 2024 Invited Speaker

Malaria in India: How shifting epidemiology and changes in parasite transmission are challenging the road to elimination

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[2]*Department of Biomedical Engineering, Johns Hopkins University, Whiting School of Engineering, UNITED STATES*

Abstract Content

Malaria in India has declined over the past ~30 years, with an estimated 91% reduction in number of cases from 1990 to 2022. Recent projections indicate a continued decline in cases with the potential for reaching zero indigenous cases before 2030, the goal of the National Framework for Malaria Elimination 2016–2030. The decrease in burden has changed malaria epidemiology and transmission across the country, challenging the road to elimination and underlining the need to roll-out novel surveillance and control tools to ensure continued progress. For example, *Plasmodium* infections are more likely to be asymptomatic and submicroscopic, which complicates early diagnosis and prompt treatment, one of the stalwarts of the NFME program. With partnerships between several Indian and US- and UK-based institutes, research as part of the NIH-funded Center for the Study of Complex Malaria in India has documented the changing face of malaria epidemiology in India since 2010 and tested the effectiveness of tools such as reactive case detection and Odisha State’s Durgama Anchalare Malaria Nirakaran (malaria control in inaccessible areas) “malaria camps”. Our research and discoveries during the 14 years of the Center highlight what can be achieved with continuous, long-term funding, and underscore the importance of continuing basic and translational research on this important disease.

Abstract Reference: 21004
Mode of Presentation: Invited Speaker - Plenary
Topic: ICTMM 2024 Invited Speaker

Genomic epidemiology and phenotypic diversity of malaria parasites

David Conway*[1]

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Abstract Content

Research on malaria has been transformed by analyses of parasite genomes. Over the past 25 years, since the first complete genome sequences were made public, there has been accelerated impact on understanding molecular and cellular processes of infection and disease. Over the same period, using independent approaches malaria has been reduced in some parts of the world, while the burden remains very high in others. It is urgent that understanding of parasite biology and genomics should lead to improved diagnostic, therapeutic and preventive tools, and some promising approaches will be highlighted. Of equal importance, more recent scale up of population level genomic analyses has illustrated how existing tools may be better applied and targeted in specific situations, and some of these advances will be illustrated. Remaining challenges include understanding complex parasite phenotypes, and host-parasite interactions that affect virulence and transmission, indicating the importance of large-scale population studies for the future.

Abstract Reference: 21005
Mode of Presentation: Invited Speaker - Plenary
Topic: ICTMM 2024 Invited Speaker

Public Health Implications of Inter-Species Transmission of SARS-CoV-2

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Abstract Content

The coronavirus disease 2019 (COVID-19) pandemic, caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), represents the most devastating global infectious disease catastrophe in a century and continues to affect millions worldwide. The virus has redefined our understanding of viral zoonotic transmission, particularly its interspecies spread. Evidence reveals SARS-CoV-2's ability to infect a broad range of animal species, with documented human-animal-human transmission. We discovered widespread natural infection in white-tailed deer in the USA—the first instance of SARS-CoV-2 in a free-living animal. In addition, multiple instances of infections have been observed in captive and free-living animal species across the globe. The virus is now known to infect at least one species in nearly every mammalian order. The ongoing circulation of SARS-CoV-2 in non-human animal hosts poses substantial risks, including the emergence of novel variants and recombination with endemic coronaviruses. Additionally, there is evidence of continued circulation of ancestral SARS-CoV-2 lineages in animal populations long after they disappeared from human circulation. These developments underscore the urgent need for a coordinated One Health approach to monitor interspecies transmission and mitigate zoonotic spillover risks. This seminar will explore the public health implications of interspecies transmission of SARS-CoV-2, focusing on its evolutionary trajectory in animal hosts and emphasizing the vital role of integrated surveillance in addressing these challenges.

SYMPOSIUM

CALL FOR SYMPOSIUM

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Abstract Reference: 20821
Mode of Presentation: Symposium
Topic: Call for Symposium

Perspectives from a low-resource clinical diagnostic lab for the detection of zoonotic malaria

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Abstract Content

In the Malaysian clinical setting, microscopy remains the reference standard for screening and diagnosis of zoonotic malaria. It is also currently the only method that allows both observation of parasite morphology and quantification. The looming threat of zoonotic malaria, in particular *P.knowlesi*, has brought to light the need for more skilled microscopists. Despite conventional light microscopy being known as a 'low-resource' tool, maintenance of highly skilled personnel are vital for malaria microscopy to be effective. The core of this talk will be to share experiences and lessons learnt from a resource-limited diagnostic laboratory in Sabah, located within an area endemic for *P.knowlesi.* The talk will begin with a brief introduction on our facilities and services. This will be followed by a discussion on the challenges of maintaining diagnostic capability whilst balancing quality amidst limited resources, ending with the solutions we have employed to overcome them.

Abstract Reference: 20778
Mode of Presentation: Symposium
Topic: Call for Symposium

The challenge of zoonotic malaria in Sabah, Malaysia

Kamruddin Ahmed*[1]

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Abstract Content

In 2004, a large cluster of patients with *Plasmodium knowlesi* malaria were detected in Sarawak state of Malaysia. Subsequently by analyzing archival samples, it was proved that infection with this parasite has occurred in Malaysia at least since the 1990s. Since 2008, Malaysia has reported more than 25,795 cases of knowlesi malaria and about 61 deaths. Malaysia has shown a tremendous achievement in controlling human malarial parasites, since 2018 no indigenous case of human malaria has been reported. However, *P. knowlesi* malaria remains a major challenge to control, particularly in Sabah one of the two states of Malaysia situated in Borneo Island. Every year Sabah has been reporting the highest number of *P. knowlesi* malaria from Malaysia. The reasons for the increase of *P. knowlesi* malaria are not known however, we've identified some potential factors which might be contributing to this increase. Based on those we've recognized several measures which might be useful for zoonotic malaria control: (i) Development of point of care diagnostics and proactive surveillance; (ii) Intervention strategies based on advanced data analytics; (iii) Inter-sectoral cooperation; and (iv) Community engagement with involvement of women. More studies are needed to implement these measures to control zoonotic malaria.

Abstract Reference: 20824
Mode of Presentation: Symposium
Topic: Call for Symposium

Plasmodium pitheci infections in wild orangutans (*Pongo pygmaeus*) in West Kalimantan, Borneo

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Abstract Content

Bornean orangutans, categorized as critically endangered by the IUCN, are threatened with extinction. A potential additional threat to vulnerable populations is the risk of infectious diseases such as malaria. Natural infections with *Plasmodium* spp., sometimes with high prevalence, are widely reported in populations of great apes within their range, although clinical implications are unknown. Altered conditions in disturbed/human-modified habitats as well as anthropogenic climate changes affect host behaviour and ecology of threatened populations of orangutans, and their vectors. These changes might affect *Plasmodium* spp. transmission dynamics, potentially increasing the risk of detrimental malaria health effects. This study was conducted in a population of wild Bornean orangutans undergoing rehabilitation at a Rescue Rehabilitation Centre (RRC) in West Kalimantan, Borneo. The study spanned over a decade of observations, and evaluated health impacts as well as epidemiological characteristics of orangutan malaria caused by *Plasmodium pitheci*. Moderate to severe illness was detected in 14% of infected orangutans, providing evidence that this parasite can be pathogenic in orangutans as their natural host. Diagnostic criteria and treatment of acute malaria illness was defined and suggested to work similarly as in humans. Furthermore, the study investigated aspects of malaria immunity in orangutans which is influenced by age and exposure, suggesting the existence of a natural non-sterilising immunity that affects malaria outcomes and resembles that in humans. In a rapidly changing environment, conservation strategies for free-roaming orangutan populations or at RRCs might need to include consideration of vulnerability to *P. pitheci*.

Abstract Reference: 20979
Mode of Presentation: Symposium
Topic: Call for Symposium

Zoonotic Plasmodium among primates in Southeast Asia: Prevalence, spatial distribution and risk factors for infection

Reuben Sharma*

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Abstract Content

Zoonotic malaria is of major concern in Southeast Asia and poses a serious challenge to malaria control and elimination in the region. The major sylvatic non-human primate reservoir hosts (*Macaca* spp.) are widespread and have adapted to various natural and human-altered habitats. With the increasing anthropogenic alterations in the landscape, many species of wild animals, including Macaques are displaced from their natural habitat. This has significantly altered the transmission dynamics and risk factors for infection of various zoonotic diseases. The present study highlights aspects of zoonotic malaria in Southeast Asia, including spatial distribution patterns, molecular epidemiology, and risk factors for infection among non-human primates. It also addresses the potential impact of anthropogenic habitat alteration and landscape fragmentation on the infection with zoonotic *Plasmodium* spp. among Long-tailed Macaques (*Macaca fascicularis*), with emphasis on studies conducted in Peninsular Malaysia and Borneo. The increasing prevalence of zoonotic *Plasmodium* infection among synanthropic Macaques poses a significant risk for urban transmission; a situation awaiting only the presence of competent mosquito vectors.

Abstract Reference: 20802
Mode of Presentation: Symposium
Topic: Call for Symposium

The evolution of zoonotic malaria

Richard Culleton*[1]

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Abstract Content

Zoonotic malaria occurs when a malaria parasite species of non-human primates infects humans. *Plasmodium knowlesi*, a parasite of macaque monkeys in Southeast Asia is now the major cause of human malaria in Malaysia, and it has recently been discovered that other macaque malaria parasite species can also cause disease in humans. Malaria parasites are consummate host-switchers, with the evolutionary history of the genera *Plasmodium* influenced by many examples of parasite promiscuity. By tracing the evolutionary history of multiple species, I will attempt to explain how today's 'human' malaria parasites evolved to parasitise *Homo sapiens*, and discuss how malaria parasites are particularly suited to jumping species barriers.

Abstract Reference: 20829
Mode of Presentation: Symposium
Topic: Call for Symposium

Highlighting malaria in Uganda with an assessment of an associated risk of infection within semi-captive chimpanzees

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Abstract Content

In this presentation, I first review our team's past work on public health mapping initiatives in Uganda to monitor malaria and intestinal schistosomiasis amongst preschool-aged children and their mothers. Drawing upon general observations along the shoreline of Lake Victoria as well as seminal infection dynamic studies that detected treatment failure(s) against *Plasmodium falciparum*, *Plasmodium ovale* & *Plasmodium malariae*, I place attention on the unusual setting of the Ngamba Island Chimpanzee Sanctuary (NCIS). Here, within this semi-captive setting, just under 40 rescued chimpanzees are held. Like humans nearby, these animals are vulnerable to malaria and intestinal schistosomiasis. Indeed, over the last two decades, regular monitoring of these animals' health has been undertaken; most recently this year, an analysis of *Plasmodium* spp. within faeces and blood took advantage of real-time PCR assays. Analysis of preliminary results points towards cryptic infections in certain animals, with the pro and con of faecal detection assays discussed. Our appraisal is then set within the newly recognised deeper evolutionary origins of malaria within non-human primates, alongside today's interplay between animal conservation and anthropozoonosis.

Abstract Reference: 20025
Mode of Presentation: Symposium
Topic: Call for Symposium

Hybridization in Urogenital Schistosomiasis (HUGS) in Malawi: Connecting human schistosomes, and their hybrids, with bovine transmission

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Abstract Content

In southern Malawi, the putative origin(s) of newly described *Schistosoma haematobium-mattheei* hybrid human schistosomes was assessed upon a seminal molecular parasitological survey of local cattle. Using miracidia hatch test (MHT) and carcass inspection at slaughter, mean prevalences of bovine schistosomiasis, in 338 and 155 sampled cattle, were 49.1% (95% CI: 43.7-54.6%) and 10.3% (95% CI: 6.0-16.2%), respectively. Significant spatial heterogeneities were observed, with approximately 2.0% of infected cattle, and only those from Mangochi District, shedding *S. haematobium-mattheei* and/or *S. haematobium* miracidia in feces. This is the first formal incrimination of these hybrid and human schistosomes in contemporary bovine transmission. To quantify schistosome (re)infection dynamics, where a *S. haematobium-mattheei* hybrid was present, we undertook a novel pilot GPS-datalogging sub-study within a specific herd of cattle (n=8) on the Lake Malawi shoreline. Concurrently, we conducted a praziquantel (40 mg/kg) treatment efficacy check across these animals, with stepped-up fecal sampling. Whilst praziquantel treatment was effective in the short-term, by six weeks reinfection was was first noted with all animals again shedding schistosome eggs in their faeces by three months. To surmise, infections with *S. mattheei* are particularly common in cattle and demonstrate a previously cryptic burden of bovine schistosomiasis. Within Mangochi District, bovine transmission of both *S. haematobium-mattheei* hybrids and *S. haematobium* are now incriminated, with unequivocal evidence of contemporary zoonotic spill-over. Future control of urogenital schistosomiasis here in southern Malawi needs to develop, then successfully integrate, a One Health approach with appropriate mitigating strategies to reduce and/or contain bovine schistosomiasis transmission.

Abstract Reference: 20832
Mode of Presentation: Symposium
Topic: Call for Symposium

Integrating home self-sampling for female genital schistosomiasis, HPV, HIV and Trichomonas: Baseline results from the Zipime Weka Schista Study in Zambia

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Abstract Content

Around 40 million women living in Sub-Saharan Africa (SSA) are affected by female genital schistosomiasis (FGS), a chronic gynaecological disease caused by the waterborne parasite, *Schistosoma haematobium (Sh)*. FGS is associated with infertility, dyspareunia and symptoms mimicking sexually transmitted infections. Awareness of the disease is largely absent in endemic communities despite growing evidence of increased prevalence of HIV and suggestion of increased cervical dysplasia, the precursor of cervical cancer (CC). Conventional FGS diagnosis is challenging, as it relies on costly equipment and high-level specialised training seldom available in resource-limited countries. Accurate estimation of disease burden is therefore hindered. Genital self-sampling for the diagnosis of female genital schistosomiasis (FGS) was a novel and bold strategy piloted in 2018 in the BILHIV study in Zambia. Results of the study revealed that parasite DNA detection of *Schistosoma haematobium*, from self-sampling strategies were comparable to those samples obtained by a trained midwife. Self-sampling strategies have already been validated for the detection of oncogenic human papillomavirus (HPV) genotypes, the etiological agents of CC and HPV point-of-care diagnostic tests are now commercially available Genital self-swabs are well accepted by participants and are known to increase compliance across settings. The ongoing Zipime Schista Study! In Zambia is a longitudinal cohort study aiming to include multiple-pathogen screening through self-sampling (Sh, HPV) and offering self-testing for HIV and STIs. This strategy is coupled with novel molecular assays that are field deployable and can provide a scalable cost-effective strategy. The study design and preliminary results will be presented.

Abstract Reference: 20843
Mode of Presentation: Symposium
Topic: Call for Symposium

Unravelling parasitic syndemics: Female genital schistosomiasis and trichomoniasis among women in Southern Malawi

Dingase Kumwenda*[1], Lucas Cunningham, J. Russell Stothard, Sekeleghe A. Kayuni, Bright Mainga, David Lally, Priscilla Chammudzi, Donales Kapira, Gladys Namacha, Alice Chisale, Tereza Nchembe, Luis Kinley, Ephraim Chibwana, Bessie Ntaba, Gilbert Chapweteka, Waleke Khumalo, Henry Chibowa, Victor Kumfunda, John Archer, Alexandra Juhasz, Sam Jones, John Chiphwanya, Peter Makaula, E. James LaCourse, Janelisa Musaya

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Abstract Content

Female Genital Schistosomiasis (FGS) is a neglected tropical disease often misdiagnosed as a sexually transmitted infection (STI) due to similar symptoms. The MORBID-FGS study revealed that 27% of women with schistosomal eggs in Malawi had hidden FGS. This longitudinal study, part of the Hybridisation in Urogenital Schistosomiasis (HUGS) project, investigated FGS prevalence and co-existence with trichomoniasis among women in Mangochi and Nsanje districts. To determine the prevalence of FGS and its co-existence with trichomoniasis among women in Malawi, within the HUGS study. Eighty-eight women aged 18 and above with microscopic evidence of schistosoma eggs in their urine were enrolled. They underwent colposcopic examination, tissue sampling, DNA analysis, cervical cancer screening, and ultrasound examinations. FGS was detected in 18.2% of women on microscopy, 47.1% on colposcopy, and 54.0% on qPCR. Five women had S. mattheei co-infections. Strikingly, 73.3% had Trichomonas vaginalis co-infections, and 42.5% had detectable Human papilloma virus (HPV). All women with cervical tissue biopsies had histologically confirmed FGS. These results indicate a high burden of FGS and trichomoniasis among women in this region. The importance of screening for FGS when treating women for STIs in schistosomiasis-endemic areas is also highlighted. It also calls for the integration of FGS screening and treatment into existing sexual and reproductive health services.

Abstract Reference: 20846
Mode of Presentation: Symposium
Topic: Call for Symposium

Malawi's approach in controlling genital schistosomiasis

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Abstract Content

Genital schistosomiasis (GS) is a neglected tropical disease affecting both men and women. In Malawi, efforts to combat GS have gained momentum through multi-sectoral coordination and integrated approaches. Key policy measures include incorporating female genital schistosomiasis (FGS) into national guidelines for sexually transmitted infections (STIs). This integration aims to raise awareness, improve diagnosis, and ensure proper care for affected individuals. Additionally, addressing male genital schistosomiasis (MGS) remains crucial, although specific policies for MGS are less documented. Challenges include misdiagnosis due to symptoms resembling other STIs. Training programs for clinicians and health workers play a vital role in early detection and care. Malawi's commitment to eliminating GS underscores the importance of country-owned solutions in the fight against neglected diseases.

Abstract Reference: 20826
Mode of Presentation: Symposium
Topic: Call for Symposium

Pilot studies on female and male genital schistosomiasis in Cameroon

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Abstract Content

The magnitude of female genital schistosomiasis (FGS) and male genital schistosomiasis (MGS) is still unknown in Cameroon. Furthermore, knowledge about these neglected diseases is limited among health staff. FGS is associated with HIV infection and is a risk factor for HIV acquisition. To assess the level of FGS and the feasibility of gynecological screening, preliminary investigations were conducted in two different primary care settings in the East region of Cameroon. A comparative cross-sectional study was conducted among HIV positive women in HIV clinics and in the general population through mobile pop-up clinics. For MGS, a study was conducted in two villages endemic for schistosomiasis in the Adamawa region to investigate the impact of *Schistosoma haematobium* or *S. mansoni* infection on the reproductive function of men of reproductive age. A medical examination was performed to measure the testes' circumference and evaluate genital tract pathologies. The results showed that typical FGS lesions were present in more than half of women examined. For the MGS investigation, the results demonstrated that infection with *S. haematobium* or *S. mansoni* was associated with low production of the reproductive hormone testosterone and may be a significant cause of male infertility. The presentation will highlight and discuss some of the key findings and the need for large-scale studies on FGS and MGS in Cameroon.

Abstract Reference: 20976
Mode of Presentation: Symposium
Topic: Call for Symposium

Putting a spotlight on *Trichomonas vaginalis* and exploring genomic markers associated with drug resistance

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Abstract Content

Trichomonas vaginalis is the most common non-viral sexually transmitted infection and gives rise to trichomoniasis. The disease is associated with adverse pregnancy outcomes and low birthweight babies. However, only a subset of *T. vaginalis* infections are symptomatic in women and the majority of men with *T. vaginalis* infections are asymptomatic. In Africa where the disease might be present alongside urogenital schistosomiasis, like *Schistosoma haematobium,* the parasite disrupts the epithelial membrane of the genitourinary tract, thereby compromising the first line of defense against HIV and other sexually transmitted viral agents. Women with *T. vaginalis* infections are both more susceptible to acquisition of HIV as well as transmission to their sexual partners. More broadly, there are concerns about medicines becoming less effective. At CDC, whole genome sequencing of a collection of 37 *T. vaginalis* isolates possessing varying degrees of drug resistance (low, medium, and high – as determined by *in vitro* assay to establish Minimum Lethal Concentrations for each isolate) was used to detect genetic markers that may be associated with resistance to 5-nitroimidazoles. This class of drug is the only family of medicines approved by the US Food and Drug Administration for oral treatment of trichomoniasis. Analysis of data suggests that there is no single marker of resistance but instead several genes that contribute to a resistance phenotype. These data are consistent with the observation that trichomonad resistance to 5-nitroimidazoles is relative rather than dichotomous. Nevertheless, more resistant isolates fall within the Type II *Trichomonas* parasite genetic grouping than Type I. In addition to improving treatment algorithms, whole genome sequencing could also be useful to identify markers associated with pathology and better delineate virulence factors associated with HIV transmission, FGS, and adverse outcome of pregnancy.

Abstract Reference: 20844
Mode of Presentation: Symposium
Topic: Call for Symposium

Burden of Male Genital Schistosomiasis (MGS) in Malawi

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Abstract Content

Male genital schistosomiasis (MGS) remains an often-overlooked chronic consequence of urogenital schistosomiasis in endemic areas of sub-Saharan Africa. Furthermore, this is not fully described in zoonotic and hybrid schistosomiasis. Surveys were conducted among men living in endemic areas of Southern Malawi to assess the prevalence and associated morbidity of MGS. Upon recruitment in 2017 and 2023 surveys, demographic, health and socio-economic data were collected. Semen samples were collected and analysed to determine the schistosome infection. Direct microscopy of semen and its sediments (after centrifugation) were conducted and examined by molecular DNA analysis with novel and established real-time PCR assays. From 2017 surveys, 376 fishermen (median age: 30 years) were recruited and below 10% reported experiencing MGS symptoms. MGS prevalence was 10.4% (n=114) by semen microscopy and 26.6% (n=64) by real-time PCR. Nine (6.9%, n=130) had abnormalities on ultrasonography, with two having prostatic and testicular nodules. Subsequent analyses on follow-up indicated variable detection dynamics, with fewer abnormalities observed. Twenty-two men (median age: 22 years) were recruited in 2023 and 11 (50.0%) had Schistosoma ova in semen while 16 (72.7%) were positive by real-time PCR. Five men with MGS had S. mattheei, three had S. mansoni while one had mixed infection of S. mansoni and possible S. haematobium-S. mattheei hybrid. MGS caused by human, zoonotic and hybrid schistosomes are prevalent in endemic areas. More awareness among local communities and healthcare professionals, improved availability and accessibility of advanced diagnostics, treatment and control interventions are required and advocated.

Abstract Reference: 20471
Mode of Presentation: Symposium
Topic: Call for Symposium

The hidden risk of simian malaria rising to the fore

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Abstract Content

Simian malaria from wild non-human primates is increasingly recognized as an important public health threat and barrier to malaria elimination. Non-human primates host diverse malaria parasite populations, some of which can cause severe and fatal malaria in people. The zoonotic malaria *Plasmodium knowlesi* is now the only indigenous cause of malaria in Malaysia with human cases reported across Southeast Asia. Similarly, human cases of simian malaria have been reported in South America and Brazil. While these parasites can have complex transmission cycles, with simian parasites spilling over into human populations and back into wildlife populations, evidence suggests most of the human burden in Southeast Asia is due to zoonotic spillover driven by environmental change. The existence of a wildlife reservoir and primarily outdoor biting mosquito populations challenges poses a major challenge to malaria control. Within this presentation, we review the drivers and distribution of simian malaria, identify priorities for surveillance and control and discuss implications for malaria control and elimination policy globally.

Abstract Reference: 20438
Mode of Presentation: Symposium
Topic: Call for Symposium

Tamping down pockets of residual malaria among forest goers, mobile- and migrant populations at remote forested areas in northern Cambodia

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Abstract Content

Cambodia has made an impressive progress in reducing malaria incidence and mortality, aiming at the elimination of all malaria species by 2025. Guided by the National Center for Parasitology, Entomology and Malaria Control, and funded by The Global Fund, Malaria Consortium delivers adaptive and responsive malaria testing, treatment, and preventative quality services to unreached communities. Forest goers, indigenous-, mobile and migrant populations, rangers and soldiers are most at-risk of malaria, due to their highly mobile nature in forested areas and across international borders, their often-limited access to malaria services and exposure to the vectors. Locally recruited Mobile Malaria Workers (MMWs), entrusted by their community and peers, provide malaria services to these hard-to-reach populations. Screening activities are tailored to the local and seasonal movement patterns, the activities of the population and malaria epidemiology. Through community dialogue meetings, remote populations are taking ownership of malaria elimination. MMWs provide services at Malaria Posts, strategically placed at entry points of deep forests and mountain ridges. Other MMWs perform outreach activities in the deep forest and at remote (family) plantations, often with overnight stay, hereby bringing the quality care closer to the at-risk populations. By reviewing quantitative evidence, operational experience and local knowledge, the Malaria Consortium team responds swiftly and delivers the most targeted interventions possible. This model – with community members as key actors – has demonstrated that flexible, well targeted, and tailored interventions remain a key strategy to achieve malaria elimination in forested and border areas with intense migration.

Abstract Reference: 20929
Mode of Presentation: Symposium
Topic: Call for Symposium

Sharing experience on *Anopheles stephensi*: What Pakistan can offer?

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Abstract Content

In Pakistan, *Anopheles culicifacies* is primary malaria vector in the rural areas of Pakistan while historically, *An. stephensi* is reported as urban vector in Pakistan since 1960’s. Studies in late 1990’s concluded that *An. stephensi* may be a more important vector than previously believed *An. culicifacies* in Pakistan. Increasing adaptability of *An. stephensi* to new areas including urban environments, bi-modal” population dynamics, wide range of breeding habitats, non-homogeneity and high vector competence, and potential challenges in control, pose a dreadful risk to global motivations to malaria elimination. Pakistan with a remarkable experience of dealing *An. stephensi* since 1960’s has a strong surveillance system monitoring spatio-temporal distribution and susceptibility level to insecticides of local vector species. The major interventions viz., indoor residual spray, insecticides treated nets, larval source management, and community engagement are producing significant decline in vector population and disease incidence. World Malaria Report 2021 acknowledged 40% reduction of estimated malaria cases in Pakistan by 2020 against the baseline of 2015. Country developed Malaria Elimination strategy (2021-2035) targeting *Malaria Free Pakista*n focusing a strong vector surveillance and control to achieve this goal. To meet research and capacity building needs in vector surveillance and control, Pakistan has established National Entomological Reference Laboratory. Country developed National Plan of Action (2024-2028) which clearly describes country’s vision and priorities for sustainable management of VBDs. Experience and knowledge developed by Pakistan can be shared with other countries of the region to eliminate malaria and other VBDs.

Abstract Reference: 20801
Mode of Presentation: Symposium
Topic: Call for Symposium

Capacity strengthening for arbovirus preparedness in Africa through South-South exchange programme

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Abstract Content

Arboviruses, particularly dengue, are emerging threats representing a global public health problem. A 2022 WHO report indicated that Africa faces serious capacity shortfalls in preparedness to deal with arboviruses. To assist in addressing the capacity shortfalls, the FCDO-funded "Resilience Against Future Threats" (RAFT) project launched an initiative including two rounds of South-South Exchange Visits (SSEV) between several African countries, Thailand and Mexico. SSEV-1 was hosted in Thailand in October 2022, collaborating with Thailand's national vector-borne disease program and academic institutions. We brought key representatives from five African countries, including Tanzania, Cote d’ivoire, Burkina Faso, Uganda and Nigeria, to Thailand, for exposure to expertise on advanced methods in disease and vector surveillance, community engagement, policy development, as well as research priorities. SSEV-2 was conducted in November 2023 in Cameroon, collaborating with Cameroon’s national epidemiological surveillance unit, Ministry of Public Health Cameroon and academic institutions. We invited key representatives from four selected African countries, including Tanzania, Cameroon, Cote d’ivoire and Burkina Faso, and the representatives from Thailand and Mexico to Cameroon. The meeting focused on risk assessment and mitigation of arbovirus disease transmission and preparedness of outbreak response for arbovirus diseases. The lessons learnt highlighted the need for effective planning and coordination, capacity strengthening on arboviruses in diagnosis and case management, ensuring correct timing commitment from partner institutions and key stakeholders, and adequate financing. The process we developed resulted in a rich exchange of knowledge and understanding about arbovirus challenges and created platforms for collaboration in research and information-sharing.

Abstract Reference: 20360
Mode of Presentation: Symposium
Topic: Call for Symposium

Trypanosomes in Southeast Asia: From veterinary perspective and its zoonotic possibility

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Abstract Content

One of the most economical destruction diseases in veterinary and medical importance transmitted by biting insect vectors known as trypanosomosis, which is caused by flagellate protozoa parasite in the genus *Trypanozoon*. *Trypanosoma evansi* is considered as the predominant trypanosome species infecting mammals endemic in south east asian countries. This parasite causes trypanosomosis in various species of mammals. Infection in mammals leads from mild symptoms in resistance hosts to death in susceptible hosts. *Trypanosoma evansi* has been less considered as a zoonotic parasite in humans due to the presence of trypanocidal protein called Apolipoprotein L1 (APOL1) in human and non-human primates. However, there were *T evansi* confirmed human cases reported in India and Vietnam. The zoonotic infections caused by *T evansi* are frequently reported in rural areas but did not trigger onward human-to-human transmission. In those two laboratories *T evansi* confirmed human cases out of seven cases; one case was an immunodeficient patient with the presence of APOL1 mutation variants, but the other one was a healthy patient with native APOL1. There were genetic population studies of APOL1 variants in different human races. This presentation is presenting the prevalence of trypanosomes infection from a veterinary perspective, the diagnosis constraints, the link to zoonotic potential trypanosomosis, the ability to cure the infection in animals and humans in Southeast Asia and its challenges.

Abstract Reference: 20427
Mode of Presentation: Symposium
Topic: Call for Symposium

An update on zoonotic malaria in Southeast Asia: Insights from veterinary viewpoints

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Abstract Content

Annual malaria cases in the WHO South-East Asia Region have significantly declined from 22.8 million in 2000 to 5.2 million in 2022, reflecting substantial progress in combating human malaria. Nearly 46% of all cases in the region were attributed to *Plasmodium vivax*. Despite this regional success, certain countries, such as Thailand, experienced a 24.3% increase in indigenous malaria cases, rising from 10,155 in 2022 to 16,675 in 2023. Southeast Asia is recognized as an endemic region for zoonotic malaria and continues to face substantial challenges in malaria elimination due to naturally occurring human infections by zoonotic species of malaria parasites, including *Plasmodium knowlesi*, *P. cynomolgi*, *P. inui*, and *P. fieldi*. While efforts to control and eliminate human malaria caused by the four common *Plasmodium* species have been the primary focus since the turn of the millennium, there is an escalating rise in natural human infections by simian malaria parasites. Notably, *P. knowlesi*, *P. cynomolgi*, and other potentially zoonotic species, such as *P. inui*, *P. inui-like*, *P. fieldi*, *P. coatneyi*, and *P. simiovale*, are increasingly reported in Southeast Asia. This rise poses a significant challenge to regional malaria control and elimination efforts. Furthermore, the current status of malaria in primate populations in this region is largely unknown due to the difficulty of monitoring wildlife movement and relocation. An update on zoonotic malaria in Southeast Asia from a veterinary perspective will be discussed in the presentation.

Abstract Reference: 20367
Mode of Presentation: Symposium
Topic: Call for Symposium

Current situation of animal leptospirosis in Southeast Asia

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Abstract Content

Leptospirosis is a major public health problem in Southest Asia caused by infection of bacteria genus *Leptospira*. The transmission is through contact with infected animal urine contaminated in the soil or water. The infection in human shows clinical sign of influenza-like illness. It can be self-limited or induce a serious disease that leads to multi-organ failure which a potential death if not treatment. In animal, this disease found in many species of mammals including dog, cat, cattle, sheep goat and wild animals. It causes broad range of clinical effects, from mild, subclinical infection to multiple-organ failure and death. In livestock resulting in abortion, decreased fertility and milk drop. Data on animal leptospirosis in the country of SE Asia were sought and reviewed from online articles and the scientific literatures. SE is the endemic area of leptospirosis particularly high incidence in Thailand, Malaysia, Veitnam, and Loas. There were many countries have reported the serpoprevalence, molecular prevalence and serovars distribution in livestock and other domestic animals. The seroprevalence in livestock of Thailand was 11.5%, commonly serovars were serovars Ranarum and Sejroe in cattle, Mini, Sejroe and Bratislava in buffaloes, Ranarum, Pomona, and Bratislava and Mini in pig, and Shermani, and Ranarum in sheep and goat[1]. In bullfighting cattle, seroprevalence and molecular positive were 27.00% and 13%, respectively, common serovars were Shermani and Ranarum[2]. Molecular detection determined 7.81% in stray cat and 0.54% in stray dog[3]. In Malaysia, overall seroprevalence of Livestock was 11.75%, which showed the highest prevalence in cattle (14.16%), common finding serovars were Hardjo-bovis, Hebdomadis and Pomona[4]. Seroprevalence in working dogs was 3.1%, which many serovars including cterohaemorrhagiae, Canicola, Pomona, Grippotyphosa, Australis, Bataviae, Javanica, Tarassovi, Hebdomadis, Lai, and Pyrogenes[5]. In Indonesia, the cattle 3.7% were seropositive, and the most common serovars were Hardjo, followed by Icterohemorrhagiae. In the Philippine, overall seropositive in animals was 95.5% which the topmost prevailing serovar infecting were: Tarassovi for water buffaloes); Patoc for cows; Manilae for dogs; Poi for pigs[6]. In Laos, *Leptospira* spp. was detected by molecular technique in animal from wild life trade 20.1%[7]. In Vietnam, the overall, the seroprevalence of leptospirosis in swine was 21.05% [8]. The prevalence of animal leptospirosis was remarkably variable depend on animal species, study design, laboratory methodology, and associated risk factor such as environmental, climate and farm practices. From this review determined that animal leptospirosis was found in many countries of SE lead to animal health problem and national economic loss. However, Asian trading should be considering on trade policy for minimize leptospirosis transmission between the nations.

Abstract Reference: 20458
Mode of Presentation: Symposium
Topic: Call for Symposium

Zoonotic vector-borne diseases in Southeast Asia

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Abstract Content

Zoonotic vector-borne diseases (ZVBDs) are infectious diseases in animals that can be transmitted to humans through vectors. Pets, livestock, and wildlife can serve as reservoir hosts for ZVBDs. In a study conducted in Thailand, 665 blood samples from pigs were analyzed for the presence of vector-borne pathogens. Results showed that 37.1% of the pigs were infected with hemoplasmas. Sequencing analysis revealed the presence of four species of porcine hemoplasmas, including Mycoplasma suis, Mycoplasma parvum, Candidatus Mycoplasma haemosuis, and a putative novel species. However, Trypanosoma evansi and Japanese encephalitis virus were not detected in this pig population. In Northern Vietnam, 489 blood samples from dogs and cats were examined, with a low hemoplasma infection rate of only 0.81%. Two species were identified, namely Mycoplasma haemocanis and uncultured Mycoplasma spp. A separate investigation in Thailand focused on wildlife as reservoir hosts for tick-borne pathogens. Screening of 449 tick pools revealed the presence of bacteria and protozoa in 66.37% of the samples. Four species of ticks were identified, with Anaplasma showing the highest infection rate at 55.23%, followed by Babesia and Theileria at 29.62% and 16.26%, respectively. These findings provide valuable insights for developing programs aimed at treating, preventing, and controlling ZVBDs. Further research is needed to understand the transmission dynamics of these pathogens by vectors and to enhance our knowledge of the relationships among pathogens, vectors, and hosts.

Keywords: Anaplasma, Babesia, Hemoplasma, Southeast Asia, Theileria, Vector, Zoonosis

Abstract Reference: 20693
Mode of Presentation: Symposium
Topic: Call for Symposium

Current situation on zoonotic soil-transmitted helminths in Southeast Asia

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Abstract Content

Zoonotic soil-transmitted helminths (STHs) remain a significant public health challenge in Southeast Asia. These infections, caused by parasitic worms such as *Toxocara* spp., *Trichuris* spp., *Strongyloides,* and *Ancylostoma* spp., are prevalent in regions with poor sanitation and hygiene practices. The transmission of these helminths from animals to humans exacerbates the public health burden, particularly in rural, underdeveloped, and agricultural areas. Recent studies highlight the endemic nature of zoonotic STH infections, with the prevalence of STH in Southeast Asia ranging from 1-89.5% in dogs and between 1-71% in cats, whereas hookworm was the most common parasite in these regions. In Thailand, the overall prevalence of STH in dogs and cats was 14.6% and 26.2%, while hookworms was the most common parasite, followed by roundworms and whipworms, respectively. The incidence of *A. ceylanicum, T. canis, T. cati,* and *T. trichiura* in dogs and cats highlights the risk of environmental contamination and zoonotic transmission to the human population. Despite ongoing control efforts, including mass drug administration and improved sanitation initiatives, challenges such as drug resistance and environmental contamination persist. Comprehensive strategies integrating One Health approaches, which consider the interconnected health of humans, animals, and the environment, are essential for effective control in the region. Enhanced surveillance, public health education, and intersectoral collaboration are critical to mitigating the impact of these neglected tropical diseases in Southeast Asia.

Abstract Reference: 20275
Mode of Presentation: Symposium
Topic: Call for Symposium

The epidemiological landscape of Leishmania infection in Thailand: A comprehensive overview

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Abstract Content

Leishmaniasis presents a significant public health issue, impacting not only those with compromised immune systems, such as HIV patients, but also the broader, immunocompetent population including blood donors. It's vital to discern its spread and influencing factors within these groups to tailor effective preventative measures. This multi-location study in Thailand aimed to determine the epidemiology of leishmaniasis among HIV-infected patients and blood donor population. Cross-sectional and cohort studies were conducted at tertiary-care hospitals. The prevalence of *Leishmania* infection among HIV infected patients were 25% in Trang, 5% in Chiang Rai, and 8% in Satun in 2016, 2018, and 2020, respectively. The incidence of Leishmania infection was 3% in Trang and 13% in Satun in 2019 and 2022, respectively. In 2023, 19% of blood donors in Trang were found, predominantly with *L. martiniquensis*. Key risk factors for HIV patients included age, intravenous drug use, low CD4 cell counts, and high viral loads, whereas for blood donors, living in stilt houses was a significant risk factor. The prevalence and incidence of Leishmania infection among HIV-infected patients and blood donors in Thailand are significant. These findings underscore the necessity for integrated care and targeted interventions to mitigate this infection and enhance public health outcomes. Further research and collaborative efforts are crucial for developing effective prevention and control strategies for Leishmania infection in the HIV-infected Thai population. Moreover, it underscores the need for integrating comprehensive Leishmania screening protocols into blood donation processes, particularly in endemic regions.

Abstract Reference: 20439
Mode of Presentation: Symposium
Topic: Call for Symposium

Current knowledge of an emerging leishmaniasis in Thailand and its causative agents: *Leishmania* (*Munidia*) spp.

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Abstract Content

Leishmaniasis is a neglected parasitic disease that has been traditionally known to be transmitted by phlebotomine sand flies. In the past, Thailand was considered as a non-endemic area of this disease. However, autochthonous cases of leishmaniasis have been continuously reported in Thailand since 1996, particularly in Northern and Southern Thailand. Most cases were diagnosed with *L. martiniquensis* or *L. orientalis*, both belonging to the newly erected subgenus *Mundinia*. Interestingly, recent evidence demonstrated that such two autochthonous Leishmania species could fully complete metacyclic development in *Culicoides sonorensis* biting midge, not *Phlebomous stantoni* sand fly. This laboratory finding indicates that *Leishmania* (*Mundinia*) spp. are most likely to be spread by *Culicoides* midges rather than sand flies. To incriminate *Culicoides* as a natural vector of leishmaniasis, one of Killick-Kendrick's criteria, namely anthropophilic behavior, needs to be fulfilled. However, evidence of human feeding in *Culicoides*, particularly in the leishmaniasis-affected areas has never been demonstrated. Therefore, we applied next-generation sequencing based on vertebrate 16S mitochondrial rRNA gene region to demonstrate the host preference of engorged *Culicoides* collected from the endemic areas. The results indicated that several species of *Culicoides* can feed on humans and several peridomestic and wild hosts such as cows, deer, pigs, and chickens. In conclusion, our metagenomic investigation fulfills the criteria of Killick-Kendrick, incriminating *Culicoides* biting midges as important vectors of *Mundinia* leishmaniasis in Thailand.

Abstract Reference: 20277
Mode of Presentation: Symposium
Topic: Call for Symposium

Potential animal reservoirs of *Leishmania martiniquensis* and *Leishmania orientalis*: Review and update situation in Thailand

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Abstract Content

Leishmaniasis is a neglected tropical disease caused by *Leishmania, in the* subgenus *Leishmania*, *Viannia, and Mundinia*. *Leishmania (Mundinia), previously named L. enriettii* complex, *is* responsible for human and animal leishmaniasis. During the last 15 years, autochthonous human cases, caused by *L. (Mundinia) martiniquensis* and *L. (Mundinia) orientalis,* have been increasing continuously in Thailand, raising the question of potential animal reservoir. In Thailand, only black rat (*Rattus rattus*) had been previously notified as the natural reservoir, in which the DNA of either species were presented in the blood, liver, or spleen of captured one from the patient's house.However, the evidence of zoonotic transmission is more promising when the animal cutaneous leishmaniasis (CL), caused by *L. martiniquensis,* were reported in horses and cows residing in Florida, Germany, and Switzerland. Although *Leishmania* antibodies were detected in various mammals residing in the endemic areas of Thailand, such as cattle, buffaloes, cats, and dogs, the transmissibility of the parasites is suspicious. Additional investigations in the endemic areas of Northern Thailand convinced the dog as the potential reservoir of *L. martiniquensis,* in which *Leishmania* DNA was detected in dog peripheral blood by nPCR. Surprisingly, an autochthonous clinical CL in a dog with a nodule on the internal ear pinna was firstly presented, in which the amastigotes were examined in the skin biopsy, and *Leishmania*isolation cultivation were successfully using Grace's insect medium. The species of *L. martiniquensis* was confirmed by molecular techniques and sequencing, and genetic analyses of ITS1 and *cytochrome* b gene were elucidated.

Abstract Reference: 20297
Mode of Presentation: Symposium
Topic: Call for Symposium

Kinetoplastid DNAs of *Leishmania orientalis* and *Leishmania martiniquensis* in Thailand

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Abstract Content

Kinetoplast DNAs (kDNAs) form networks of hundreds of interlocked DNA circles that require complex RNA editing in trypanosomatids, including *Leishmania*. The kDNAs have been reported to play a role in drug resistance, adaptation, and survival of *Leishmania*. *Leishmania orientalis* and *Leishmania martiniquensis* are frequently observed species in Thailand, and their kDNAs have not been examined. Our research aimed to investigate the maxicircle and minicircle DNAs of *L. orientalis* strain PCM2 and *L. martiniquensis* strain PCM3 isolated in Thailand using hybrid genome sequencing technologies and bioinformatic analyses. The kDNA sequences were assembled using the SPAdes hybrid assembler from the Illumina short-read and PacBio long-read data. The circularized maxicircle and minicircle DNAs were confirmed by BLASTn and rKOMICs programs and were annotated by BLASTn before the comparative genomic and phylogenetic analysis. The maxicircle DNAs of both *Leishmania* species were closely relayed to *Leishmania enriettii* strain LEM3045, and the phylogenetics of their minicircle DNAs showed monophyletic separation from those of other known *Leishmania* species. Our first report on the complete maxicircle and minicircles of *L. orientalis* and *L. martiniquensis* will help improve diagnosis methods and further explore this parasite population genetics in Thailand and related regions.

Abstract Reference: 20267
Mode of Presentation: Symposium
Topic: Call for Symposium

Simplified colorimetric and florescent quantitative LAMP assay for detecting Leishmania infection in asymptomatic patients with HIV

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Abstract Content

Asymptomatic visceral leishmaniasis patients have continuously increased, especially among HIV co-infected cases who are at risk to develop further symptoms of leishmaniasis. Risk populations mostly live in rural communities with limited resources of laboratory equipment. Therefore, a simple, sensitive and reliable diagnosis is crucially needed. In our experiments, a highly sensitive and selective determination of *Leishmania* among asymptomatic *Leishmania/*HIV co-infected patients was successfully developed to simultaneously interpret and semi-quantify using color (SYBR green I), colorimetric precipitates (gold-nanoparticle probe; AuNP-probe) and fluorescence (SYBR safe dye and distance-based paper device; dPAD) in one-step loop-mediated isothermal amplification (LAMP) assay. The sensitivities and specificities of the detection methods were equivalent and had reliable performances achieving as high as 94.4%. Detection limits were 10^2 parasites/mL (0.0147 ng/µL) which were 10 times more sensitive than other related studies. Hence, a simplified colorimetric and florescent quantitative LAMP assay is reliably fast, simple, inexpensive and practical for field diagnostics to point-of-care settings in resource-limited areas. The assay can be set up in all levels of healthcare facilities, particularly in low to middle income countries, to empower leishmaniasis surveillance as well as prevention and control.

Abstract Reference: 20460
Mode of Presentation: Symposium
Topic: Call for Symposium

Research and application with new methods for rapid detection of anisakis in seafood based on nucleic acid amplification

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Abstract Content

Food-borne parasitic diseases (FBPDs) have emerged as a global public health concern. Subsequently, rapid and accurate diagnosis of food-borne parasites is crucial to prevent FBPDs. The detection of nucleic-acid is an accurate molecular diagnostics method frequently leveraged for FBPDs diagnosis. Recently, increasing demands for POCT have been put forward for nucleic acid detection. CRISPR/Cas associated biosensors have been shown to have great potential in sensing applications due to their high sensitivity and high base resolution.However, the signal reporter system containing two organic fluorescent dye pair is limited by high cost and less stability. In contrast, functional nanomaterials exhibit robust stability, excellent optical properties and low preparation cost, making them suitable reporters.In this study, a MoS2 nanosheets (NSs) improved CRISPR/Cas12a-based biosensing platform was constructed for the first time to detect food-borne parasites. MoS_2 NSs were used as fluorescence quenchers and single-stranded DNA (ssDNA) discriminated carrier to construct CRISPR/Cas signal reporter system. The combination of recombinase polymerase amplification with MoS_2 NSs modulated CRISPR/Cas12a helped achieve attomolar sensitivity for nucleic acid detection within 35 min. Moreover, the results were obtained using a portable apparatus, enabling visual detection at the point of care. The practical applicability of this biosensing platform was successfully achieved through the detection of anisakis in real samples. This study provides novel insights into exploring the feasibility of two-dimensional nanomaterials based reporter in the CRISPR/Cas12a system, as well as offers a reliable tool for on-site monitoring of parasites.

Abstract Reference: 20322
Mode of Presentation: Symposium
Topic: Call for Symposium

Prevalence of *Clonorchis sinensis* metacercariae in *Pseudorasbora parva* across various regions of China

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Abstract Content

To investigate the prevalence of *Clonorchis sinensis* metacercariae in *Pseudorasbora parva* in different regions of China, a comprehensive survey was conducted from August 2022 to January 2024. The survey covered 12 sampling sites, located in East China, South China, Central China, Sichuan, and Shanxi provinces. Identification of *C. sinensis* metacercariae in *P. parva* specimens involved multifaceted approaches, combining morphology of metacercariae, 16S rDNA marker, detection of the eggs and adult worms collected from the rats' feces on 25 days after metacercariae infection. Results showed that out of the 665 *P. parva* samples examined, 277 were positive with metacercariae. These positive samples collected from Fuyang in Anhui Province (24/32), Ningde in Fujian Province (5/19), Hengzhou in Guangxi Zhuang Autonomous Region (6/6), Puyang in Henan Province (22/22), Yantai and Qingdao in Shandong Province (122/124), Hanzhong in Shaanxi Province (95/193), and Chengdu in Sichuan Province (2/30) respectively. These findings suggest the presence of a complete *C. sinensis* life cycle in the ecosystems of these regions, highlighting the risk of *C. sinensis* infection after the consumption of raw or undercooked *P. parva* and may also the related freshwater fish contain the metacercariae. Additionally, the study confirmed the utility of the 16S rDNA gene as a molecular marker for the identification of trematodes, which, when combined with the morphological characteristics, can effectively identify the species of metacercariae in the freshwater fish.

Abstract Reference: 20425
Mode of Presentation: Symposium
Topic: Call for Symposium

Immunosuppressive ability of *Trichinella spiralis* adults can ameliorate type 2 inflammation in a murine allergy model

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Abstract Content

There is an increase in the global incidence of allergies. The hygiene hypothesis and the old friend hypothesis reveal that helminths are associated with the prevalence of allergic diseases. The therapeutic potential of *Trichinella spiralis* (*T. spiralis*) is recognized; however, the stage at which it exerts its immunomodulatory effect is unclear. We evaluated the differentiation of bone marrow-derived macrophages stimulated with *T. spiralis* excretory-secretory products. Using an ovalbumin-induced murine model, *T. spiralis* was introduced during three allergy phases. Cytokine levels and immune cell subsets in the lung, spleen, and peritoneal cavity were assessed. We found that *T. spiralis* infection reduced lung inflammation, increased anti-inflammatory cytokines, and decreased Th2 cytokines and alarms. Eosinophil, CD11b$^+$ dendritic cells, and interstitial macrophage recruitment to the lung was significantly suppressed, whereas Treg cells and alternatively activated macrophages increased in *T. spiralis* infection groups compared with that of the ovalbumin group. Notably, when *T. spiralis* was infected prior to ovalbumin-challenge, intestinal adults promoted CD103$^+$ dendritic cells and alveolar macrophages proportions. *T. spiralis* strongly suppressed type 2 inflammation, and adult maintained lung immune homeostasis.

Abstract Reference: 20426
Mode of Presentation: Symposium
Topic: Call for Symposium

A point-of-care testing assay for clonorchiasis using a EuNPs-CsTR1 fluorescent probe-based immunoassay

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Abstract Content

Clonorchis sinensis is one of the most important fish-borne zoonotic parasitic worms, and is distributed in several countries with more than 15 million people infected globally. However, the lack of a point-of-care testing (POCT) method is still the critical barrier to effectively prevent clonorchiasis. With the application of novel fluorescent nanomaterials, the development of on-site testing methods with high signal enhancement can provide a simple, precise and inexpensive tool for disease detection. In this study, Eu-(III) nanoparticles (EuNPs) were used as indicative probes, combined with *C. sinensis* tandem repeat sequence 1 (CSTR1) antigen to capture specific antibodies. Afterward, the complex binds to mouse anti-human IgG immobilized on the test line producing a fluorescent signal under UV light. The EuNPs-fluorescent immunoassay (EuNPs-FIA) was successfully constructed, and it enabled both qualitative determination with the naked eye under UV light and quantitative detection by scanning the fluorescence intensity on the test line and control line. A total of 133 clinical human sera were used in this study. For qualitative analysis, the cut-off value of fluorescence for positive serum was 31.57 by testing 74 known negative human samples. The assay had no cross-reaction with other 9 parasite-infected sera, and could recognize the co-infection sera of *C. sinensis* and other parasites. The sensitivity and specificity of EuNPs-FIA were both 100% compared with KK method. Taking advantage of its high precision and user-friendly procedure, the established EuNPs-FIA provides a powerful tool for the diagnosis and epidemiological survey of clonorchiasis.

Abstract Reference: 20421
Mode of Presentation: Symposium
Topic: Call for Symposium

Revealing the dynamic whole transcriptome landscape of *Clonorchis sinensis*: Insights into the regulatory roles of noncoding RNAs and microtubule-related genes in development

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Abstract Content

Clonorchis sinensis is a significant zoonotic food-borne parasite that causes a range of hepatobiliary diseases, which in severe cases can even lead to cholangiocarcinoma. To explore new diagnostic and treatment strategies, the dynamic RNA regulatory processes across different developmental stages of *C. sinensis* were analyzed by using whole-transcriptome sequencing. The chromosomal-level genome of *C. sinensis* was used for sequence alignment and annotation. In this study, we identified a total of 59,103 RNAs in the whole genome, including 2,384 miRNAs, 25,459 mRNAs, 27,564 lncRNAs and 3,696 circRNAs. Differential expression analysis identified 6,556 differentially expressed mRNAs, 2,231 lncRNAs, 877 miRNAs and 20 circRNAs at different developmental stages. Functional enrichment analysis highlighted the critical role of microtubule-related biological processes in the growth and development of *C. sinensis*. And coexpression analysis revealed 97 lncRNAs and 85 circRNAs that were coexpressed with 42 differentially expressed mRNAs that associated with microtubules at different developmental stages of *C. sinensis*. The expression of the microtubule-related genes dynein light chain 2 (DLC2) and dynein light chain 4 (DLC4) increased with *C. sinensis* development, and DLC2/4 could be inhibited by albendazole. Finally, by constructing competing endogenous RNA (ceRNA) networks, the lncRNA-miRNA-mRNA and circRNA-miRNA-mRNA regulatory relationships were constructed, and the ceRNA networks of MSTRG.14258.5-novel_miR_2287-newGene_28215 and MSTRG.14258.5-novel_miR_2216-CSKR_109340 were verified. This study suggests, through whole transcriptome sequencing, that the context of microtubule regulation may play an essential role in the development and growth of *C. sinensis*.

Keywords: *Clonorchis sinensis*, microRNA, long noncoding RNA, circular RNA, competing endogenous RNA, microtubule

Abstract Reference: 20830
Mode of Presentation: Symposium
Topic: Call for Symposium

Updates on epidemiology, pathogenesis, and control of the human liver fluke, *Opisthorchis viverrini* infection

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Abstract Content

Human liver fluke infection caused by *Opisthorchis viverrini* is a major foodborne trematodiasis in the Lower Mekong Basin, including Thailand, Laos, Cambodia, and central Vietnam, with over 10 million people infected. The infection is associated with several hepatobiliary diseases, including cholangiocarcinoma. Over the past decade, significant updates have emerged regarding the epidemiology, disease pathogenesis, and control of the infection. Recently, a new occurrence site of *O. viverrini*in Myanmar has been reported, and high infection rates are increasingly documented in Cambodia. Notably, liver fluke co-infection with *Helicobacter pylori* enhances disease pathogenesis. Specifically, *O. viverrini* serves as a reservoir for the carcinogenic bacteria, as it possesses receptors for *H. pylori*, leading to severe pathology. Persistent periductal fibrosis in opisthorchiasis post-praziquantel treatment is associated with persistent infection with cagA-positive *H. pylori*. Despite liver fluke control programs being implemented in these countries, *O. viverrini* infection remains high in certain endemic areas. Its complex life cycle, involving multiple hosts and environments, complicates control using conventional methods. A new control strategy, known as the "**Lawa model**," using the EcoHealth/One Health approach, was introduced in the Lawa Lake area in Thailand with great success. This strategy is documented in the national agenda against liver fluke and cholangiocarcinoma. Internationally, the "Lawa model" is one of two showcases for helminth control recognized by WHO/NZD4. The One Health approach has been recommended for the control of foodborne trematode infections by the WHO Western Pacific Region.

Abstract Reference: 20921
Mode of Presentation: Symposium
Topic: Call for Symposium

Omics of *Schistosoma haematobium*: An example of the importance of understanding helminth pathogenesis

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Abstract Content

A better understanding of the pathogenesis of helminths is crucial to improving diagnostics and development of vaccines. In this presentation we will focus on the pathogenesis of the world's most prevalent blood fluke, *Schistosoma haematobium*, which lays highly inflammatory eggs in the bladder and other pelvic organs. This leads to bladder carcinogenesis, bladder fibrosis-induced kidney failure, and increased HIV susceptibility. We will discuss how development of tractable mouse models of egg-induced bladder and vaginal pathogenesis, combined with omics approaches, has led to discoveries regarding key pathways likely involved in carcinogenesis and enhanced sensitivity to HIV infection.

Abstract Reference: 20865
Mode of Presentation: Symposium
Topic: Call for Symposium

Bridging the gap: Schistosomiasis vaccines and the One Health approach

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Abstract Content

Helminthic infections, such as those caused by Schistosoma spp. and soil-transmitted helminths, afflict nearly 25% of the global population. In tropical and subtropical regions, these infections are major public health challenges, affecting large proportions of the population. Among the neglected tropical diseases, helminthic infections have far-reaching impacts on human and animal health, reflecting the interrelation of ecosystems, human societies, and animal populations. Vaccine development against helminth infections is a promising route for their control and eventual elimination. Here, we discuss the challenges and progress in developing helminth vaccines, focusing on key antigenic targets, formulation of vaccine candidates, immunogenicity, and protective efficacy assessment. Furthermore, we discuss in detail the complex considerations in vaccine deployment, including equity in distribution, community engagement, and impact sustainability, which are relevant to One Health principles. Rigorously addressing challenges from these diseases, we hope to ensure a better future by enhancing the health of humans, animals, and the environment.

Abstract Reference: 20811
Mode of Presentation: Symposium
Topic: Call for Symposium

Functional genomics advance understanding of the pathobiology of schistosomiasis

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Abstract Content

Functional genomics methods are needed in the arena of the Neglected Tropical Diseases, especially for helminth parasites, to facilitate basic and transformational studies to improve global public health. Gain-of-function phenotypes would be valuable in this context. Aiming to advance this field, we identified genome safe harbor (GSH) sites in the chromosomes of the human blood fluke, *Schistosoma mansoni*, and developed methods for transgene insertion and to characterize transgene performance following homology directed insertion at the schistosome GSH. Thereafter, we inserted into a GSH a transgene encoding a coronavirus neutralizing antibody, which was expressed and secreted in the blood of schistosome infected mice. The progress reported here can be expected to advance functional genomics for species of the Platyhelminthes - including free living model species of planarians and should be adaptable to helminths generally.

Abstract Reference: 20950
Mode of Presentation: Symposium
Topic: Call for Symposium

Differential roles of small extracellular vesicles and microvesicles from *Opisthorchis viverrini* in human cholangiocytes cell proliferation

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Abstract Content

Chronic infection with *Opisthorchis viverrini* is a significant public health issue in the Mekong River Basin countries, strongly associated with the development of cholangiocarcinoma (CCA). However, the precise mechanisms through which *O. viverrini* contributes to CCA remain largely elusive. This study aims to elucidate these mechanisms by characterizing the extracellular vesicles (EVs) released by *O. viverrini* (*Ov*EVs) and investigating their roles in host-parasite interactions using proteomic and transcriptomic analyses. Our findings reveal that *Ov*EVs isolated at 120,000 x g (120k *Ov*EVs) significantly promoted cell proliferation in H69 cells, while those isolated at 15,000 x g (15k *Ov*EVs) did not show such effects. A detailed proteomic analysis highlighted distinct differences in the composition of these EV populations, potentially explaining their varied biological impacts. Furthermore, analysis of miRNAs in the 120k EVs and computational prediction of their interactions with human host genes suggested their involvement in pathways related to inflammation, immune response, and apoptosis. This representative to demonstrate the specific roles of different EV populations in the pathogenesis of parasitic helminths. It marks a crucial step towards understanding the mechanisms underlying opisthorchiasis and the development of associated liver fluke infection-related malignancies.

Abstract Reference: 20651
Mode of Presentation: Symposium
Topic: Call for Symposium

New diagnostic tools for case detection and management

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Abstract Content

Diagnostic tests to detect *P. vivax* (Pv) and P. *falciparum* (Pf) malaria have challenges in performance and operational feasibility, creating a barrier to accurate detection and clinical care. New diagnostic solutions capable of high sensitivity detection of Pv and Pf infection are needed to overcome challenges of: 1) limited sensitivity to infections of low parasite density, typical of *Plasmodium vivax* and asymptomatic malaria infections, 2) diagnostic evasion (false negative test results) as seen in Pf infections with gene deletions. Next-generation rapid diagnostic tests (RDTs) have improved limits of detection for Pv-specific lactate dehydrogenase (LDH) and allow single-line detection of Pf through combined Pf histidine-rich protein 2 (HRP2) and Pf-specific LDH detection, thus allowing detection even in cases of *hrp2/3 gene* deletion. Analysis of analytical sensitivity of new RDTs as compared to WHO-prequalified RDTs is presented. Further implications on clinical performance for these new RDTs are discussed, addressing gene deletions in *P.falciparum,* symptomatic versus asymptomatic case detection, reliable *Plasmodium* speciation, and diagnosing individuals with recent exposure to *P.vivax* infections. While RDTs can detect blood stage malaria with improving sensitivity, other strategies are still needed, particularly to address individuals at risk of *P.vivax* relapse and support equitable access to radical cure with Tafenoquine and Primaquine and safe use guidance through glucose-6-phosphate dehydrogenase deficiency (G6PDd) testing of individuals with this common enzymopathy for whom radical cure is contraindicated. New point-of-care tests for G6PDd are entering the market and the product pipeline will be discussed.

Abstract Reference: 20806
Mode of Presentation: Symposium
Topic: Call for Symposium

Introducing new products. Operational challenges for programs and clinics, the importance of community engagement. Cambodia case study, equal access to safe radical cure.

Soy Ty Kheang*[1]

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Abstract Content

As Cambodia approaches the last mile in malaria elimination, the disease burden is increasingly localized in remote villages, community around forest edge areas, and among marginalized populations. *Plasmodium vivax* has become the predominant cause of malaria in a population with a burden of G6PD deficiency, which contraindicates the use of the two curative treatment options, primaquine and tafenoquine. Implementing malaria elimination strategies relies heavily on reliable rapid diagnostic tests (RDT) to identify both passive and active malaria infections, as well as point-of-care tests for G6PD deficiency to treat *P. vivax* cases. Malaria elimination is also dependent on successful community engagement. With the recent availability of point-of-care tests for G6PD deficiency, Cambodia has transitioned to providing access to universal radical cure treatments for *P. vivax* cases. The operational experience of adopting new diagnostic tools for *P.vivax*, including tests for G6PD deficiency, the lessons learned, and current gaps will be discussed during the session.

Abstract Reference: 20804
Mode of Presentation: Symposium
Topic: Call for Symposium

Elimination: Targeting *Plasmodium vivax* in an elimination setting: challenges and opportunities for introduction of new diagnostic products in a country with low burden. Vietnam case study

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Abstract Content

In Vietnam, a diminishing trend in malaria case load has been witnessed year over year. The *Plasmodium vivax* cases accounted for more than 46% of total detected cases in 2023. The provision of radical cure strategies to treat both the blood and dormant liver stages of the parasite could support malaria elimination by 2030. In settings with low disease burden, introduction an scale-up of new commodities such as diagnostic products require new considerations to ensure their sustained appropriate uptake. Experience in Vietnam in introducing point-of-care quantitative glucose-6-phosphate dehydrogenase (G6PD) testing into malaria case management practices to support radical cure is described.

Abstract Reference: 20808
Mode of Presentation: Symposium
Topic: Call for Symposium

Challenges in malaria case detection, pre-existing limitations and emerging threats in Asia-Pacific region

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Abstract Content

Despite significant gains in malaria control and elimination across the Asia-Pacific in recent decades, major challenges in our ability to track, prevent and treat malaria remain. The current gold standard of field malaria diagnosis, microscopy, is limited by a shortage of skilled microscopists and materials in hard-to-reach areas. As such, malaria diagnosis in the Asia-Pacific is primarily performed by community health workers who can access hard-to-reach areas and populations and perform malaria diagnosis using rapid diagnostic tests (RDTs). However, with the recent decline of malaria transmission in the Asia-Pacific, the role and motivation of community health workers as well as their malaria annual blood examination rates has declined. Residual parasite reservoirs need to be detected and eliminated to prevent ongoing transmission. However, the cornerstone of malaria diagnosis, conventional RDTs, have sub-optimal sensitivity to detect low density asymptomatic infections which prevail in the Asia-Pacific. RDTs (nor any other field deployable diagnostics) cannot detect hypnozoites – the dormant asymptomatic liver-stages of *Plasmodium vivax*, discriminate between imported or indigenous cases or between relapses and reinfections, nor detect *P. knowlesi*, an emerging zoonotic infection transmitted from macaques to humans. Furthermore, conventional RDTs are beginning to fail due to deletions in the *P. falciparum* target antigen gene (*hrp2/3*). To detect and eliminate all malaria infections as well achieve malaria elimination, new highly sensitive tools and testing strategies which can detect and track the diversity of *Plasmodium* spp., low density or asymptomatic infections, or *P. vivax* dormant liver-stage infections are urgently required.

Abstract Reference: 20805
Mode of Presentation: Symposium
Topic: Call for Symposium

Health economic considerations: The value proposition for new diagnostic products to support malaria control and elimination

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Abstract Content

Health economic considerations are crucial when adopting new diagnostic products, especially in the context of malaria elimination, where funding is likely to be limited. Selecting malaria diagnostics in this environment should be based on multiple value propositions, such as cost-effectiveness, affordability, and economies of scale. Evaluating different dimensions of value for new malaria diagnostic tools helps policymakers make investment decisions that maximize health benefits within financial constraints. This approach is illustrated through a case study on the cost-effectiveness of point-of-care G6PD diagnostic tests for Plasmodium vivax (Pv) radical cure in Laos. Among four different implementation strategies for primaquine radical cure, strategies using G6PD tests were found to be cost-effective when considered against the willingness to pay threshold of 1 Gross Domestic Product per capita in Laos. Sensitivity analysis showed lower cost-effectiveness with lower adherence rates to primaquine and smaller numbers of Pv cases reported at a health facility. Economies of scale and affordability were tested in a budget impact analysis, which showed that only half a million US$ would be needed when G6PD tests were rolled out selectively based on the number of Pv cases reported in each health facility. In contrast, an indiscriminate rollout approach, where case numbers per health facility are not considered, was found to be more expensive and less effective.

Abstract Reference: 20795
Mode of Presentation: Symposium
Topic: Call for Symposium

Opportunities and challenges of pathogen taxonomy using shotgun metagenomics – lessons from the pathogen exchange at the human wildlife interface study

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Abstract Content

The recent COVID-19 pandemic is a stark reminder of the human and economic consequences of newly emerging zoonotic pathogens. To prevent future epidemics/pandemics and their devastating consequences, we must engage with communities most at risk of emerging pathogens and develop context-specific, acceptable, feasible ways to rapidly identify pathogens with epidemic/pandemic potential as they arise. Combined with zoonotic host and vectors, this offers the potential to facilitate early, rapid clinical and public health action at source. But how to do this is unclear and is a contemporary, priority area for Global Health Research. Taking three geographically distinct forest-fringe communites in Central and Northern Sulawesi, we conducted cross-sectional surveys of reported febrile illnesses. In addition vector trapping and non-human primate sampling were conducted. We combined standard molecular techniques with long-read sequencing (Oxford Nanopore Technology). We discuss the findings from this research program, delivered across a pandemic, with reference to sampling, bioinformatic pipelines and the outcomes. The learnings from such field work are important to drive forward our ability to apply pathogen agnostic strategies in a OneHealth approach. The challenges of contemporary "nearer to point of care" genomic analysis are discussed, along with the limitations of shotgun metagenomics. We use as an example simian malarias, but the implications translate across the taxonomic landscape.

Abstract Reference: 20664
Mode of Presentation: Symposium
Topic: Call for Symposium

Acute febrile illness in Makassar and adjacent areas

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Abstract Content

Introduction: The prevalence of acute febrile illness is notably high in Makassar and surrounding areas; however, information on causative etiologies is limited. This study aims to gather data on undiagnosed acute fever cases in primary healthcare and Type B referral hospitals, identifying the causes of undifferentiated febrile illnesses from 2017 to 2022. Methods: We enrolled 881 cases, and blood samples were collected from patients with acute fever (≥38°C for ≤7 days) without any major symptoms of respiratory or gastrointestinal infection from two primary health centers and two Type B referral hospitals in Makassar, Maros, and Gowa, South Sulawesi. Routine hematological exams and rapid tests for NS1 Ag, IgM, and IgG were conducted on-site, while samples were sent to the Eijkman Laboratory in Jakarta for polymerase chain reaction (PCR) molecular analysis. Results: Results showed that 282 cases (31.9%) were dengue, 22 cases (2.5%) were chikungunya, 16 cases (1.8%) were leptospirosis, and four cases (0.4%) were rickettsiosis. The remaining 556 samples (63.1%) were undiagnosed. Conclusion: In conclusion, there is still a big gap in knowledge regarding the causative agents of acute febrile illness in Makassar and adjacent areas, which remain primarily undiagnosed (62.3%), while dengue (31.9%) was the most frequently diagnosed cause of acute fever cases.

Keywords: acute febrile illness, dengue virus, Indonesia

Abstract Reference: 20724
Mode of Presentation: Symposium
Topic: Call for Symposium

Evidence of Aedes-transmitted arboviruses co-distributed in Makassar City with the presence of mosquito vectors as potential emerging diseases in the area

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Abstract Content

The prevalence of undiagnosed fever in Makassar City and neighboring areas, based on a survey in 2017-2021 was >60%. Dengue is the most prevalent arbovirus infection in the area. Despite the same mosquito vectors, there were no official reports on Chikungunya and Zika infections. Several independent serology surveys were performed on healthy children and adults to explore the possibility of Chikungunya and Zika virus distribution, along with dengue, using IgG ELISA assays. Entomology surveys were performed to check the presence of mosquito vectors, *Aedes aegypti* and *Aedes albopictus,* in five locations in Makassar City and the neighboring districts. Serology surveys: DENGUE seropositive: children under 5 years old: 59/181 (32.6%), pregnant women: 18/55 (32.7%), blood donors: 65/71, (91.6%). ZIKA seropositive: children under 5 years old: 3/181 (1.7%), pregnant women: 46/139 (33.1%). CHIKUNGUNYA seropositive: children under 5 years old (1.7%), healthy adults: (33.1%). MIX infection (Zika and Dengue) seropositive: children under 5 years old: 2/181 (1.1%), pregnant women: 12/139 (8.6%). Mosquito surveys: *Ae. albopictus* was present in 5 different landscapes (urban business area, urban residential area, semi-urban area, rural lowland, and rural highland area) surveyed, while *Ae.aegypti* present in four landscapes, but absent in the rural highland area. Despite no official reports on Chikungunya and Zika virus infections, there was evidence of their distribution, along with Dengue virus, in Makassar and neighboring areas. The presence of mosquito species vectors in most of the landscape types shows the potential of Chikungunya and Zika viruses causing emerging diseases.

Abstract Reference: 20616
Mode of Presentation: Symposium
Topic: Call for Symposium

Oligonucleotide aptamer as a promising approach for developing accurate diagnostic tools and therapeutics in tropical diseases

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Abstract Content

The utilization of oligonucleotide aptamer-based technology has great potential as a strategy for translating medical advancements from the laboratory to clinical practice. Oligonucleotide aptamers, known as “chemical antibodies," have proven to be superior in diagnostic and therapeutic capabilities compared to antibody-based tools due to their high stability, low production cost, and low immunogenicity. Oligonucleotide aptamers are novel biomolecules renowned for their exceptional specificity and affinity. Oligonucleotide aptamers have been extensively utilized in tropical diseases for the rapid detection of viruses and as a therapeutic strategy for antiviral applications. This approach has resulted in the development of aptamer-based biosensors (aptasensors) and antiviral agents for treating infections. Aptasensors necessitate a mechanism that can identify the interaction between viral molecules and aptamers in virus-infected cells, blood, and other body fluids. From a therapeutic perspective, aptamers are used to specifically target either viral particles or host cell receptors. Their purpose is to hinder the contact between the virus and host cells or to disrupt the life cycle of the virus within infected cells by selectively binding to intracellular viral proteins. Moreover, oligonucleotide aptamers are also widely investigated as a drug-delivery nanoparticle and a new potential tool for precision medicine. Despite the abundance of studies on virus detection and treatment, there is a scarcity of commercially accessible aptamer-based products for clinical diagnosis and therapy. The study of aptamers is an evolving field. Further exploration is needed to provide a more comprehensive understanding of aptamer research and development.

Keywords: Oligonucleotide aptamer, chemical antibodies, aptasensors, precision medicine

Abstract Reference: 20796
Mode of Presentation: Symposium
Topic: Call for Symposium

Bioinformatics – The pros and cons of short and long read sequencing

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Abstract Content

The advancement in sequencing technology promises more accurate results at a reduced cost, revolutionising biology and medicine. However, users need to be aware of the potential pitfalls of various technologies and critically evaluate what is required for their projects and what is achievable within individual labs. Next-generation sequencing (NGS), such as Illumina, produces highly accurate short reads (100–250 paired-end reads) at high depth. Mature software, workflows, and pipelines exist to analyse such data. However, due to the short nature of these reads, the resulting sequences may not be unique enough to yield adequately high confidence in some circumstances. Long-read sequencing technologies, such as Nanopore and PacBio, are increasingly accurate per base but suffer from indels due to a lack of a time dimension in data acquisition. This can have catastrophic consequences if not accounted for, particularly in genome (or metagenome) assembly. The software for long-read data analysis is newer, constantly evolving, and rarely optimized. Additionally, high-end GPUs and significant amounts of RAM and storage, typically part of high-performance computing clusters, are required for the analysis of long-read data, which may be out of reach for some labs, especially considering the financial costs (cloud computing vs buying hardware). Moreover, computational expertise is required to analyse sequencing data, which should be factored into project planning.

Abstract Reference: 20985
Mode of Presentation: Symposium
Topic: Call for Symposium

The transmission dynamics of zoonotic malaria

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Abstract Content

Despite efforts to eliminate malaria in Malaysia, the emergence of zoonotic malaria caused by the simian parasite *Plasmodium knowlesi* remains a significant public health concern, particularly in Malaysian Borneo. *P. knowlesi* malaria is primarily transmitted by forest-dwelling *Anopheles* mosquitoes, with long-tailed macaques (*Macaca fascicularis*) and pig-tailed macaques (*M. nemestrina*) serving as the main hosts. Genetic and genomic studies have identified two distinct subpopulations of *P. knowlesi* in Malaysian Borneo, each associated with a different macaque species, and a third unique subpopulation in Peninsular Malaysia. These findings reveal the complex transmission dynamics of *P. knowlesi* and highlight unexpected variations in their evolutionary trajectories. A genotyping PCR assay was developed to distinguish the two dimorphic forms of *P. knowlesi* infections in Malaysian Borneo, showing a predominance of infections associated with long-tailed macaques, accounting for two-thirds of total human infections. Demographic data indicate that adult males are most susceptible, often due to agricultural activities. Infections linked to long-tailed macaques are primarily associated with farming near residential areas and forest fringes, while pig-tailed macaque infections are more common with activities in deep forest areas. Continuous monitoring of *P. knowlesi* subpopulation frequencies and environmental changes, including the identification of infection hotspots, is crucial to anticipate shifts in zoonotic malaria epidemiology. These insights are essential for developing new strategies to control this zoonosis and protect public health, emphasizing the need for ongoing epidemiological surveillance and targeted public health interventions.

Abstract Reference: 20646
Mode of Presentation: Symposium
Topic: Call for Symposium

An update on schistosomiasis

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Abstract Content

Despite the prolonged and sustained programs to reduce the impact of human schistosomiasis, these vascular parasites persist as important pathogens of humans and domestic animals. Ongoing efforts to reduce disease burden of the schistosomes have met with many successes, but we are far from reaching a state of sustained control, let alone complete eradication of the agents of schistosomiasis from many countries in the world. Dare we still say that our inability to reduce the impact of these parasites reflects a still limited understanding of schistosomes? Or do we know enough about the parasites now and just need to implement control strategies more effectively? While both sides of such an argument have merit, this presentation will investigate the former argument. The presentation will focus on the growing bodies of data on the host specificity of schistosomes, both for their definitive and intermediate hosts. Schistosomiasis must be seen as a One Health problem and should be addressed with a. multi-pronged approach informed by ongoing epidemiological and bimolecular research.

Abstract Reference: 20537
Mode of Presentation: Symposium
Topic: Call for Symposium

Emerging human fascioliasis in Southern and Southeastern Asia

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Abstract Content

Human fascioliasis is emerging in southern and southeastern Asia at present, with increasing patient reports from Pakistan in the West up to Vietnam in the East. In this wide region, *Fasciola gigantica* is the cause of endemicity in livestock since old times. Lymnaeid transmitting species differ according to biogeographical regions, with *Radix auricularia* superspecies in Pakistan, additionally *R. luteola* in India and Bangladesh, and *R. viridis* in southeastern Asia. Human fascioliasis emergence appears linked to increasing livestock prevalences due to (i) ruminant importation from other countries because of the increasing demand of rapidly growing human populations, (ii) numerous livestock movements, including transborder corridors, due to the uncontrolled small-scale household farming practices, and (iii) man-made introduction of *F. hepatica* with imported livestock leading to frequent hybridization. The emergence scenario in southern China and Vietnam resembles northeastern India and Bangladesh, whereas in Pakistan it is linked to increasing monsoon rainfall within climate change combined with an impact of an extensive irrigation system. Past human-guided movements of pack animals along the western Grand Trunk Road and the eastern Tea-Horse Road explain the *F. gigantica* mtDNA results obtained. Physicians should be aware about these emerging scenarios, clinical pictures, diagnostic techniques and treatment. Government authorities must appropriately warn health professionals, ensure drug availability and improve livestock control.

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Abstract Reference: 20688
Mode of Presentation: Symposium
Topic: Call for Symposium

Emerging zoonotic filarial infections in the Asia Pacific

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Abstract Content

Zoonotic filariases are significant yet often neglected tropical diseases caused by filarial parasites of the family Onchocercidae, which are transmitted from animals to humans via arthropod vectors. The filarial nematodes most associated with zoonotic filariases are *Brugia* spp., *Dirofilaria repens*, and, to a lesser extent, *Dirofilaria immitis*. However, the limitations of the largely used microscopy-based techniques in identifying novel or cryptic species have hindered our understanding of the role of zoonotic filariases in the Asia Pacific region. Recently, there has been a rapid increase in the number of human cases infected with zoonotic filariases in this region. Using molecular methods, dogs have been identified as reservoirs of zoonotic *Dirofilaria* sp. hongkongensis and potentially a novel species of *Brugia* in Sri Lanka. Analyses of human and dog blood infected with *Brugia*-like microfilariae using a nanopore sequencing-based metabarcoding assay demonstrated that the *Brugia* infecting humans were identical to those infecting dogs in Sri Lanka. In this talk, I will provide information on the emergence of zoonotic filariases in the Asia Pacific and discuss their impact in the era of mass drug administration.

Abstract Reference: 20517
Mode of Presentation: Symposium
Topic: Call for Symposium

Project Wolbachia - Singapore

Chee-Seng Chong*[1], Lee-Ching Ng[1], Jue-Tao Lim[2], Cheong-Huat Tan[1], Shuzhen Sim[1], Judith Chui Ching Wong[1], Chia-chen Chang[1], Yee-Ling Lai[1], Kathryn Vasquez[1], Youming Ng[1], Caleb Lee[1], Lu Deng[1], Li-Yun Tan[1], Grace Chain[1], Mohammad Faizal Zulkifli[1], Jonathan Liew[1], Borame Sue Dickens[3]

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Abstract Content

Project *Wolbachia* involves the release of irradiated male *Aedes aegypti* infected with *Wolbachia*, a maternally inherited endosymbiotic bacterium, to suppress the wild-type population. Due to cytoplasmic incompatibility, mating between *Wolbachia*-infected males and wildtype non-infected females yield non-viable eggs. Since the start of Project *Wolbachia* in 2016, the National Environment Agency (NEA) has observed positive results across study sites where more than 90 per cent reduction of the *Aedes aegypti* population has been observed. Data from 2019 to 2022 indicates that residents living in areas with at least one year of releases are up to 77 per cent less likely to be infected with dengue. This demonstrates the potential of *Wolbachia* suppression technology for strengthening dengue control in tropical cities, where dengue burden is the greatest.

Abstract Reference: 20794
Mode of Presentation: Symposium
Topic: Call for Symposium

Mosquito control in the 21st Century

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Abstract Content

Despite numerous annual vector control interventions, mosquitoes that transmit pathogens remain a formidable threat to human populations, particularly in resource-limited regions. The alarming rise of insecticide resistance has catalysed the development of a diverse array of innovative strategies, including genetic, symbiont-based, and chemical approaches, to combat mosquito-borne diseases. This presentation will delve into the cutting-edge tools and techniques that have emerged in the 21st century, focusing on the vectors of malaria, dengue, Zika, and Chikungunya. Attendees will gain insights into the critical considerations and challenges associated with these new interventions. This talk also aims to set the stage for the pivotal contributions of the other speakers in this symposium, fostering a comprehensive understanding of the current landscape and future directions in mosquito-borne disease prevention.

Abstract Reference: 20612
Mode of Presentation: Symposium
Topic: Call for Symposium

Making virus-resistant mosquitoes

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Abstract Content

Genetic control methods are being developed for several major insect pest species, based on genetic modification of the insect pest followed - after considerable laboratory work - by release of modified insects into target population(s). Modifications may aim to reduce the numerical size of the pest population (“population suppression”) or to reduce the vector competence of insects carrying the novel genetic trait (“refractory insects”). This talk focuses on the latter, **how to reduce the ability of *Aedes aegypti* to transmit key viruses such as dengue virus, Zika virus and Chikungunya virus**. A further practical consideration is how to get such a heritable modification into a wild vector population at a high enough allele frequency to have a significant effect on vectorial capacity, and hence potentially an epidemiological impact. While mass-release of modified insects may work well in some cases, especially for some small or accessible target populations, in many cases more self-sustaining genetic systems - gene drives - are likely essential. CRISPR/Cas9-based artificial selfish DNA elements (“gene drives”) have recently been described that might be capable of spreading through an entire species or species complex - though current designs would likely be neutralised by mutation, e.g. target site mutation, before reaching every individual. At York we are aiming to develop “local” gene drives that will sustainably modify a target population but not invade other populations of the same species. Principles, progress and some limitations will be discussed.

Abstract Reference: 20809
Mode of Presentation: Symposium
Topic: Call for Symposium

The next-generation Sterile Insect Technique for mosquito elimination

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Abstract Content

Insecticide resistance, warming climate, and global trade are expanding the distribution and abundance of the mosquito, resulting in recent surges of mosquito-borne diseases. The urgency of the mosquito problem revived the interest in biological approaches for mosquito suppression, such as Sterile Insect Technique (SIT) and *Wolbachia* Insect Incompatibility Technique (WIIT) as well as novel Genetic Modification (GM) approaches. SIT and WIIT rely on massive repeated releases of sex-sorted and ‘sterilized’ adult male mosquitoes, and failed to reach the scale due to their exuberant costs and poor efficacy. Alternatively, novel GM approaches based on releases of fertile GM mosquitoes are failing at the larger scale due to natural selection and/or facing strong regulatory barriers. We have developed the next-generation SIT (ngSIT) that combines the safety of traditional SIT with the precision and efficacy of CRISPR gene knockouts. The CRISPR components are separated into two GM mosquito strains, each expressing Cas9 or multiple guide RNAs separately. The genetic cross between these strains actives CRISPR in the generated ngSIT eggs that develop hands-free into sex-sorted and sterilized male mosquitoes. The egg generation and the ability to release and store *Aedes aegypti* pgSIT eggs increase a production output by 100x relative to that of adult mosquitoes and decrease deployment costs while making possible global logistics. Due to precision-guided genetic knockouts, ngSIT consistently leads to mosquito male sterility and does not sacrifice male fitness, longevity, and competitiveness in the environment. Finally, ngSIT is a technology platform and can be ported into diverse mosquito species.

Abstract Reference: 20816
Mode of Presentation: Symposium
Topic: Call for Symposium

Investigating the robustness of gene drives for mosquito control

Tony Nolan*[1]

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Abstract Content

Mosquito control through gene drive involves the deliberate introduction and spread of altered genetic traits into a population, in order to reduce its potential to transmit pathogens. In recent years great strides have been made in developing an array of different gene drives that have demonstrated proof-of-principle in the laboratory, showing strongly biased rates of inheritance that can rapidly spread an introduced trait to fixation. Were these successes to transfer to a field setting they would represent a transformative tool that is self-sustaining, species-specific, non-toxic and offering benefit to all, regardless of access to healthcare. In addition to the regulatory challenges that such a transformative technology will have to address, there are still technical challenges that can be addressed in order to make this technology even more effective and more robust to resistance. I will talk about some of these aspects, including how to find additional genetic targets for gene drive in the malaria mosquito, and how to investigate, and ameliorate, the effect of potential genetic barriers to gene drive penetrance in a population.

Abstract Reference: 20762
Mode of Presentation: Symposium
Topic: Call for Symposium

Development of triple artemisinin-based combination therapies for malaria

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Abstract Content

Artemisinin-based Combination Therapies (ACTs) are first-line treatments for malaria. However, artemisinin and partner drug resistance are prevalent in the Greater Mekong Subregion, even as these countries move towards malaria elimination. Recent reports of artemisinin resistance in African countries are worrisome and call for urgent action to prevent further emergence or spread of resistance. Triple ACTs (TACTs), combining artemisinin with two currently available partners drugs, could provide one of the last remaining safe and effective treatments for malaria that can be deployed rapidly. TACTs were tested in a clinical study titled Tracking Resistance to Artemisinin Collaboration II (TRACII), providing the first clinical proof of concept of TACTs. Results of the TRACII trial led to the "Development of Triple Artemisinin Combination Therapies (DeTACT)" project, which takes a holistic approach to provide further evidence needed for deployment of TACTs. Two TACTs were developed and tested in a placebo-controlled, randomized, partially-blinded trial for safety, tolerability and efficacy in eight African countries and two Asian countries. Preliminary results from Cambodia and Bangladesh indicated that TACTs are safe, well-tolerated and highly efficacious. Mathematical modeling studies indicated that deployment of TACTs could prevent or delay artemisinin resistance and thereby reduce treatment failures. Studies to explore the market positioning of TACTs in the GMS demonstrated the readiness of countries to explore strategies to deploy TACTs when they become available. One of the TACTs has now been developed into a fixed-dose combination and will be taken forward into a clinical trial and approval by a stringent regulatory authority.

Abstract Reference: 20464
Mode of Presentation: Symposium
Topic: Call for Symposium

Dose optimization of tafenoquine for radical cure of *Plasmodium vivax* malaria

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Abstract Content

Tafenoquine (an 8-aminoquinoine) is an alternative radical curative treatment to primaquine acting against the dormant liver stage of *Plasmodium vivax* (the hypnozoite). Tafenoquine has the considerable advantage of single dosing as compared to a 7 or 14-day course of primaquine to achieve radical cure. The recommended tafenoquine dose of 300mg was shown to be inferior in radical curative efficacy to a total primaquine dose of 3.5mg/kg in Southeast Asia; 74% versus 93% respectively. The comparator 3.5mg/kg total primaquine dose is the standard and most commonly used dose globally, but in Southeast Asia and the Western Pacific, higher doses of primaquine are needed for radical cure. Pharmacometric meta-analysis of data from the phase 3 pre-registration trials supports a 50% dose, which is predicted to more than halve the relapses. The Southeast Asia Dose Optimisation of Tafenoquine (SEADOT) trial aims to determine whether a 50% increase in tafenoquine dose provides better efficacy against recurrent *P. vivax* infection at 4 months than the currently recommended tafenoquine dose.

Abstract Reference: 20714
Mode of Presentation: Symposium
Topic: Call for Symposium

The role of community health workers for malaria elimination in Myanmar

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Abstract Content

Malaria in South-east Asia is now predominantly in remote and difficult to access communities, mainly in Myanmar, which has the majority of malaria reported cases in the region. Access to quality health care services for these communities is very difficult. Most villagers had access only to untrained informal health care providers who did not have malaria tests. Patients with undifferentiated fever, received a variety of inappropriate treatments and malaria transmission continued unabated. To address this, a large number of Community Health Workers (CHWs) were trained to test and treat malaria in their community. This dramatically decreased malaria and eliminated falciparum malaria in most communities within a few years. Early treatment with ACT plus primaquine promptly decreased gametocytaemia and thus transmission. When transmission is low a continued uptake of services is crucial as every person with fever needs to be tested for malaria if elimination is to be attained. But "malaria only" services decline in popularity as people are reluctant to consult services which are increasingly unlikely to help them. With a malaria positivity rate of 1%, 99 out of 100 fever patients will not receive treatment if the CHW only treats malaria. Expanding health services, including management of other common causes of fever, was key in getting local populations with fever to visit the CHW, where they could be tested for malaria, or receive treatment for other diseases if the malaria test was negative. This can improve rural health care while ensuring continued progress towards the elimination of malaria.

Abstract Reference: 20698
Mode of Presentation: Symposium
Topic: Call for Symposium

Design and implementation of a cluster-randomized trial assessing mass vaccinations and mass drug administrations on falciparum malaria transmission in 100 endemic villages in Southeast Asia

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Abstract Content

Community-level malaria elimination tools such as targeted mass drug administration (MDA) have demonstrated short-term effectiveness in Asia. However, untreated parasitaemic individuals can readily re-introduce infections. R21/MatrixM is the second WHO-approved vaccine against falciparum malaria, has more than 70% protective efficacy, is well tolerated and safe. In 2025 a factorial, cluster-randomized controlled trial in Bangladesh will allocate 100 villages (approximately 10,000 population) between four study arms: vaccines, MDA, combined vaccines and MDA, or controls receiving the standard of care. MDA and vaccines will be given over 3 months, with a booster vaccination at 12 months. The primary objective is to evaluate effectiveness over two years against falciparum infections identified by passive case detection and prevalence surveys. A multi-faceted community engagement is being implemented to improve coverage and acceptability. A collaboration is being established between researchers and local partners including health authorities, local NGOs, the EPI programme, and the community health workers who will assist in implementing the trial. Novel materials for communication are created taking into consideration the multi-ethnic communities and vulnerable populations such as migrants and illiterate groups. The study site is a remote, forested region with small, isolated communities and multiple challenges for conducting research, hence the establishment of consortium to implement the trial and a long period of community sensitization. The integration of mass vaccination with R21/MatrixM alongside targeted mass drug administration aims to achieve prolonged interruption of malaria transmission. Tailored, effective community engagement is essential for this strategy to succeed.

Abstract Reference: 20823
Mode of Presentation: Symposium
Topic: Call for Symposium

The intensified 'last mile' elimination approach in Cambodia

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Abstract Content

Cambodia has made significant strides in malaria elimination in recent years. This progress was almost impeded by a steep increase in cases reported between 2017 and 2018, with 46,590 and 63,186 cases, respectively. This rise in cases prompted the National Malaria Control (CNM), with support from the WHO, to implement an Intensification Plan (IP) in October 2018 in 30 health center catchment areas within nine operational districts (ODs) where malaria transmission was primarily occurring. In 2019, the Intensification Plan 2 (IP2) was expanded to encompass 36 health centers in 12 ODs. CNM and WHO developed the Last Mile Elimination focus response package to accelerate elimination in these remaining hotspots in 2020. The Last Mile response package, a comprehensive set of activities, has been in place since November 2020. Its core interventions include community engagement, TDA, IPTf, weekly active fever screening (AFS), top-up of long-lasting insecticide-treated nets (LLINs), and the recruitment of VMWs/MMWs, where deemed necessary. This package aims to detect, investigate, and clear all foci with sustained, local transmission of P. falciparum or mixed cases. When a locally acquired case of P. falciparum or a mixed infection of P. falciparum is identified in a village, a focus investigation is triggered to determine the Last Mile intervention package for that focus, demonstrating its effectiveness in targeted response. Since the implementation of the Intensification Plans, cases in the country have decreased steadily (93%) alongside significant increases in the number of diagnostic tests performed, around 26%.

Abstract Reference: 20851
Mode of Presentation: Symposium
Topic: Call for Symposium

Managing febrile patients in remote communities: Stakeholders' perspectives and experiences in Bangladesh, Cambodia and Laos

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Abstract Content

This study explores and compares the perspectives and experiences of domestic and international stakeholders regarding the management of febrile patients in remote communities across Bangladesh, Cambodia, and Laos. Febrile illnesses are common and pose significant health challenges in these regions due to limited healthcare infrastructure and access. Through qualitative interviews with healthcare providers, community health workers, community leaders, health sector managers and implementers, the research identifies key barriers and facilitators in the diagnosis, treatment, and management of febrile conditions, considering commonalities and differences across the study settings and national health systems. Stakeholders highlighted issues such as inadequate medical supplies and diagnostics, lack of trained personnel, and difficulties in accessing healthcare services for referral of patients, resulting in delayed care or inappropriate management practices such as the widespread use of antibiotics to treat viral infections. Stakeholders also emphasized the importance of community-based health services, the potential of innovative strategies such as digital health, and the need to account for epidemiological change in the communities. The findings underscore the need for targeted interventions to strengthen healthcare systems, enhance training programs for healthcare workers, and develop community-based solutions to effectively manage febrile illnesses in remote settings.

Abstract Reference: 20441
Mode of Presentation: Symposium
Topic: Call for Symposium

Community perceptions of health-related risk factors, health status, and healthcare service in rural Southeast Asia: Insights from a cross-sectional household survey in Bangladesh, Cambodia, and Thailand

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Abstract Content

The South and Southeast Asia Community-based Trials Network conducted a household health survey in 2022-2023 across rural Bangladesh, Cambodia, and Thailand, assessing disease prevalences and identifying community-perceived concerns about health and healthcare. Using two-stage cluster sampling, participants of all ages were recruited. Data on adult ($\geq$ 15 years) were collected through questionnaire interviews, covering their disease history- to be confirmed by laboratory tests- and concerns. Preliminary analysis of adults (Bangladesh: n=1166, Cambodia: n=953, Thailand: n=1199) showed the highest self-reported prevalence of raised cholesterol, hypertension and diabetes in Thailand (hypertension:25.2%, cholesterol: 17.2%, diabetes: 10.2%), followed by Cambodia (hypertension:13.1%, cholesterol: 4.2%, diabetes: 4.6%) and Bangladesh (hypertension:10.9%, cholesterol: 0.8%, diabetes:4.3%). Fever in the past 30 days was the highest in Bangladesh (13.0%), followed by Cambodia (3.6%) and Thailand (0.4%). Women were more likely to have hypertension in Bangladesh (13.8% VS 6.9, $p<0.001$) and Cambodia (15.9 VS 9.8, $p=0.006$), diabetes (5.5% VS 2.2, $p=0.006$) in Bangladesh, and raised cholesterol (19.9% VS 13.6%, $p=0.005$) in Thailand. Bangladeshi adults with hypertension more likely to have fever recently (21.3 VS12.0%, $p=0.004$). Healthcare cost was the leading concern in Cambodia (82.1%) and Bangladesh (46.1%). Bangladeshi adults with hypertension were more likely to report this concern (57.5% VS 44.7%, $p=0.006$). In Thailand, no specific concern was most commonly reported (38.8%), followed by healthcare delivery timeliness (20.9%), especially among those with hypertension (24.9% VS 19.3%, $p=0.038$) and diabetes (29.8% VS 18.7%, $p=0.008$). This survey highlights the varied disease prevalence and community-concerns across countries, underscoring the need for tailored healthcare interventions.

Abstract Reference: 20485
Mode of Presentation: Symposium
Topic: Call for Symposium

Estimating causes of community deaths using electronic verbal autopsies within South and Southeast Asia Community-Based Trial Network (SEACTN) research programme

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Abstract Content

Low- and lower-middle-income Asian countries have limited mortality statistics and large numbers of deaths occur outside of the healthcare system without cause of death (COD) identified. Cause-specific mortality data are critical in developing public health policies, allocation resources and accessing healthcare programs. Along with a rural febrile illness etiology study of South and Southeast Asia community-based trial network (SEACTN), electronic verbal autopsies (VA) were performed to better understand the underlying major COD in these underserved populations. Using standardized WHO VA tools and ICD-10 codes assigned by physician review, mortality surveys were conducted at selected rural sites in Bangladesh, Myanmar, Lao PDR, Thailand, and Cambodia between 2021 and 2023. To minimize recall bias, interviews were conducted three to six months after a death. Of the 3,246 deaths reported across the sites, 3,083 (94%) were adults. In all countries, male deaths outnumbered female deaths. The majority of cases (75%) died at home followed by hospital deaths accounting for (17%). The deceased were treated in a variety of healthcare facilities, primarily at the government hospitals and health centers. Non-communicable diseases predominated at all sites, and digestive system (mainly contributed by males aged 15-59 years), cardiovascular disease, and neoplasms were top three leading COD among adults. Our research concluded that cost-effective interventions targeting the growing burden of non-communicable diseases should be implemented throughout the region. To monitor disease epidemiology over time, VA should be incorporated into national surveys or surveillance, as well as countries' civil registration and vital statistics systems.

Abstract Reference: 20807
Mode of Presentation: Symposium
Topic: Call for Symposium

Aetiology of febrile illness in South and Southeast Asia investigated by patients' blood screening using multiplex real-time (RT-) PCR assays

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Abstract Content

Acute febrile illness is a common symptom for which patients seek healthcare services. Inaccurate diagnosis and a multitude of undifferentiated diseases lead to delayed or inappropriate treatment, which escalate antibiotic-resistance in pathogens. We investigated the aetiology of febrile illness across Southeast Asia to inform targeted intervention and point-of-care tests tailored to these underserved areas. Here we describe preliminary findings from molecular assays carried out on EDTA whole blood samples from febrile patients recruited at secondary hospitals between June 2022 and March 2024 for septicemia screening using multiplex real-time (RT-)PCR targeting rickettsiosis, leptospirosis, scrub typhus, flavivirus and alphavirus fevers. A 0.5 millilitre of patient blood was used to prepare nucleic acid. The detection limits of each infection were 20 (leptospirosis, scrub typhus, and Japanese encephalitis) or 200 (rickettsiosis, dengue, chikungunya, and zika) copy numbers per millilitre of blood. Of 1,896 samples from Chiang Rai, Tak and Suvannakhet, 91 dengue (4.9%), 52 scrub typhus (2.7%), 15 leptospirosis (0.8%), six rickettsiosis (0.3%), and one chikungunya (0.6%) were detected. In Suvannakhet, the most commonly detected pathogen was dengue (74/1,252,5.9%) and Tak (12/85,14.1%), while scrub typhus was common in Chiang Rai (41/599,6.8%). In Suvannakhet, dengue cases peaked in September 2022 and July 2023. Notably, the peak in 2023 was three times higher than in 2022. In Chiang Rai, scrub typhus cases were found between June 2022 and March 2023 at a median of 4.5 cases a month (interquartile of 1.75– 6 cases). This suggested that different study areas uniquely require diagnosis, treatment and disease controls.

Abstract Reference: 20781
Mode of Presentation: Symposium
Topic: Call for Symposium

The epidemiology of acute febrile illness in rural South and Southeast Asian primary care

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Abstract Content

In South and Southeast Asia, malaria is no longer the principal cause of acute febrile illness (AFI) but little is known about the contemporary epidemiology of AFI, especially in rural areas where most of the population live. This study aimed to define the main AFI syndromes, and their clinical management and outcomes in rural primary care settings across five countries (Bangladesh, Cambodia, Laos, Myanmar, and Thailand). Observational study of patients with AFI recruited between 2021–2023. Data collection was performed electronically by village health workers/village malaria workers and in primary health centres serving seven geographically-defined study sites. At enrolment, demographic, clinical, and management data were obtained. Patients were followed up 28 days later to obtain data on further care-seeking and determine outcomes. Causative syndromes were assigned algorithmically using rules developed through expert consensus. Over 80,000 patients of all ages were recruited, with the median symptom duration being two days. Upper respiratory tract infections (URTI) comprised approximately two-thirds of all AFI cases, with fever of unclear source contributing a further quarter. Malaria was negligible at all sites except in Myanmar and neighbouring Tak province in Thailand. Antibiotic prescribing and hospital referral were poorly targeted, and self-medication before and after enrolment was common. Nevertheless, mortality and hospital admission rates were negligible. In rural primary care settings, the bulk of AFI is attributable to URTI and has good outcomes. There is much scope to improve AFI management, such as through algorithm-based digital health interventions to support clinical decision-making.

Abstract Reference: 20611
Mode of Presentation: Symposium
Topic: Call for Symposium

Spot sepsis: prediction of disease severity in young children with acute febrile illnesses in resource limited settings

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Abstract Content

Infections remain the leading cause of preventable childhood mortality in low- and middle-income countries. Reliable guidelines to help community healthcare providers identify children whom may benefit from referral to higher-level care are lacking. This talk presents findings from a multi-country prospective observational cohort study (Spot Sepsis; NCT04285021) which recruited children under the age of five presenting with acute febrile illnesses in Bangladesh, Cambodia, Lao PDR, Indonesia, and Vietnam. The primary outcome was death or vital organ support within two days of enrolment. Weighted logistic regression was used to quantify predictive performance of individual host biomarkers and assess their ability to risk stratify children presenting with acute infections in resource-limited community settings and decentralised models of care. 3,423 children were recruited, of whom 133 (0.4% weighted prevalence) met the primary outcome. sTREM-1 demonstrated the best predictive performance (AUC 0.86; 95% CI 0.82-0.90), which was consistent across sites (AUCs 0.84-0.89) and pre-specified subgroups: presenting syndromes (AUCs 0.84-0.87); microbiologically-confirmed infection (AUC 0.88); and prediction horizons from ≤4 hours to >48 hours (AUCs 0.85-0.93). The four leading biomarkers (sTREM-1, sFLT-1, Ang-2, and PCT) all demonstrated better discrimination than WHO Danger Signs (AUC 0.75; 95% CI 0.71-0.80), the current standard of care for guiding referral from the community. Host biomarkers reflecting immune activation, endothelial dysfunction, and inflammation demonstrate promise for risk stratification of childhood infections in resource-limited community settings in Asia. Further work is required to understand whether biomarker measurements can add value to the clinical assessments of community healthcare providers.

Abstract Reference: 20565
Mode of Presentation: Symposium
Topic: Call for Symposium

From a lab to diagnosis and treatment: Lesson learned from the studies of the brain-infecting amoeba and *Plasmodium falciparum*

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Abstract Content

Strategies for coping with persistent parasitic diseases shall include interdisciplinary research. This talk selects two different approaches to address unmet needs in drug testing against *Plasmodium falciparum* and rare brain-eating amoeba. Despite effective treatment of falciparum malaria, *P. falciparum* arrests growth in response to artemisinin. The growth-arresting parasites survive and cause malaria recrudescence. The standard microscopy fails to detect this stage. Here, we demonstrated the use of cell-permeable, DNA-binding fluorophores to distinguish the false death, that is growth-arrested, artemisinin-resisting stage, from true dead parasites. This method is a simple assay applicable for monitoring artemisinin resistance. Secondly, free-living amoeba *Balamuthia mandrillaris* is highly fatal and there is no curative treatment. Here, we applied organoid, which is a three-dimensional cell culture of stem cells. By using cerebral organoids, the amoebicidal effect of the repurposed drug nitroxoline was confirmed. Together, a cooperative project with other disciplines may provide a new solution to the long-existing problem in the diagnosis and treatment of parasitic diseases.

Abstract Reference: 20649
Mode of Presentation: Symposium
Topic: Call for Symposium

Environmental DNA approach in Eco Health/One Health towards eradication of opisthorchiasis

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Abstract Content

Opisthorchiasis, caused by *Opisthorchis viverrini* (Ov) affects more than 10 million people in the lower Mekong River Basin, chronic infection by Ov is related to cholangiocarcinoma and constitutes a major health problem. The main countermeasure against Ov in endemic areas is treatment of infected people based in coproparasitological tests, however no consistent reducing on the Ov prevalence has been observed. Prophylactic measures include avoiding the consumption of fish with metacercaria. Though, it is a difficult task once the presence of metacercaria in fish is not detectable by naked eyes and there is a lack of tests for detection of Ov infected fish and areas/sites with risk of infection by fish ingestion. We developed an environmental DNA approach for detecting parasite DNA in environmental water, allowing us to better understand habitats of Ov and the infection dynamics with high accuracy, and sensitivity. Using eco-epidemiological eDNA data, it is possible to determine hotspots of environmental contamination by the parasite and predict active transmission sites. Due to the zoonotic nature of Ov, possessing animal reservoirs such as dogs and cats, the life cycle of Ov in the community cannot be completely stopped without measures against such non-human hosts, and if Ov remains in the environment, reinfection to humans can easily occur. Furthermore, dogs' behavior showed daily water contact, confirming dogs as an important factor in Ov life cycle perpetuation, spreading Ov eggs in the environment. Technical advances in eDNA detection and its outcomes will be presented in a prospective study in Lao-PDR.

Abstract Reference: 20585
Mode of Presentation: Symposium
Topic: Call for Symposium

Multi-OMICS approaches for drug development in parasitic diseases

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Abstract Content

Schistosoma mekongi is a major causative agent of human schistosomiasis in Southeast Asia. With reliance on praziquantel (PZQ) and emerging resistance, identifying new drug targets is critical. Due to limited knowledge of its molecular biology, we employed proteomics, phosphoproteomics, and kinomics approaches to identify potential drug targets. We focused on sex-specific differentially expressed proteins, phosphoproteins, and kinases, which play crucial roles in female maturation and egg production. Mass spectrometry-based quantification revealed 174 and 156 differentially expressed proteins in male and female worms, respectively. Male-biased proteins are involved in actin filament-based processes, microtubule-based processes, biosynthetic processes, and homeostatic processes. Female-biased proteins are related to biosynthetic processes, organelle organization, and signal transduction. Phosphorylation, which regulates key signaling pathways for parasite growth and reproduction, presents a viable intervention point. We identified 88 male- and 44 female-biased phosphoproteins in the *S. mekongi* phosphoproteome. Protein kinases (PKs), particularly focal adhesion kinase (FAK), have emerged as promising drug targets. Transcriptomic and proteomic analyses identified FAK as essential for cellular processes in *S. mekongi*. Molecular docking simulations and in vitro assays showed that FAK inhibitors, especially FAK inhibitor 14 and PF-03814735, exhibit significant anti-parasitic activity with low toxicity to human cells. These results position FAK as a potential target for novel anti-schistosomal therapies, warranting further *in vivo* validation. This study provides a strategic framework for developing new treatments to combat schistosomiasis and reduce its global impact.

Abstract Reference: 20663
Mode of Presentation: Symposium
Topic: Call for Symposium

Integrative molecular biological analysis to identify *Schistosoma mekongi* candidates for the development of diagnostics and vaccines

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Abstract Content

Schistosoma mekongi, causing schistosomiasis in humans, is a significant public health concern in Southeast Asia. While praziquantel is the primary treatment, the emergence of resistance necessitates the development of alternative diagnostics and vaccines. However, the biology and molecular biology of S. mekongi remain poorly understood, with limited genes and proteins available in public databases. Integrative analyses of transcriptomics, proteomics, and peptidomics of S. mekongi have been introduced. These efforts have identified several candidate molecules, some of which have been characterized using bioinformatics, molecular biology, and immunology approaches. These findings will aid in the development of new diagnostics and vaccines.

Abstract Reference: 20470
Mode of Presentation: Symposium
Topic: Call for Symposium

Overview of an eAsia and NHMRC partnership grant on eliminating *Schistosoma mekongi* in Laos and Cambodia

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Abstract Content

Schistosoma mekongi is endemic in Cambodia and Lao PDR and prevalence in these countries have ranged from 0.6% to 33%. While the prevalence is now considerably lower, particularly in Cambodia, than when control programs began, the parasite persists despite yearly mass drug administration (MDA) of Praziquantel. While *S. mekongi* is a zoonosis, with dogs and pigs previously identified as potential hosts, the role these animals play in transmission has not been fully elucidated. The Mekong region has been identified as one of the regions most vulnerable to climate change. Changing rainfall and climatic patterns due to climate change will lead to shifts and potential expansion of schistosomiasis to new areas and increased transmission, due to the impact climate change will have most particularly on the intermediate snail host. Thus, we believe it is a perfect time to push towards elimination before the effects of climate change on the epidemiology of the parasite can be felt. We hypothesise that by implementing and adapting and developing a health education package combined with WASH, MDA, diagnostics, environmental monitoring, monitoring potential animal hosts, and spatial and mathematical models for targeting *S. mekongi*, we can provide a blueprint for the rapid elimination of *S. mekongi* in the Mekong area before the effects of climate change can be felt, and use mathematical models to show the success of the developed intervention in achieving this aim. Here I will present an overview of the project and the tools we will develop during this project.

Abstract Reference: 20695
Mode of Presentation: Symposium
Topic: Call for Symposium

Seasonality of schistosomiasis infection risk and the dynamics of environmental DNA detection

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Abstract Content

Schistosomiasis is a water-borne disease that poses a significant threat to human health in agricultural areas of endemic countries affecting especially the less empowered and people in a situation of social vulnerability. The presence of snail host and *Schistosoma* in freshwater bodies indicate active disease transmission. Currently, environmental monitoring is done via snail survey and microscopic examination, a laborious and highly technical method. As pointed out by WHO/NTD road map there is a need for improvement in the tools for surveillance of transmission foci to achieve the goal of schistosomiasis elimination by 2030. Shifting the strategy to a holistic One Health approach, we are using environmental DNA (eDNA) for improved sensitivity and accuracy in detecting hosts and parasites. The technique could increase by 8-fold the detection of snails and accurately detect *Schistosoma* eDNA in water samples. Clustering of schistosomiasis-positive households are observed around eDNA-positive sites, supporting there is a focal disease transmission. We will present our findings and insights on the dynamics of eDNA in an endemic area and their eco-epidemiological implications for the surveillance and control of schistosomiasis.

Abstract Reference: 20632
Mode of Presentation: Symposium
Topic: Call for Symposium

***Schistosomiasis mekongi*: An overview**

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Abstract Content

Schistosomiasis mekongi is endemic along the Mekong river and its tributaries in the lower Mekong basin, and is caused by infection with the blood fluke *Schistosoma mekongi*. Endemic areas are found in Cambodia, Laos, and previously Thailand. An estimated 140,000 people are at risk of infection in both Laos and Cambodia. Untreated, infection can result in sever disease outcomes. Early observations on patients in 1957 revealed severe intestinal and hepatosplenic disease. High mortality rates and widespread disease were reported from the provinces of northern Cambodia (Stung Treng and Kratie´) and southern Lao PDR (Champasack) in the early 1970s and 1990s. Control programmes built around mass drug administration (MDA), with praziquantel, and combined with information and education campaigns, were carried out in both countries which continue today. These efforts resolved the public health problem of schistosomiasis mekongi and led to a significant reduction in transmission. In Lao PDR, the interventions started in the late 1980s, but suffered several interruptions which permitted transmission to resume. Today, a number of small foci continue to show substantial prevalence rates despite ongoing MDA. The snail intermediate host, Neotricula aperta, is present in the Mekong River and some of its tributaries. There is evidence that the snail might not yet have reached its full geographical distribution, particularly in the light of climate change which is expected to impact greatly on the Mekong area, emphasising the need to sustain vigilance. Here I will present an overview of schistosomiasis mekongi in Laos and Cambodia.

Abstract Reference: 20655
Mode of Presentation: Symposium
Topic: Call for Symposium

Elimination efforts of *Schistosoma mekongi* in Cambodia

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Abstract Content

Schistosomiasis mekongi has been identified as endemic in Cambodia and Laos since the early 1960's, although the exact species, *Schistosoma mekongi*, was not identified until the late 19170's. In Cambodia, schistosomiasis is transmitted in the provinces of Kratie and Stung Treng where approximately 80 000 individuals are estimated to be at risk of infection. Similar to *S. japonicum* infection results in sever hepatosplenic disease. The infection is distributed along a limited part of the Mekong River, regulated by the focal distribution of the intermediate snail host Neotricula aperta. Although more sensitive diagnostics imply a higher figure, the current use of stool examinations suggests that only about 1500 people are presently infected, and cases of severe morbidity are no longer reported. Control activities based on mass drug administration resulted in strong advances, and prevalence was reduced to less than 5% according to stool microscopy. Even so, transmission continues unabated, and the true number of infected people could be as much as 10 times higher than reported. Complicating the matter, *S. mekongi* has been noted as a zoonosis, with dogs previously been recognized to play a role in schistosomiasis transmission in Cambodia, although the importance of that role is undetermined. Here I will present an overview of elimination efforts in *Schistosoma mekongi* in Cambodia.

Abstract Reference: 20625
Mode of Presentation: Symposium
Topic: Call for Symposium

A glimpse into the occurrence of strongyloidiasis and challenges for its control in India

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Abstract Content

The approach towards strongyloidiasis has shifted from a disease relevant only in immunosuppressed population to a disease targeted for control as a public health problem. The recent estimates indicate that more than 600 million people are infected with *Strongyloides stercoralis* worldwide. There is a lack of studies specifically focusing on strongyloidiasis from India, and the earlier analyses indicated an overall estimated prevalence of about 6% in community- and 11% in hospital-based studies from the country. However, recent works reveal that the burden of infection is much higher, ranging from 15 to 36% in different geographical regions of the country. Though a variety of risk factors are known for the development of severe strongyloidiasis, such as corticosteroid therapy, malignancy, etc., it needs to be emphasized that there may be situations where the immunosuppressed status of an individual may remain obscure, especially in settings of developing and underdeveloped world with inadequate infrastructure for elaborate diagnostic workup for immunosuppression. *S. stercoralis* is also likely to be affecting immunocompetent individuals and may be an important cause of chronic morbidity like other soil transmitted helminth (STH) infections. It is also important to understand the molecular epidemiology of *S. stercoralis* and the zoonotic aspects of its transmission to implement effective control strategies. Finally, though the control of human strongyloidiasis has been clubbed under the umbrella of STH control programmes, the disease poses some unique challenges which need to be addressed before its control can be achieved.

Abstract Reference: 20476
Mode of Presentation: Symposium
Topic: Call for Symposium

Ending the neglect – Setting the platform for strongyloidiasis elimination in Australia

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Abstract Content

Strongyloidiasis is a disease of poverty, intimately linked to inadequate sanitation, lack of clean water and poor hygiene, as well as limited access to health care and preventive measures. It is caused by parasitic nematodes and considered to be the most neglected of the neglected tropical diseases. There are two main Strongyloides species that cause human infection; *Strongyloides stercoralis* and *Strongyloides fuelleborni*. In Australia, *S. stercoralis* is the infecting species that disproportionately affects remote Indigenous communities, with the prevalence ranging from 10-60%, although the true extent is unknown. Infection ranges from asymptomatic to fatal. The lifecycle and transmission are complex with both a parasitic cycle and free-living cycle. This is further complicated by autoinfection and the possibility of zoonotic transmission. These factors coupled with less than ideal diagnostics, and treatment options where there is evidence of treatment failures, the spectre of emerging resistance and the inability to prevent reinfection, all have implications for control and elimination efforts. The complexity of transmission, underlying causes and deficiencies in knowledge, treatment and diagnostics means there is no “quick fix” for strongyloidiasis in Australia (and the world). Multiple disciplines and sectors spanning the community, human and veterinary health, education and the environment will be required to come together to defeat this disease of the poor that should not be in Australia. It is therefore, our central thesis that strongyloidiasis is a zoonotic neglected tropical disease of public health importance in Australia and that an integrated interdisciplinary “One Health” approach is required for its elimination.

Abstract Reference: 20841
Mode of Presentation: Symposium
Topic: Call for Symposium

Real-time PCR for diagnosing and monitoring treatment effect of *Strongyloides stercoralis* infection in endemic and non-endemic settings

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Abstract Content

Molecular methods for the diagnosis of *Strongyloides stercoralis* infections have been used in several countries reporting differences in performance depending used reference technique and the setting in which the study was conducted. In a recent retrospective study in the Netherlands, the diagnostic data collected over a period of more than 15 years in two hospitals with a different patient population were analyzed. A total of 19179 PCR results were available, *S. stercoralis* DNA was detected in 149 specimens from 103 patients. PCR results of follow-up samples was available of 46.6% of the patients of those the first follow-up fecal sample was negative in 79% of the cases. Serology showed a positive result in 70 of 74 (94.5%) patients in which a serum sample was available. *Strongyloides stercoralis* real-time PCR is an efficient tool for the diagnosis of strongyloidiasis and monitoring treatment efficacy.

Abstract Reference: 20437
Mode of Presentation: Symposium
Topic: Call for Symposium

Lateral flow rapid diagnostic test for *Strongyloides stercoralis* infection: A review on its evaluations and applications

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Abstract Content

Strongyloides stercoralis, one of the most neglected NTDs, infects about 600 million people worldwide. Challenges in diagnosing *S. stercoralis* infection include the lack of a gold-standard test and standardization of detection methods. The low and intermittent *Strongyloides* larvae output in stool poses difficulties in the parasitological diagnosis of suspected people. Serology is more sensitive than faecal and molecular methods, thus often used in diagnosis despite some limitations. A serological test in a rapid diagnostic test (RDT) format would support control programs needing a field-applicable test and developing countries with limited resources. SsRapid is a prototype point-of-care (POC) lateral flow cassette test that uses recombinant NIE antigen and specific IgG4 detection. The presentation review the evaluations and applications of the RDT in Southeast Asia performed in Malaysia, Thailand, and Indonesia. Additionally, it will inform on the field and laboratory studies conducted in Iran and several countries in South America and Europe. Overall, the RDT shows good diagnostic performance and may fill the gap for a rapid test for *strongyloidiasis.*

Abstract Reference: 20768
Mode of Presentation: Symposium
Topic: Call for Symposium

An integrated vector management strategy for the control of simian malaria in Malaysia and Thailand

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Abstract Content

Due to increases in simian malaria transmission to humans in Asia, management and prevention strategies must be vector- or human-centric. An integrated vector management plan for control of simian malaria requires a code of practice with guidelines for managing mosquitoes in forests and agro-forestry landscapes, which can guide stakeholders in reconciling priorities and decisions for sensitive sites depending on the local context. The evidence base of recent entomological studies in semi-field systems, forest ecotype, and mathematical modeling that describes mosquito behaviour to experimental data sets is reviewed in the context of the Mekong regional landscape. Modelling studies parameterizing the impact of etofenprox-treated clothing, picaridin topical repellents, transfluthrin spatial repellents, as well as combined interventions are discussed. Products within these classes can be delivered to more at-risk individuals using social behaviour change and communication strategies, collecting implementation outcomes on factors that enable or prevent sustained uptake including willingness to pay for these products alone and in combination with other protective measures, including chemoprophylaxis. The area-wide approach to managing forest mosquitoes of the Leucosphyrus group necessitates a variety of approaches, including innovative tools within delimited areas to ensure co-ordinated and co-operative management through the efforts of a revitalised community participation health programme (Sukarelawan Penjagaan Kesihatan Primer or SPKP) in Malaysia or Village Health Volunteers in Thailand. Further research is needed to evaluate these technologies for addressing gaps in protection such as day-biting or outdoor-biting mosquitoes, in Malaysian and Thailand settings where LLINs and IRS are not suitable.

Abstract Reference: 20750
Mode of Presentation: Symposium
Topic: Call for Symposium

Sampling efficacy of moving sweep net collection of *Aedes albopictus* (Skuse) (Diptera: Culicidae) in a rubber plantation ecotype

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Abstract Content

Vector surveillance requires representative sampling of mosquito populations to support decision-making. We compared the effectiveness of Moving-Sweep net Collection (MSC) and Human Landing Catch (HLC) of *Aedes albopictus*, an arbovirus vector, and determined the parity status. Both methods were concurrently conducted in three rubber tree plots over four replicates, during 07:00-10:00h and 14:00-17:00h in the dry season. Collectors rotated daily for six days per replicate. For MSC, a collector systematically conducted slow walks along transect rows of trees and sweep net collections at every fifth tree for 3 minutes, while another collector performed stationary HLC and collected mosquitoes landing on exposed legs with an aspirator. Parity status was determined by ovarian dissections. Negative binomial regression was used to evaluate the effectiveness of collection methods. Analysis of variance was then utilized for parity status. Among 1,863 mosquitoes collected, 823 and 1,040 were *Ae. albopictus* and non-*Ae. albopictus*, respectively. Higher numbers of *Ae. albopictus* were collected in the afternoon than in the morning (IRR= 0.292, df= 1, 95% CI= 0.231–0.369, P<0.001) particularly in plots near houses (IRR= 0.335, df= 2, 95% CI= 0.218–0.379, P<0.001) with no significant difference between methods (IRR= 0.924, df= 1, 95% CI= 0.741–1.153, P=0.485). Parous mosquitoes were significantly higher than nulliparous mosquitoes in the afternoon (F= 17.695, df= 1, P=0.006) but not significantly different in morning collections (F= 3.098, df= 1, P=0.129). In conclusion, MSC caught a representative sample of *Aedes* vectors as HLC and were found concentrated in anthropized areas of a rubber plantation ecotype.

Abstract Reference: 20506
Mode of Presentation: Symposium
Topic: Call for Symposium

Dirus Complex Species Identification PCR (DiCSIP) improves identification of *Anopheles dirus* complex from Greater Mekong subregion

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Abstract Content

The *Anopheles dirus* complex plays a significant role as malaria vectors in the Greater Mekong Subregion (GMS), with varying degrees of vector competence among species. Accurate identification of sibling species in this complex is essential for understanding malaria transmission dynamics and deployment of effective vector control measures. However, the original molecular identification assay, Dirus Allele Specific PCR (AS-PCR) targeting the ITS2 region have pronounced non-specific amplifications leading to ambiguous results and misidentification. This study investigates the underlying causes of these inconsistencies and develops new primers for accurate identification. Despite several optimizations, the Dirus AS-PCR continued to produce inaccurate identifications, particularly for *Anopheles dirus*, *Anopheles scanloni*, and *Anopheles nemophilous*. Subsequently, in silico analyses pinpointed problematic primers with high GC content and multiple off-target binding sites. Through a series of in silico analyses and laboratory validation, a new set of primers for Dirus Complex Species Identification PCR (DiCSIP) has been developed. DiCSIP primers improve specificity, operational range, and sensitivity for accurate identification of five complex member species found in the GMS. Validation with laboratory and field *An. dirus* complex specimens demonstrated that DiCSIP could correctly identify all samples while the original Dirus AS-PCR misidentify *An. dirus* as other species when used with different thermocyclers. The DiCSIP assay offers a significant improvement in *An. dirus* complex identification, addressing challenges in specificity and efficiency of the previous ITS2-based assay. This new primer set provides a valuable tool for accurate entomological surveys, supporting effective vector control strategies to reduce transmission, and prevent the re-introduction.

Abstract Reference: 20388
Mode of Presentation: Symposium
Topic: Call for Symposium

Multidisciplinary evaluation of malaria transmission and effectiveness of vector control methods in the Balombo region, Angola

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Abstract Content

Sub-saharan Africa bears a disproportionate burden of malaria, and alone account for 96% of the death recorded worldwide (WHO, 2023). Angola is the 5th country most impacted by malaria, experiencing a 40% increase in cases since 2015. In the Balombo region, where malaria is meso-endemic, a vector control program and multidisciplinary study have been ongoing since 2007. To assess the program's impact, cross-sectional parasitological and entomological surveys were conducted during both dry and rainy seasons. Entomological surveys were done by trapping *Anopheles* adult mosquitoes in nine villages of the Balombo region. Then, they were identified morphologically and molecularly (PCR). Parasitological surveys were done by collecting fingertip blood drops from villagers for thick and thin smears, and Rapid Diagnostic Tests, to evaluate *Plasmodium* species prevalence. Additionally, the percentage of long-lasting insecticidal nets use per village was estimated. Results revealed changes in the *Anopheles* fauna, with *An. gambiae* s.s. replacing *An. funestus* in some villages. Despite vector control efforts, a notable increase in *Plasmodium* prevalence occurred. Moreover, *Plasmodium falciparum* is no longer the only species infecting villagers. *Plasmodium malariae, Plasmodium ovale,* and even *Plasmodium vivax* have also been identified. In conclusion, changes in the epidemiological malaria context in the Balombo region are undergoing. Despite the implementation of vector control measures, infection rates continue to rise, accompanied by changes in both *Plasmodium* and *Anopheles* species composition. These results underline the importance of regular and long-term malaria surveillance to respond effectively to the evolving challenges posed by malaria in Africa over the past decade.

Abstract Reference: 20374
Mode of Presentation: Symposium
Topic: Call for Symposium

Malaria control in Angola and immunological markers as indicator of vector control effectiveness

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Abstract Content

On a global scale, progress in the elimination of malaria remains uneven. Some countries have met the goal to reduce malaria incidence or even eliminate it, while other countries such as Angola are facing a resurgence of the disease with an increase in mortality since 2011. Angola is now among the 10 countries with the highest number of reported malaria cases (3.4%) and deaths (2.4%) in the world, respectively ranking 5th and 10th among the African countries (WHO 2022). In the context of mesoendemic malaria in villages in the Balombo region of Angola, our study aims to identify factors promoting malaria transmission with the goal of improving malaria control and reducing the malaria burden in 9 villages. Our objectives are to increase our knowledge on the *Plasmodium* species circulating in the region, as well as the *Anopheles* vector species present in each village, their biting behavior and role in *Plasmodium* transmission. An immunological marker based on the analysis of the specific IgG response to *Anopheles* salivary peptide (gSG6-P1) by ELISA tests, in human blood samples, is also used to estimate the mosquito-biting pressure to which the population of each village is subjected in relation to the percentage use of long-lasting insecticide-treated nets (LLINs). This analysis is allowing an estimation of the efficacy of the vector control method implemented. This multidisciplinary project aims to improve malaria control in an area, and country, particularly affected by the disease and where children pay the heaviest price.

Abstract Reference: 20292
Mode of Presentation: Symposium
Topic: Call for Symposium

Important vector-borne diseases in AECs and implications for control

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Abstract Content

The Asian Economic Countries (AECS) comprise ten nations, many of which are facing infectious diseases. Globally, vector-borne diseases account for more than 17% of all infectious diseases, causing over 600,000 deaths annually. They can be caused by parasites, bacteria, or viruses. Several vector-borne diseases are endemic in some of these AEC countries, including malaria, filariasis, and various arboviruses. Malaria and filariasis, parasitic infections transmitted by mosquito vectors, are predominantly found along international borders, posing significant challenges to elimination efforts. The most prominent malaria problem is currently observed along the borders between Thailand and Malaysia, as well as Thailand and Myanmar, among others. Additionally, other AECS countries such as Indonesia and Malaysia are also encountering malaria issues. Countries implementing elimination programs often struggle to succeed in border regions, a situation common among nations sharing borders.

Abstract Reference: 20213
Mode of Presentation: Symposium
Topic: Call for Symposium

Plasmodium falciparum asexual and sexual stage activity of ivermectin and its interactions with antimalarial drugs

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Abstract Content

Ivermectin is not only an anthelminthic drug, but also an endectocide, killing mosquitoes when feeding on ivermectin treated individuals. Studies evaluating mass drug administration of ivermectin show a reduction in mosquito survival and human malaria incidence. The current study investigated the effect of ivermectin on the asexual and sexual erythrocytic stages of *Plasmodium falciparum*. The susceptibility of asexual erythrocytic stage *P. falciparum* to ivermectin and its metabolites (M1, M3 and M6) were investigated using a SYBR green-1-based assay. The mean (SD) 50% inhibitory concentration (IC50) of ivermectin was 0.81 (0.15) mM for artemisinin-sensitive and 0.81 (0.13) mM for artemisinin-resistant parasites (P=0.574). Ivermectin metabolites were less active than the ivermectin parent compound (P<0.001). Pharmacodynamic interactions of ivermectin with artemisinin, ACT-partner drugs and atovaquone were evaluated using a chequerboard assay. No synergistic or antagonistic interactions were observed with any combination. Sexual stage activity of ivermectin in artemisinin-resistant *P. falciparum* stage V gametocytes was studied using a *P. falciparum*gamete formation assay (PfDGFA). Mean (SD) IC50 was 23.85 (4.53) mM for male gametocytes and 40.91 (9.51) mM for female gametocytes, showing higher susceptibility of the male gametocytes (P<0.001). In conclusion, *P. falciparum* asexual and sexual stage activity of ivermectin was only shown at submicromolar and micromolar concentrations, which is higher than the expected ivermectin plasma concentrations after treatment. There were no pharmacodynamic interactions between ivermectin and antimalarial drugs, suggesting that ivermectin can be added to antimalarial drugs in mass drug administration targeting malaria elimination without compromising antimalarial activity.

Abstract Reference: 20838
Mode of Presentation: Symposium
Topic: Call for Symposium

Pharmacometric properties and mosquito-lethal effects of ivermectin

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Abstract Content

Ivermectin is an antiparasitic drug, but it also has mosquito-lethal properties. This can be advantageous during mass drug administration with the aim to eliminate malaria. To optimise the use of ivermectin, it is crucial to understand the pharmacokinetic and pharmacodynamic properties of ivermectin and its metabolites. The objective of this study was to develop a pharmacokinetic/pharmacodynamic model to quantify the relationship between the concentration of ivermectin and its mosquito mortality. The model was constructed using data from two healthy volunteer trials (n=26). Drug concentrations of ivermectin and three newly identified metabolites were quantified using LC-MS/MS. In addition, blood from volunteers were fed to mosquitos, and mosquito mortality was measured. All the collected data were evaluated using nonlinear mixed-effects modelling in Pumas AI. The pharmacokinetic properties of ivermectin and its metabolites were described by the developed model. Body weight was included using an allometric function on all clearance and volume parameters. Co-administration of the antimalarial drug dihydroartemisinin-piperaquine was shown to decrease the elimination of ivermectin. Mosquito mortality was modelled with an Emax-model, accounting for both ivermectin and metabolite concentrations. *An. minimus* mosquitoes was substantially more sensitive to ivermectin compared to *An. dirus*. A pharmacokinetic/pharmacodynamic model of ivermectin and its metabolites was developed successfully, and this model was used to simulate several different dosing scenarios for ivermectin treatment and for mass drug administration. This work could be used to inform the design of future clinical trials and to guide malaria elimination campaigns.

Abstract Reference: 20594
Mode of Presentation: Symposium
Topic: Call for Symposium

From channel interactions to field trials: Updates on ivermectin for malaria control

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Abstract Content

Ivermectin is a novel vector control tool for malaria as ivermectin-treated humans or animals are lethal to blood-feeding *Anopheles* mosquitoes, the vectors of malaria. In fruit flies and nematodes, the target for ivermectin is the Glutamate-Gated Chloride (GluCl) ion channel. However, *Anopheles* GluCl channel and ivermectin interactions have not been well characterized. Preliminary work with the Southeast Asian malaria vectors, *Anopheles dirus* and *Anopheles minimus*, suggests novel ivermectin-GluCl interactions that were not identified previously from nematode models. Recent field trials with standard ivermectin formulations mass administered to people and/or livestock indicate that longer lasting ivermectin formulations may be required for effective malaria control. We have recently completed field evaluation of commercially available standard and long-lasting ivermectin formulations in cattle and buffalo in a malaria endemic setting in rural Indonesia. Duration of mosquito-lethal effect against wild *Anopheles* with standard ivermectin lasted for 8 and 16 days, and with long-lasting ivermectin for 56 and 72 days, in buffalo and cattle respectively. Nine Southeast Asian *Anopheles* species were captured in abundance high enough to calculate the lethal concentration that kills 50% of mosquitoes including: *An. Aconitus*, *An. Annularis*, *An. Barbirostris*, *An. Flavirostris*, *An. Kochi*, *An. Maculatus*, *An. Sundaicus*, *An. Tessellatus*, and *An. Vagus*. These species are primary, secondary, and potential malaria vectors in Southeast Asia and have never been evaluated for ivermectin susceptibility previously. These results indicate that this long-lasting ivermectin formulation in livestock may be an ideal addition to mass human treatment for malaria control.

Abstract Reference: 20529
Mode of Presentation: Symposium
Topic: Call for Symposium

A trial of mass ivermectin administration to reduce malaria transmission in Thailand

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Abstract Content

A cluster-randomized trial was conducted to evaluate the impact of ivermectin mass drug administration on malaria transmission in Thailand. The study, initiated in 2017, began with site selection through malaria mass blood surveys across four endemic sites in western and southern Thailand. Surat Thani province was chosen as the study site, followed by baseline malaria surveys in 2019 to inform the final design of the cluster-randomized intervention trial. The trial involved 10 treatment clusters and 10 control clusters, with a total of 6,551 participants. Three mass drug administrations (MDAs) were conducted in May, June, and July of 2022, achieving 62-70% coverage in the treatment arm. The impact of the intervention on malaria transmission was evaluated through a series of human mass blood surveys and mosquito collection using human landing capture before, during, and after the three MDAs. Results of the trial, including feasibility assessment, safety evaluation, and efficacy, will be described and discussed.

Abstract Reference: 20584
Mode of Presentation: Symposium
Topic: Call for Symposium

The role of the automated hematology analyzer XN-31

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Abstract Content

The gold standard for malaria diagnosis is to prepare a blood smear for microscopy to identify *Plasmodium* species. However, this method is time-consuming and labor intensive, and requires skill to perform microscopic examination with high accuracy. Rapid Diagnostic Tests (RDTs) are widely used because they are easy to handle and can be performed in 15 minutes. However, the sensitivity of the RDTs is inferior to other methods. The PCR method has excellent sensitivity, but it takes 2-3 hours to obtain results. Sysmex Corporation has developed the automated hematology analyzer XN-31 to overcome these issues. The XN-31 can detect and quantify *Plasmodium* -infected RBCs to aid malaria diagnosis. The number of Malaria Infected RBC (MI-RBC#) is counted and %parasitemia (MI-RBC%) is calculated in about 1 minute. Information on *Plasmodium* species and their developmental stage can also be obtained for research purposes. The operator does not require skilled lab-techniques and is faster in producing results than the other conventional methods. Prompt diagnosis leads to proper treatment. The potential contribution of the XN-31 to malaria elimination will be pointed out in this symposium.

Abstract Reference: 20562
Mode of Presentation: Symposium
Topic: Call for Symposium

AD22: A promising malaria vaccine antigen and target for monoclonal antibody drugs

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Abstract Content

Enolase, a glycolytic enzyme from *Plasmodium falciparum*, has been identified as a potent antigenic target in convalescent-phase malaria patients. We synthesized a 22-residue peptide, AD22, derived from *P. falciparum* enolase, to evaluate its vaccine potential. Our studies revealed that polyclonal antibodies induced by AD22 in rabbits significantly inhibited the growth of *P. falciparum in vitro* in a dose-dependent manner and localized to the merozoite surface. These antibodies reduced *P. berghei* sporozoite invasion of Hep G2 cells by 66%. Mice immunized with AD22 and alum showed increased specific antibody levels and improved survival rates following *P. berghei* challenges. Additionally, *Aotus* monkeys immunized with AD22 and Freund adjuvant demonstrated notable reductions in parasitemia upon challenge with *P. falciparum* FVO strains. We are also developing fully humanized monoclonal antibodies targeting AD22 for severe or drug-resistant malaria, with one clone showing 73% growth inhibition *in vitro*. Mice infected with *P. berghei* and treated with these antibodies survived significantly longer than control mice. This research highlights the potential of AD22-based vaccines and therapies as innovative contributions from Japan to global malaria control efforts.

Abstract Reference: 20717
Mode of Presentation: Symposium
Topic: Call for Symposium

Malaria-LAMP：Simple and rapid molecular diagnostics for malaria elimination

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Abstract Content

Here, we introduce molecular diagnostics for malaria (Malaria-LAMP), in which an isothermal DNA amplification method called LAMP (loop-mediated isothermal amplification) is used in the DNA amplification step. The Malaria-LAMP consists of three types of LAMP reagent kits: Pan-LAMP, Pf-LAMP, and Pv-LAMP. Pan-LAMP is designed to detect all five species of *Plasmodium* that infect humans; meanwhile, Pf-LAMP and Pv-LAMP are specifically designed to detect *Plasmodium falciparum* and *Plasmodium vivax*. The sensitivity of the Malaria-LAMP combined with a simple DNA extraction technology named PURE (Procedure for Ultra Rapid Extraction) has found to be a few parasites per microliter of peripheral blood. Therefore, this combination of PURE and Malaria-LAMP enables the detection of *Plasmodium* parasites circulating in asymptomatic parasite-carriers with very low-level parasitemia. Moreover, these products are designed to be simple and robust enough to provide solutions for the decentralization of screening activities. This decentralization is critical for facilitating the last mile for malaria elimination in the regions where the disease is nearly eliminated. During the symposium, we will showcase the impact of Malaria-LAMP in collaboration with the Japanese authority and some private companies to achieve true malaria elimination.

Abstract Reference: 20644
Mode of Presentation: Symposium
Topic: Call for Symposium

Integrated vector management

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Abstract Content

Vector Control (VC) is a very important tool to fight against malaria and other vector-borne diseases. An innovative approach, including the development of new products, is essential to achieve the goal of malaria elimination. Sumitomo Chemical has been playing a significant role in introducing new Long-Lasting Insecticidal Nets (LLINs), Indoor Residual Spraying (IRS), Larvicides and other VC products for the last 25 years. Mitsui Chemical Crop & Life Solutions introduced a new IRS in 2023. However, from the private sector point of views, finding a balance between return on investment and social contributions is always a challenging issue. In addition, there are other obstacles such as insecticide resistance in vector mosquitoes as well as changes in their behavior (e.g., outdoor biting). An integrated approach is required to address these challenges effectively. Japanese companies are expected to play key roles in driving innovation in the VC sector.

Keywords: Vector control, Innovation, Malaria eliminiation, Insecticide resistance, Japanese companies

Abstract Reference: 20600
Mode of Presentation: Symposium
Topic: Call for Symposium

Global issues for malaria elimination to which Japan can contribute.

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Abstract Content

Attention to infectious disease control as a global diplomatic issue was underscored at the G8 Kyushu-Okinawa Summit in 2000 in Japan. This catalyzed the "Okinawa Infectious Diseases Initiative" and the establishment of the "Global Fund" in 2002. At the East Asia Summit in 2014, Asia-Pacific leaders committed to achieve a malaria-free region by 2030, a target also embraced by the African Union in 2016. Achieving "Zero Malaria" by 2030, as outlined in the WHO's "Global Technical Strategy for Malaria 2016-2030", necessitates novel approaches, new tools and improved implementation of existing strategies. Key innovations include Sumitomo Chemical's WHO-certified "Olyset® Net" and "SumiShield™ 50WG" insecticides. Additionally, Sysmex Corporation's "XN-31 Automated Hematology Analyzer" approved in Japan in 2020, offers rapid and sensitive malaria diagnostics, while Eiken Chemical's "Malaria-LAMP" method provides a simple and highly sensitive bedside diagnosis solution. Indeed, effective policies are essential to ensure access to quality health services for everyone in need. Continued academic research, including vaccine development at the National Center for Global Health and Medicine (NCGM), shows significant potential. The non-profit organization Malaria No More Japan (MNMJ) champions these innovations through advocacy, partnerships, and the Zero Malaria 2030 Campaign, ensuring these vital tools reach those who need them most. As these examples illustrate, Japanese innovation stands at the forefront of the global fight against malaria, with the potential not only to reach but to exceed the ambitious targets set for 2030. Through relentless innovation and collaboration, Japan is setting a dynamic course towards eliminating malaria globally.

Abstract Reference: 20842
Mode of Presentation: Symposium
Topic: Call for Symposium

Accelerating towards zero vivax malaria – the Vivax Serology Partnership (VISPA)

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Abstract Content

A key challenge for elimination of malaria in the Asia-Pacific region is the high proportion of infections caused by *Plasmodium vivax.* To overcome this hurdle, we need innovative tools that specifically detect people with hidden *P. vivax* hypnozoites. A novel panel of serological markers of recent infection have recently been validated to identify people with hypnozoites who go on to have a relapsing infection. Clinical studies in Indonesia have shown that serological markers can detect people that carry hypnozoites with high sensitivity and specificity (85% each) and prevention of relapsing *P. vivax* infection is achieved by treating sero-positive individuals. Mathematical models are being employed to determine how best to use PvSeroTaT in different epidemiological settings and in-depth consultations with policy makers are being undertaken to guide evidence generation and implementation. To translate our findings and accelerate malaria elimination in our region we have established the Bill and Melinda Gates Foundation funded "Vivax Serology Partnership" (VISPA). This symposium will highlight both the science behind this invention and the progress towards its translation into a novel public health intervention.

Abstract Reference: 20748
Mode of Presentation: Symposium
Topic: Call for Symposium

The efficacy of serological screen and treatment to prevent *Plasmodium vivax* incidence among schoolchildren in North Sumatra, Indonesia: A randomized-controlled trial

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Abstract Content

Introduction. Elimination of *Plasmodium vivax* is challenging because of its dormant stage. Serological assay may identify individuals who are likely to carry hypnozoites. This study aims to evaluate the efficacy of serological screen and treatment (PvSeroTAT) to reduce recurrent parasitaemia of *P. vivax*. Methods. An open label randomized controlled trial was conducted during February 2022-May 2023 in Batubara regency, North Sumatra, Indonesia. Schoolchildren aged 6-15 years were randomly allocated (1:1) to either the intervention or control arm. The intervention arm underwent serological screening for *P. vivax* exposure over previous 9 months. Those found positive received radical cure (daily 1mg/kgBW primaquine for 7 days). In both arms, children who became ill and positive for malaria by microscopy anytime during the study were treated according to national guideline. All participants were followed for 9 months, with *P. vivax* incidence measured by microscopic examination. Result. 1133 schoolchildren from 11 schools were enrolled, with 811 were available for analysis. Cumulative incidence of *P. vivax* was 0.009 versus 0.031 for intervention and control arm, respectively. The protective effect of PvSeroTAT was 70% (p=0.03, 95%CI=0.11-0.90). Among seropositive children who received radical cure (n=34), none became positive during follow-up, compared to 7 of 34 in those untreated (p=0.011). Meanwhile, *P. vivax* incidence among seronegative children was comparable between both arms (0.010 and 0.017, p=0.547). Discussion. PvSeroTAT reduces risk of *P. vivax* recurrent parasitaemia. Scaling up this intervention could significantly impact on malaria transmission. Conclusion. PvSeroTAT is a novel intervention that offers an alternative approach for malaria elimination.

Abstract Reference: 20499
Mode of Presentation: Symposium
Topic: Call for Symposium

Guiding the development of evidence-based policy and implementation guidelines for the introduction and uptake of *Plasmodium vivax* serological testing and treatment strategies in the Asia Pacific region

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Abstract Content

Plasmodium vivax is major challenge to the 2030 malaria elimination targets of countries in the Asia Pacific region. New tools to address the large reservoir of undetectable *P. vivax* infections are required. Validated *P. vivax* serological markers are a promising tool for identifying populations and individuals at high risk of relapsing infections, thereby guiding the administration of effective treatment. To ensure the timely integration of these new approaches into policy and practise it is essential to understand country-level priorities, health systems enablers, barriers and readiness to adopt and implement new tools effectively and sustainably. The Vivax Serology Partnership (VISPA) is undertaking collaborative policy consultations with key stakeholders to inform National Malaria Control Programs on programmatic implementation and uptake of *P. vivax* serological testing and treatment (*Pv*SeroTAT). Interviews and focus groups will explore the acceptability, feasibility and health systems readiness for *Pv*SeroTAT within two use case scenarios; 1) diagnosing relapse risk to guide radical cure and 2) population screening of recent *P. vivax* infections/ hynozoite carriage for programmatic applications. Policy consultations will develop priority use cases for countries within the two use case scenarios. These will explore themes such as leadership and planning, community awareness and information, tool introduction and regulatory processes, funding mechanisms for sustainable implementation and workforce capacity. The findings will be used to inform and co-develop roadmaps for country level policy change including possible test and treat approaches and critical evidence required to drive decision making and uptake of the *PvSeroTAT*.

Abstract Reference: 20735
Mode of Presentation: Symposium
Topic: Call for Symposium

Quantifying the impact of novel intervention strategies to accelerate *Plasmodium vivax* elimination efforts in high endemic malaria in Papua, Indonesia

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Abstract Content

Malaria in the Papua region contributes to almost 90% of all reported malaria cases in Indonesia. Persistent *Plasmodium vivax* infections particularly challenge Indonesia's malaria elimination efforts. This parasite may cause relapses weeks or months after the primary infection. Current presumptive antirelapse treatment for patients presenting with relapsing malaria fail to disrupt transmission. Tools that directly target *P. vivax* hypnozoite reservoir and asymptomatic infections are needed. A serological diagnostic tool has been developed and evaluated to detect potential carriers of hypnozoites and recent *P. vivax* infections. We will simulate a range of intervention scenarios with a serological diagnostic tool for mass screen-and-treat strategy, mass campaign that can reach and treat asymptomatic cases with radical cure at high coverage, and G6PD testing. We will quantify the impact of all scenarios to the reduction of *P. vivax* prevalence and the number of averted *P. vivax* clinical using an individual-based model of *P. vivax* malaria. We aim to identify the optimal deployment strategies that can accelerate *P. vivax* elimination efforts in high and low endemic settings. We will quantify the required G6PD tests and treatment doses for a range of deployment strategies. We will use the existing *P. vivax* mathematical transmission model with both human and mosquito compartments and calibrate for the Papuan settings using data from the epidemiological studies and surveillance program in Papua. Our study plans to demonstrate the added benefit of combining interventions and inform future programmatic guidelines and implementation for malaria elimination. Initial findings will be presented later.

Abstract Reference: 20636
Mode of Presentation: Symposium
Topic: Call for Symposium

Plasmodium vivax serological exposure markers to uncover hidden malaria infections

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Abstract Content

A key challenge for elimination of malaria in the Asia-Pacific and the Americas is the high proportion of infections caused by *Plasmodium vivax*. This is due to a hidden parasite stage in the liver, hypnozoites, that are responsible for maintaining transmission in communities. To overcome this hurdle, we need innovative tools that specifically detect people with hidden *P. vivax* hypnozoites. Our novel strategy has been to measure antibodies induced in response to infection, rather than the parasites themselves. Through studies in the Asia-Pacific and Americas, we identified and validated a novel panel of serological markers of recent infection. To translate our findings and accelerate malaria elimination in our region we have established the Bill and Melinda Gates Foundation funded “Vivax Serology Partnership” (VISPA). The major objective of VISPA is to provide the evidence to introduce serology-based identification and drug treatment interventions into global national policy and to develop novel point of contact diagnostic tools based on our serological test. This presentation will introduce both the science behind this invention and the progress towards its translation into a novel public health intervention.

Abstract Reference: 20634
Mode of Presentation: Symposium
Topic: Call for Symposium

Serological markers predict *Plasmodium vivax* relapses in a returning Indonesian soldier cohort

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Abstract Content

Plasmodium vivax elimination is hindered by relapses from latent liver-stage parasites (hypnozoites), but no available diagnostic tools can detect hypnozoites. *P. vivax* blood-stage infections induce strong antibody response after infection that decay slowly over time. Antibodies may allow identification of recent exposure to *P. vivax* and thus at risk of carrying hypnozoites. This study aimed to test the ability of eight antibody signatures to predict relapse risk. Two cohorts of soldiers who returned from a 9-month deployment in a malaria-endemic area between 2018 and 2022 to a malaria-free area were screened (n = 553). Blood sampling was done at start of enrolment, then every two weeks and at times of febrile symptoms for up to 6 months. *P. vivax* relapses were detected using microscopy and PCR, and the eight antibody signatures were captured using validated antigens by Luminex MAGPIX platform. A random forest classification algorithm was trained to classify soldiers exposed to *P. vivax* during the previous nine months. Relapses occurred in 128 soldiers with heterogeneity between Cohort 1 (25/269, 9%) and Cohort 2 (103/284, 35%). Our diagnostic tool had 86% sensitivity and specificity at identifying future relapses using blood samples from recruitment day. Soldiers who relapsed had higher median antibody titers for most of the serological markers. These results demonstrate the ability of serological markers to identify people at risk of relapse. We discuss the implications of these results for the development of a novel public health intervention *P. vivax* serological testing and treatment (PvSeroTAT) for relapse prevention.

Abstract Reference: 20591
Mode of Presentation: Symposium
Topic: Call for Symposium

Point-of-care G6PD testing and short course primaquine for the radical cure of *Plasmodium vivax* - the rationale and design of the SCOPE study

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Abstract Content

Plasmodium vivax causes recurrent episodes of malaria that exerts a significant public health burden in the Asia Pacific region. Current treatment strategies rely on a prolonged course of daily primaquine (PQ) administered over 14 days, but use of this approach is undermined by poor adherence to completing a full course and the risk of severe haemolysis in patients with Glucose-6-Phosphate Dehydrogenase (G6PD) deficiency. Novel tools and treatment have recently become available that will transform this landscape. One option is the use of a short course PQ regimen in which a high daily dose of PQ (1mg/kg/day) is administered over 7 days (PQ7). Whilst this regimen has good efficacy under trial settings it is associated with an increased risk of gastrointestinal intolerability and haemolysis. The latter can be ameliorated by screening patients with a point-of-care G6PD test (SD Biosensor) prior to PQ administration. Early clinical review on day 3, can also encourage patients to complete treatment or detect early signs of adverse effects so that treatment can be curtailed. The safety, efficacy and feasibility of this strategy is currently being assessed in the SCOPE study, a large scale implementation study conducted in Indonesia and Papua New Guinea. In this presentation the rationale and design of the SCOPE study and its potential to inform better tolerated and more effective case management of patients with *P. vivax* malaria will be presented.

Abstract Reference: 20749
Mode of Presentation: Symposium
Topic: Call for Symposium

How in vitro and in vivo vivax malaria models can help us understand the outcome of past *Plasmodium vivax* clinical studies with tafenoquine and design the next set of studies

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Abstract Content

Plasmodium vivax causes over 4 million malaria cases annually and is increasingly prevalent in areas also affected by *P. falciparum*. Treating *P. vivax* requires elimination of both the acute blood and the dormant liver (hypnozoites) stages infections (known as radical cure). 8-aminoquinolines (8-AQs), such as primaquine (PQ) and tafenoquine (TQ), are the only approved treatments for hypnozoites. PQ is administered over 7-14 days with either chloroquine (CQ) or an artemisinin-based combination therapy, while TQ is a single-dose treatment administrated with CQ. Phase III trials (DETECTIVE and GATHER) supported TQ's approval from the US-FDA and Australian-TGA and now from several *P. vivax* endemic countries. These studies showed that TQ is active when co-administered with CQ. In the TQ INSPECTOR Phase III trial carried out in Papua, Indonesia, which tested TQ with dihydroartemisinin-piperaquine (DHA-PQP) instead of CQ, failed to confirm radical cure as previously observed with CQ in previous studies carried out in other areas of the world (South-East Asia, South America and Ethiopia). Subsequent pre-clinical studies replicated the trial's results, showing that while CQ and PQP synergize with PQ and TQ, DHA interferes with this synergy. These findings explain the INSPECTOR study's outcome and validate the use of *in vitro* and *in vivo* assays to explore TQ's interactions with other potential partner drugs.

Abstract Reference: 20549
Mode of Presentation: Symposium
Topic: Call for Symposium

Point-of-care testing for G6PD deficiency: From clinical evidence to operational performance, opportunities and limitations

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Abstract Content

Primaquine has historically been given over 14 days for the radical cure of *Plasmodium vivax* malaria, but alternative treatments such as Tafenoquine and shorter courses are being evaluated and adopted across malaria-endemic countries. These shorter courses require screening for glucose-6-phosphate dehydrogenase (G6PD) deficiency prior to administration. Until recently, diagnosis of G6PD deficiency has primarily relied on moderate to high complexity laboratory assays but recently, point-of-care tests for G6PD deficiency have expanded testing to populations without access to laboratory-based assays. One such test is the STANDARD G6PD Test (SD Biosensor, South Korea). A pooled performance analysis of this test with data from Bangladesh, Brazil, Ethiopia, India, Thailand, the United Kingdom, and the United States was conducted. Across over 4200 study participants, the STANDARD G6PD Test demonstrated a sensitivity of 100% (95% Confidence Interval (CI): 97.5%-100%) for G6PD deficient cases with <30% activity and 77% (95% CI 66.8%-85.4%) for females with intermediate activity between 30%-70%, as compared to the spectrophotometry reference testing. Specificity was 98.1% (95% CI 97.6%-98.5%) and 92.8% (95% CI 91.6%-93.9%) for G6PD deficient individuals and intermediate females, respectively. Based on this diagnostic performance data, this analysis concludes that the STANDARD G6PD Test enables safe access to drugs that are contraindicated for individuals with G6PD deficiency. This presentation will explore the implications of the test on treatment access and user considerations for uptake and use within malaria-endemic settings.

Abstract Reference: 20682
Mode of Presentation: Symposium
Topic: Call for Symposium

Point-of-care G6PD testing and short course primaquine for the radical cure of *Plasmodium vivax* - Lessons learnt from SCOPE stage 1

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Abstract Content

The SCOPE study is investigating the feasibility of implementing a revised case management package for patients with *P. vivax* malaria at 10 health facilities in Indonesia and Papua New Guinea (PNG). The package includes a point-of-care G6PD activity test prior to treatment with primaquine and subsequent prescription of high dose (7 mg/kg total) primaquine over 7 or 14 days to eligible patients. This revised case management is combined with education prior to treatment and a community-based clinical review at day 3 to encourage treatment adherence and facilitate early detection and management of adverse events. SCOPE is nearing completion of the initial Stage 1 safety study. Stage 2 will focus on the large-scale feasibility and effectiveness of the revised case management package. Both stages contain in-depth social science and health economics components. In this presentation the key lessons learnt during Stage 1 in Indonesia and PNG will be presented and explored. These experiences relate to the training and roll-out of G6PD testing across health facilities and community-level observations regarding primaquine administration according to G6PD activity. The presentation will explore the challenges and successes of conducting day 3 community-based follow up to detect early signs of primaquine-induced haemolysis. Preliminary insights regarding patient education, understanding of G6PD deficiency and drug adherence will be presented, with a discussion of how these insights could be integrated into Stage 2 for scale-up.

Abstract Reference: 20626
Mode of Presentation: Symposium
Topic: Call for Symposium

Operational feasibility of Appropriate *Plasmodium vivax* radical cure after G6PD testing in Thailand

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Abstract Content

Plasmodium vivax is the major obstacle to malaria elimination in Thailand. Prevention of relapse of *P. vivax* with 8-aminoquinolines (tafenoquine/primaquine) is critical; however, both drugs can cause hemolysis in glucose-6-phosphate dehydrogenase (G6PD) deficient individuals. This study evaluated the feasibility of providing appropriate radical cure following quantitative G6PD point-of-care testing in routine care. A prospective, observational, multi-centre, longitudinal study was conducted across seven sites in Yala and Mae Hong Son provinces. Eligible patients were ≥16 years old with uncomplicated *P. vivax* malaria. G6PD activity was quantified using the SD Biosensor point-of-care device. Healthcare providers prescribed radical cure (tafenoquine single dose / daily primaquine / weekly primaquine) in line with G6PD enzyme activity. Patients were followed up on days 5 and 14. Hospital admissions were reviewed to identify cases of acute hemolytic anemia. Of 187 patients enrolled in the study, all patients were tested for G6PD activity. According to G6PD status, appropriate use or non-use was 100% (95%CI 96.6, 100 [132/132]) with tafenoquine, 100% (95%CI 95.7, 100 [104/104]) with daily primaquine and 99.5% (96.7, 99.9 [186/187]) with weekly primaquine. None of the suspected cases of drug-induced acute hemolytic anemia were confirmed. Thai Health systems are adaptive and incorporate changes to well established routines, including systematically applying a new diagnostic and treatment algorithm. Provision of appropriate radical cure following quantitative G6PD testing was operationally feasible within Thailand's public health system, without observation of concerning adverse events. These results support the implementation of this treatment algorithm in routine care.

Abstract Reference: 20552
Mode of Presentation: Symposium
Topic: Call for Symposium

Field testing of Wolbachia deployment for dengue control in Indonesia

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Abstract Content

Indonesia is one of the countries in the world where dengue is hyperendemic. The number of dengue cases continues to increase annually, despite the government's implementation of a multitude vector control initiatives. The development of the Wolbachia-infected *Aedes aegypti* mosquito technology commenced at the end of 2011. The research process in Indonesia was conducted in a series of stages, including safety and feasibility testing, small-scale release, efficacy testing, and small-scale program implementation. A cluster-randomized trial was conducted from 2016 to 2020, which involved the deployment of wMel-infected *Aedes aegypti* mosquitoes. The trial consisted of 12 intervention clusters and 12 control clusters that were randomly assigned. The intervention's efficacy was evaluated using a test-negative design. This study reveals evidence of efficacy in reducing dengue infections in humans by up to 77% and efficacy against hospitalization by up to 86%. A project implementation model was implemented in two additional districts of Yogyakarta Province because of this significant success. Currently, the Ministry of Health of the Republic of Indonesia is adopting this technology as a complementary measure to prevent dengue infections by piloting this method in five additional cities throughout the nation.

Abstract Reference: 20771
Mode of Presentation: Symposium
Topic: Call for Symposium

Characterising the native resident Wolbachia strains of *Anopheles* mosquitoes and exploitation for malaria control

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Abstract Content

The use of Wolbachia as a novel vector control strategy has been highly successful, with demonstrated impact on disease prevalence in field trials targeting *Aedes* mosquitoes. Long thought to be absent from natural populations of *Anopheles* mosquitoes, which are highly effective malaria vectors, *Wolbachia* based interventions have proven challenging. Our recent discovery of natural high density Wolbachia strains in populations of *Anopheles moucheti* and *Anopheles demeilloni* has reinvigorated efforts to create transinfections in medically relevant *Anopheles* mosquitoes. Here we present our work demonstrating high density maternally transmitted strains of Wolbachia in *An. moucheti* and *An. demeilloni* from sub-Saharan Africa, providing concrete evidence for resident *Wolbachia* strains in this genus. In addition, we report on our recent endeavours working with these novel strains of *Wolbachia* in the lab, thereby providing a tractable source of *Wolbachia* for further experiments. We discuss our findings in the context of developing novel *Wolbachia*-based control approaches in *Anopheles* to reduce the burden of malaria and our recent insights on the molecular mechanisms induced by *Wolbachia* to interfere with pathogens.

Abstract Reference: 20498
Mode of Presentation: Symposium
Topic: Call for Symposium

Discovery and development of CorA - A new anti-Wolbachia drug

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Abstract Content

The bacterial RNA polymerase inhibitor Corallopyronin A (CorA) kills Gram-negative *Wolbachia* endobacteria of filarial nematodes that cause onchocerciasis (river blindness) and lymphatic filariasis (elephantiasis). Depleting the essential endosymbionts causes worm sterility and slowly kills adult worms. Using the *Litomosoides sigmodontis* infection model in Mongolian gerbils, we demonstrated that CorA depletes *Wolbachia* >2-logs and is macrofilaricidal with a 2-week regimen and can be further reduced to ten days by administering CorA and albendazole; a significant advance over the current 4-week doxycycline regimen. We also demonstrated macrofilaricidal activity using the *Onchocerca ochengi* mouse model. Non-GLP *in-vitro* toxicity tests demonstrated CorA is non-toxic and pharmacologically safe; *in vivo* toxicity studies in rats and dogs measured a maximal tolerated dose of 1000 mg/kg. Seven-day repeated dose studies in rats and dogs demonstrated no prohibitive safety issues: NOEL (dog)= 50 mg/kg; LOAEL (rat)=250 mg/kg, predicted HED=4 mg/kg. The upscaled production processes are established at a GMP-CMO to produce drug substance for the phase 1 trial material. Using amorphous solid dispersion, we developed two solid oral formulations with increased stability (>3 months at 30 °C, >6 months at 5 °C) and oral bioavailability (mouse >59%, dog >53%). With funding from the EU and GHIT, GLP toxicology studies will be started in 2024. After finalizing the pre-clinical work, we plan to enter clinical phase 1 in 2026. Successful development of CorA will not only provide a new treatment for filarial infections, but could provide new treatments for antimicrobial resistant infections with *Neisseria gonorrhoeae* or *Staphylococcus aureus*.

Abstract Reference: 20568
Mode of Presentation: Symposium
Topic: Call for Symposium

Targeting Wolbachia for curative therapy of human and veterinary filariasis

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Abstract Content

Lymphatic filariasis (affecting 65 million people) and onchocerciasis (affecting 21 million people) are leading causes of global morbidity. Heartworm disease is caused by *Dirofilaria immitis*, with multiple vectors supporting a global distribution in the tropics and sub-tropics, with seasonal transmission in more temperate climates. Current control efforts are hindered by the lack of a safe macrofilaricidal/adulticidal drug. A clinically validated approach for delivering macrofilaricidal activity is to target the *Wolbachia* bacterial endosymbiont of the causative nematodes. The filarial nematodes responsible for these diseases have evolved a mutualistic dependency on *Wolbachia*, which is essential for larval and embryo growth and development, transmission of the parasite through their insect vectors and the longevity of adult parasites, enabling therapeutic targeting of *Wolbachia* to deliver prophylactic, transmission blocking and macrofilaricidal outcomes. The anti-*Wolbachia* consortium (A-WOL) has screened more than 2 million drugs and compounds from the human pharmacopeia, focused anti-infective and large diversity libraries to identify 6 novel anti-*Wolbachia* chemotypes with suitable drug-like qualities. The first industrial scale screening of 1.3 million compounds in partnership with AstraZeneca delivered 20,000 hits and a further 10 novel chemotypes as promising new leads, showing a more rapid kill rate compared with all other anti-wolbachial drugs. A radical improvement to targeting *Wolbachia* occurs via a drug synergy between a common anthelmintic drug (albendazole) and all different classes of antibiotics in the A-WOL portfolio. Using the drugs in combination reduces the length of treatment required opening up the opportunity to scale-up this approach at the community level.

Abstract Reference: 20648
Mode of Presentation: Symposium
Topic: Call for Symposium

Scaling up implementation of Wolbachia mosquito releases for the sustainable control of dengue and other arboviral diseases

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Abstract Content

The confluence of a warming climate, urbanization and global mobility is escalating the threat of dengue and other arboviruses for communities and health systems throughout the tropics and subtropics, with 5.5 billion people predicted to be at risk by 2050. Conventional vector control strategies have been unable to curb the spread and intensification of dengue outbreaks, and there is an urgent need to integrate new evidence-based tools into dengue control programs. The World Mosquito Program (WMP) is a global not-for-profit initiative that partners with governments and communities to implement an innovative public health intervention that protects communities from arboviral diseases by introducing the naturally occurring insect bacterium *Wolbachia* into *Aedes aegypti* populations. *Wolbachia* significantly reduces the ability of *Ae. Aegypti* to transmit dengue and other arboviruses and is self-sustaining in the mosquito population after short-term releases. We will discuss the global evidence for the acceptability, feasibility, public health impact and cost-effectiveness of *Wolbachia* deployments in 14 Asia-Pacific and Latin American countries, reaching >11 million people since 2011. Considerations will be discussed for accelerating programmatic scale-up of *Wolbachia* to achieve global control targets and enhance pandemic preparedness against mosquito-borne disease, including: integration with existing control programs; regulatory pathways; ndustrializing mosquito production and distribution; evaluating long-term effectiveness; and financing.

Abstract Reference: 20467
Mode of Presentation: Symposium
Topic: Call for Symposium

Deployment of Wolbachia strain wAlbB sharply decreases dengue incidence in Malaysian disease hotspots

Cheong Yoon Ling[*8], Ary Hoffmann[1], Nazni Wasi Ahmad[2], Wan Ming Keong[3], Noor Afizah Ahmad[2], Nick Golding[1], Nicholas Tierney[5], Jenarun Jelip[3], Perada Wilson Putit[3], Norhayati Mokhtar[3], Sukhvinder Singh Sandhu[6], Lau Sai Ming[6], Khadijah Khairuddin[6], Kamilan Denim[3], Norazman Mohd Rosli[7], Hanipah Shahar[7], Topek Omar[7], Muhammad Kamarul Ridhuan Ghazali[2], Nur Zatil Aqmar Mohd Zabari[2], Mohd Arif Abdul Karim[2], Mohamad Irwan Saidin[2], Muhammad Nizam Mohd Nasir[2], Tahir Aris[8], Lee Han Lim[2], Steven P. Sinkins[9], Farah Diana Ariffin[8], Steven P. Sinkins[9]

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Abstract Content

The field releases of *w*AlbB *Aedes aegypti* males and females in Malaysia were initiated in 2017 as a research project in 6 dengue hotspots. Since 2019, the *Wolbachia* replacement strategy has been operationalised as part of the National Dengue Prevention and Control Programme in more than 30 dengue hotspots in several states in Malaysia such as Kuala Lumpur, Selangor, Putrajaya, Penang, Kelantan, Malacca, Pahang, Johore and Negeri Sembilan. Community engagement is mandatory in all localities prior to *w*AlbB *Ae. aegypti* release. Some of the localities are showing stable high *Wolbachia* frequency after seven years. Deployment of *Wolbachia* strain *w*AlbB *Ae. aegypti* in Malaysia sharply decreased the dengue incidence of 62.4% (confidence intervals 50-71%) in 20 operational release sites and research sites. The vector control and prevention activities such as source reduction and dengue awareness campaign are conducted as part of the vector control activities in all release sites. The successful *Wolbachia* invasion depends on ensuring the fitness of *Wolbachia* mosquitoes, natural boundaries around the release sites and cessation of space spraying activities in *Wolbachia* release sites. The *Wolbachia* strain *w*AlbB has proven effective at comparatively high ambient temperatures. Further expansion of *Wolbachia* release sites will enable greater impact of reduction in dengue incidence.

Abstract Reference: 20593
Mode of Presentation: Symposium
Topic: Call for Symposium

Building African expertise in genetic-biocontrol approaches for malaria control and elimination in Africa

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Abstract Content

Mosquito with gene drives represent one of the transformative tools for malaria elimination in Africa. The combined impact of climate change and continuous increase of insecticides resistance by targeted malaria vectors that are expected to increase the number of people at risk to malaria by 300 million by 2030, clearly necessitate the need for new and transformative tools. While gene drives offer one of the options to address these challenges, its development and implementation requires sustained capacity building to African stakeholders including scientists. Ifakara Health Institute in Tanzania, is pioneering the development of genetic modified and gene drive mosquitoes locally under the collaborative Transmission zero (T0) program that aim to develop mosquitoes that cannot carry malaria parasite (population modification). Through its milestones, the T0 program aim to build in-country and regional capacity on transgenesis research, infrastructure development such as mosquito containment facilities, and communication and engagement with stakeholders including regulators. Of importance, Ifakara Health Institute, has continued to establish recommended biosafety facilities for containing gene drive mosquitoes, investing in training in-country scientists at level of MSc and PhDs, support other East Africa countries that aim at researching the use of gene-drive for malaria elimination. Further development and future field release of gene-drive mosquitoes will require sustained capacity building and strengthening on technical local expertise, contained research infrastructures, collaborative communication and engagement programs with all relevant stakeholders including regulators and policy makers.

Abstract Reference: 20837
Mode of Presentation: Symposium
Topic: Call for Symposium

The role of regional leadership in supporting research and uptake of novel approaches to malaria control

Phone Si Hein*[1], Leo Braack*

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Abstract Content

Mosquito-borne diseases such as malaria and dengue continue to pose significant public health threats. To provide long-lasting, affordable, and sustainable solutions, new and innovative approaches like gene drives are necessary. Regional leadership is essential to promote research, development, and adoption of these novel vector control methods. Leaders can coordinate initiatives across environmental science, public health, and community engagement sectors, and advocate for policies that prioritize innovative research. Supporting research requires establishing proper regulatory frameworks, securing funding, and fostering partnerships between academic institutions, research groups, and industry. Gaining community acceptance and addressing concerns about new technologies necessitate effective stakeholder engagement. Regional leaders can build trust and transparency among communities, policymakers, and scientists. The role of leaders also includes encouraging workshops, training programs, and collaborative research efforts to enhance expertise in new innovative technologies. Learning from successful implementations can provide valuable insights for developing and scaling new strategies. In conclusion, regional leadership plays a crucial role in advancing the development and adoption of novel vector control methods, ensuring their effective implementation and long-term viability in reducing the incidence of mosquito-borne diseases.

Abstract Reference: 20789
Mode of Presentation: Symposium
Topic: Call for Symposium

How to gain legitimacy with local communities in research project? Case of target malaria project

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Abstract Content

For more than 10 years, Target Malaria has been conducting research on genetically modified mosquitoes as a complementary means of controlling malaria. The goal of this research is to provide a complementary solution to existing methods of combating malaria which unfortunately continues to claim many victims. Based on guidance documents, Target Malaria has been implementing its engagement strategy for more than 10 years, which adapts to the context of the countries of intervention. The operationalization of this engagement strategy made it possible to make the understanding of research less complex at the stakeholder level, particularly the local communities directly impacted by the research. in the context where the civil society organizations are vocal, and claim more accountabilities, one of the major challenges of implementing the project, was to obtain legitimacy from local communities who are directly impacted by the project's actions to establish relationships of trust and promote collaboration. To do this, stakeholder engagement and communication were the essential pillars to be implemented. Engagement with stakeholders thus made it possible to establish a relationship of trust with stakeholders. This commitment, supported by transparent communication with communities demystified the complexity of the project in the eyes of the stakeholders who took ownership of it.

Keywords: research, stakeholder, engagement, communication, legitimacy engagement strategy, Target Malaria

Abstract Reference: 20563
Mode of Presentation: Symposium
Topic: Call for Symposium

Project Wolbachia – Singapore: Lessons learned from piloting and scaling a novel vector control tool

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Abstract Content

To enhance resilience against dengue, Singapore complements conventional source reduction with releases of male *Wolbachia*-infected *Aedes aegypti* mosquitoes to further suppress vector populations. Project *Wolbachia* – Singapore currently covers ~480,000 households (about a third of all Singapore households). Results have been promising: towns with at least a year of releases show more than 90 percent reduction in *Aedes aegypti* mosquito population, and residents are up to 77 percent less likely to acquire dengue. Piloting and scaling the *Wolbachia* suppression approach has required the development of a multidisciplinary programme with an ecosystem of interdependent components, including stakeholder engagement, risk assessment, surveillance systems, innovation in engineering and automation, and robust quality assurance. This talk will highlight key considerations and lessons learned from our experience.

Abstract Reference: 20715
Mode of Presentation: Symposium
Topic: Call for Symposium

ELFN2 mediated autophagy is important for Toxoplasma to proliferate in pig cells

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Abstract Content

Pigs are one of the most sensitive farm animals to *Toxoplasma gondii* infection, which leads to abortions and still birth in sows, causing huge economic losses. In addition, as a major foodborne pathogen, *Toxoplasma* contaminated pork is a major source of human infections. Therefore, reducing the infection rates or parasite burdens in pork is of particular importance. To better understand the interactions between *Toxoplasma* and the pig host, a gene inactivation mutant library covering all protein coding genes in pigs was constructed in PK15 cells using CRISPR/Cas9. Then, the library was screened for mutants that are resistant to *Toxoplasma* infection. A number of mutants were obtained and one of them, which lacked a functional ELFN2 gene, was studied further. The results indicate that ELFN2 is an important mediator of metabolic interactions between *Toxoplasma* and pig cells. PK15 cells lacking ELFN2 were defective in autophagy and accumulated high levels of lipid droplets, therefore preventing the salvage of host lipids by the parasites. As such, proliferation of Toxoplasma parasites in ELFN2$^-$ mutants were significantly reduced. Taken together, these results suggest that Toxoplasma parasites actively hijack host autophagy to satisfy their nutritional needs.

Abstract Reference: 20396
Mode of Presentation: Symposium
Topic: Call for Symposium

Host vimentin functions in *Toxoplasma gondii*-induced brain damage and the therapeutic potential of probiotics

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Abstract Content

Toxoplasma gondii is an opportunistic pathogen that forms cysts in various tissues including the central nervous system (CNS) in immunecompetent hosts. Vimentin is a cytoskeletal protein and functions in maintaining cell contractility and mediating cell adhesion, and regulating immunity. *T. gondii* acute and chronic infection models were established in both wild-type (WT) and vimentin knockout (*vim-/-)* mice. *Vim-/-* mice exhibited reduced resistance to *T. gondii* infection, while WT mice showed higher rates of cyst formation in the brain, enhanced neuronal apoptosis, and more severe cognitive impairment and depressive tendencies. WT mice displayed increased BBB permeability, with more significant upregulation of brain chemokines and adhesion molecules. Notably, intercellular adhesion molecule-1 (ICAM-1), with the assistance of vimentin, facilitated *T. gondii* adhesion and invasion of vascular endothelial cells. These effects promote *T. gondii* entry into the blood-brain barrier (BBB). WT mice experienced severe dysbiosis of gut microbiota and intestinal inflammation during infection, with a decrease in *Lactobacilli* species. Serum metabolite analysis revealed a significant decrease in *Lactobacilli* metabolites, including indole-3-lactic acid (ILA) after infection. Transplantation of *Lactobacillus murinus* and *L. gasseri* in WT mice resulted in increased secretion of IFN-γ and IL-10 in serum. Furthermore, in non-infected conditions, oral administration of ILA promoted the activation of AhR signaling pathway, thereby increasing the number of CD8$^+$ T cells in peripheral blood and leading to significant inhibition of *T. gondii* proliferation in the gut and extraintestinal dissemination. This intervention reduced brain cyst numbers, alleviated brain inflammation, and decreased the number of apoptotic neurons.

Abstract Reference: 20229
Mode of Presentation: Symposium
Topic: Call for Symposium

Reprogrammed macrophages with Toxoplasma macrophage migration inhibitory factor and its translation medicine application

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Abstract Content

Macrophage therapy for liver fibrosis is on the cusp of meaningful clinical utility. Due to the heterogeneities of macrophages, it is urgent to develop safer macrophages with a more stable and defined phenotype for the treatment of liver fibrosis. Herein, we developed a new macrophage-based immunotherapy using macrophages stably expressing a pivotal cytokine from *Toxoplasma gondii*, a parasite that infects approximately two billion people. We found that *Toxoplasma gondii* macrophage migration inhibitory factor-transgenic macrophage ($M\varphi^{tgmif}$) showed stable fibrinolysis and strong chemotactic capacity. $M\varphi^{tgmif}$ effectively ameliorated liver fibrosis and deactivated aHSCs by recruiting $Ly6C^{hi}$ macrophages *via* paracrine CCL2 and polarizing them into the restorative $Ly6C^{lo}$ macrophage through the secretion of CX3CL1. Remarkably, $M\varphi^{tgmif}$ exhibited even higher chemotactic potential, lower grade of inflammation and better therapeutic effects than LPS/IFN-γ-treated macrophages, making macrophage-based immune therapy more efficient and safer. Mechanistically, *Tg*MIF promoted CCL2 expression by activating the ERK/HMGB1/NF-κB pathway, and this event was associated with recruiting endogenous macrophages into the fibrosis liver. Our findings do not merely identify a viable immunotherapy for liver fibrosis, but also suggest a therapeutic strategy based on the evolutionarily designed immunomodulator to treat human diseases through modifying the immune microenvironment.

Abstract Reference: 20505
Mode of Presentation: Symposium
Topic: Call for Symposium

In vivo CRISPR screens identify Toxoplasma genes encoding secreted and non-secreted virulence factors

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Abstract Content

The research field to identify and characterize virulence genes in *Toxoplasma gondii* has been dramatically advanced by a series of *in vivo* CRISPR screens. Secreted virulence factors of Toxoplasma to survive in immune-competent hosts have been extensively explored by in vivo CRISPR screen methods, whereas their requirements in immune-deficient hosts are incompletely understood. Furthermore, those of non-secreted virulence factors are further enigmatic. Here we develop an in vivo CRISPR screen system to enrich not only secreted but also non-secreted virulence factors in virulent Toxoplasma-infected C57BL/6 mice. Notably, combined usage of immune-deficient Ifngr1$^{-/-}$ mice highlights genes encoding various non-secreted proteins as well as well-known effectors such as ROP5, ROP18, GRA12, and GRA45 as interferon-γ (IFN-γ)-dependent virulence genes. The screen results suggest a role of GRA72 for normal GRA17/GRA23 localization and the IFN-γ-dependent role of UFMylation-related genes. In addition, we further identified two candidates, TgGTPase and TgRimM, which are localized in the cytoplasm and the apicoplast, respectively. Both genes are essential for parasite virulence and widely conserved in the phylum Apicomplexa. Collectively, our study demonstrates that host genetics can complement in vivo CRISPR screens to highlight genes encoding IFN-γ-dependent secreted and non-secreted virulence factors in Toxoplasma.

Abstract Reference: 20444
Mode of Presentation: Symposium
Topic: Call for Symposium

Phospholipid-mediated regulation of calcium homeostasis and lytic cycle in Toxoplasma

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Abstract Content

Phosphatidylserine (PtdSer) and phosphatidylthreonine (PtdThr) are lipids attributed to calcium-regulated gliding locomotion and motility-dependent invasion and egress events in *Toxoplasma gondii*. However, the synthesis and importance of PtdSer in the parasite remains poorly understood. It is also unclear how these lipids regulate calcium homeostasis in the parasite. Here, we show that conditional depletion of PtdSer synthase (PSS) and sarcoendoplasmic reticulum calcium- ATPase (SERCA) in the endoplasmic reticulum of tachyzoites abrogates the lytic cycle due to impaired cell division and gliding motility. The base-exchange-type PSS enzyme produces PtdSer, rapidly converted to phosphatidylethanolamine (PtdEtn). The PSS-depleted mutant exhibits a lower abundance of the major ester-linked PtdEtn species with concurrent accrual of host-derived ether-PtdEtn species. Most phosphatidylthreonine (PtdThr) species were repressed; however, the PtdSer remained largely unaltered, likely driven by the serine-exchange reaction of the PtdThr synthase (PTS). On the other hand, the PTS-knockout mutant lacks PtdThr but displays a proportionally higher content of PtdSer, further asserting a functional relation between the two lipids. Furthermore, PTS mutant is impaired in calcium homeostasis and gliding motility but ectopic expression of SERCA restored its lytic cycle, suggesting a physiological dependence of the calcium pump on the endoplasmic reticulum's lipid milieu. Our extended work on structure modeling of SERCA and ligand docking with an in-house library comprising >5000 chemicals identified 'drug-like' ATP mimics (RB-15, NR-301) inhibiting the parasite growth. In a nutshell, we reveal SERCA as a druggable lipid-assisted calcium pump and physiologically vital repurposing of PtdSer and PtdThr in a clinically relevant intracellular pathogen.

Abstract Reference: 20540
Mode of Presentation: Symposium
Topic: Call for Symposium

Zoonotic malaria: Journey to discovery and lessons learnt

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Abstract Content

This introductory talk for the Symposium entitled ‘Parasites, Wildlife and One Health’ will begin with the reasons that prompted us to study atypical ‘*Plasmodium malariae*’ infections in the Kapit Division of Sarawak, Malaysian Borneo. This will be followed by descriptions of the experimental work that was undertaken which led to the discovery in Sarawak of a large focus of human infections with *P. knowlesi*, a malaria parasite typically found in nature in long-tailed and pig-tailed macaques. It will end with the lessons that were learnt during this journey.

Abstract Reference: 20922
Mode of Presentation: Symposium
Topic: Call for Symposium

Unravelling risk factors for a foodborne zoonotic parasite

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Abstract Content

Taenia solium is a foodborne zoonotic parasite transmitted between pigs and people and is a major cause of acquired epilepsy (neurocysticercosis) in endemic countries. Key risk factors for transmission are well known and include free ranging pig systems, low sanitation/hygiene practices and ingestion of raw/undercooked, yet sustained control in endemic regions has yet to be achieved. A need for increased knowledge of the social/cultural context within these regions is often cited as a requirement for sustained control. To better understand community socio-cultural behaviours related to these risk factors a rapid qualitative assessment was developed and undertaken in three northern provinces of Lao PDR. Group discussions, key interviews and observations by the research team were conducted in 42 villages with a total of 421 community members participating in the assessment. Results from the qualitative assessment have identified aspects of community behaviour not previously reported or described, which influence the continued transmission of *T. solium* between pigs and people. This knowledge will be vital for developing future intervention strategies in Lao PDR which may provide sustainable control. This methodology is also easily adaptable for other endemic regions/countries.

Abstract Reference: 20617
Mode of Presentation: Symposium
Topic: Call for Symposium

Metagenomic profiling of microbial pathogens and potential symbionts from tick collected in Thailand

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Abstract Content

Ticks are efficient vectors of multiple pathogens responsible for human diseases. They are also significant vectors of disease-causing pathogens in domestic and wild animals, ranking second to mosquitoes globally. Over 100,000 human illnesses worldwide are attributed to tick-borne pathogens annually. These pathogens include bacteria, viruses, and protozoa, which can cause severe and sometimes fatal diseases such as Rickettsioses, severe fever thrombocytopenia syndrome virus, and babesiosis. Moreover, ticks also carry non-pathogenic bacteria, which promote tick development and reproductive success. These endosymbionts can influence the physiology and survival of their tick hosts, enhancing their capacity to transmit pathogenic microbes. This study aims to collect tick specimens from dogs and cattle in Thailand and investigate tick-associated pathogens and microbiomes using full-length 16S rRNA amplicon sequencing with Oxford Nanopore Technologies (ONT). By employing this advanced sequencing technique, we aim to understand ticks' microbial communities, identifying pathogenic and non-pathogenic bacteria. The 16S rRNA full-length sequencing gene provides sufficient taxonomic resolution to accurately identify bacterial communities at species and strain levels, facilitating detailed insights into the diversity and composition of tick microbiomes. Through this approach, we expect to uncover the prevalence of various tick-borne pathogens in domestic animals in Thailand and to characterise the beneficial endosymbionts that support tick populations. This knowledge will contribute to a better understanding of the epidemiology of tick-borne diseases and the potential for controlling tick populations by targeting their symbiotic relationships. Ultimately, this research will enhance our ability to predict, prevent, and manage tick-borne diseases in both human and veterinary contexts.

Abstract Reference: 20134
Mode of Presentation: Symposium
Topic: Call for Symposium

Human infections by simian malaria parasites of *Plasmodium knowlesi* and *Plasmodium inui* in Indonesian Kalimantan provinces bordering Malaysian Borneo

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Abstract Content

Over the past 20 years, Kalimantan has seen a remarkable decline in malaria due to Indonesia's national strategic plans and policies against malaria. This low prevalence, however, contrasts sharply with *Plasmodium knowlesi* infections, which continue to be prevalent throughout Malaysia Borneo. Given that both regions have a similar epidemiological risk of zoonotic malaria infection and share the same natural habitat, this situation appears incongruous. We used molecular approaches to undertake active and passive malaria surveillance in West, East and North Kalimantan provinces bordering Malaysian Borneo between November 2020 and April 2021, and a questionnaire survey regarding factors contributing to potential zoonotic malaria transmission in each household. Blood samples were taken from 1,125 respondents aged 1 to 87 years old who attended health facilities and from those who lived in malaria risk areas. Phylogenetic analysis of 18S rRNA genes revealed that the prevalence of malaria was low (0.7%) with four human *Plasmodium* sp infections (2 *P. vivax* and 2 *P. malariae*), three simian *Plasmodium* infections (2 *P. knowlesi* and 1 *P. inui*) and one unidentified species. From 639 respondents representing each household, 64.2% of respondents slept at home every night, 63.8% lived more than 500 meters away from the forest, 36.2% of respondents lived near or within the forest and 15.8% experienced the presence of monkeys within 500 meters of their house. This study emphasises the necessity of conducting extensive surveys to investigate the disparity between the low zoonotic malaria infections in these regions and those in Malaysian Borneo.

Abstract Reference: 20453
Mode of Presentation: Symposium
Topic: Call for Symposium

The epidemiology and elimination of schistosomiasis in the Philippines

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Abstract Content

Despite decades of control efforts centered on treatment of cases and preventative chemotherapy through mass drug administration (MDA), the parasitic blood fluke *Schistosoma japonicum*, the causative agent of schistosomiasis, remains highly endemic across communities in the Philippines with severe public health and socioeconomic burdens. More than a quarter of endemic villages in the country have a prevalence of >5% as of 2018 with new endemic areas being discovered in the past decade. The complicated, multi-host, life cycle of the parasite is intertwined with the agricultural, domestic and recreational activities of endemic communities; many of them associated with poverty. Thus, schistosome distribution and transmission are at the intersection of environmental, socioeconomic and biological factors and schistosomiasis cannot be eliminated solely by MDA. Current control strategies in the country have recently shifted to an integrated One Health approach, targeting the different aspects of the disease epidemiology to sustainably eliminate schistosomiasis in humans and other mammalian hosts, intermediate snail hosts, and the environment.

Abstract Reference: 20720
Mode of Presentation: Symposium
Topic: Call for Symposium

Multiplex serology for tropical fever diagnostics

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Abstract Content

Febrile illnesses in tropical regions pose a major public health challenge due to the variety of pathogens that cause fever and their overlapping symptoms. Common febrile illnesses include malaria, dengue, chikungunya, Zika, leptospirosis, and typhoid fever. Current diagnostic methods are typically designed to detect one pathogen at a time, which can delay diagnosis and treatment and lead to severe outcome. This study introduces a multiplex diagnostic tool using bead-based immunological assay that can simultaneously detect multiple pathogens from a single sample with the potential to improve the speed and accuracy. We have developed a multiplex panel, using commercial antigens, formulates to detect antibodies against DENV, CHIKV, ZIKV, JEV, *Plasmodium vivax*, *Plasmodium falciparum*, and SARS-CoV-2. To further enhance diagnostic efficiency and comprehensiveness, we explore biomarkers for locally endemic diseases to expand diagnostic panel and tailor to the specific disease burden of the population. Our team has successfully produced pathogen-specific recombinant antigens for detecting scrub typhus, rickettsioses, and leptospirosis, which are not commercially available. Preliminary antigen validation and performance evaluation were conducted using the Luminex® xMAP Intelliflex system. These advancements represent a significant step towards creating a comprehensive diagnostic tool that offers efficient, cost-effective, and extensive antibody profiling, addressing the complex landscape of febrile illnesses in tropical regions.

Abstract Reference: 20385
Mode of Presentation: Symposium
Topic: Call for Symposium

Forest-dwelling mosquito of *Anopheles barbirostris* group as predominant vector in highly endemic zoonotic malaria regions in Sarawak, Malaysian Borneo

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Abstract Content

Plasmodium knowlesi is recognised as one of the simian parasites that cause zoonotic malaria in Sarawak. More than a decade ago, *Anopheles latens*, a forest-dwelling mosquito, was the predominant species and responsible in transmitting *P. knowlesi* to humans in Kapit Division, Sarawak. Recent entomological surveys conducted have incriminated *Anopheles donaldi* of the Barbirostris Group and *Anopheles latens* of the Leucosphyrus Group in Lawas district, and both *An. roperi* and *An. collessi* of the Umbrosus Group in Betong district as the vectors of *P. knowlesi* and other zoonotic malaria parasites in Sarawak. Over the years, Kapit Division undergoes significant changes in land use due to deforestation and urbanisation. Our study endeavour to foresee the possible shift in the zoonotic malaria vectors in this region due to these environmental modifications. A total of 1134 anopheline specimens were collected through human landing catch and resting collection approaches within the forest fringes, farms and areas where macaques have been sighted. Of these, *An. donaldi* (67.8%) was found to be the predominant species, followed by *An. latens* (11.7%) and *An. maculatus* (9.9%). Further molecular analysis of the heads and thoraces revealed that 18 mosquitoes were positive for simian malaria parasites. More than half of these were *An. donaldi*, which was confirmed by the newly developed PCR assay to accurately identify this mosquito species. Overall, this entomological survey suggests that over the years, *An. donaldi* mosquito has gradually replaced *An. latens* as the predominant vector of simian malaria parasites in the Kapit Division.

Abstract Reference: 20321
Mode of Presentation: Symposium
Topic: Call for Symposium

The use of technology-driven biosafety tools for the enhancement of disease risk management in facilities across Southeast Asia

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Abstract Content

Laboratory accidents and pathogen escapes often stem from operational errors caused by insufficient training or fatigue of workers. Risk assessments serve as pivotal instruments for identifying and mitigating hazards associated with laboratory activities involving infectious substances. Implementing appropriate risk management strategies is requisite to reducing the risk to a level where harm to both the individual and community is minimal or negligible. The introduction of technology-based risk management tools emerges as a promising approach to enhance the efficacy of biosafety risk assessments and programs. Two simple, pathogen-agnostic risk prediction software tools, WHO Biosafety Risk Assessment Tool (RAST) and Sandia National Labs Biosafety Risk Assessment Model (BioRAM), will be evaluated for usability and application across different laboratory facilities. RAST, a mobile application, provides an initial risk evaluation and control recommendations, while BioRAM, an open-source software, analyses safety control measures in the facility to determine a residual risk outcome. The initial risk outcomes from both tools will be compared with pathogen-specific risk assessments in the WHO SEARO Risk Assessment Manual (RAM), to validate tool performance. BioRAM will be utilized to further analyze residual risk differences in facilities reflecting diverse biosafety standards across Southeast Asia. Assessing tool performance against traditional risk assessment methods and different lab contexts presents valuable insights for improving biosafety protocols and practices. Integrating technology-driven tools into biosafety management programs can allow for an evidence-based understanding of risk mitigation efficacy, advances in the current biosafety training landscape, and proactive prevention of biosafety incidents.

Abstract Reference: 20375
Mode of Presentation: Symposium
Topic: Call for Symposium

Liver fluke's secret weapon: Unveiling extracellular vesicles in disease and vaccine hope

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Abstract Content

Infection with Liver fluke, *Opisthorchis* viverrini, is major risk factor for cholangiocarcinoma and is classified as Class I carcinogen causing by their excretory/secretory products, particularly extracellular vesicles (EVs). These vesicles play a role in inducing pathogenesis within host cells by delivering cargos like proteins, and potent nucleic acids, such as microRNAs. The precise mechanism by which cholangiocytes internalize these EVs remains unclear. Studies on the uptake mechanisms and impacts of *O. viverrini* EVs using proteomic methods show that EVs induce cell proliferation and cytokine production promote tumorigenic microenvironment to the host cell. Gene editing technologies, such as CRISPR/Cas, were used to modify key molecules like tetraspanins (*Ov*-TSPs), specifically *Ov*-TSP-2, which are integral to the EVs' uptake process. Moreover, vaccine development using *Ov*-TSPs and whole *Ov*EVs are investigated in animal models, indicating their potential as an effective protective vaccine against the parasite which is reduce the worm burden and parasite fitness.

Abstract Reference: 20669
Mode of Presentation: Symposium
Topic: Call for Symposium

Spatial distribution of major helminths across the Lower Mekong Basin

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Abstract Content

Neglected Tropical Diseases (NTDs), especially helminthic infections, represent a significant public health burden in rural regions of low and middle-income nations. The Lower Mekong Basin, encompassing Thailand, Lao PDR, Cambodia, and Vietnam, exhibits a high prevalence of the liver fluke *Opisthorchis viverrini* and soil-transmitted helminths (STH). Opisthorchiasis caused by *O. viverrini* has been an enduring concern in this area, with chronic heavy infections leading to serious complications like liver cirrhosis, portal hypertension, and cholangiocarcinoma. Spatial analyses reveal significant clustering of *O. viverrini* infections along the Mekong River, persisting in Lao PDR and central Vietnam. STH infections are especially prevalent among children and malnourished populations, contributing to increased morbidity and mortality throughout the Lower Mekong Basin. In Thailand, opisthorchiasis caused by *O. viverrini* and STH are major helminthic diseases, exhibiting varying prevalence rates and geographical distributions. This study utilized nationwide survey data on *O. viverrini* and STH infections in Thailand from 2019, obtained from the Ministry of Public Health. Bayesian model-based geostatistical approaches were employed to identify environmental, climatic, and socioeconomic factors driving the transmission of *O. viverrini* and STH, and to predict high-risk areas within the country. The risk of opisthorchiasis and STH infections was found to be correlated with various environmental, climatic, and socioeconomic factors. The high-risk areas were identified for *O. viverrini* in the Northeast region, while STH displayed higher risks in the southern part of Thailand. Understanding the spatial epidemiology and distribution of these helminthic infections is crucial for designing and implementing effective control and prevention programs.

Abstract Reference: 20645
Mode of Presentation: Symposium
Topic: Call for Symposium

Integrated helminth control using the Lawa model One Health approach and the Magic Glasses in Thailand

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Abstract Content

Helminthiases caused by soil-transmitted helminths (STH) and human liver flukes are major public health problems in the Lower Mekong Basin. A 2019 national survey in Thailand revealed over 7 million people had helminth infections despite control programs over the past 30 years. We conducted a survey on helminthic infections and implemented a new integrated control program using the One Health Lawa model in the community, alongside the “Magic Glasses” for school children. Our study included six villages and three schools in Chaiyaphum province, which has the highest incidence of cholangiocarcinoma in the country. Baseline stool surveys in humans showed a high prevalence of Opisthorchis viverrini (OV) infection at 36.6% (max. 59.5%), followed by Strongyloides stercoralis (5.7%), minute intestinal flukes (5.5%), and other STHs. Reservoir and intermediate hosts showed OV infection prevalence of 12.1% in cats, 0.9% in dogs, and 8.8% in fish. No OV infection was found in Bithynia snails. We implemented interventions for liver fluke and STH using the Lawa model, including anthelminthic treatment, targeted health education, village health volunteer (VHV) training, door-to-door education by VHVs, daily broadcasts, pamphet distribution, billboard installation, and cooking classes. School-based education included the Magic Glasses program with cartoons, pamphlets, competitions, and class discussions. Cats and dogs were treated with anthelminthics. This integrated program increased community knowledge on liver fluke and STH infections. Initial lessons emphasize the need for STH education and local authority engagement for sustainable control.

Abstract Reference: 20475
Mode of Presentation: Symposium
Topic: Call for Symposium

The Helminth Elimination in the Lower Mekong (HELM) research program overview

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Abstract Content

Opisthorchis viverrini (OV) and soil-transmitted helminths (STH) are two of the most common helminth-related Neglected Tropical Disease (NTDs) in the Lower Mekong Basin. Although MDA is the cornerstone of the control programs to reduce morbidity caused by these infections, this approach has limitations in preventing re-infections. It requires additional measures such as reservoir host treatment, improved hygiene and health education to reinforce its impact. The Helminth Elimination in the Lower Mekong (HELM) Research Program aims to examine the impact of a scalable multi-component One Health Elimination program that combines human Praziquantel (PZQ)/Albendazole (ALB) treatment with a program that includes the "Magic Glasses" and the "Lawa Model". This research program is pioneering the WHO NTDs 2030 roadmap by simultaneously integrating multiple interventions, targeting multiple diseases across multiple countries.

Abstract Reference: 20650
Mode of Presentation: Symposium
Topic: Call for Symposium

Helminth Elimination in the Lower Mekong (HELM) baseline prevalence of major helminthiases in Lao PDR, Cambodia, and Thailand

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Abstract Content

The Southeast Asian region, the Lower Mekong Basin in particular, have the highest reported prevalence of OV and among the highest prevalence of STH infections, with only Sub-Saharan Africa having similar prevalence of STH infections. STH infections present a significant public health challenge in Southeast Asia, where it is estimated that approximately 113 million infections exist, although uncertainty in the sensitivities of commonly used diagnostic techniques means that the true prevalence could be higher. Thailand, Cambodia and Lao PDR are among the countries in the Lower Mekong Basin with ongoing STH and OV transmission and are in different stages towards elimination. In terms of STH prevalence, Thailand is much further along than Cambodia and Lao PDR with prevalence in endemic areas in the northeast region up to 4% and in the South up to 11% compared to Cambodia and Lao PDR which both exceed 40% in many endemic areas. Here, we present the baseline prevalence of the major helminth infections in Lao PDR, Cambodia, and Thailand utilizing the data from the HELM cluster randomized controlled trial (cRCT) to evaluate the impact of combining PZQ/ALB treatment with a multi-component elimination programme that comprises the *Magic Glasses* and the *Lawa Model* compared to PZQ/ALB treatment alone for the elimination of major helminthiases in the Lower Mekong Basin.

Abstract Reference: 20753
Mode of Presentation: Symposium
Topic: Call for Symposium

Advancing high-throughput mosquito sex separation technology for mosquito control program

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Abstract Content

Effective control of *Aedes* mosquitoes is crucial for mitigating the transmission of vector-borne diseases. The *Wolbachia*-based Incompatible Insect Technology (IIT) presents a promising approach, involving the release of male *Wolbachia-infected Ae. aegypti* to suppress field populations. However, the success of the IIT program hinges on the precise separation of male and female mosquitoes, posing a challenge due to the absence of turn-key technology for large scale operations. To address this challenge, the Project *Wolbachia* – Singapore team has developed innovative solutions by integrating mosquito biology, precision engineering, environmental control, and artificial intelligence. These solutions optimize larvae rearing conditions and standardize pupal size distribution of male and female mosquitoes, to achieve high-throughput production of male mosquitoes with minimal female contamination through high-precision mechanical separation. This breakthrough enables the development of a robust and scalable IIT strategy for controlling *Aedes* mosquito populations.

Abstract Reference: 20712
Mode of Presentation: Symposium
Topic: Call for Symposium

Sterile Insect Technique integrated with prerelease treatments suppresses *Aedes aegypti* populations in an urban setting in Indonesia

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Abstract Content

The implementation of the sterile insect technique (SIT) in areas with high-density target mosquito populations throughout the year is challenging. This study evaluated the effectiveness of releasing radio-sterilized male *Aedes aegypti* mosquitoes subjected to prerelease treatments in a highly urbanized area. A mark–release–recapture (MRR) trial was conducted to assess the performance of sterile male mosquitoes. The MRR results revealed that the life expectancy of irradiated mosquitoes was 1.2–8.8 days, and that their mean dispersal distance was 60.0–64.3 m. The estimated wild male population ranged from 1,475 to 2,297 male mosquitoes/ha. In the SIT trial, sterile male *Ae. aegypti* mosquitoes were released at a rate of 9,000 male mosquitoes/week/ha for 24 weeks. Prerelease treatments including chemical fogging (Fludora Co-Max EW) and breeding site removal were employed at the release site. A buffer zone was established by applying residual insecticide (K-Othrine PolyZone SC) and releasing sterile male mosquitoes. In the SIT trial, relative to control sites, the site with sterile male mosquitoes had considerably greater sterility in the field population (greater by 53%), resulting in reductions in the ovitrap index (OI) (66% and 80%), ovitrap density index (ODI) (45% and 70%), and number of wild female mosquitoes recaptured (54%) at the release site. Furthermore, our survey revealed that community engagement activities are pivotal for improving SIT knowledge and acceptance among participating residents. Overall, this study underscores the critical role of an integrated vector management when the SIT is implemented in highly urbanized areas.

Abstract Reference: 20931
Mode of Presentation: Symposium
Topic: Call for Symposium

Pilot field trials of boosted Sterile Insect Technique against *Aedes* invasive species in Europe

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Abstract Content

Aedes invasive species are a great concern for public health in Europe, particularly *Aedes albopictus* and *Ae. aegypti*. They both cause severe nuisance worldwide and their vectorial capacity for many diseases such as dengue, chikungunya and Zika viruses is a permanent threat. Their management is complex and requires the combination of several control tools. Recently, we proposed to boost the Sterile Insect Technique (SIT) by coating the sterile males with pyriproxyfen before release. Small scale trials (phase II) of the boosted Sterile Insect Technique (boosted SIT) have been implemented against *Ae. albopictus* in Spain and against *Ae. aegypti* and *Ae. albopictus* in Reunion island, France, in 2021 within the ERC project Revolinc, and more recently (2023) using intermittent releases in Greece. Boosted sterilized males releases lead to a strong (>80%) reduction of mosquito densities in all sites where it was tested. These promising results constitute a significant advance, and we propose boosted-SIT approach as a new component of integrated management of the Asian tiger mosquito. Its ability to prevent dengue is now under testing at a larger scale (phase III trial) in Reunion island, within the OPTIS project, funded by the EU FEDER funds, the Reunion region and the French Ministry of Research. Private companies are also under development to apply this strategy at an operational scale.

Abstract Reference: 20972
Mode of Presentation: Symposium
Topic: Call for Symposium

Community-oriented approach to managing mosquito-vectors and resistance to insecticides in Cameroon: the potential role of new tools

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Abstract Content

It is estimated that more than 67% of Cameroon's urban population lives in slums which are prone to mosquito breeding sites, and the situation is far from improving as these neighborhoods are growing at an annual rate of 5.5%. However, it is not known how this rapid and uncontrolled urbanization affects the patterns of vector populations and disease transmission across urban versus rural areas. Therefore, we conducted a review of studies carried out over the two last decades in 65 locations across the country and identified seventeen mosquito species involved in the transmission of ten diseases with differential profiles between urban and rural areas. These include eleven species mainly involved malaria transmission (45-67% prevalence), five species in arbovirus transmission (14-30% dengue fever prevalence) and one species in the transmission of malaria and Lymphatic filariasis. *Anopheles* spp. and *Aedes aegypti* species frequencies significantly increased in urban areas over the time, while remaining at considerable frequencies in rural areas. Furthermore, there was an increase in mosquito-borne diseases prevalence associated with the acquisition of resistance mechanisms (such as Kdr 1014F and 1014S resistant alleles, detoxication genes) by the vectors, coupled with their vectorial capacity and competence, as well as the abusive insecticide use in agriculture. These findings suggested that vector-borne disease control approaches in Cameroon should integrate new tools, community educational campaigns and insecticide resistance management strategies against malaria and other co-emerging/re-emerging mosquito-borne diseases such as dengue and Zika in urban areas, or against lymphatic filariasis and Rift Valley fever in rural areas.

Abstract Reference: 20167
Mode of Presentation: Symposium
Topic: Call for Symposium

Prevention of dengue infection use Wolbachia in the aedes mosquito

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Abstract Content

Many innovative way to control Dengue had been done, such as breeding source activities conducted by community, namely 3 M activities to reduce the morbidity and training to medical to reduce the mortality rate. Indonesia through UGM conducted research for Wolbachia. Showed it’s efficacy to decrease Dengue cases in Yogyakarta (2020). Result of Cluster Randomized Trial Control Trial (CRCT) in 2017, was effective in reducing dengue cases by 77%, also effective in reducing dengue incidence of 4 strains (DENV 1 - 4), as well as can reduced hospitalization by 86% (Utarini, Adi et al. 2021) .The MoH decided to implement the use of Aedes with Wolbachia in 5 cities with that is Bandung Bontang Semarang West Jakarta and Kupang. Placing the bucket with Aedes with Wolbachia eggs in the people homes at a distance of 75 meter. Every 2 weeks the water and egg are replaced for 12 times. Monitoring was carried out, if the mosquito population more than 40 %, release was stopped Semarang, Bontang and Kupang began in November 2023, Bandung and West Jakarta will begin on 2024. Some obstacles found during implementation such as communication and coordination with local government, inter sector and local community leader, the hot climate make eggs damage, community volunteers, disbelieve from the community, circulating the negative issue in the community.

Abstract Reference: 20993
Mode of Presentation: Symposium
Topic: Call for Symposium

Rising parasites, stagnant protocols: Bridging the gap in foodborne parasitology for a warmer world

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Abstract Content

Foodborne parasites have evolved to exploit the food web, often utilizing cold-blooded intermediate hosts or vectors, which are predominantly invertebrates, to reach our plates. This complex lifecycle, coupled with global warming, suggests a likely increase in the prevalence and population of these parasites. However, the adequacy of current food safety protocols, particularly in developed countries, remains questionable. Many of these protocols were established in the 20th century, a time when the focus was on controlling and eradicating parasites. Since then, there has been a noticeable decline in the training of skilled parasitologists capable of addressing the emergence of new, climate-driven parasitic threats. This presentation explores case studies to highlight the existing knowledge gaps and the urgent need to modernize our approach to foodborne parasitology, ensuring that safety measures keep pace with the evolving landscape of parasitic infections.

Abstract Reference: 21006
Mode of Presentation: Symposium
Topic: Call for Symposium

Food borne parasites in India - Epidemiology, burden and diagnostics

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Abstract Content

Food borne parasitic infections impact populations in low resource settings with poor access to networked WASH facilities disproportionately. In addition, lack of awareness, poor implementation of or lack of standards and policies for hygienic practices, increased animal-human mixing and some cultural practices increase these risks. This can lead to enteric infections with a range of protists (Cryptosporidium, Giardia, Entamoeba) and helminths (Ascaris, Trichuris, Taenia and others) that cause 1) diarrheal disease or 2) subclinical infections which lead to anemia and malnutrition in young children and other vulnerable populations as well as 3) invasive infections such as hydatid disease, fascioliasis and cysticercosis. In this talk, using examples from a range of cases seen at a large quaternary care hospital in southern India over the last two decades, the burden, epidemiology and diagnostics of these endemic food borne parasitic infections will be discussed.

Abstract Reference: 21007
Mode of Presentation: Symposium
Topic: Call for Symposium

Foodborne outbreaks caused by parasites and viruses: An update on impact and prevention measures

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Abstract Content

Consumption of foods that lack a “kill” step such as cooking, can pose a risk for acquiring parasitic and viral illnesses. That includes fresh and frozen vegetables and fruits that are normally consumed raw. Among these parasites and viruses, *Cyclospora cayetanensis*, the agent of human cyclosporiasis, and the Hepatitis A virus represent important foodborne pathogen that causes impactful outbreaks in the US and Canada. In 2022 and 2023, two US multistate outbreaks linked to consumption of fresh and frozen organic strawberries involved the same Hepatitis A genotype. In terms of public health impact, several seasonal *Cyclosporiasis* outbreaks have occurred US and Canada over the last decade. In 2023, these outbreaks affected 2,272 individuals in multiple states of the US. These outbreaks events have triggered a comprehensive response from public health and regulatory authorities. This presentation will provide an update on the global impact of foodborne outbreaks caused by viruses and parasites.

Abstract Reference: 21008
Mode of Presentation: Symposium
Topic: Call for Symposium

The modernization of foodborne and diagnostic parasitology and virology: The current impact, elimination, control, and opportunities in the next decade

Momar Ndao*[1], Alexandre da Silva[2], Sitara Ajjampur[3], Shokoofeh Shamsi[4]

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[4]*Charles Sturt University, AUSTRALIA*

Abstract Content

The risk for parasitic and viral foodborne illnesses continues to rise worldwide for many reasons. Consumption of foods that lack a “kill” step such as cooking, can pose a risk for acquiring parasitic illnesses. That includes vegetables that are normally consumed raw as well as raw fish and meat. Among these parasites and viruses, *Cyclospora cayetanensis*, the agent of human cyclosporiasis, *Trypanosoma cruzi*, agent of Chagas disease, and hepatitis A virus represent important foodborne pathogens that causes impactful yearly outbreaks globally. Since cyclosporiasis outbreaks affect between 1,000 to more than 2,000 individuals every year, public health, and regulatory agencies in collaboration with stakeholders, are working on multidisciplinary efforts to control these events. The objective of this session is to update the audience about how foodborne parasitology and virology is changing with these new trends that have a global impact. The talks will also cover aspects of efforts that will be required over the next decade to reduce and ultimately eliminate the burden of these foodborne diseases at global levels.

SPONSORED SYMPOSIUM

SPONSORED SESSION

Abstract Reference: 20690
Mode of Presentation: Symposium
Topic: Sponsored Session

Zoonotic intestinal nematodes of pets - Overview and prevention

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Abstract Content

Infections with soil-transmitted helminths (STHs) affect billions of animals and people worldwide, resulting in a disease burden of ∼4 million disability adjusted life years in humans. Hookworm disease alone affects nearly half a billion people in underprivileged communities. Disease control relies heavily on reducing morbidity through periodic treatment targeting at-risk populations. However, the success of these programs is hindered by rapid re-infection rates associated with persistent reservoirs and the low sensitivity of conventional diagnostic techniques. Moreover, in the Asia Pacific region, the presence of animals in close proximity to human dwellings contributes to environmental contamination with zoonotic STHs. In this presentation, I will provide an overview of our research aimed at improving STH control. This includes improved methods to assess the effectiveness of WHO-recommended control strategies and the development of innovative point-of-care diagnostics. Additionally, I will share data on the development and implementation of a multidisciplinary One Health intervention program for the control of zoonotic STHs in Cambodia. Finally, I will present results from the development of novel multi-host transmission models involving dogs, cats, and humans for controlling zoonotic parasites. Our findings demonstrate that One Health interventions, targeting both animals and humans, could suppress prevalence in humans to ≤ 1% by the end of 2030, even with only modest coverage of the animal reservoir. These findings show that the adoption of a transdisciplinary One Health approach is central to monitoring zoonotic infections and the success of intervention strategies, which can ultimately aid in reducing morbidity in animal and human populations.

Abstract Reference: 20718
Mode of Presentation: Symposium
Topic: Sponsored Session

Zoonotic malaria in Sarawak

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Abstract Content

Sarawak is home to many nonhuman primates that harbor malaria parasites that are of public concern due to their zoonotic capability. The zoonotic capabilities of these parasites bridged by the presence of opportunistic vectors that are not host specific transcend the monkey-to-human host barrier. Seven species of malaria parasites; *Plasmodium inui*, *P. inui*-like, *P. knowlesi*, *P. cynomolgi, P. coatneyi, P. fieldi, and P. simiovale*, have been identified infecting the macaques of Sarawak. Of these, *P. knowlesi* is recognized as the fifth malaria parasite to cause malaria in humans. Recently, the zoonotic capabilities of *P. inui*, *P. inui-like*, *P. simiovale*, as well as *P. knowlesi* and *P. cynomolgi* were demonstrated to naturally infect indigenous communities living along forest fringes or cohabiting with non-human primates. A total of 8473 indigenous knowlesi cases were reported between 2011 to 2019 only in Sarawak, with seven districts from the southeastern border reporting the most number of cases. Studies highlighted that working men, 20-49 years of age, and older women, 50 years and above, are more prone to knowlesi infection. The factors contributing to the elevated propensity of zoonotic malaria transmission among the locals in Sarawak include loss of habitat of macaques or cohabitation and anthropogenic activities coupled with the vector composition, abundance, and biting behavior. Therefore, further epidemiological and entomological studies are required to help mitigate the transmission of zoonotic malaria in Sarawak.

Abstract Reference: 20736
Mode of Presentation: Symposium
Topic: Sponsored Session

Tuberculosis in Sarawak: Bridging the gap

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Abstract Content

Tuberculosis (TB) is a preventable disease caused by *Mycobacterium tuberculosis*. Annually, about 10 million people get TB, with 1.5 million people dying from it. The disease is present globally, affecting people in low- and middle-income countries. The incidence rates are highest in South-East Asia (SEA) Region countries. It is a major public health concern in Malaysia, with cases increasing by 17% in 2022 (25,391) from 2021 (21,727). It is of particular concern in Sarawak. Next to Selangor and Sabah, Sarawak reported the highest number of cases (3,234) in 2023 where the incidence rate was over 120 per 100,000 compared with the national estimates of 113 per 100,000, with disparities observed in demography. The problem of latent TB infection (LTBI) is also of concern as it forms a major reservoir for new active TB cases in the state. Curbing their burden is in line with the National Tuberculosis Strategic Framework for End-TB 2021-2030. In 2023, over 3,000 cases were identified via surveillance work with 93% administered preventive intervention. Tackling the problem of TB in Sarawak requires addressing the gaps that were identified, namely identification of cases, costs of tests, stigma associated with the disease and knowledge about the disease. In collaboration with the State Health Department and the communities affected, the Sarawak Infectious Disease Centre (SIDC) aims to close this gap by bringing the lab to communities to support TB surveillance and help healthcare services determine the drivers of TB in various community settings.

Abstract Reference: 20978
Mode of Presentation: Symposium
Topic: Sponsored Session

Feral cats and dogs, and synanthropic wild mammals as potential reservoirs of zoonotic parasites in Southeast Asia

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Abstract Content

Zoonotic disease is on the rise globally and is of major concern in Southeast Asia. Urbanization and anthropogenic landscape alterations have drastic impacts on the transmission dynamics of many zoonotic diseases, as there is an increase in feral domestic and synanthropic wild mammals that subsist in these human-altered habitats. These mammals also act as a bridge between zoonotic pathogens circulating in the sylvatic cycle and domesticated companion animals. The transmission of zoonotic parasites to humans may be through arthropod vectors, direct contact, or ingestion of infective stages. The present study investigates the diversity and prevalence of potentially zoonotic parasites that are harboured by feral/stray cats and dogs, as well as wild mammals living in close proximity to humans in Southeast Asia. Gastrointestinal parasites including various genera of protozoa and helminths are among the major groups of zoonotic parasites that pose a significant risk to humans due to environmental contamination by these feral and wild mammals. Arthropod-borne parasites comprise mainly of haemoprotozoa and filarid worms. Tissue-dwelling protozoa including *Toxoplasma* is also of major concern in the region. With the global increase in the population of feral/stray cats and dogs, it is imperative that in depth studies be conducted in order to appreciate their role in the epidemiology and transmission of zoonotic parasites, in order to prevent infections among humans and domestic companion animals.

Abstract Reference: 20986
Mode of Presentation: Symposium
Topic: Sponsored Session

New approaches in the control of ecto and endoparasites of dogs and cats

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Abstract Content

Parasiticides acting on endo- or ectoparasites represent the first segment of the global animal health market, accounting for around 25% of the market. Parasitic infections are among the most significant diseases worldwide. Parasites (e.g. fleas, tick, mites, gastro-intestinal worms, heartworm, lungworms) are common in companion animals and, due to their possible zoonotic nature, represent threats to human health. There are 900 and 400 million of pet dogs and cats, respectively, on earth. Controlling parasites of companion animals not only protect them but also protect human population. During discovery, an intensive search is conducted to identify active molecules. This is followed by the development phase until registration which includes formulation, PK/PD data, efficacy, safety, and production quality and will last from 6 to 8 years. The processes involved in the discovery and development of veterinary antiparasitics compare well with those used in human pharmaceutical industry. However, the veterinary field takes can perform studies directly on the target hosts/species. Isoxazolines are the latest group of insecticides-acaricides and a true innovation and success story. For companion animals, current products for the treatment of ectoparasites provide efficacy against fleas, ticks, and mites for a period of at least 1 month. Nematodicides (mainly belonging to macrocyclic lactones) mainly target gastrointestinal nematodes, heartworm, and lungworms. Tapeworms are treated via the use of praziquantel. Due to multiparasitsim in dogs and cats, the most recent formulations are endectoparasiticides. Innovation also includes easiness to administer, with oral palatable formulations in dogs and topical formulations for cats.

Abstract Reference: 20987
Mode of Presentation: Symposium
Topic: Sponsored Session

Small molecule inhibitor from SBC Natural Product Library for inhibition of SARS-CoV-2

Barbara Anak Ngikoh[*1], Mitchel Constance George[1], Jorim Ujang[1], Lau Ching Ching[1], Siti Muhaini Binti Haris Fadzillah[1], Julian Voong[1], Velnetti Linang[1], Felicia Chin Yien Yin[2], Angelesa Runin[1], Michele Mejin[1], Peter Morin Nissom[2], Yeo Tiong Chia[1]

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Abstract Content

The Natural Product Library (NPL) maintained by the Sarawak Biodiversity Centre (SBC) boasts a diverse array of extracts sourced from plant and microorganism species found in Sarawak. In this study, we conducted a screening strategy aimed at assessing pre-fractionated extracts from NPL for their efficacy against three key mechanisms of SARS-CoV-2: Spike Protein – ACE2 interaction, 3-chymotrypsin-like protease (3CLPro), and papain-like protease (PLPro). Our primary objective is to identify natural compounds with potential inhibitory properties for antiviral therapeutic applications. A total of 5,012 prefractionated extracts have been obtained and subjected to a one-dose primary screening protocol. Hits extracts were determined through 2-standard deviation threshold. A total of 87, 63 and 121 hits were found against Spike:ACE2, PLPro and 3CLPro, respectively. Further selection through Liquid Chromatography Mass Spectrometry (LCMS-TASQ)-based dereplication strategy was done to maximize the potential for unknown antiviral compound discovery. A compound identified designated as PLT95 was identified as promising molecule against 3CLPro. Our findings offer a starting point for compound efficacy study for treatment of patients infected with SARS-CoV-2 or coronavirus with similar pathogenic mechanism.

Keywords: Natural Product Library (NPL); SARS-CoV-2; compound discovery

Abstract Reference: 20989
Mode of Presentation: Symposium
Topic: Sponsored Session

Japanese encephalitis: Is it really rare? Or are we just not aware?

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Abstract Content

Japanese Encephalitis (JE) is often perceived as a rare disease in Southeast Asia, including Malaysia. However, this perception may be misleading due to underreporting, misdiagnosis, and the lack of widespread surveillance. JE is a mosquito-borne viral infection that can cause severe neurological damage and has a high mortality rate, particularly in children. Despite the availability of vaccines, JE continues to pose a significant public health challenge in endemic regions. This presentation will explore the true burden of Japanese Encephalitis in Malaysia and Southeast Asia by examining current epidemiological data, highlighting the gaps in surveillance, and discussing the potential factors contributing to the underestimation of JE cases. We will delve into the environmental, socio-economic, and behavioral factors that facilitate JE transmission and discuss the role of vector control and vaccination programs in mitigating its impact. By reassessing the perceived rarity of JE, this talk aims to raise awareness and encourage more robust surveillance and prevention efforts to better protect vulnerable populations in the region. This discussion will be crucial for public health professionals, researchers, and policymakers to re-evaluate the current understanding of JE and to develop more effective strategies for its control and prevention in Southeast Asia.

Abstract Reference: 20994
Mode of Presentation: Symposium
Topic: Sponsored Session

Japanese encephalitis: Are we just unaware?

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Abstract Content

The majority of Japanese encephalitis (JE) infections are asymptomatic, but when neurological symptoms do occur, the disease can be severe, with a high fatality rate. After an incubation period of 4 to 14 days, initial symptoms are usually nonspecific, including fever, lethargy, vomiting, and headache. Over the next several days, patients may experience behavioral changes, focal neurological deficits, and movement disorders, eventually progressing to impaired consciousness and coma. Recovery is typically slow, with neurological function gradually improving over several weeks. Currently, there is no specific antiviral treatment for JE. However, supportive care - such as controlling increased intracranial pressure, managing seizures, ensuring fluid balance, providing respiratory support, and preventing secondary infections - has significantly improved survival rates and outcomes. Vaccination against JE is an effective method for reducing the incidence of the disease. The JE chimeric virus vaccine (JE-CV) induces seroconversion in 99% of adults within four weeks of a single dose, with 84% maintaining protective antibody levels after five years. Antibody persistence models suggest that 85.5% of individuals remain seroprotected for up to 10 years. In toddlers, a JE-CV booster results in seroprotection rates of 98% after five years.

Abstract Reference: 20997
Mode of Presentation: Symposium
Topic: Sponsored Session

The burden of malaria and dengue: On ongoing fight with vector control solutions

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Abstract Content

Envu is a company built not from the ground up but on a foundation of 50 years of environmental science experience. This rich history gave rise to leading vector control innovations and brands including K-Othrine® products, Resigen®, Aqua Resigen®, Fludora® products and many others. One of those products is K-Othrine Polyzone: developed by Envu containing a polymer-enhanced suspension concentrate aqueous formulation. This proprietary polymer technology protects the active ingredient from weather, rainfall and mechanical abrasion. When applied correctly, the active ingredient remains available for several months on treated surfaces to control vectors of malaria and dengue. In a local study conducted in Sabah (Tenom district) and Sarawak (Julau district) against vectors of knowlesi malaria, it was found that K-Othrine Polyzone showed residuality for an average of six months and knowlesi malaria cases dropped by 28% and 46% in the two years. Another study was conducted against dengue vectors in a locality in Selangor, which showed an average of three months residuality and a reduction of about 88% in dengue cases when compared to previous year. Here in Envu, we fully leverage our industry-leading capabilities to stay ahead of evolving threats. Mosquito vectors are always adapting to better suit their environments, evading threats, and finding new ways to challenge us and our methods. We at Envu are focussed leaders, committed to 360 innovation to deliver more broad range of solutions to meet the evolving nature of pest-transmitted diseases.

Abstract Reference: 21003
Mode of Presentation: Symposium
Topic: Sponsored Session

Achieving zero dengue deaths: Roles of early diagnosis in patient management

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Abstract Content

Dengue Fever remains a significant public health challenge, particularly in tropical and subtropical regions. Despite advancements in medical science, dengue continues to cause substantial morbidity and mortality. Each year, an estimated 390 million dengue infections occur globally, resulting in up to 36,000 deaths1. In 2024 alone, over 12 million cases and more than 8,000 dengue-related deaths have been reported from 86 countries2. This lecture explores the critical role of early diagnosis in the effective management of dengue patients, aiming to achieve the ambitious goal of zero dengue deaths. Early diagnosis is pivotal in identifying severe cases promptly, allowing for timely intervention and appropriate patient management. However, early diagnosis can be challenging due to the similarity of dengue symptoms to other febrile illnesses, often leading to delayed identification and treatment. Additionally, predicting which patients will develop severe dengue is complex and requires careful monitoring and understanding of warning signs. This presentation will discuss the latest diagnostic techniques, including rapid diagnostic tests (RDTs), which enhance the accuracy and speed of dengue detection. Additionally, the lecture will highlight the importance of clinical vigilance and the integration of diagnostic tools in routine healthcare practices. By examining case studies and recent research findings, we will illustrate how early diagnosis can significantly reduce the risk of complications and improve patient outcomes. The lecture will also address the challenges and barriers to implementing early diagnostic strategies in resource limited settings and propose solutions to overcome these obstacles. Ultimately, this lecture aims to underscore the necessity of early diagnosis as a cornerstone in the fight against dengue, advocating for its widespread adoption to save lives and achieve the goal of zero dengue deaths.

ORAL PRESENTATION

Oral Presentation

Abstract Reference: 20004
Mode of Presentation: Oral Presentation
Topic: One Health 2

Investigating geographical clusters of leptospirosis in Pangandaran, West Java, Indonesia

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Abstract Content

Leptospirosis is one of the neglected zoonotic diseases in many tropical developing countries, including Indonesia. This research aimed to investigate epidemiological features and the spatial clustering of the recent leptospirosis outbreaks in Pangandaran, West Java. The study analysed data on individual-level leptospirosis notifications between September 2022 to May 2023. Global Moran I coefficient and local indicator for spatial association (LISA) were applied. Comparative analysis was performed to characterise the identified hotspots of leptospirosis relative to its neighbourhoods. A total of 172 reported leptospirosis in 40 villages from 9 sub-districts in the District of Pangandaran were analysed. Of these, 132 cases (76.7%) were male. The median age was 49 years (interquartile range [IQR]: 34-59 years). Severe outcomes including renal failure, lung failure, and hepatic necrosis were reported in up to 5% of the cases. A total of 30 patients died, resulting in the case fatality rate [CFR] was 17.4%. Moran's *I* analysis showed significant spatial autocorrelation (I=0.293; p-value=0.002). LISA's results identified 7 High-High clusters (hotspots) in the southwest, with the total population at risk was 26,184 people. The hotspots had more cases among older individuals (median of age 51, IQR: 36-61 years; $p<0.001$), more farmers (79%, p=0.001), and more evidence of the presence of rats (p=0.02). A comprehensive One Health intervention should be targeted towards these high-risk areas to control the transmission of leptospirosis. More empirical evidence is needed to understand the role of climate, animals, and sociodemographic characteristics on the transmission of leptospirosis in the area studied.

Abstract Reference: 20034
Mode of Presentation: Oral Presentation
Topic: One Health 1

Insect succession and decomposition pattern on pig carrion during warm and cold seasons in KwaZulu-Natal province of South Africa

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Abstract Content

With the aim of identifying insects with potential value as indicator species in postmortem interval (PMI), the location or season of death of human or monogastric animals, two medium-sized large white pigs were used for the study during cold and warm seasons. Five stages of decomposition and their durations were observed and described in the pig carcasses during both seasons. Carcasses were first colonized by flies from seven taxa during fresh stage. *Chrysomya marginalis* (Wiedemann) (Diptera: Calliphoridae), *Chrysomya albiceps*, (Wiedemann) (Diptera: Calliphoridae) and *Musca domestica* (Walker) (Diptera: Calliphoridae) were recorded as the overall dominant adult flies found on the carcasses in both seasons. Colonization by beetles began during the bloated stage in the warm season and active stage in the cold season. *Dermestes maculatus* (DeGeer) (Coleoptera: Dermestidae) and *Necrobia rufipes* (De Geer) (Cleridae) were the most abundant beetles in both seasons. Flies and beetles were generally abundant during the warm seasons as compared to the cold season. However, the difference was only significant for beetles. The highest number of flies were recorded in the bloated stage for both seasons, however they were reduced in the active stage which coincided with the introduction of predatory beetles. The arrival time of the different arthropod species and their association with different stages of decomposition during both seasons pointed to their value in estimating the PMI in forensic investigations in the locality of KwaZulu-Natal, South Africa. Consequently, they can potentially be useful in the estimation of PMI and other cases of criminal investigations.

Abstract Reference: 20042
Mode of Presentation: Oral Presentation
Topic: Parasitology - Molecular Parasitology

The efficacy of genetic marker GRA7 in identifying the specific type of *Toxoplasma gondii* from direct clinical samples of cerebrospinal fluid HIV/AIDS patients

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Abstract Content

Cerebral toxoplasmosis is a disease that affects immunocompromised individuals, usually the HIV/AIDS. The severity of the disease might be linked to T. gondii genotype. Highly virulent strains of the parasite are frequently linked to a greater occurrence and more severe instances of the disease in humans. Genetic markers are required to figure out the genotype, and many studies have used genetic markers, especially the dense granule proteins. Our previous investigation on GRA6 showed no positive results, prompting researchers to explore GRA7 instead. The objective of this study was to evaluate the use of GRA7 for determination of T. gondii genotype from cerebrospinal fluid of HIV/AIDS patients wth toxoplasma encephalitis in Cipto Mangunkusumo hospital, Jakarta. Nested PCR of GRA7 were carried out on 69 CSF orignated from the HIV/AIDS patients with cerebral disorders and confirmed for toxoplasmosis through positive ELISA IgG and 5' SAG2 PCR. Positive amplicon of GRA7 PCR underwent sequencing. DNA sequences were verified, blasted,aligned to Toxoplasma type 1, 2 and 3 reference sequences available from NCBI gene bank, then put into phylogenetic analysis for type determination. GRA7 PCR positive result was obtained in 34 out of 69 CSF samples (49,3%). Six samples were selected for sequencing. Phylogenetic tree analysis by maximum likelihood of 1000 replication, resulted in three samples of type 1 and the rest of atypical strain. GRA7 can be an alternative to GRA6 for the determination of the T. gondii genotype directly from cerebrospinal fluid.

Keywords: Genotyping, Toxoplasma gondii, genetic marker, GRA7, HIV/AIDS

Abstract Reference: 20045
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 1

Analysis of the effect of primaquine dose on the efficacy, safety, and tolerability of patients with *Plasmodium vivax* malaria in Ethiopia

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Abstract Content

Plasmodium vivax causes relapsing episodes of malaria that can cause significant morbidity, mortality, and ongoing transmission. The elimination of *P. vivax* requires widespread deployment of a safe and effective radical cure. The only hypnozoitocidal drug for the dormant liver stages available in Ethiopia is primaquine, which can cause severe drug-induced haemolysis in G6PD-deficient patients. A recent global individual patient data pooled analysis demonstrated that patients treated with a high total dose of primaquine (7 mg/kg) had half the risk of *P. vivax* recurrence within 180 days than patients treated with low total dose primaquine (3.5 mg/kg). The Ethiopian Ministry of Health has requested Ethiopian-specific data to quantify the benefit of change in antimalarial policy. A systematic review of clinical studies will be undertaken to assess the safety and efficacy of daily primaquine regimens in patients with uncomplicated *P. vivax* malaria. Investigators of eligible studies were invited to share individual patient data, which will be collated. The effect of total primaquine dose and the duration of the primaquine regimen on the risk of recurrence will be explored by time-to-event analysis including multivariable Cox regression analysis. The presence of gastrointestinal symptoms and clinically relevant haemolytic events will be assessed according to the effect of daily primaquine dose. Data from five of six eligible studies, including over 1,000 patients are available. The analysis of these data will assess the risks and benefits of high total dose primaquine in Ethiopia. Complete results and its implications for policy change will be presented.

Abstract Reference: 20054
Mode of Presentation: Oral Presentation
Topic: Entomology - Vector and Vector-Borne Diseases

DNA barcode of KFD vectors in India: *Haemaphysalis spinigera* and *Haemaphysalis turturis*

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Abstract Content

Ticks are significant vectors of several diseases such as Kyasanur forest disease (KFD), Lyme disease, Babesiosis etc. Identifying tick species with certainty is crucial to prevent tick-borne diseases and DNA barcoding provides a significant advancement in this field. While, the molecular characterization and DNA barcoding has been done in few genera of ticks, the evolutionary genetics and DNA barcoding of *Haemaphysalis spinigera* and *Haemaphysalis turturis* (vectors for KFD, deadly viral haemorrhagic fever) is not well studied. In this study, we analysed the samples of both species collected from different regions of India along with outgroup species using multi-marker (*16S*, *COI and ITS2*) approach. These sequences are analysed based on genetic divergences and neighbour-joining phylogenetic relationships among all tick-species. Our results revealed that *COI* and *ITS2* are reliable markers for species distinction, however *16S* could not discriminate between both species. A DNA barcoding system was developed for *H. spinigera* and *H. turturis* as both the species were making their own monophyletic clade, and no matching sequences were found in BOLD database. Therefore, the phylogenetic pattern and uniqueness of generated sequences of COI and ITS2 gene justifies their divergence from other species of *Haemaphysalis* genus and allocate them to be considered as a successful barcode of *H. spinigera* and *H. turturis*. This barcode would help many taxonomers or non-taxonomers to easily identify these two species of *Ixodida* based on DNA sequences. However, additional research is needed to resolve the deficiency in the information of 16S genetic region of several species of ticks.

Abstract Reference: 20055
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 1

An eco-epidemiological analysis of the malaria situation from 2004 to 2023 in two southern endemic pockets of India

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Abstract Content

Currently, India is in malaria elimination stage. In this context, analysing malaria epidemiological data of endemic pockets is important. In the present investigation, malaria prevalence in two endemic coastal localities of India viz., Besant Nagar (Chennai district) and Pamban (Ramanathapuram district) was analysed from 2004 to 2023 and correlated with the highest maximum temperature. The analysis showed that the malaria cases (P.v. and P.f.) were directly proportional to the temperature increase. Malaria cases remarkably increased from 2004 to 2011 and subsequently, both *P.v.* and *P.f* cases were drastically reduced till 2023. *P.v.* was higher than *P.f.* and the male population was found to be more affected. Mixed infection of *P.v.* and *P.f.* was observed only in the Besant Nagar site (0.3%). The most affected age group was the adult age group (15 years and above) in both Besant Nagar (76.1%) and Pamban (69.5%). *Anopheles stephensi* (Liston) is the urban vector in India responsible for malaria transmission in Chennai areas (urban coastal). Our survey in Pamban areas (Southern tip of India) recorded the presence of *An. stephensi* apart from the local vector *An. culicifacies*. Improved surveillance, complete treatment and integrated vector control correlated with a declining trend of malaria in both the coastal sites.

Keywords: Coastal Malaria, *Anopheles stephensi* invasion, Malaria elimination challenges

Abstract Reference: 20057
Mode of Presentation: Oral Presentation
Topic: Entomology - Mosquito Vectors

Future warming could trigger Himalayan expansion of *Anopheles stephensi* while preserving the range of *Anopheles culicifacies* in India: An ensemble ecological niche modelling approach

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Abstract Content

Control and elimination of malaria cannot be achieved without accounting for the distribution and abundance of its primary vectors – the Anopheline mosquito. As the world continues to warm, it is imperative to understand how these species may respond to future changes in climate, as shifts in their geographic distribution could alter the epidemiology of malaria in India. The present study aims to contribute to this broader goal by investigating the potential impacts of climate change on the geographic distribution of two important malaria vectors in India – *An. stephensi* and *An. culicifacies*. The study employs an ensemble ecological niche modelling approach to identify the present and future climatic/ecological suitability (based on 19 bioclimatic variables and 3 ecological variables) for the two vectors using known locations of occurrence obtained from previous literature. This was then used to model the present (1975 – 2020) and future (2030s, 2050s and 2070s) distribution range of the two species under three scenarios of climate change (RCP 2.6, RCP 4.5 and RCP 8.5). Under all three scenarios, suitability for *An. stephensi* is predicted to decline in the central and eastern parts of India, however significant increase in range is projected in the lower terai regions of Himalayas by 2050s and 2070s, a result of future warming. *An. culicifacies* is widely distributed across the country and does not appear to be affected significantly by future climate change, though some increase in range is projected in the Thar desert region due to changes in precipitation based variables.

Abstract Reference: 20065
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 1

Differentially expressed miR-3158-3p microRNA in severe malaria: from discovery to validation

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Abstract Content

Case fatality rates for *Plasmodium falciparum* (*Pf*) severe malaria (SM) remain unacceptably high in malaria-endemic countries. Sequestration of *Pf*–infected erythrocytes in vital organs and the associated inflammation leads to organ dysfunction. This study validated the potential of hsa-miR-3158-3p microRNA, released upon organ damage, as a biomarker of SM and its complications including cerebral malaria (CM). Our previous studies involving Mozambican children and Indian adults established the association of this microRNA with SM, CM, and magnetic resonance imaging (MRI) features indicating poor outcomes in CM. However, these studies omitted asymptomatic malaria patients (i.e., infections without clinical symptoms) and non-malarial febrile illnesses. Inclusion of these cases is necessary to confirm the specificity of hsa-miR-3158-3p association with SM and CM and to further strengthen its role as a biomarker of SM or CM. In the present study, plasma levels of hsa-miR-3158-3p, determined by quantitative reverse transcriptase PCRs, correlated with disease severity in *Pf* malaria patients ($p<0.0001$) and were associated with CM ($p<0.0001$). Remarkably, hsa-miR-3158-3p levels on admission discriminated CM patients from those with severe non-cerebral, uncomplicated, asymptomatic malaria cases, as well as non-malarial febrile illnesses, with an AUC of 81% to 100% ($p<0.0001$). These findings support hsa-miR-3158-3p as a promising CM biomarker, potentially replacing MRI for CM monitoring and clinical management.

Abstract Reference: 20070
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 1

Assessment of factors affecting non-usage of bed nets by women of reproductive age group in India: Insight from a demographic health survey

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Abstract Content

As a pivotal tool in malaria prevention, understanding the dynamics shaping the adoption of Bed nets is imperative for public health strategies. This study delves into socio-economic factors, educational backgrounds, and regional disparities impacting non usage of bed nets. By scrutinizing data from National Family Health Survey (NFHS), it aims to provide a nuanced understanding of barriers and drivers. States were grouped into regions based on Annual Parasite Index (API). Descriptive statistics as well as univariate and multilevel logistic regression analyses were used on the datasets of NFHS 5 to identify factors associated with usage of Bed nets. Usage of Bed nets was 5.20%, 27.15% and 39.87% in states with API 1, 2 and 3 respectively. When compared with usage, the odds of non-usage of bed nets were higher among women of all age groups with highest being in 15 to 19 years (aOR: 1.51). Similarly, it was highest among women with No education (aOR: 1.70). Moreover, those residing in states belonging to API 1 had the highest odds of non-usage (aOR: 11.99). Higher number of household members and lack of children under five years of age was associated with higher odds of non-usage (aOR: 1.57) and (aOR: 1.24) respectively. Pregnancy was a protective factor (aOR: 0.95). Similar studies was conducted in Africa using Health Surveys and they had similar results. Multiple factors are contributing for non-usage of bed nets among women which can be the focus of the targeted interventions.

Abstract Reference: 20136
Mode of Presentation: Oral Presentation
Topic: One Health 1

Dynamics of helminthic infections in epidemic and epizootic systems of Bangladesh

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Abstract Content

Given a growing international commitment to control helminthiasis, there is an urgent need to intensify case detection from various reservoir hosts. This study aimed to reveal the dynamics of helminths in the epidemic and epizootic systems of Bangladesh with the concept of One Health. We employed a combination of methods including copromicroscopy, scanning electron microscopy, experimental sedation, culture, and molecular approaches. Specimens (human stools, animal feces, and soils) were collected from the three ecological areas (Dhaka, Sylhet, and Chattogram) in Bangladesh. The ecological zone shared by host communities was found rich in a diversity of helminths, of which some are extensively shared across the host species. Human, animals, and soils showed an overall prevalence of 31.7%, 59.3%, and 52.5% respectively. Diverse species of helminths include *Ascaris*, *Trichuris*, *Capillaria*, hookworms, *Hymenolepis*, *Enterobius*, *Rhabditis*. *Toxocara*, *Spirometra*, opisthorchiid, *Fasciola*, *Paramphistomum*, roundworms, taeniid were detected. *Ascaris* and *Toxocara* were the predominant parasites in human and soil respectively. Frequently observed helminths in animals vary according to host species. For the first time in Bangladesh, nematodes, i.e., *Rhabditis* sp. from human, *Agriostomum* sp. from goat, *Ancylostoma ceylanicum* from soil, and cestode species *Spirometra decipiens* were reported from lion. This study also developed a context-based method for geohelminths recovery and the method proved feasible in terms of field applicability and egg recovery rate. This study provides the overall infection status of helminths in humans, animals, and soils from three tropical ecological settings. This pattern would help us understand helminth propagation, environmental persistence, and transmission.

Abstract Reference: 20138
Mode of Presentation: Oral Presentation
Topic: Virology

Probing fisetin: Profiling a potential antiviral shield against chikungunya

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Abstract Content

Chikungunya is a viral disease that causes fever and joint pain in humans. Over 110 countries in Africa, Asia, Europe and the Americas have been affected since chikungunya virus (CHIKV) was isolated in Tanzania in 1952. Fisetin has a known anti-CHIKV capacity with a multi-pathways mechanism. This presentation discusses the profiling of fisetin for antiviral development against CHIKV as good profiling contributes to expediting the antiviral development process. Throughout the profiling journey, both *in-silico* and *in-vitro* approaches were utilized. The *in-silico* approach offered profiling of binding affinity, binding site, residue interaction, conformational, binding mode and drug-like properties. The *in vitro* approaches allowed us to delve deeper into the dose-dependent anti-CHIKV capacity, the Toll-like receptor-mediated innate immune response and apoptosis mechanisms. Fisetin demonstrated a great binding affinity (-9.2 kcal/mol) towards CHIKV nsP3 protein, establishing stable and flexible interaction with the key residues of nsP3 macro-domain. At 30 μM fisetin reduced CHIKV-E1 RNA copy number by ~1000-fold in Huh7 cells. It promoted early and prolonged viral clearance by increasing the expression and phosphorylation of IRF3 and IRF7, resulting in the increase of antiviral effectors and response. Fisetin recovered cells from CHIKV-induced apoptosis as apoptotic hallmarks (morphology and DNA fragmentation) and biomarkers (caspases, PARP and Bcl-2) were significantly dampened. On-going researches are actively evaluating the oxidative stress and autophagy mechanisms, and challenge against CHIKV in a mice model to complete the profiling.

Abstract Reference: 20141
Mode of Presentation: Oral Presentation
Topic: Entomology - Mosquito Vectors

Morphology, sexual dimorphism and developmental changes of the larval salivary glands in dengue vector mosquitoes *Aedes* spp. (Diptera: Culicidae)

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Abstract Content

Dengue is the most widespread mosquito-borne viral disease of humans worldwide. *Aedes aegypti* is one of the most common and invasive mosquito species worldwide and major vector of dengue, chikugunya, Zika and yellow fever. The present study deals with structural morphology, sexual dimorphism and developmental changes of larval (1st to 4th instar) salivary glands in *Aedes aegypti* and *Aedes albopictus* for the first time in Bangladesh. The larval salivary glands were dissected in Ringers solution, then fixed in Carnoy's solution. Images were captured using Zeiss Stemi 305 SZ microscope with Zeiss Axiocam 105 color camera. The gland is comprised of two elongated asymmetrical lobes, located at anterolateral position in larval thorax. The lobes are connected anteriorly into a slender duct known as salivary duct. Development of larval (1st to 4th instar) salivary glands is by cell-growth which are polytene cells containing polytene chromosomes. A remarkable feature is that, salivary glands are also sexually dimorphic in larval stage, i.e. male and female larva can be distinguished by examining their lobes morphology. Salivary glands of the vector mosquitoes are very much important for their roles in blood feeding and pathogen transmission to vertebrate hosts. Developmental changes of salivary glands in 1st to 4th instars clearly express their structural and functional differences that enable females to engage successfully in disease transmission and hematophagy. Further study of polytene chromosomes are in progress to find out chromosomal inversions which are very common in *Aedes* species and are considered as an important factor contributing to speciation.

Abstract Reference: 20145
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 1

Antimicrobial resistance of Enterococci among dairy farmers

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Abstract Content

Farmers, particularly those engaged in animal husbandry, represent a high-risk group for antimicrobial resistance (AMR) due to their close and continuous interaction with animals. Hence, this study aims to investigate the resistance patterns of Enterococci among dairy farmers in Selangor, Malaysia. A cross-sectional study was conducted among dairy farmers of 10 randomly selected farms. Samples were collected from nasal swab, hand swab (pre- and post-washing) and oral swab. VITEK-2 system was used for bacterial identification and antimicrobial susceptibility testing. A total of 64 enterococcal isolates were recovered, with *Enterococcus faecalis* (n=36) being the predominant species, followed by *E.faecium* (n=11). Approximately 37% of workers displayed persistent Enterococcus isolation even with handwashing, while 32% showed post-washing isolation despite no pre-washing bacterial presence. About 69% of the isolates exhibited resistant to one or more tested antibiotics with the highest resistance were observed towards quinupristin/dalfopristin (52%), followed by tetracycline (34%). All isolates were susceptible to vancomycin. Multi-drug resistance was reported at 16% which was predominantly from nasal samples.The susceptibility of all isolates to vancomycin is reassuring since it remains a critical antibiotic in treating gram positive infections. Persistence of isolates despite handwashing and the predominance of multidrug resistance in nasal samples are concerning observations. These findings shed light into the importance of strengthening biosecurity practices among farmers. Hence, multifaceted interventions are imperative in addressing AMR effectively.

Abstract Reference: 20146
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 1

The aggregated protein dye YAT2150: an irresistible antimalarial drug with multiple targets in *Plasmodium falciparum* is also strongly active against *Leishmania infantum*

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Abstract Content

YAT2150 is a first-in-class, fast-acting antiplasmodial drug with an inexpensive, easy and rapid synthesis (two steps), and a long shelf life (months) at room temperature. YAT2150 binds protein aggregates and reduces the aggregation of *Plasmodium*'s proteome according to thioflavin T assays. YAT2150's presumed mode of action (inhibition of protein aggregation in the parasite) will likely target multiple proteins, hampering rapid resistance evolution by the pathogen. Moreover, YAT2150 belongs to a novel chemical family where no other antimalarial has been described to date. Resistant parasites to YAT2150 did not emerge *in vitro* after 60 days of incubation. Transcriptomic (RNAseq) and proteomic (Cellular Thermal Shift Assay) analyses identified several significantly up- and down-regulated transcripts and stabilized/destabilized proteins upon YAT2150 treatment of *Plasmodium falciparum* cultures. Although no particular drug targets could be singled out, several of the identified proteins have been found to be involved in key cellular processes like carbohydrate metabolism, parasite invasion and vesicular transport. We have synthesized several YAT2150 derivatives with IC_{50} <40 nM and selectivity index >1000. Remarkably, YAT2150 is also highly active against *P. falciparum* gametocytes (>10 times more potent than primaquine) and against *Leishmania infantum* (IC_{50} 500 nM). The results presented herein support an antiparasitic mechanism based on the disruption of multiple molecular targets by interfering with the formation of protein aggregates or condensates. Our results postulate YAT2150 as an irresistible antimalarial drug deserving attention in a likely future scenario of widespread resistance to current front-line antimalarial and antileishmanial treatments. Funding: PID2021-128325OB-I00, PDC2022-133085-I00, PID2020-118127RB-I00 (MICIU/AEI/10.13039/501100011033), 2021-SGR-00357, 2021-SGR-00635.

Abstract Reference: 20150
Mode of Presentation: Oral Presentation
Topic: Virology

Assessing mortality in COVID-19 adult patients receiving low molecular weight heparin (LMWH): Considerations for applying Padua Prediction Score (PPS) and IMPROVE Score

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Abstract Content

Both therapeutic and prophylactic doses of LMWH have been shown to reduce mortality rate in hospitalized COVID-19 patients, but their use is associated with an increased risk of bleeding. Careful use of LMWH requires emphasizing specific evaluated criteria. To evaluate PPS for predicting venous-thrombosis-(PPS_{VTE}), IMPROVE score for thrombosis-($IMPROVE_{VTE}$) and bleeding-($IMPROVE_{BRS}$), as well as their accuracy in predicting overall survival. This retrospective study was conducted at Rajavithi Hospital, 2021-2022, investigated the association between each score and outcomes. The study analyzed evidence of bleeding, thrombosis, and overall survival to assess the potential impact of LMWH on these outcomes. Of the 73 patients enrolled, 60.3% were female. The median age was 64.0 (IQR= 54.5-73.5 years). During hospitalization, 16 patients (21.9%) developed VTE, 41.1% with bleeding events, and 53.4% died. For predicting mortality rate, high $IMPROVE_{VTE}$ with an AUC of 0.762, high PPS_{VTE} (AUC=0.699) and high $IMPROVE_{BRS}$ (AUC=0.641). Combining thrombosis and bleeding risk score showed increased predictive power among patients with both high PPS_{VTE} and high $IMPROVE_{BRS}$ had an AUC= 0.725, which was higher than the combination of high $IMPROVE_{VTE}$ and high $IMPROVE_{BRS}$ (AUC=0.628). Combinations of high bleeding and thrombosis scores were significantly associated with worse overall survival compared to individuals with low risk ($p < 0.005$ for each combination). Among adult patients with COVID-19 infection and low underlying risk factors, those received LMWH showed a statistically significant association with lower mortality rates. This finding warrants further investigation to determine the causal relationship and potential clinical implications.

Abstract Reference: 20153
Mode of Presentation: Oral Presentation
Topic: Parasitology - Molecular Parasitology

Characteristic and genomic analysis of *Acanthamoeba endosymbionts* and the effects to the hosts

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Abstract Content

Acanthamoeba spp. are commonly free-living in the environments, however they can cause sight-threatening keratitis, or even the fatal granulomas amoebic encephalitis. Moreover, *Acanthamoeba* spp. can also serve as hosts for protection and residence of amoeba-resisting bacteria (ARB). Two *Acanthamoeba* VGH9 and VGH12 isolates harboring ARB9 and ARB12 respectively had been axenically isolated from two *Acanthamoeba* keratitis patients in Taiwan. Both *Acanthamoeba* isolate belong to genotype T4 based on 18S rDNA BLAST. The ARB9 and ARB12 belong to two different Genus Holosporaceae and Candidatus Paracaedibacteraceae, according the 16S rDNA BLAST, respectively, which cannot grow in Luria-Bertani broth and nutrient broth in vitro alone without *Acanthamoeba* served as hosts. Therefore, these two ARBs are considered to be endosymbionts. Nevertheless, after treating with rifampin or doxycycline, the *Acanthamoeba* TVGH12 with ARB12 changed cell morphology becoming rounding-up and detached which showing the cytopathic effects. Whereas, *Acanthamoeba* TVGH9 with ARB9 grew well without morphology change as same as *Acanthamoeba* ATCC30010 negative control. On the other hand, when *Acanthamoeba* spp. changed growth medium from PYG to RPMI for nutritional study, the cell membrane of *Acanthamoeba* TVGH9 with ARB9 began loss of cell integrity shown necrosis-like cell feature after 6 hours, whereas other *Acanthamoeba* spp. were growth well and remained cell integrity. Therefore, the distinct interaction features caused by different ARBs in free-living amoebas may provide some preliminary information for further studies of antibiotic effect, nutrition requirement, pathogen spreading and future amoebic disease control.

Abstract Reference: 20155
Mode of Presentation: Oral Presentation
Topic: Water & Food Borne Parasites

Insights and development of a multi-epitope vaccine against *Opisthorchis viverrini*: Integrating immunoproteomic and immunoinformatics analyses in host-pathogen dynamics

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Abstract Content

Opisthorchis viverrini is a liver fluke prevalent in the Great Mekong Subregion (GMS), particularly affecting northeast Thailand, where it leads to cholangiocarcinoma (CCA) development in humans. Current treatment modalities rely on praziquantel but faces challenges due to rapid reinfection and lifestyle factors. Vaccine development is crucial for disease control. We performed comparative immunoproteomic analysis using resistant and susceptible host models. The resistant host exhibited a strong immune response to the paramyosin (Pmy) protein. Immunoinformatics was employed to identify B-cell and T-cell epitopes within the myosin protein tail domain of Pmy protein, strategically positioned at the host-parasite interface. The resistant host showed a significant immune response to the Pmy protein during the developmental stages of *O. viverrini*. Computational modeling revealed potential B-cell and T-cell epitopes within the myosin protein tail domain and with acceptable results, indicating its suitability for vaccine design and *in vitro* and *in silico* analysis. The multi-epitope vaccine design showed promise in inducing protective humoral and cellular immune responses, suggesting its potential effectiveness against *O. viverrini* infection. Integration of immunoproteomics and immunoinformatics provides a powerful approach for vaccine development against *O. viverrini*. By identifying key surface proteins and epitopes, we can target crucial interactions between the parasite and the host. The multi-epitope vaccine design holds the potential to induce a proper immune response. The combination of immunoproteomics and immunoinformatics offers a promising strategy for accelerating vaccine development. This approach may have broader implications for addressing helminth diseases and overcoming challenges related to drug resistance.

Abstract Reference: 20158
Mode of Presentation: Oral Presentation
Topic: Parasitology and Microbiology

Cat scratch disease presenting with thrombocytopenic purpura and lymphadenopathy in a child

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Abstract Content

A 5-year-old girl was admitted with a week of fever and left neck swelling, followed by petechial rashes on her lower limbs on the day of admission. No other bleeding tendencies were noted. Her history included exposure to household cats and being scratched by a kitten two weeks prior to symptom onset. On arrival, her temperature was 37.6°C. Physical examination revealed a painless neck swelling with erythema and petechial rashes on both lower limbs, without visible cat scratch marks or organomegaly. Initial laboratory workup revealed isolated thrombocytopenia with a platelet count of 2 x 10^9/L and normal inflammatory markers. Histopathological examination of tissue obtained from an incision and drainage procedure revealed necrotizing granulomatous changes. Pus cultures and polymerase chain reaction (PCR) assays for mycobacterium tuberculosis and atypical mycobacteria were negative, along with negative interferon gamma releasing assay (IGRA) and normal chest radiograph. The diagnosis of cat scratch disease (CSD) was established through positive Bartonella henselae PCR from pus samples and significantly elevated Bartonella henselae serology titres (IgM and IgG at 1:512). The child was treated with azithromycin and trimethoprim-sulfamethoxazole, along with intravenous immunoglobulin (IVIG). This led to significant improvement in platelet counts and an uneventful recovery. This case underscores the complexity of diagnosing CSD, particularly when presenting with thrombocytopenic purpura without the typical signs of cat scratches and highlights the necessity of considering CSD in the differential diagnosis of unexplained lymphadenopathy and thrombocytopenia in children with a history of cat exposure.

Abstract Reference: 20159
Mode of Presentation: Oral Presentation
Topic: Water & Food Borne Parasites

Investigation of waterborne parasites in natural recreation rivers in Hulu Semenyih, Selangor, Malaysia

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Abstract Content

Water-borne diseases remain a major cause of morbidity and mortality worldwide. Waterborne parasites like parasitic protozoans can be contracted while washing, bathing, drinking contaminated water, eating food contaminated with parasites. This study was carried out to investigate presence of various waterborne parasites in a few natural recreations rivers in Hulu Semenyih, Selangor, Malaysia. The research method employs a comprehensive water sampling from six rivers near Hulu Sememyih. In each sampling sites, three water samplings were collected and the pH, temperature and Biochemical Oxygen Demand (BOD) was measured. Next, for parasite screening, the water samples were concentrated using a 0.22µm pump filter, followed by Trichrome stain and acid fast stain to detect parasites. The parasites were confirmed using a light microscope. The results indicated presence of *Blastocystis hominis* in four sampling sites and presence of *Cryptosporidium* spp in two sampling sites. The BOD reading was high at certain points where by abundance of parasites were high and Colilert test indicated positive. This study evaluates the correlation between water quality indicators and parasite prevalence, providing valuable insights into the factors contributing to parasite contamination in recreational waters. The findings of this investigation are crucial for enhancing public health awareness and implementing effective management strategies to mitigate the risks associated with waterborne parasites in recreational river areas. By understanding the prevalence and distribution of these parasites, policymakers and stakeholders can develop targeted interventions to safeguard the health and well-being of recreational water users in Hulu Semenyih and similar environments worldwide.

Abstract Reference: 20163
Mode of Presentation: Oral Presentation
Topic: Veterinary Health

Molecular prevalence of haemoparasites and their associations with Mafriwal cattle's age groups

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Abstract Content

Understanding the prevalence and impact of haemoparasitism, the tick-borne diseases in livestock is crucial for effective management and control strategies. This study aimed to investigate the molecular prevalence of haemoparasites and their relationship with the age group of Mafriwal cattle. Blood samples were obtained from calves (n=92), yearlings (n=95), lactating cows (n=90), and dry cows (n=94) for microscopic and molecular identification of haemoparasites. Prevalence rates were determined by the ratio of infected samples to the total observed samples. Odds ratio and Fisher's exact test were used to analyse the association between haemoparasitism and age groups of Mafriwal cattle. *Babesia bigemina* emerged as the most prevalent haemoparasite in cases of monospecies infection (20.8%), while co-infection of *Anaplasma marginale* and *B. bigemina* showed the highest molecular prevalence (36.4%). Significant associations of haemoparasitism were detected between calves and yearlings ($p<0.001$, Odds ratio = 21.340, 95% CI = 3.200 – 907.871), lactating cows ($p<0.01$, Odds ratio = 6.600, 95% CI = 1.808 – 36.516), and dry cows ($p<0.001$, Odds ratio = 10.457, 95% CI = 2.363 – 96.242). However, calves and yearlings were found to be 2 to 4 times more likely to be co-infected with multiple haemoparasite species compared to the older age groups. In conclusion, Mafriwal cattle exhibited susceptibility to haemoparasitism with advancing age, yet younger calves were more prone to co-infection with multiple haemoparasite species. These findings contribute to our understanding of susceptibility patterns of Mafriwal cattle to haemoparasitism across various stages of life, providing valuable insights for targeted intervention strategies.

Abstract Reference: 20166
Mode of Presentation: Oral Presentation
Topic: Veterinary Health

Isolation of blood parasites in zoo animals: A 30-year data

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Abstract Content

Blood parasites isolated from Zoo Negara Malaysia were reviewed during 1980–2023. The zoo animals were purchased or donated. Literature records of parasites from zoo animals in Malaysia were reviewed, resulting in a list of 59 species belonging to 14 different groups. Parasites obtained in this paper include blood nematodes (*Brugia pahangi*, *Cardiofilaria pavlovskyi*, *Dirofilaria immitis*, *D. repens*, *Loxodontofilaria asiatica*, *Setaria cervi* and *Thelezia sp.*) and blood protozoa (*Babesia bovis*, *Plasmodium knowlesi*, *Trypanosoma evansi* and *Lankesterella sp*.). The blood parasites were incidental findings. During the routine medical examination of the zoo animals, no treatments were done for the positive cases, only preventive medicines were adopted for certain species of animals such as carnivores and pinnepedias. Ivermectin was administered monthly. In a Clouded Leopard from the Johor Zoo, we isolated double infection of blood nematodes and was not treated. We isolated *Loxodontofilaria asiatica* in a Malayan Elephant and was not treated. Monthly blood smear examination revealed the decreased microfilaria count. Eventually the population of *Loxodontofilaria asiatica* completely disappeared, indicating no sufficient sex ratio of the microfilaria to multiply. We isolated *Trypanosoma evansi* from the Sumateran Rhinoceros at Sungai Dusun, it was too late to save them. Prevention of the mosquitos were undertaken. The breeding sites were identified and the vectors eliminated. The surrounding spaces of the enclosures were cleaned periodically to avoid mosquito breeding. The zoo was concerned about the welfare of the visitors to avoid mosquito bites.

Abstract Reference: 20171
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 1

The mode of action study of DHLC, an ultrapotent new antimalarial

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Abstract Content

Malaria is a mosquito-borne disease caused by five *Plasmodium* spp. in humans that has a significant health impact in the tropics with more than 200 million cases annually, including half-million deaths. More than 90% of malaria cases were inflicted by *Plasmodium falciparum* (*Pf*) infections. There is a continuous need to identify new antimalarial agents, especially with a novel mechanism of action as *Pf* has developed full or partial resistance toward all antimalarial compounds, including chloroquine (CQ) and artemisinin (ART). We previously reported the identification of a new antimalarial, Dihydrolucilactaene (DHLC) from *Fusarium* sp. 97-94 that is highly active against *Pf* 3D7 (wild-type) and *Pf* K1 (CQ resistant) strains. The present study aimed to understand the mode of action of DHLC. The erythrocytic stage-specific profile determination revealed that the *Pf* trophozoites stage was the most sensitive to DHLC, followed by ring and schizont stages, which is different from the stage-specific profile of ART and CQ, indicating distinctive modes of action. Subsequently, DHLC-resistant *Pf* strains were generated via continuous exposure to sub-lethal DHLC concentration and whole genome sequencing was performed to identify DHLC plausible molecular target(s). Mutation of a gene encoding an unknown essential conserved *Pf* membrane protein was detected in the genome of DHLC-resistant strains generated from two independent attempts, suggesting this protein is the possible target of DHLC. This protein was never reported as the target of any antimalarials, hence, we put forward DHLC as a prime drug lead for future antimalarial drug development.

Abstract Reference: 20173
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 1

Geographical landscape of antimicrobial resistance in non-typhoidal salmonella

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Abstract Content

Nontyphoidal *Salmonella* is a leading bacterial cause of gastroenteritis in humans and increasing drug-resistant strains have worsened the effectiveness of antibiotic treatments. The emergence and propagation of antimicrobial resistance (AMR) in *Salmonella* are strain-specific and vary by source and geographical region. Genomic analysis, such as whole genome sequencing (WGS), is a robust platform to characterize the bacteria's genome in terms of data on serotypes, antibiotic resistance genes, virulence factors, plasmids, and single nucleotide polymorphisms. In this study, we aim to investigate the geographical spread of AMR genes and the diversity of nontyphoidal *Salmonella* isolates between humans, animals, and the environment. The WGS data on *Salmonella* from selected countries were downloaded from the National Center for Biotechnology Information (NCBI) and underwent bioinformatic analysis. Our findings revealed that AMR gene transmission in *Salmonella* is geographically dependent and a high number of multidrug resistances were found. This study provides useful knowledge to strengthen the prevention strategies to limit AMR contamination within/between humans, animals, and the environment towards the One Health concept.

Abstract Reference: 20174
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 1

Plasmodium falciparum genomic intelligence in Mozambique for decision making

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Abstract Content

Genomics is driving some of the most ground-breaking surveillance approaches. To reduce the gap in genomic surveillance application for public health action in Mozambique, we operationalized a country-wide sampling strategy and an amplicon sequencing panel targeting 165 *P. falciparum* microhaplotypes and 15 drug resistance genes. In 2023, we estimated a very low prevalence (0.15%) of infections carrying *hrp2/3* deletions (that code for the antigens detected by most rapid diagnostic tests [RDTs] used in Africa), absence of *pfk13* validated/candidate markers of artemisinin partial resistance, and no increased *pfpm2* copy numbers (associated with piperaquine resistance). However, a high prevalence (92%) of *pfdhfr/pfdhps* quintuple mutants (associated with therapeutic resistance to sulphadoxine-pyrimethamine, used for chemoprevention) was observed; <1% A581G *pfdhps* mutations were detected. A spatial genetic structure across the country was associated with larger fractions of closely related infections within than between regions. A probabilistic approach that combines travel duration and genetic relatedness identified 24% of the malaria cases in Magude and Matutuine pre-elimination districts (Maputo Province) as imported, mostly from the southern Inhambane Province. Finally, declines of malaria transmission following elimination activities in Magude were accompanied by genetic diversity reductions. These results support continued use of HRP2-based RDTs and artemisinin-based combination therapies, call for close monitoring of chemopreventive drug efficacy, identify Inhambane as an important transmission source for pre-elimination southern areas, and support genetic diversity as a metric for intervention impact assessment. Overall, data demonstrate how equitable deployment and genomic surveillance use can achieve an immense potential benefit to human health.

Abstract Reference: 20181
Mode of Presentation: Oral Presentation
Topic: Veterinary Health

An autochthonous case of canine cutaneous leishmaniasis in Northern Thailand

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Abstract Content

In the last decade, the *occurrences of* autochthonous human leishmaniasis cases, caused by *Leishmania (Mundinia) martiniquensis*, have been increasing continuously in Northern Thailand. *The precise identity of domesticated animal reservoirs remains uncertain; however, only the black rat (Rattus rattus) has been previously identified as the natural reservoir*. Here, we describe a novel case report of cutaneous leishmaniasis that appears for the first time in a dog residing in Chiang Mai Province, Northern Thailand. A nodule with 0.5 cm in diameter was presented on the right internal ear pinna, in which the amastigotes were detected by skin biopsy, suggesting the *Leishmania* parasites. *Leishmania isolation and cultivation were successfully harvested in Grace's insect medium supplemented with 30% fetal bovine serum.* The PCR and sequencing of the internal transcribed spacer 1 (ITS1) region of small subunit ribosomal RNA gene, minicircle kinetoplast DNA gene, and *cytochrome* b gene (CYTB), classified the respective isolate as *L. martiniquensis.* Based on this finding, we performed the monthly blood collection for health check and parasitism. Parasitemia was detected only once following the case presentation, exhibiting no significant systemic clinical symptoms, as confirmed by blood tests assessing liver and kidney function, as well as abdominal radiographic and ultrasonographic examinations. In conclusion, we posit that dogs could potentially serve as reservoirs, thereby potentially contributing to the transmission of leishmaniasis in Thailand. Epidemiological studies will assess *L. martiniquensis* prevalence and risk factors in Thai domestic animals near the canine index case and other areas affected by human leishmania outbreaks.

Abstract Reference: 20185
Mode of Presentation: Oral Presentation
Topic: One Health 2

Antimalarial prescribing practice in Eastern Indonesia: A prescription analysis

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Abstract Content

Artemisinin-based Combination Therapy (ACTs) has been introduced since 2013 for the treatment of uncomplicated malaria in Indonesia. However, the quality of prescriptions of ACT in public health facilities has never been evaluated. This study aimed to determine the quality of prescription for uncomplicated malaria in primary health centers and hospitals in two malaria highly endemic districts in Eastern Indonesia. Retrospective review of prescriptions and medical records was conducted between June and December 2017 to assess whether antimalarial drug prescriptions were in-line with the national guideline. Descriptive statistics were performed using SPSS 23.0. A total of 836 prescriptions for laboratory-confirmed malaria were reviewed. ACTs were prescribed in 92.2% prescriptions. Of all, 89.2% used correct combination of ACTs. ACTs were prescribed in 90.5% of malaria falciparum cases, 88.6% in malaria vivax, and 85% in mixed malaria. Correct dosage was found in 35.8% of ACTs prescription for malaria falciparum, 59.3% of malaria vivax, and 47.1% of mixed malaria. Incorrect dosage were mostly over-dosage, i.e. 66.5% in malaria falciparum, 59.1% in malaria vivax and 37.1% in mixed malaria. Under-dosage was found in 30.7% malaria falciparum, 37.1% in malaria vivax and 88.9% in mixed malaria. Incorrect ACTs prescriptions in primary health centers and hospitals are still prevalent, especially overdosage in ACTs prescriptions for malaria falciparum and vivax, which might be due to overestimation of the severity of the infection, particularly as the area is malaria endemic. Continuous medical education and training are essential to ensure adherence to guidelines.

Abstract Reference: 20186
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 1

Mosquito ferritin and its crucial role in iron metabolism and *Plasmodium* survival

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Abstract Content

Vector is very crucial for disease propagation as plasmodium spends the maximum time of its life cycle inside the vector. Vector survival and disease progression are largely dependent on blood feeding and iron metabolism. Ferritin is a ubiquitous cage-like protein, acting as a primary iron storage for almost all organisms. While its function remains almost similar across different species, its structural complexity varies widely as we go down the evolutionary scale. We found that ferritin expression is highly dependent (up-regulation) on mosquito diet (blood-meal ingestion), we also discovered that ferritin is transporting iron to ovaries and playing a crucial role in egg development. As ferritin plays a pivotal role in mosquito iron metabolism, we targeted ferritin at different stages of mosquito life-cycle by using ferritin selective and broad iron chelators, and the larvicidal effect was observed at even 15.6 ppm LD50.When the same iron chelators fed to adult female post-blood meals, the no. of oocytes decreased significantly. In summary all our data suggests that ferritin plays a crucial role in mosquito iron metabolism, and it could be used as a potential insecticidal target. The other objective of this study is to explore how plasmodium sequesters iron from the mosquito for its survival, and in my presentation, I will showcase all our recent findings related to mosquito iron metabolism and its crosstalk to plasmodium.

Abstract Reference: 20189
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 1

Exploring harmala alkaloids as novel antimalarial agents against *Plasmodium falciparum* through bioinformatics approaches

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Abstract Content

Caused by the *Plasmodium* parasite, malaria remains a significant global health challenge, with *Plasmodium falciparum* accounting for approximately 50% of cases and posing a considerable threat. Despite strides in control measures, malaria continues to cause an estimated one million deaths annually. The intricate lifecycle of *P. falciparum*, involving both vertebrate hosts and *Anopheles* mosquitoes, complicates eradication efforts. Resistance of the parasite to existing antimalarial drugs, coupled with medication toxicity, necessitates innovative therapeutic approaches. Recent research has revealed that an alkaloid, harmine, produced by an endophytic gut bacterium of *Anopheles* mosquitoes, can impede the transmission of the malarial parasite to humans by inhibiting a crucial life stage. This study investigates harmala alkaloids, sourced from plants and bacteria such as *Peganum harmala*, as potential alternatives to conventional antimalarial drugs. Notably, harmine and harmaline have shown promising antimalarial activity by inhibiting the essential enzyme protein kinase 4 (PK4), vital for the parasite's survival. These compounds exhibit lower toxicity, effectively inhibiting both the blood stage growth and transmission of the parasite. Employing *in silico* methodologies, including ADME analysis, molecular docking, MD simulation, and toxicity analysis, this study identifies harmala alkaloids as potential inhibitors against crucial *P. falciparum* proteins. Targeting proteins essential for the parasite's survival, paralleling established drugs like pfCRT protein, establishes a basis for developing effective antimalarial treatments. The comprehensive screening of harmala alkaloid molecules opens avenues for the pharmaceutical industry to tackle challenges related to drug resistance and toxicity, offering a promising route for biorational management of malaria.

Abstract Reference: 20195
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 1

Development of a system evaluating expression of an exogenously introduced SICA protein on infected red blood cell surface by *Plasmodium knowlesi*

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Abstract Content

Malaria cases caused by *Plasmodium knowlesi* have been increasingly reported in Southeast Asia. *P. knowlesi* infection can be fatal. Hence, it is necessary and important to understand the molecular basis of its virulence and pathogenicity to develop better intervention strategies. A post-mortem examination of human *knowlesi* malaria cases has shown sequestration of *P. knowlesi*-infected red blood cells (Pk-iRBCs) in the blood vessels of certain organs. This phenomenon, which has been proposed to be associated with disease severity, is likely mediated by the cytoadhesion of iRBCs to vascular endothelial cells. Recently, we discovered one molecule from the Schizont Infected Cell Agglutination (SICA) protein family, which mediated the cytoadhesion of *P. knowlesi*-iRBCs to human umbilical vein endothelial cells (HUVECs), and we named it SICA-HUVEC. To evaluate if the exogenously introduced SICA-HUVEC is exposed on the iRBCs, we added an HA-tag at the N-terminal of SICA-HUVEC and a Myc-tag at its C-terminal (termed HA-SICA-HUVEC-Myc). HA-SICA-HUVEC-Myc on the iRBC surface was detected with anti-HA antibodies and retained the binding activity to HUVECs. The established system is useful to further characterize SICA-HUVEC and to screen chemicals with the aim of inhibiting the expression of parasite-derived molecules on the iRBC surface, which reduces the binding activity of the iRBCs and thereby the parasite virulence. We present the results of one Proof of Principle experiment.

Abstract Reference: 20208
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 1

Influence of TLR Polymorphism on the dynamic changes in the levels of circulating cytokines in *Plasmodium vivax* clinical isolates: Indicator for vaccine designing

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Abstract Content

Malaria is categorized into symptomatic or asymptomatic on the basis of clinical manifestations and symptomatic malaria is further divided into complicated and uncomplicated malaria. Earlier studies on influence of TLR polymorphisms on the levels of circulating cytokines are rare. So, present study, elucidate association between innate and adaptive immune responses and their role in severity of disease in *P.vivax* isolates. 65 *P.vivax* clinical isolates and 20 Healthy controls were collected and DNA was extracted. Polymorphisms in TLR1 (I602S), TLR6 (S249P) and two promoter regions of TLR9 T- (1486)-C and T-(1237)-C were detected through PCR-RFLP. Levels of circulating cytokines (IFN-Ɣ, TNF-α, IL-6 and IL-10) were measured by using ELISA from serum samples. Association between TLR genotype and alterations in levels of cytokines was detected by unpaired t-test and $p<0.01$ was considered statistically significant. Among the studied TLRs genetic variation for TLR 1 (I602S), TLR6 (S249P) and promoter region of TLR9 T-(1237)-C were >10% while for promoter region of TLR 9 T-(1486)-C variation was present in 27.7% of complicated and 36.5% of uncomplicated cases.Significant associations for TNF-α and IL-6 were absent for TLR 9 T-(1486)-T variants While in case of IL-10 and IFN-γ significant decline was observed in genotype TLR 9 1486T . Influence of SNPs in promoter region of TLR9 T-(1486)-C on the IL-10 and IFN-γ production indicates association of adaptive and innate immune response and their role in disease severity. It would be used as an indicator for vaccine designing as well as designing tools for control and elimination of malaria in future.

Abstract Reference: 20212
Mode of Presentation: Oral Presentation
Topic: Parasitology - Molecular Parasitology

Benzimidazole resistance and mutations in the hookworm *β-tubulin* isotype 1 gene

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Abstract Content

Benzimidazole resistance among soil-transmitted helminths is an emerging concern that can undermine pharmacological interventions like Mass Drug Administration (MDA) programs. Single Nucleotide Polymorphisms (SNPs) in the β-tubulin isotype 1 gene that alter the protein's amino acid constitution confer resistance. This research aimed to determine the resistance-associated SNPs in different hookworm species and assess their effects on β-tubulin-benzimidazole interaction *in silico.* A systematic review was conducted to synthesize peer-reviewed evidence on the occurrence of resistance-associated mutations and document their geographical distribution. β-tubulin isotype 1 proteins of *Ancylostoma ceylanicum, A. caninum, A. duodenale,* and *Necator americanus* were modeled to contain the reported SNPs and were docked with Albendazole, Mebendazole, Oxfendazole, and Fenbendazole. Binding affinities and docking positions were evaluated. Seven benzimidazole resistance-associated SNPs were reported among several hookworm species: Q134H, F167Y, E198A, E198K, E198V, F200Y, and F200L. SNPs have occurred in the United States, Canada, Brazil, Haiti, Australia, New Zealand, Kenya, Ghana, Mozambique, and Tanzania. No reports were found in Asia. The *in silico* docking study revealed that the SNPs cause alterations in the β-tubulin-benzimidazole binding interactions. F200L and E198K mutations in hookworm β-tubulins were shown to significantly weaken the binding affinities and change the binding positions of the benzimidazole drug ligands. Mutations in the hookworm β-tubulin isotype 1 gene due to resistance-related SNPs alter benzimidazole ligands' binding efficiency potentially causing resistance. The occurrence of these SNPs in Asia and their contributions to benzimidazole resistance should be explored further.

Abstract Reference: 20219
Mode of Presentation: Oral Presentation
Topic: Entomology - Vector and Vector-Borne Diseases

From lemongrass to ICU: The unsuspecting threat of a lethal chigger bite

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Abstract Content

Scrub typhus is endemic in Malaysia; however, there are challenges in recognizing and reporting the illness. We report a fatal case of laboratory-confirmed scrub typhus. Subject is a 33-year-old lady who presented with fever for one week, associated with vomiting, loose stool, and chest discomfort. She had history of a visit to a health clinic and was treated with antibiotics but symptoms did not abate. She was a worker in lemongrass farm with possible exposure to rodents. She arrived at the emergency department critically ill, was admitted to ICU and electively intubated due to respiratory failure. Blood investigations show a positive dengue serology IgG and IgM. Full blood count showed leucocytosis with thrombocytopenia. C-reactive protein was elevated 234 mg/L and blood film for malaria parasite was negative. Subsequently, leptospirosis serology IgM was positive. Subject was started on benzylpenicillin for treatment of leptospirosis. Infectious disease consultation was requested and upon assessment, there was presence of eschar near subject’s inguinal region. Other systemic examinations were unremarkable. Scrub typhus treatment including intravenous azithromycin and doxycycline were initiated. After two days in ICU subject deteriorated and passed on. Rickettsial PCR that was sent from ICU confirmed scrub typhus infection. Scrub typhus is an important differential diagnosis of acute febrile illness in Malaysia and clinicians should have high suspicion in investigating for this infection especially in cases of undifferentiated fever and risk of occupation exposure to rodents, that can harbour lethal chiggers – bites of which can prove lethal.

Abstract Reference: 20221
Mode of Presentation: Oral Presentation
Topic: Water & Food Borne Parasites

Unveiling the pathogenesis of *Opisthorchis viverrini* -Associated kidney injury: Insights from *in vivo* and *in vitro* investigations

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Abstract Content

Opisthorchiasis, caused by *Opisthorchis viverrini* (OV), is prevalent in the lower Mekong basin, where chronic kidney disease (CKD) rates are also high. Studies indicate that a third of chronic opisthorchiasis cases present CKD symptoms, yet the precise impact and mechanisms of OV infection on the kidney remain inadequately explored. Therefore, our study aims to elucidate the novel mechanisms of OV-induced kidney injury, both *in vivo* and *in vitro*. The study comprised two parts: an ultrastructural examination of the kidneys of chronically infected hamsters and a non-contact co-culture experiment involving *O. viverrini* and renal tubular epithelium HK-2 cells. Our findings revealed that chronic OV infection in hamsters was associated with podocyte foot process effacement and loss of glomerular slit diaphragm integrity. Co-culture experiments with HK-2 cells demonstrated reduced cell viability when exposed to 10 OV adult worms, with a slight impact observed at lower worm numbers. Flow cytometry analysis indicated increased cell apoptosis induced by excretory proteins from 10 OV adult worms, with ultrastructural analysis revealing apoptotic and necrotic features in HK-2 cells, including chromatin clumping and apoptotic body formation, alongside observed reactive oxygen species (ROS) generation. These findings suggest that *O. viverrini* adult worms induce ROS production and oxidative stress in multiple types of renal cells, leading to cellular injury and death in podocytes and renal tubular cells. Further clinical investigations into *O. viverrini* infection and kidney complications are warranted.

Abstract Reference: 20228
Mode of Presentation: Oral Presentation
Topic: One Health 1

Oral myiasis caused by *Chrysomya bezziana* (Diptera: Calliphoridae) infestation in a quadriplegic patient at Hospital Canselor Tuanku Muhriz

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Abstract Content

Myiasis, the infestation of human tissues and organs by fly larvae, is a well-documented condition primarily observed in the skin, and affects both animals and individuals residing in developed and developing regions. However, its occurrence within the oral cavity, termed oral myiasis, remains comparatively rare. This case study discusses an uncommon manifestation of oral myiasis involving palatal mucosal tissue. The patient, a 35-year-old quadriplegic Malay male, presented at Hospital Canselor Tuanku Muhriz with extensive oral myiasis affecting the palatal region, characterized by multiple ulcerations. Third-instar fly larvae were detected within the ulcers. A total of 83 larvae were removed through bedside procedures and oral hygiene maintenance conducted twice daily over a five-day period. Subsequent microscopic identification confirmed that the larvae were *Chrysomya bezziana*, an obligatory parasite. Investigation indicated various predisposing factors contributing to the infestation, including malnutrition, inadequate oral hygiene, neurological disability, and persistent mouth opening due to immobility. Prompt diagnosis and a comprehensive interdisciplinary approach involving dental and medical practitioners were imperative for successful management.

Abstract Reference: 20232
Mode of Presentation: Oral Presentation
Topic: One Health 2

Plasmodium cynomolgi and *Plasmodium inui*: Potential new challenges in combating zoonotic simian malaria

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Abstract Content

The elimination of malaria in Southeast Asia has become more challenging due to rising knowlesi malaria cases. Besides, naturally occurring human infections with *Plasmodium cynomolgi* and *Plasmodium inui* adds another dimension of complexity in malaria elimination in this region. Unfortunately, data on vectors which are responsible for transmitting this zoonotic disease is very limited. Thus, this study aims to investigate the entomological parameters of the simian malaria vectors and to examine the genetic diversity and evolutionary pattern of their simian *Plasmodium*. All the captured *Anopheles* mosquitoes were dissected and mosquitoes which were positive with simian *Plasmodium* were subjected to nested PCR targeting 18S SSU rRNA gene to examine the genetic diversity and evolutionary pattern of their simian *Plasmodium*. Our study revealed that the *Anopheles* Leucosphyrus Group mosquitoes are highly competent vectors, as evidenced by their high parity rate, survival and sporozoite infections in these mosquitoes. Besides, haplotype analysis on *P. cynomolgi* and *P. inui* from this study had shown close relationship between simian *Plasmodium* from the *Anopheles* mosquitoes with its vertebrate hosts. Furthermore, population genetic analysis showed significant negative values suggesting both *Plasmodium* species are undergoing population expansion. In conclusion, *P. cynomolgi* and *P. inui* are highly prevalent in mosquitoes and they demonstrated close genetic relationship with their vertebrate hosts, suggesting ongoing transmission between the vectors, macaques, and humans. With constant microevolutionary processes, there are risks for both the simian *Plasmodium* to emerge and spread as a major public health problem, following the trend of *P. knowlesi* in Southeast Asia.

Abstract Reference: 20244
Mode of Presentation: Oral Presentation
Topic: Virology

Immunity bypassed: Emergence of equine-like G3 and porcine-like G9 rotavirus strains in Sarawak with the potential to escape vaccine-triggered immunity

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Abstract Content

Rotavirus is the leading cause of paediatric acute gastroenteritis globally, especially in children 5 years old and below. WHO recommends the inclusion of rotavirus vaccines in national immunisation programs, whereas rotavirus vaccination is implemented based on voluntary policy in Malaysia. Mutations derived from neutralising epitopes residing on the outer capsid and spike proteins are deemed to cause rotavirus to escape immunity. Characteristics of the current rotavirus strains in Malaysia remain unknown, leading to a lack of understanding of rotavirus epidemiology and vaccine compatibility. This study sought to determine the genetic relatedness of Sarawak rotaviruses with global strains and to determine the antigenic coverage and epitope compatibility of Rotarix and RotaTeq vaccines with the Sarawak rotaviruses via in silico analysis. A total of 89 stool samples were collected from pediatric patients (≤5 years old) with acute gastroenteritis at private hospitals in Kuching, Sarawak. Rotavirus was detected using reverse transcription-polymerase chain reaction. Positive amplicons were analysed using nucleotide sequencing before phylogenetic analyses and assessment of epitope compatibility. Genotyping revealed G1P[8] (1/13; 7.7%), G3P[8] (3/13; 23%), G9P[4] (1/13; 7.7%), and G9P[8] (3/13; 23%), G9P[X] (1/13; 7.7%), GXP[4] (1/13; 7.7%), and GXP[8] (3/13; 23%) in samples. All wild-type Sarawak rotavirus strains, except G1, showed variations in their phylogenetic and antigenic epitope characteristics. Based on this in silico analysis, it is concluded that rotavirus vaccines may not confer protection against acute rotavirus gastroenteritis due to significant epitope mutations, suggesting the vaccines to be updated to include rare and emerging genotypes.

Abstract Reference: 20249
Mode of Presentation: Oral Presentation
Topic: One Health – General 1

Investigating the role of ectoparasites on rats as potential vectors for disease transmission to humans: A cross-sectional survey in Semarang City, Indonesia

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Abstract Content

Rats and ectoparasites can be vectors and reservoirs of human diseases. Information on rat species and ectoparasite infestation in rats is crucial for control measures and prevention against potential zoonotic diseases. This study aims to describe the presence of rats and ectoparasites in densely populated settlements and markets in Semarang City. A total of 100 traps were set up over 3 days in traditional markets and settlements around the market. Rats were captured using bait such as pindang, roasted coconut with a live trap as the capture tool. Variables studied include trap success, rat species diversity, ectoparasite density, and ectoparasite species. Data analysis was performed descriptively in the form of frequency distribution tables. Trap success in densely populated settlements and markets in Semarang City was 11.94%. In traditional market areas and densely populated settlements in Semarang City, R. norvegicus (89.8%; 70.1% respectively) and R. tanezumi (9.443; 29.8%) rats were found. Ectoparasites found in densely populated settlements and markets in Semarang City are Xenopsylla cheopis fleas and mites of the Echinolaelaps echidninus and Laelaps nuttalli species. There were 84 fleas (41.38%). The general flea index was 0.41 and the specific flea index was 1.67. The density of rats along with ectoparasites indicates a high risk potential in transmission based on rats and ectoparasites.

Abstract Reference: 20250
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 1

The interactions of malarial cysteine proteases, falcipains, with their natural substrate hemoglobin and endogenous inhibitor falstatin

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Abstract Content

Malarial proteases constitute an important class of enzymes essential for various events in the parasite life cycle. Cysteine proteases, especially falcipains, are primarily involved in the degradation of hemoglobin, the principal source of nutrients for blood stage plasmodium parasites. Our study, through a combination of bioinformatic and mutagenesis analysis, has identified a single amino acid within both falcipains, falcipain-2 (FP2) and falcipain-3 (FP3), crucial for mediating interactions with hemoglobin. This approach is beneficial as the identified residue lies at an exosite protruding away from the active site, thus would likely be less prone to drug pressure. Further, we characterized the interactions between falcipains and their natural macromolecular inhibitor, falstatin. Falstatin, an inhibitor of cysteine proteases (ICP), is unique as compared to its homologs as only a single loop (termed BC loop) is sufficient for the inhibition of falcipains. Our current study suggests that falstatin interacts with FP2 in a multimeric form with ten units of falstatin interacting with ten units of FP2 in a 1:1 stoichiometry. Furthermore, bioinformatic analysis of the falstatin-alone multimeric complex suggested a symmetric decameric structure, an observation also supported by preliminary biophysical analysis. Putative residue interactions required for falstatin multimerization have been identified, and are currently being explored via mutagenesis experiments. Together, our study characterized novel exosite interactions of FP2 with hemoglobin, which could have chemotherapeutic applications, and with the ICP falstatin, to further our understanding of the protease-inhibitor interactions.

Abstract Reference: 20251
Mode of Presentation: Oral Presentation
Topic: One Health – General 1

Mapping the impact of climate variability on leptospirosis transmission in Semarang City: A spatio-temporal analysis (2019-2023)

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Abstract Content

Amidst the increasing global climate change, Semarang City faces new challenges in controlling leptospirosis, which is vulnerable to changes in rainfall patterns and temperature. Limited knowledge of how climate change affects the spatio-temporal patterns of leptospirosis transmission necessitates comprehensive analysis from 2019 to 2023 to identify the relationship between climate variability and case distribution. One hundred ninety-four cases (2019-2023) in Semarang City were mapped using GPS and ArcView and then interpreted with spatial analysis. R program was employed to analyze temporal data with a 1-3 month time lag. The majority of cases were male (69.6%). Spatial analysis indicated that most cases were in low-lying areas <47 masl (85.1%), with poor wastewater disposal facilities (81.4%), densely populated housing (72.2%), high rainfall >220 mm/month, presence of rats around the house (100%), flood profile (85.05%), and poor waste conditions (67.5%). Minority cases were found in tidal water profile areas (22.2%) and the presence of vegetation (10.8%). Over the past five years, there has been a significant relationship and symmetry between temporal patterns and cases, wherein an increase in rainfall at lag 2, humidity at lag 1, and floods at lag 1 led to an increase in leptospirosis cases. Cross-sectoral cooperation is vital in concluding integrated prevention and control measures, including improving sanitation infrastructure, environmental monitoring, and rodent population management, to reduce the risk of leptospirosis transmission influenced by climate change.

Keywords: Leptospirosis, Spatio-Temporal, climate change,

Abstract Reference: 20274
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 1

Estimating the relative importance of imported malaria in driving local transmission in Bhutan using Hawkes Processes

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Abstract Content

Bhutan is aiming for malaria elimination certification in 2025. This study aimed to understand how importation drives local transmission in Bhutan. Information on geo-located individual-level laboratory-confirmed malaria cases between 2016 and 2020 was obtained from the Bhutan Vector-borne Disease Control Program. Records included the date of diagnosis and treatment, type of cases classified as indigenous or imported, and malaria species. Hawkes Processes were used to study the role of imported malaria in local transmission in Bhutan. We imposed 15 days delay for a mosquito to become infectious in the model. There were 285 cases during the study period and 58.6% (159) were imported malaria. 71.1% (113) of these imported cases were *Plasmodium vivax* and 73.6% (117) were from India. The model suggested that a person remains infectious for 8 days for *Plasmodium falciparum* malaria but over 19 days for *Plasmodium vivax.* The background intensity from imported malaria cases was much greater for *P. vivax* cases (maximum 0.17) resulting in more importations than *P. falciparum* cases (maximum 0.06). However, model fitting suggested that local *P. falciparum* transmission was mainly driven by importations but additional factors such as relapse played a role for *P. vivax*. Imported malaria cases are key drivers of transmission within Bhutan, with most cases since 2016 being *P. vivax*. Control programmes should be devised to target interventions towards the *P. vivax* strain and test those who are more likely to bring in imported malaria cases or acquire it from those who travel.

Abstract Reference: 20279
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 1

The role of immune-inflammatory markers in children with complicated and uncomplicated malaria in Enugu, Nigeria

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Abstract Content

There is currently insufficient data regarding immune parameters and relationship with severity of malaria infection in Enugu, Nigeria where the disease and its management are extremely costly. This study was conducted to determine the relationship between malaria severity and some immune-inflammatory markers among malaria-infected children in Nigeria. The study adopted a case control design. Eligible children were categorized into 3 groups — complicated, uncomplicated and healthy children. Pro-inflammatory cytokines –interferon-gamma (INF-γ) and tumor necrosis factor-alpha (TNF-α); and anti-inflammatory cytokine — interleukin-10 (IL-10) were assayed using ELISA technique, while immune cell ratios — neutrophil lymphocyte ratio (NLR) and monocyte lymphocyte ratio (MLR) were calculated from full blood count results. The overall mean age of the participants was 7.3 ±3.4 (range: 6 months - 12 years) and the male-female ratio was 1:1. There was no significant difference between the ages of the three groups ($P = 0.44$). The Mean levels of INF-γ, TNF-α, and NLR were higher in complicated than uncomplicated malaria ($p < 0.001$); and higher in uncomplicated malaria than healthy children ($p < 0.001$). There was a positive correlation between NLR and INF-γ ($r = 0.815$; $p = 0.003$), as well as NLR and INF-γ ($r = 0.745$; $p = 0.002$). Complicated malaria is associated with higher levels of certain immune-inflammatory biomarkers. NLR correlates positively with pro-inflammatory cytokines and could be used as a cost-effective approach of assessing malaria severity and prognosis in settings where proinflammatory biomarkers are expensive or not readily accessible.

Abstract Reference: 20280
Mode of Presentation: Oral Presentation
Topic: Parasitology

Countrywide implementation of G6PD testing for *Plasmodium vivax* malaria treatment in Cambodia: Challenges and potential solutions

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Abstract Content

Plasmodium vivax is the predominant cause of malaria across the Greater Mekong Subregion challenging malaria elimination. *P. vivax* recurrences can arise from reactivation of the parasite's dormant liver stage (hypnozoites) weeks to months after an initial infection. The only drugs that kill hypnozoites can cause severe hemolysis in Glucose-6-Phosphate Dehydrogenase (G6PD) deficient individuals. The STANDARD G6PD test (Biosensor) is a new point-of-care diagnostic to identify patients at risk. To explore the countrywide implementation of the Biosensor in Cambodia, a mixed methods study was conducted in three high-burden provinces. Quantitative data were gathered from routine surveillance records (January 2021-March 2023). Interviews and focus group discussions were conducted among 142 participants, followed by thematic analysis. The main challenge to implementing G6PD testing was referral to a health center following malaria diagnosis by community health workers (CHW); only 49.2% (437/888) of patients reached health centers for G6PD testing. Influencing factors included road conditions and long distances to health centers compounded by the cost of seeking further care and patients' perceptions of vivax malaria and its treatment. Although the use of the Biosensor by CHWs could overcome these challenges, there is hesitancy among stakeholders given the resources required, concerns about CHWs' capacity, and risk of hemolysis associated with treatment in the case of misdiagnosis. Our findings suggest that bringing treatment closer to patients, through CHWs using the Biosensor, would improve access to radical cure for vivax malaria, but the successful implementation of the device at community level will require strategies to address stakeholders' concerns.

Abstract Reference: 20294
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 1

Efficacy of *Curcuma amada* against a model cestode parasite of poultry: Cytological and ultrastructural studies

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Abstract Content

Helminthiasis is an acute problem amongst small ruminants and poultry birds globally. Anthelmintic drug resistance has triggered research on alternative anthelmintic strategies involving phytochemicals which has revealed a number of prospective plants as curatives. The present study focuses on the anthelmintic activity of Ethanolic crude extract (ECE) of Aamada (*Curcuma amada*) rhizome and compares its effectiveness with Praziquantel (PZQ), a broad-spectrum drug. The live worms were selected and incubated at 39°C in different petri-plates with media containing different dosages of ethanolic crude extract (ECE), in PBS with 0.1% DMSO. The incapacitated model parasites, following treatment with the most efficacious dose of the ECE and PZQ were processed for further studies. Observations using scanning electron microscope (SEM) and transmission electron microscope (TEM) reveal structural and cellular alterations in the treated parasites compared to control group. These alterations include breakage in the proglottid wall, distortion in scolex and neck and damage to organelles. Furthermore, the study explores the effects of ECE on the cellular level by preparing single cell suspensions. Analysis includes cell viability, DNA damage and mitochondrial condition assessment. Significant result was obtained in the treated worms compared to the control. The results of *in vitro* experiments clearly indicated the promising potential as well as the efficacy of ECE of pulp of the rhizome of Aamada, as an anthelmintic. Studies on the changes in the cell cycle of the parasite cells in future would facilitate the characterization of the germinative cells in cestodes and would confirm our pre-obtained results.

Abstract Reference: 20298
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 1

Development and optimization of AI-based models for automated mosquito identification

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Abstract Content

Mosquito identification often requires expert knowledge and can be time-consuming. To address this, we developed a low-cost, AI application for mosquito identification. The project also aims to create a centralized image database to support AI model training and validation. Dataset of 950 images of insectary-reared dead mosquitoes from various species, including *Anopheles stephensi*, *Anopheles culicifacies*, *Aedes aegypti*, *Aedes albopictus*, and *Culex*, was compiled using: USB microscopes, digital-single-lens-reflex (DSLR Nikon-D5300) camera, and smartphone cameras, (Redmi 9A/iPhone). Images were taken from various angles and orientations to ensure diversity. Dataset was augmented and split into training, validation, and test sets. Convolutional neural network (CNN) models of varying configurations were trained, starting with a 16-layer sequential-CNN at 256x256 resolution. Other models used more layers and higher resolutions, 1024x1024 pixels. The 16-layer CNN achieved accuracy of 10%. A 32-layer model with 224x224 pixel resolution improved accuracy to 16%, while a similar model at 1024x1024 reached 36%. ResNet-50 and VGG-16 had test accuracies of 12% and 18%, respectively. A 32-layer sequential CNN with 1024x1024 resolution showed substantial increase, achieving 75% test accuracy. The results indicate that source, resolution, and model complexity are critical to achieving higher accuracy. Significant jump to 75% test accuracy with high-resolution images suggests that quality data and optimized model configurations are key. Results show promise for automated mosquito identification, with a top test accuracy of 75%. Future work will focus on expanding dataset and refining model configurations to enhance accuracy, providing practical applications in mosquito surveillance and vector control

Abstract Reference: 20299
Mode of Presentation: Oral Presentation
Topic: Parasitology

Exploring the role of *Opisthorchis viverrini* helminth defense molecules (HDM) in shaping host immunity

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Abstract Content

The interaction between hosts and parasites plays a crucial role in determining the pathogenesis of helminth infections. Excretory/Secretory products, including Helminth Defense Molecules (HDMs), have been proposed as contributors. Previous studies have demonstrated that HDMs are expressed at every stage of host infection and serve diverse biological functions across various trematode species. Previous studies showed that *Fasciola hepatica* Helminth Defense Molecule-1 inhibit LPS function by reducing the level of cytokines production. Conversely, *Clonorchis sinensis* HDM was found to bind to LPS without neutralizing the production of inflammatory cytokines. This study aimed to explore the functional properties of this molecule in the carcinogenic liver fluke *Opisthorchis viverrini*. An in vitro study was conducted to investigate the effect of HDM from *O. viverrine* (OvHDM) on LPS-induced inflammation. We used the OvHDM C-terminal synthetic peptide and incubated it with LPS from *Escherichia coli*. The peptide and LPS were co-cultured in RAW 246.7 macrophage cell lines, then TNF-α production was measured by the ELISA technique. The results showed that OvHDM increased the level of LPS-induced TNF-α production. The study reveals the immunomodulatory potential of OvHDM, with OvHDM enhancing TNF-α production when interacting with LPS. These suggest species-specific variations in HDMs function among parasitic helminths, underscoring the need for further research to understand these interactions for potential therapeutic strategies.

Abstract Reference: 20302
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 1

Health system needs for malaria elimination in the Greater Mekong Subregion: A qualitative study

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Abstract Content

Countries in the Greater Mekong Sub-region (GMS) committed to eliminate malaria by 2030 and implemented malaria elimination activities to interrupt the onward transmission. It is important to explore the perspectives of stakeholders on implementation of malaria elimination activities in the GMS to understand the health system needs. Qualitative interviews were conducted in Lao PDR, Myanmar and Vietnam with National Programme managers (n=2), and personnel from public sector (n=7), implementing partners (n=12), and technical agency (n=1). The study participants were recruited purposively. Reflexive thematic analysis was undertaken. Stakeholders highlighted the importance of continuous funding support for malaria elimination. Adequate and sustainable funding mechanisms such as a government-led funding and/or a community-initiated trust fund should be in place to avoid interruption in malaria elimination activities should the external fundings decline or stop. Stakeholders also highlighted the need for strengthening malaria microscopy since existing rapid diagnostic tests could not identify all the four main human malaria parasites and had questionable diagnostic accuracy in some cases. Moreover, tailored interventions for high-risk groups, dedicated staff for malaria elimination, highly sensitive surveillance systems, political commitment and support were also needed for a successful malaria elimination program. Findings from this study provided an understanding on how the malaria elimination strategies are being implemented in the GMS. This study also highlighted that a malaria elimination program requires various health system inputs at different levels. It is important to assess whether these requirements are already in place before hosting malaria elimination activities.

Abstract Reference: 20304
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 2

Spatio-temporal analysis of malaria in Central Vietnam from 2018 to 2022: A Bayesian approach

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Abstract Content

Malaria remains a public health challenge in Central Vietnam. We aimed to assess correlations between environmental and climatic factors in the district with malaria cases. We analyzed malaria cases in Central Vietnam between 2018 and 2022. Environmental and climatic data were extracted from Google Earth Engine. A multivariable Zero-inflated Poisson regression was conducted within a Bayesian framework, utilizing spatial and spatiotemporal random effects and estimated using Bayesian Markov Chain Monte Carlo simulation with Gibbs sampling. *Plasmodium falciparum* risk increased by five times (95% credible interval [CrI] 4.37, 6.74) for each 1-unit increase ofnormalized difference vegetation index (NDVI) without lag and by 8% (95% CrI 7%, 9%) for every 1ºC increase in maximum temperature (TMAX) at a 6-month lag. While a decrease in risk of 1% (95% CrI 0%, 1%) for a 1 mm increase in precipitation with a 6-month lag was observed. A 1-unit increase in NDVI at a 1-month lag was associated with a four-fold increase (95% CrI 2.95, 4.90) in risk of *P. vivax*. Additionally, the risk increased by 6% (95% CrI 5%, 7%) and 3% (95% CrI 1%, 5%) for each 1ºC increase in daytime land surface temperature with a 6-month lag and TMAX at a 4-month lag, respectively. Spatial analysis showed a higher mean malaria risk of both species in Central Highlands and southeast parts of Central Vietnam. Environmental, climatic risk factors, and spatial clusters of malaria were identified. This finding is crucial for designing adaptive strategies for eliminating malaria in Vietnam.

Abstract Reference: 20305
Mode of Presentation: Oral Presentation
Topic: Entomology - Vector and Vector-Borne Diseases

Vector-borne diseases and biodiversity: Upsurge of simian malaria

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Abstract Content

Emerging infectious diseases are increasing worldwide, while human activities are drastically reducing biodiversity. These concurrent patterns appear to be strongly linked as species diversity may play an important role in the modulation of pathogen transmission through the dilution effect. Biodiversity changes and loss may simultaneously decrease the dilution effect and amplify vector-borne disease transmission. The upsurge of simian malaria in Southeast Asia is a good model for understanding the mechanisms involved in this increase in human cases. The study is conducted in four locations near the Cambodian and Malaysian borders, in areas with forested foothills and the presence of macaques. Surveys are done both in forested areas and human settlements. Molecular methods are used to identify *Anopheles* vector species and simian *Plasmodium* in humans and mosquitoes. Expected results will allow the identification of *Anopheles* vector species of simian parasites, which are not known in Thailand. The comparison of *Plasmodium* transmission in vectors and humans, in forested *versus* village areas, will provide information on the level of simian malaria risk in both types of environments, high *versus* low biodiversity respectively. This study will provide a better understanding of the impact of deforestation and human behavior on epidemic risk in a One Health context. Finally, the results will help lowering the burden of simian malaria by implementing vector control strategies.

Abstract Reference: 20311
Mode of Presentation: Oral Presentation
Topic: Veterinary Health

Evaluation of molecular-based techniques for detection and quantification of *Fasciola hepatica* infection from faecal samples of experimentally infected cattle

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Abstract Content

Fasciola hepatica causes substantial losses in global ruminant livestock. Due to increasing drug resistance, improved diagnostics are imperative. Traditional methods have limitations, prompting exploration of molecular alternatives. This study compared FEC with molecular techniques (cPCR, LAMP, qPCR) for diagnosing *F. hepatica* in experimentally infected cattle. Ninety-four female beef cattle aged 6-12 months were infected with 500 metacercariae each. Faecal samples were collected 12 weeks later and analysed using FEC. DNA was extracted from faeces and subjected to cPCR, LAMP, and qPCR to detect *F. hepatica*. Non-infected dairy cattle samples served as negative controls. The sensitivity of conventional cPCR, LAMP, and qPCR was 86.2%, 87.2%, and 96.8%, respectively, comparable to FEC (97.9%). Similarly, all molecular methods demonstrated a specificity of 97.5%, while FEC exhibited 100% specificity. The molecular methods demonstrated high sensitivity and specificity, suggesting that these tools might be a viable alternative diagnostic test to FEC. FEC also showed good sensitivity and specificity in this study, however, the ease of use and large-scale application potential of molecular methods overcomes the limitation of FEC. Molecular methods, with their high sensitivity and specificity, have the potential to serve as promising substitutes to FEC for diagnosing *F. hepatica* infection in cattle.

Abstract Reference: 20320
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 2

A personal protection package for reducing malaria transmission among forest-going mobile and migrant populations in Cambodia and Lao PDR: A stepped-wedge cluster-randomised controlled trial with nested mixed methods study

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Abstract Content

In Greater Mekong Subregion, routine malaria protective measures such as long-lasting insecticidal bed-nets do not prevent all infectious mosquito bites among high-risk populations such as forest-going mobile and migrant populations (MMPs). Evidence of the effectiveness, acceptability and feasibility of a personal protection package tailored to MMPs in reducing malaria transmission is required to inform the regional malaria elimination toolkit. A personal protection package of long-lasting insecticidal hammock net, picaridin insect repellent and health communication pamphlet was distributed to MMPs in an open stepped-wedge cluster-randomised controlled trial conducted in 488 villages (60 in Cambodia and 428 in Lao PDR) from March 2022 to February 2023. Baseline (n=760) and endline (n=650) surveys, four focus group discussions (n=6-8/discussion) with MMPs who received the package and in-depth interviews (n=5) with health stakeholders were conducted. Over the duration of the trial, 9.62% (159/1,652) and 4.23% (1,621/34,300) of participants in Cambodia and Lao PDR tested positive for malaria, respectively. There was an absolute reduction in total malaria infection rates among MMPs who received the package in Lao PDR of 2.90% (7.00% in control and 4.10% in intervention periods). Knowledge, attitude and personal protection practices improved among MMPs in endline compared to baseline surveys. MMPs showed willingness to continue using the package as it is convenience to use in their workplace. Overall, the personal protection package is effective in reducing malaria prevalence among MMPs, acceptable to MMPs and health stakeholders, and could be considered for national and regional scale up to achieve regional malaria elimination.

Abstract Reference: 20325
Mode of Presentation: Oral Presentation
Topic: Parasitology and Microbiology

Prevalence and phylogenetic analysis of *Toxoplasma gondii* in feline, pigs, vegetables, and environmental samples from Chandigarh region, India

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Abstract Content

Toxoplasma gondii (*T. gondii*) is an obligate intracellular zoonotic protozoan parasite and a cause of zoonosis, food-borne & waterborne pathogen. So, current study aimed at detecting the possible occurrence or prevalence of *T. gondii* in animals and environment from Chandigarh region using different molecular and serological techniques. A total of 500 pigs (250 tissue and 250 blood), 100 cat faeces, 100 soil, 100 water and 500 vegetable samples were processed for DNA extraction and then subjected to Conventional PCR, Real-Time PCR, and Real-Time LAMP for detection of *T.gondii*. Double antibody sandwich ELISA was performed for detection of anti-*T. gondii* IgG levels in pigs. Further, phylogenetic analysis was performed using MEGA software for the *T. gondii* isolates obtained from the study. The molecular prevalence of *T.gondii* was found to be 27.6% in pigs, 47% in cats, 18% for water samples, 9% for soil samples and 6.6 % for vegetable samples. 65.6 % seroprevalence was found in pigs. The phylogenetic analysis revealed that the *T. gondii* isolates from our study were clustering with other *T. gondii* isolates from Iran, Mexico and also with patients *T. gondii* isolate from North Indian region. In the current study, we documented the first report from India to detect *Toxoplasma gondii* in pigs, cats, soil, water and vegetables samples using Real-Time PCR and Real-Time LAMP. Overall findings from the current study indicate detection of *Toxoplasma gondii* in environmental matrices and animals is of utmost importance to prevent its spread in humans.

Abstract Reference: 20344
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 1

Shielding soldiers: Unveiling the power of treated uniforms and repellents against mosquito vectors

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Abstract Content

This study evaluated the effectiveness of military uniforms treated with etofenprox and permethrin, along with metofluthrin spatial repellent, in preventing mosquito biting. The evaluation was conducted in large mosquito enclosures (LMEs) in Thailand against malaria and dengue vectors. The study's primary outcomes centered on landing inhibition, mortality, delayed mortality at 24 hours, and blood feeding inhibition. Volunteers wore treated military uniforms and spatial repellents within the LMEs, while untreated uniforms served as the control. Six interventions were tested, each pairing different treatments to assess their impact on mosquito behavior. The research utilized the human landing catch method alongside a randomized crossover design. The interventions consistently decreased landing rates across all three mosquito species. While most interventions reduced landing rates for *Ae. aegypti*, etofenprox treated uniforms alone were not as effective for this species. *Aedes albopictus* displayed significantly reduced landing rates for all interventions compared to the control, with variations between treatments. Similarly, *An. dirus* consistently demonstrated reduced landing rates across all interventions, signifying the impact of insecticide-treated uniforms on this particular species. Additionally, these interventions effectively reduced blood feeding rates across all three species. Survival rates at 24 hours after exposure were decreased for all tested mosquito species in treated chambers. The study demonstrates the effectiveness of etofenprox and permethrin-treated military uniforms in reducing landing rates, blood feeding, and survival of *Ae. aegypti*, *Ae. albopictus*, and *An. dirus*. This research provides valuable insights for preventing insect bites, especially in malaria and dengue vector control.

Abstract Reference: 20346
Mode of Presentation: Oral Presentation
Topic: Entomology - Mosquito Vectors

Assessing insecticide susceptibility of *Aedes albopictus* collected from urban parks in Selangor using WHO tube tests

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Abstract Content

The threat of mosquito-borne diseases is being exacerbated in Malaysia, by the growth of insecticide resistance in mosquitoes. This study aimed to assess the insecticide susceptibility of *Aedes albopictus* collected from six urban parks of Selangor, namely Taman Tasik Section 14 Shah Alam (Petaling district), Taman Rekreasi Awam Bandar Parklands (Klang district), Taman Tasik Sri Gombak (Gombak district), Taman Teratai Awam Bandar Baru Salak Tinggi (Sepang district), Taman Banting Baru (Kuala Langat district) and Taman Tasik Puncak Bestari (Kuala Selangor district). A total of 616 ovitraps were placed between September 2021 to April 2024. Among the mosquitoes collected, 92.8% were confirmed as *Ae. albopictus*, followed by *Culex* (7.1%) and *Armigeres* (0.1%). WHO tube test was used to determine to knockdown time and mortality rate of adult mosquitoes of *Ae. albopictus*. Gombak and Sepang strains showed resistance to all tested insecticides in WHO tube test, while Klang strain was resistant to all insecticides, except bendiocarb 0.1%. Petaling and Kuala Selangor strains were resistant only to malathion 0.8%. Mosquitoes of all strains showed the longest knockdown time when treated by malathion 0.8% (KT_{50} values > 562 min). The descending order of insecticide effectiveness of WHO test was bendiocarb 0.1% > DDT 4% > permethrin 0.25% > malathion 0.8%. Based on the results, higher concentration or other insecticides of the same category should be introduced to control the vector population. The study findings provide light on the dynamics of insecticide resistance and emphasize the importance of sustainable mosquito control strategies.

Abstract Reference: 20349
Mode of Presentation: Oral Presentation
Topic: One Health 1

Emerging and reemerging parasitic diseases in Taiwan: A retrospective study of clinical case reports from 2001 - 2018

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Abstract Content

Emerging and re-emerging parasitic diseases can cause significant economic burdens at national and global levels. However, governments often underestimate or ignore these diseases, especially in developed countries. This retrospective, case-oriented study analyzed parasitic diseases reported in Taiwan between 2001 and 2018. One hundred and thirty-two eligible clinical profiles of Taiwanese patients obtained from the NCBI, Scopus, Google Scholar, and Web of Science databases and local journals according to age, sex, source of infection, symptoms, risk factors, and geographical regions were analyzed. The analysis result showed that the number/frequency of cases caused by nematodes (46.97%) or protozoa (37.88%) was significantly higher than that of trematodes (9.85%) or cestodes (5.30%) ($p < 0.0001$). Northern Taiwan (46.97%) had a significantly higher rate than Southern Taiwan (33.33%), Central Taiwan (8.33%), and Eastern Taiwan (5.30%) ($p < 0.05$). The 15-65 age group (68.94%) had a significantly higher rate than the 65-90 age group (22.73%) and the 0-15 age group (8.33%) ($p < 0.0001$). Males (70.46%) had a significantly higher number/frequency of cases than females (29.54%) ($p < 0.0001$). People who acquired the infection through the food/soil route (32.58%) or who had a low immune status (32.58%) had a higher rate than travel-related infections (15.15%) ($p < 0.001$). The present study showed that emerging/reemerging parasitic infections continue to be of great concern to the lives and health of Taiwanese citizens and, if ignored, will threaten the health of the Taiwanese people; therefore, the delineation of preventive measures by health authorities is urgently warranted.

Abstract Reference: 20350
Mode of Presentation: Oral Presentation
Topic: Water & Food Borne Parasites

Expression profile analysis of the Transient Receptor Potential (TRPM) channel, a possible target of Praziquantel in *Schistosoma japonicum*

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Abstract Content

Schistosomiasis, a major NTDs, is caused by blood flukes of the genus *Schistosoma*. *S. japonicum*, which is the cause of Asian zoonotic schistosomiasis, is endemic in China, the Philippines, and some parts of Indonesia. At present, there is no vaccine for schistosomiasis, and the control relies heavily on mass drug administration (MDA) with well tolerated drug Praziquantel (PZQ). Regarding the previous studies that demonstrated that PZQ activates the transient receptor potential (TRP) channel in *Schistosoma mansoni* (*Sm*.TRPM$_{\mathrm{PZQ}}$), the expression profile of the ortholog of this channel gene (Smp_246790.5) in *S. japonicum* (EWB00_008853) (*Sj*.TRPM$_{\mathrm{PZQ}}$) was analyzed. The relative expression of this gene in various stages of the parasite lifecycle was analyzed by qRT-PCR, and the expression of *Sj*.TRPM$_{\mathrm{PZQ}}$ was observed by immunohistochemical staining using anti-serum against the recombinant *Sj*.TRPM$_{\mathrm{PZQ}}$ protein. qRT-PCR revealed the significantly lower mRNA expression in the snail stage in comparison to other stages ($p<0.01$). The relative quantity of the *Sj.TRPM*$_{PZQ}$ expression for paired females, unpaired males, and eggs was 60%, 56%, and 68%, respectively, in comparison to paired males that showed the highest expression ($p<0.05$). Interestingly, immunostaining demonstrated that *Sj*.TRPM$_{\mathrm{PZQ}}$ is expressed in the parenchyma which contains muscle cells, neuronal cells and tegument cells in adult worms. This may support the two major effects of PZQ—worm paralysis and tegument disruption—induced by channel activation. Moreover, the channel was expressed in both the eggshell and the miracidia inside but could not be observed in sporocyst. These results correspond to the known sensitivity of *S. japonicum* to PZQ.

Abstract Reference: 20353
Mode of Presentation: Oral Presentation
Topic: Entomology - Mosquito Vectors

Species sanitation against *Anopheles darlingi* in Amazonian indigenous villages located within low-order river-floodplain systems, Brazil

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Abstract Content

Species sanitation has previously been employed successfully to control primary malaria vectors in Malaysia, Indonesia and India. We applied the species sanitation technique to specifically target *Anopheles darlingi* larvae in the Marari healthcare base hub, identified as the most significant malaria hotspot within the Brazilian Yanomami territory. Following the species sanitation approach, our study was structured in two distinct phases. The initial phase focused on acquiring precise data regarding the ecology of *An.darlingi* larvae, while the subsequent phase involved the implementation of targeted environmental management interventions against this species. Various anti larval measures were employed: 1) excavation of open earth ditches for surface drainage, 2) filling of small water bodies, 3) mechanical removal of sun-exposed floating detritus and aquatic vegetation and 4) utilization of portable water-pumps. Sun exposure was the key environmental factor influencing the occurrence of *An.darlingi* larvae and guided the selection of larval habitats for targeted environmental management interventions. Our efforts resulted in significant reductions in adult *An.darlingi* densities, with decreases of 97.1% and 74.6% in the Castanha and Monobi villages, respectively. Within the Castanha region, the number of larval habitats positive for *An.darlingi* decreased from 11 before the intervention to between zero and three during the post-intervention period. Remote indigenous villages may represent some of the last remaining malaria transmission hotspots in the Brazilian Amazon. Species sanitation could contribute to reach malaria elimination in these areas, potentially leading to the suppression of local *An.darlingi* populations or substantial reductions in their densities.

Abstract Reference: 20354
Mode of Presentation: Oral Presentation
Topic: Parasitology - Molecular Parasitology

CSF3: a novel gene regulates hepatic fibrosis causing by *Fasciola hepatica* infection based on RNA-sequencing and experimental validation

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Abstract Content

Fascioliasis is an important zoonotic disease caused by *Fasciola hepatica* which parasitic in the liver and bile ducts of ruminants such as cattle and sheep. The excretory and secretory products (ESPs) of *F. hepatica* have serious effect in causing liver fibrosis. The study was conducted to explore altered genes in Kuffer cells (KCs) which play an important role in *F. hepatica* infection. We collected adults *F. hepatica* in artificially sheep liver for vitro culture to prepare the ESPs. Whether ESPs promote liver injury was performed by injecting ESPs into the tail vein of mice, hematoxylin eosin (HE) and Masson staining was conducted. The altered genes of KCs treated with ESPs of *F. hepatica* were identified by the RNA-sequencing. Further analyses using qRT-PCR were performed to identify genes with significant up-regulation in liver infected with *F. hepatica*. As a result, obvious liver damage could be seen in *F. hepatica* infection by HE and Masson. RNA-sequencing indicated that a total of 308 genes showed significant up-regulation, and 222 genes showed down-regulation. The colony stimulating factor 3 (CSF3) was the most up-regulated gene, which was consistent with the trend of CSF3 in the sheep infected with *F. hepatica*. And the JAK/STAT pathway related to the CSF3 was enriched in KEGG analysis. In conclusion, the CSF3 may be the available gene that regulate the liver fibrosis in *F. hepatica* infection via the JAK/STAT pathway. This will provide new ideas and potential therapeutic targets for the treatment of hepatic fibrosis caused by *F. hepatica*.

Abstract Reference: 20365
Mode of Presentation: Oral Presentation
Topic: Parasitology and Microbiology

Characterization and toxicity evaluation of live versus inactivated recombinant *Bacillus subtilis* spores expressing *Acinetobacter baumannii* Ton-B protein

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Abstract Content

Previous research by MatRahim et al. (2023) investigated the use of recombinant *Bacillus subtilis* expressing *Acinetobacter baumannii* TonB protein as a prophylactic treatment for multidrug-resistant *Acinetobacter baumannii*. *Bacillus subtilis* endospores are durable and ideal for oral delivery of recombinant proteins. However, inactivating the endospores is desirable due to concerns about the shedding of recombinant GRAS spores. In the present study, we developed a method to inactivate the recombinant *Bacillus subtilis* spores expressing *Acinetobacter baumannii* Ton-B protein. Subsequently, we determine their toxicity in mice. The inactivation of recombinant GRAS bacteria was achieved through autoclaving the bacterial spores at 121°C or chemical inactivation methods such as 4% formaldehyde, Chemical X, and Chemical Y. The results showed that Chemical X is the best inactivator, with 100% inactivation within 24 hours when the inactivated products were plated on the TSA plate. The live and inactivated *Bacillus subtilis* recombinant spore was characterized by detecting the protein of interest by immunoblotting and observing the morphology through microscopy. The study found that the live and inactivated *Bacillus subtilis* recombinant spore had the protein of interest detected but had different morphologies when viewed under the light microscope and scanning electron microscope. Toxicity assessment of live and inactivated Ba*cillus subtilis* recombinant spores conducted in mice revealed that consumption of the inactivated spores did not result in acute toxicity. These results suggest that *Bacillus subtilis* recombinant spores were successfully inactivated without compromising the protein of interest and are safe for consumption. (Chemical X and Chemical Y are under IP filing)

Abstract Reference: 20366
Mode of Presentation: Oral Presentation
Topic: Parasitology - Molecular Parasitology

Leishmania exosomes enriched in polyamines drives metabolic switching in exosome mediated host macrophage polarization from M1 to M2 phenotype

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Abstract Content

Exosomes are small (~30-150nm) extracellular vesicles of endocytic origin that play a major role in host-pathogen interaction and intracellular communication. The exosomes are carriers of the unique repertoire of metabolites including Polyamine (PA). It is a polycationic molecule that is pivotal in shaping host immune-metabolic switch toward parasite survival. The present study highlights how Leishmania exosome metabolites switch polyamine biosynthesis in the host, leading to immune polarization during infection. Interestingly, our biochemical and LC/MS analysis reveals that *L. donovani* exosomes are enriched with polyamines such as spermidine and putrescine. The polyamine depletion/ inhibition study showed that parasites are heavily compromised in their growth and fitness, suggesting that PA is an essential metabolite required to create a pro-parasitic environment in the nutrient-depleted niche of the phagolysosomes as well as neutralizes the acidic environment in it. Further, we investigated the metabolic reprogramming of the *L. donovani*-derived exosome from the perspective of host macrophage (THP-1) polyamine biosynthesis. We observed that exosomes uptaken macrophages, showing M2 polarization by increasing the Arginase I expression and activity. Notably, the Leishmania exosomes contribute to the intracellular spermidine pool and induce the expression of the polyamine transporter. The study also found that exosome stimulation enhances the phagocytic index and infectivity by creating a presumptive environment for the parasite. These findings suggest that the *L. donovani* exosomes-mediated polarization of macrophages from the M1 to M2 phenotype drives the polyamine pathway instead of the iNOS pathway as reciprocal regulation of a single substrate for two enzymes.

Abstract Reference: 20370
Mode of Presentation: Oral Presentation
Topic: One Health 1

Gut bacteria and gut parasite: A bidirectional influence

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Abstract Content

Whilst the influence of intestinal microbiota has been shown in many diseases, investigations are still scarce on its role in altering the nature of other infective organisms. This study assesses the association and interaction of Blastocystis sp. and human intestinal microbiota. We investigated the gut microbiota of Blastocystis sp.-free and Blastocystis sp. ST3-infected individuals who are symptomatic and asymptomatic. We tested if the expression of phenotype and pathogenic characteristics of Blastocystis sp. ST3 was influenced by the alteration of its accompanying microbiota. Blastocystis sp. ST3 infection alters bacterial composition. Its presence in asymptomatic individuals showed a significant effect on microbial richness compared to symptomatic ones. Inferred metagenomic findings suggest that colonization of Blastocystis sp. ST3 could contribute to the alteration of microbial functions. For the first time, we demonstrate the influence of bacteria on Blastocystis sp. When Blastocystis sp. isolated from a symptomatic individual was co-cultured with bacterial suspension of Blastocystis sp. from an asymptomatic individual, the parasite demonstrated increased growth and reduced pathogenic expressions. This study also reveals that Blastocystis sp. infection could influence microbial functions without much effect on the microbiota diversity itself. This results demonstrate evidence on the influential role of gut microbiota in altering the characteristics of the parasite, which becomes the basis for the contradictory findings on the parasite's pathogenic role seen across different studies. Our study provides evidence that asymptomatic Blastocystis sp. in a human gut can be triggered to show pathogenic characteristics when influenced by the intestinal microbiota.

Abstract Reference: 20373
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 2

Plasmodium falciparum population structure in southwestern Africa, using data from Angola

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Abstract Content

In 2022, Angola ranked ninth globally for malaria deaths. Despite varying malaria prevalence among provinces (from 1% to 50%), the genetic diversity and demographics of *Plasmodium falciparum* (Pf) in Angola remain poorly understood. This work aims to address several key questions: Do Pf infections in Angolan provinces with varying levels of malaria endemicity, including hyperendemic (Cabinda, Uíge), mesoendemic-stable (Luanda, Cuanza Sul), and mesoendemic-unstable (Cunene, Namibe), differ in complexity or genetic diversity? Does Pf form a panmictic population in Angola? Does Angola, located in the southwestern Africa, harbor a parasite population distinct from neighboring countries? Parasite DNA from 112 Angolan dried blood spots underwent sequencing, and SNP identification were conducted using diverse Pf samples from Africa. Statistical methods such as FWS, Fst, PCA, and admixture analysis assessed genetic diversity and differentiation in Angola, providing insights into Pf populations across Africa. Frequency of polyclonal infections was low in all six provinces, but in Cunene and Namibe (unstable malaria transmission) they were nearly exclusively monoclonal. Fst analysis showed low but significant genetic differentiation, notably in these provinces. Angolan samples cluster with those from the Democratic Republic of Congo, and Angola hosts the largest proportion of Pf with most representative genome. In conclusion, this study reveals varying infection complexity and genetic diversity among Angolan provinces with different malaria transmission levels. The Pf population in Angola is not entirely panmictic, with genetic differentiation observed between provinces. Angola's Pf population represents the southwestern edge of the parasite's distribution in Africa and appears distinct from neighboring countries.

Abstract Reference: 20379
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 2

Community-based molecular and serological surveillance of malaria: a study among indigenous Temiar Orang Asli in Peninsular Malaysia

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Abstract Content

In Malaysia, malaria still strikes hardest in vulnerable populations living in remote and rural areas. This includes the Temiar group of Orang Asli, a remote indigenous community in Peninsular Malaysia. Integrating molecular and serological measures may improve malaria surveillance in this hard-to-reach community and inform targeted interventions and elimination responses. A cross-sectional survey was conducted in six indigenous Temiar Orang Asli settlements in Kelantan, from June to October 2019. Blood samples were tested for malaria using microscopy and molecular methods, while antibody responses to *Plasmodium falciparum* and *Plasmodium vivax* blood-stage antigens were assessed by ELISA. Age-adjusted antibody responses were analysed using a reversible catalytic model to calculate seroconversion rates (SCR). Of the 1,954 individuals who appeared healthy, no malaria parasites were found using microscopy. However, molecular testing revealed seven cases of *Plasmodium knowlesi* mono-infection (0.4%) and no human malaria species were detected. For all parasite antigens analysed from 645 samples, the proportion of seropositive individuals significantly increased with age ($p = 0.004$) and study areas ($p < 0.001$). Based on the SCRs, there was a higher level of *P. falciparum* transmission than *P. vivax* using all tested antigens, ranging from 0.032 year^{-1} (0.026–0.04) to 0.122 year^{-1} (0.093–0.16) for *P. falciparum* and 0.000 year^{-1} (0.000–0.002) to 0.019 year^{-1} (0.011–0.035) for *P. vivax*. These findings indicate low submicroscopic *P. knowlesi* infections among indigenous communities in Malaysia. Demonstrating congruence between conventional parasitological and serological measures suggests broader utility for serology monitoring and evaluating malaria transmission.

Abstract Reference: 20381
Mode of Presentation: Oral Presentation
Topic: One Health 2

Prevalence of helminths in freshwater animals in Heilongjiang Province of the People's Republic of China

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Abstract Content

Foodborne parasitic diseases distribute worldwide and seriously affect human health. In the transmission of these diseases, freshwater animals and their products are important sources of parasite infection. This project conducted a survey on freshwater animals with parasitic infections at 58 experimental sites in 13 cities in Heilongjiang Province. A total of 20596 freshwater animal samples were collected, including 30 species of fish (12455 samples), 3213 of three species of amphibious animals (3213 samples), 2121 mollusks of three species of mollusks (2121 samples) and, three species of crustaceans (2817 samples). The results showed that a total of 50 parasitic helminths were detected, belonging to 44 genera, 35 families, five classes, 15 orders, and three phyla. The total infection rate was 19.49%. The infection rates of fish, frogs, and crustaceans were 13.32%, 72.72% and 1.24%, respectively. No worms were detected in mollusks. Statistical analysis showed that *Clonorchis sinensis*, *Diplodiscus mehrai* and *Rhabdias bufonis* were the dominant species of fish and frogs. Analysis of risk factors found that nine species of zoonotic parasites including *C. sinensis* were all fish-borne and they are all in the infective stage. The logistic regression analysis found there are significant prevalent differences in different locations ($P<0.01$), and significant differences exist in certain species ($P<0.05$). In summary, this study obtained first-hand information on the prevalence of freshwater animal parasites in Heilongjiang Province, which not only provides scientific theoretical basis for the prevention and control of freshwater animal borne parasitic diseases, but also effectively responds to sudden public health events.

Abstract Reference: 20384
Mode of Presentation: Oral Presentation
Topic: Entomology – Vector and Vector-Borne Diseases

A comparative study of high-throughput screening system toxicity bioassay with air-drying time of transfluthrin-treated filter papers against pyrethroid-susceptible *Aedes aegypti* (Diptera: Culicidae)

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Abstract Content

Increasing temperature can enhance the geographic spread of and behavior of disease vector mosquitoes, exposing vulnerable populations Aedes-borne viruses and infections. To address this risk, cost-effective and sustained intervention vector control tools such as volatile pyrethroid spatial repellents may be required. This study used a high-throughput screening system toxicity bioassay (HITSS-TOX) to assess discriminating concentrations (DCs) from varied air-drying times of transfluthrin (TFT)-treated filter papers exposed to pyrethroid-susceptible *Aedes aegypti* mosquitoes. Established lethal concentrations (LCs) differed significantly between air-dried filter papers after 1 h and 24 h treatment ($P < 0.05$). Consequently, the DC of 24 h air-dried filter paper (0.42583%) was 2.8-fold higher than those of 1 h (0.15222%) and increased by 5-fold to 336 h (0.71273%) of air-dried papers.Regression analysis showed that all LCs and DCs were positively correlated with air-drying periods (LC$_{50}$: $R^2 = 0.89$, LC$_{75}$: $R^2 = 0.85$, and both LC$_{99}$ and DC: $R^2 = 0.74$; 95% CI). The results of this experiment are comparable with a recent study that used WHO tube assay which showed that the optimal air-drying period of the TFT-treated filter paper is critical as greater DC values may underestimate pesticide resistance. Due to the instability of TFT-treated papers that vary with air-drying durations, the new WHO bottle bioassay is preferred method determining mosquito susceptibility and DC to volatile insecticides that incompatible with filter papers.

Keywords: Transfluthrin, *Aedes aegypti*, High-Throughput Screening System, Air-drying time, Toxicity bioassay.

Abstract Reference: 20389
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 1

Elucidating combined effect of *Salvadora persica* L. Twig (Miswak) extracts and chlorhexidine mouthwash against multidrug resistant bacteria

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Abstract Content

Ventilator-Associated Pneumonia (VAP) poses a significant healthcare challenge, often driven by multidrug-resistant (MDR) bacteria colonizing Endotracheal Tubes (ETT) through biofilm formation, rendering these pathogens resistant to antibiotics. Chlorhexidine mouthwash (CHX) is commonly used to manage oral microbiota in ventilated patients, yet concerns exist regarding its potential mucosal damage and the emergence of Gram-negative organisms with reduced susceptibility to it. Consequently, alternative strategies are urgently needed to combat MDR infections associated with VAP. Twigs of *Salvadora persica* a traditional toothbrush tree, exhibits promising antibacterial properties due to its bioactive compounds. This study aimed to assess the combined antibacterial efficacy of *Salvadora persica* twig extract (SPE) and CHX against MDR forming biofilms on ETT. The twig was extracted using hexane via a Soxhlet apparatus. The antibacterial activity of the extracts was evaluated against *Acinetobacter baumannii*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* strains isolated from clinical specimens. Minimum Inhibitory Concentration (MIC) values were determined using the broth microdilution method, and the Fractional Inhibitory Concentration Index (FICI) was calculated via a checkerboard assay. From the results SPE and CHX had lowest MIC values of 2.5 and 0.05859mg/ml respectively and FICI values > 4 in all the tested MDR. Therefore, the combination of SPE and CHX exhibited antagonism against all the tested MDR strains, despite their individual activities. It can be concluded that the finding suggests combining these agents may not be effective for combating MDR infections in intubated patients. Further investigation is needed to know the mechanisms underlying the SPE activity on the bacteria.

Abstract Reference: 20392
Mode of Presentation: Oral Presentation
Topic: Water & Food Borne Parasites

Schistosoma japonicum Cathepsin B as potential diagnostic antigen for Asian zoonotic schistosomiasis

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Abstract Content

In this study, the diagnostic value of *Schistosoma japonicum* cathepsin B (SjCatB) was evaluated as an antigen for the early detection of *S. japonicum* infection. SjCatB is a key protease used by the cercaria to penetrate the intact skin of the host. The early exposure of this enzyme to the host immune system may elicit early production of antibodies against this molecule. The full-length coding sequence of SjCatB was retrieved from GenBank and expressed as a recombinant protein in *Escherichia coli* with an N-terminal 6xHis-tag (rSjCatB). rSjCatB was tested for its performance as an antigen in an indirect ELISA using sera collected from experimentally infected mice at >8 weeks post-infection, which showed 100% sensitivity and 95.0% specificity. The early detection of antibodies against rSjCatB was evaluated using sera from experimentally infected mice collected at 2, 4, 6 and 8 weeks post-infection. As early as 6 weeks post-infection, 2 of 4 mice tested positive in the ELISA. Furthermore, the potential of the recombinant antigen in detecting the infection was evaluated with sera collected from individuals (n=30) diagnosed with *S. japonicum* infection by stool examination, achieving a sensitivity of 86.7% and a specificity of 96.7%. Serum samples from patients with other parasitic diseases had minimal cross-reactivity with rSjCatB. Taken together, the results of this study suggest that SjCatB is a potential diagnostic antigen capable of sensitive and specific early detection of *S. japonicum* infection.

Abstract Reference: 20397
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 1

Antimicrobial and antibiofilm activities of hexane *Salvadora persica* extract against Carbapenem-resistant *Acinetobacter baumannii* (CRAB) isolated from endotracheal tube (ETT) samples

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Abstract Content

Carbapenem-resistant *Acinetobacter baumannii* (CRAB) presents a critical challenge in healthcare due to its antibiotic resilience, leading to severe infections in hospitalized patients. *Salvadora persica (S. persica)* roots, traditionally used for oral hygiene and endorsed by the WHO, offer a promising avenue for medical research. This study investigated solvent extracts from *S. persica* roots against CRAB strains from endotracheal tube samples. Hexane solvent hexane was employed using a Soxhlet apparatus. Antimicrobial activity against CRAB was evaluated using broth microdilution assays to determine minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) values. Additionally, minimum biofilm inhibition concentration (MBIC) and minimum biofilm eradication concentration (MBEC) assays were conducted to assess antibiofilm activity. Gas chromatography-mass spectrometry (GC-MS) analysis were revealed the presence of various phytochemical compounds. Hexane extract was rich in benzoic acid. Hexane extracts exhibited potent antibacterial and antibiofilm properties, with MIC and MBC values ranging from 1.56 to 3.13 mg/ml and 6.25 to 12.50 mg/ml, respectively. MBIC and MBEC values for hexane extracts were 6.25 mg/ml and 62.5 to 125.00 mg/ml, respectively. The antimicrobial and antibiofilm activities of hexane extracts were consistent across all tested CRAB strains (n=20), with MIC ranging from 1.56 to 6.25 mg/ml and MBC from 3.13 to 12.50 mg/ml. MBIC and MBEC values varied from 6.25 to 25.00 mg/ml and 12.50 to 62.50 mg/ml, respectively. Scanning electron microscopy (SEM) analysis showed reduced biofilm structure post-treatment. Hexane extracts of *S. persica* roots demonstrate potent antibacterial and antibiofilm effects against CRAB, highlighting their potential for therapeutic intervention.

Abstract Reference: 20402
Mode of Presentation: Oral Presentation
Topic: One Health – General 1

Deep learning models applied to timeseries forecasting for vector-borne diseases: A climate based perspective

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Abstract Content

The interrelationships shared between climate and vector borne diseases such as malaria and dengue are valuable for understanding the environmental impact on the disease epidemiology, while also promoting disease risk predictions. However, the complexities inherent in these climate-disease relationships are, not well understood and classical models fail to explain them sufficiently. Deep learning transformer models can expose the complex dynamics between climate and these vector-borne diseases. A transformer with attention and a temporal fusion transformer were initialized and trained with multiple climate datasets and daily to weekly case data for both malaria (1998-2022) and dengue (2000-2018) simultaneously. This promoted generalized case predictions with high accuracy over 90% for both diseases despite varying geographic locales and climate data. Physics-informed enhancements were employed to continuously update the models at specific high risk climate variable magnitudes for malaria and dengue. Results indicate over 81-95% accuracy in weekly dengue and malaria case predictions and over 95% at the daily level. With the model's ability to provide explainability, the specific contributions of each climate variable affecting case incidence are revealed, indicating that max/min temperature, rainfall, sea surface temperature and long-term variability such as the Indian Ocean Dipole and Niño indices have substantial influence. Case incidence 35-50 weeks ahead was also found to be the optimum prediction windows for these diseases when using these climate variables. As data availability increases and climate change is exacerbated, the application of AI and deep learning in disease prediction is becoming necessary.

Abstract Reference: 20422
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 1

Longitudinal population analysis and natural selection of *ama-1* gene in Indian Plasmodium falciparum isolates

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Abstract Content

High genetic diversity is a major impediment to developing a universal malaria vaccine based on *Plasmodium falciparum* apical membrane antigen-1 (*Pfama-1*). Vaccine effectiveness against heterologous forms of the antigen requires information about existing genetic diversity of gene in circulation. *Pfama-1* ectodomain was genotyped in 147 samples collected from 14 Indian states between 1993 to 2021. Polymorphic profile, structure and natural selection were assessed to explore the longitudinal variation in *Pfama-1* in Indian *P. falciparum* field isolates. In this study we identified 70 haplotypes arising from 52 polymorphic sites along with two previously unreported mutations, S498C/G and F505Y. Domain I ($\pi = 0.025$) exhibited highest genetic polymorphism, while Domain II ($\pi = 0.006$) appeared to be the most conserved across all states throughout the studied time period. Non-significant positive Tajima's D value (Taj D $= 0.945$, $p > 0.10$) was observed suggesting samples to be under balancing natural selection. Although haplotype network was complex, structure analysis showed no evidence of distinct genetic pattern state wise or changes in *Pfama-1* gene structure over time. Thus, genetic structure of *Pfama-1* in Indian field isolates is complex, exhibiting a high degree of genetic polymorphism. Domain II showing relative conservation across all states and between old and recent samples could be targeted for vaccine design. Constant pattern of *Pfama-1* gene in circulation suggests that the gene evolves independently without significant selection pressures. These findings provide fundamental insights into the prevalent genetic polymorphisms of *Pfama-1* gene in India offering valuable information for malaria vaccine design.

Abstract Reference: 20424
Mode of Presentation: Oral Presentation
Topic: Parasitology and Microbiology

Blastocystis sp. ST3 and Wnt Signaling: Evidence for causing inflammation

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Abstract Content

Wnt pathway is involved in inflammation and etiology of colorectal cancer (CRC). *Blastocystis* sp. infection has been linked with irritable bowel syndrome (IBS) and CRC. This study aimed to investigate the role of solubilized antigen of *Blastocystis* sp. subtype 3 (Blasto-Ag ST3) from IBS patients in regulating Wnt pathway of colon normal (CCD-18Co) and cancer cells (HCT116). Eight *Blastocystis* sp. ST3 isolates from non-IBS and IBS patients were used. CCD-18Co and HCT116 cells were exposed to 5 μg/ml Blasto-Ag ST3, followed by cell proliferation and migration assays. Wnt pathway analysis was conducted using the QuantiGene 2.0 Plex Magnetic Separation Assay. Cell proliferation and migration levels are significantly higher in cells exposed to IBS Blasto-Ag ST3 compared to non-IBS Blasto-Ag ST3. Wnt pathway analysis indicated that numerous canonical genes were differentially expressed in both CCD-18Co and HCT116 when exposed to IBS and non-IBS Blasto-Ag. Notably, WNT3 and WNT7A were the only genes significantly upregulated in both cell types following exposure to IBS Blasto-Ag ST3. The WNT3 and WNT7A upregulation proposes potential markers for inflammation or cancer progression in IBS patients, especially with *Blastocystis* sp. infection. Increased cell proliferation and migration with IBS Blasto-Ag ST3 exposure may exacerbate IBS symptoms and contribute to CRC development. These findings suggest a diagnostic pathway for monitoring IBS patients, especially those infected with *Blastocystis* sp.

Abstract Reference: 20431
Mode of Presentation: Oral Presentation
Topic: Parasitology - Molecular Parasitology

Csi-miR-71a delivered by *Clonorchis sinensis* extracellular vesicles suppresses liver fibrosis via targeting Scube3

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Abstract Content

Clonorchis sinensis is mainly parasitic in the hepatobiliary duct and gallbladder of humans, cats, dogs and other animals, which can cause liver fibrosis, even cholangiocarcinoma. In this study, *C.sinensis* extracellular vesicles (CsEVs) and primary mouse HSC were isolated and identification, and high-throughput sequencing was conducted to identify the miRNAs of *C.sinensis* in HSC. Csi-miR-71a was screened as the research object by Bioinformatics analysis. Then, overexpressed or inhibited recombinant plasmids of Csi-miR-71a were transfected into HSC-T6 cell or mice, to evaluate the regulatory effect of Csi-miR-71a on host liver fibrosis. The result showed that Csi-miR-71a could inhibit HSC activation, and reducing the development of liver fibrosis. Subsequently, prediction and identification of target genes of Csi-miR-71a through analysis the binding sites and the 3′ UTR, as well as perform dual luciferase reporter experiment to further verify. Scube3 was screened as the target gene of Csi-miR-71a. Flag-SCUBE3 and TβR-II-HA plasmids were constructed to Co-Immunoprecipitation, the results indicated that Scube3 could interact with TβR-II. Finally, Csi-miR-71a-mimics or Scube3 siRNA was transfected into HSC-T6 cell or mouse primary HSC to detect the expression of key protein of signaling pathway. The result showed the expression of key protein of TGF-β/Smad and PI3K/AKT signaling pathway (p-Smad2, p-Smad3, p-PI3K, p-AKT) were significantly decreased. In conclusion, Csi-miR-71a can target Scube3 to inhibit TGF-β/Smad and PI3K/AKT signaling pathway and to inhibit HSC activation, mitigate the development of liver fibrosis. This study will provide new targets and intervention strategies for the treatment of clonorchiasis.

Abstract Reference: 20434
Mode of Presentation: Oral Presentation
Topic: Parasitology

Stopping malaria parasites before they StART: aryl-acetamide compound MMV006833 inhibits lipid transfer and ring development

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Abstract Content

Efforts to eradicate malaria have stalled partly due to parasites developing resistance to many antimalarials. Therefore, new drugs with novel modes of action are urgently needed. Our laboratory recently identified an aryl-acetamide compound called MMV006833 (M833), that stops *Plasmodium falciparum* parasites from growing inside red blood cells after invasion. Parasites resistant to M833 contained mutations in the StART domain phospholipid transferase protein (PF3D7_0104200, thereafter called StART). These mutations were engineered into drug-sensitive parasites and reproduced resistance to M833. Through structure activity relationship studies, we significantly improved the potency of the compound >30-fold with the most potent analogue, W991, having a subnanomolar EC_{50}. We demonstrated direct binding of W991 to StART using three different protein-based techniques, as well as demonstrating an absence of drug binding to mutant StART proteins. Overall, our data confirms that StART is the biological target of M833 and analogues. To understand the mode of action of these compounds, invading merozoites were filmed by lattice light sheet microscopy. In the presence of StART inhibitors, merozoites were unable to transform into amoeboid rings. Further, exposing invading parasites to StART inhibitors for only 4 hours was sufficient to block ring development for at least three days. W991 also inhibited the development of oocysts in mosquitoes. Overall, we have developed the first inhibitors of StART and hypothesise that StART is involved in the transfer of lipids required for the establishment of the parasite parasitophorous vacuole membrane and for the internal reorganisation of membranes needed for the transformation of merozoites into rings.

Abstract Reference: 20440
Mode of Presentation: Oral Presentation
Topic: Veterinary Health

Molecular characterization of intestinal protozoa of dogs and cats from Bangalore region of Karnataka state, India

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Abstract Content

Gastrointestinal protozoan parasites of dogs and cats are diffused worldwide and most of them are having zoonotic significance and play an important role in maintenance of disease and act as asymptomatic carriers. Therefore, the work was taken to ascertain the prevalence of gastrointestinal protozoan parasites of dogs and cats by molecular method. The fecal samples (119 dogs) and (119 cats) in and around Bangalore region were screened by flotation, formal ether and modified Ziehl-Neelsen methods. Fifty samples were subjected to conventional and n-PCR by targeting SSU rRNA for *Entamoeba*, *Cystoisospora*, *Cryptosporidium* species and β-giardin gene for *Giardia* species. *Cryptosporidium* spp. (8), *Isospora* spp. (4), and *Entamoeba* spp. (1) were detected whereas, *Cryptosporidium* spp. (4) and *Isospora* spp. (4) were detected in each 119 faecal samples of dogs and cats respectively. In dogs, *Entamoeba* spp. (2) and *Cystoisospora* spp. (2), *Giardia* spp. (3) and *Cryptosporidium* spp. (2) whereas, *Entamoeba* spp. (4), *Cryptosporidium* spp. (2) and *Cystoisospora* spp. (7) in cats were recorded in PCR. The sequence and phylogenetic analysis of dogs isolates revealed *Cystoisospora belli*, *Cystoisospora canis*, *Cystoisospora orlovi*, *Cystoisospora ohioensis* and *Entamoeba polecki*. Whereas, in cats, *Entamoeba polecki* and *Cystoisospora felis* were generated by sequencing. Further, it confirms the existence of *E. polecki* and *C. ohioensis* in dogs and cats, recorded first time in Karnataka as well as from India. These gastrointestinal protozoan parasites are of zoonotic and individuals who are in close proximity are at significant risk. The study serves as surveillance tool and benchmark for future management efforts.

Abstract Reference: 20448
Mode of Presentation: Oral Presentation
Topic: Parasitology

Identification of tick-borne pathogens and endosymbionts in ticks by metagenomic next-generation sequencing

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Abstract Content

Ticks are blood-feeding ectoparasites that act as arthropod vectors for transmission pathogens. The aim of this study was to screen bacteria community in ticks in Korea using metagenomic next-generation sequencing and confirm the results by PCR. Questing ticks were collected from four provinces in Korea in 2021 using the flagging method. After selected 61 DNA tick pools the bacterial *16S rRNA* V3-V4 hypervariable region was amplified and sequenced using the Illumina MiSeq platform. Through conventional PCR the present of *Rickettsia*, *Ehrlichia*, and the endosymbiont *Wolbachia* were combined with sequencing analysis to confirmed the results of mNGS. In total, 6,907 ticks (534 pools) were identified as (*Haemaphysalis* spp., *H. longicornis*, *H. flava*, *I. nipponensis*, and *A. testudinarium*). Through mNGS, 240 amplicon sequence variants were identified. *Rickettsiella* and *Coxiella* were the dominant taxa, present of the pathogenic bacteria genera *Rickettsia* and *Ehrlichia*, endosymbiotic bacteria genera *Wolbachia* and *Spiroplasma* were identified. As s results of conventional PCR: *Rickettsia* was the most prevalent (61.42 %), followed by *Wolbachia* (5.05 %), and *Ehrlichia* by (4.87 %), whereas *Bartonella* was not detected. In this study, mNGS analysis revealed the presence of *Rickettsia*, *Wolbachia*, and *Ehrlichia*, in that order of abundance, and absence of *Bartonella*. These results showed same trend that were confirmed in individual tick DNA using conventional PCR. Therefore, this study provides insights of tick microbiome diversity of tick species, that can be useful for identified novel or rare microorganisms in ticks in large-scale screening studies.

Keywords: Next-generation sequencing, *Haemaphysalis*, *Wolbachia*, microbiome

Abstract Reference: 20451
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 2

How to use learning curves to evaluate the sample size for malaria prediction models developed using machine learning algorithms

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Abstract Content

Machine learning algorithms have been used to predict malaria risk and severity, identify immunity biomarkers for vaccine candidates, and determine molecular biomarkers of antimalarial drug resistance. Developing these prediction models necessitates a large training dataset to ensure reliability when applied to new individuals in the target population. Learning curves can be used to assess training dataset size by evaluating the predictive performance of a model at different training dataset sizes. These curves are agnostic to the specific prediction model, but their construction does require existing data. This presentation aims to demonstrate how to generate and interpret learning curves for malaria prediction models developed using machine learning algorithms. To illustrate the approach, training dataset sizes were evaluated to inform the design of a “mock” prediction modelling study aimed to predict the artemisinin resistance status of *Plasmodium falciparum* malaria isolates utilising *in vitro* transcription data. Data were simulated based on a previously published *in vivo* transcription dataset, and learning curves produced for two machine learning algorithms, sparse Partial Least Squares-Discriminant Analysis (sPLSDA) and random forests (RFs). At the largest training dataset evaluated (626 samples), the predictive performance (balanced accuracy) on a validation set not used for model training was 0.91 for sPLSDA and 0.81 for RFs. The shape of the learning curves indicates that adding more data to the training set could improve the RFs performance. These learning curves can be used to determine the minimum sample size required for future prediction studies and for evaluating published malaria prediction models.

Abstract Reference: 20461
Mode of Presentation: Oral Presentation
Topic: One Health – General 1

The potential of L929 cells in propagating *Orientia tsutsugamushi* originally grown in embryogenic egg

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Abstract Content

In Malaysia, scrub typhus is endemic and one of the most prevalent rickettsial infection being reported. *Orientia tsutsugamushi*, the causative agent of scrub typhus is an obligate intracellular bacterium that is transmitted to human through the bite of *Leptotrombidium* mite. This bacterium is traditionally isolated and propagated in embryonated eggs. However, the process is labour-intensive, limited scalability, and requires specialised equipment, making it less accessible for many laboratories. Another approach is to use cell culture method as a propagation host for this bacterium. In this study, we aim to evaluate the potential of *O. tsutsugamushi* which has been long adapted and kept in embryonated egg to be grown in mammalian cell cultures. Two mammalian cell lines (Vero and L929) were infected with three genotype strains of *O. tsutsugamushi* (Karp, Kato, and Gilliam) which were harvested from the embryogenic eggs culturing method. The presence *O. tsutsugamushi* determined by quantitative RT-PCR and gimenez staining at 14 days interval. After 28 days of culture, Gilliam 94 and Karp 94 grown in L929 cells showed signs of propagation, although at a slow rate. Most of the other isolates showed a little to no progress, with some showing presence of other bacteria. These findings highlighted the potential of L929 cells as an alternative propagation host for *O. tsutsugamushi*, providing a more accessible and scalable method for antigen production.

Keywords: rickettsia, scrub typhus, *Orientia tsutsugamushi*, tissue culture, intracellular bacteria

Abstract Reference: 20463
Mode of Presentation: Oral Presentation
Topic: Entomology - Mosquito Vectors

Forest restoration reduces the zoonotic vector *Anopheles balabacensis* population in Sabah, Malaysia

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Abstract Content

Anthropogenic changes to forest cover have been linked to an increase in zoonotic diseases. In many areas, natural forests are being replaced with monoculture plantations, such as oil palm, which reduce biodiversity and create a mosaic of landscapes with increased forest edge habitat and an altered microclimate. These altered conditions may be facilitating the spread of the zoonotic malaria parasite *Plasmodium knowlesi* in Sabah, on the island of Borneo, through changes to mosquito vector habitat. We conducted a study on mosquito abundance and diversity in four different land uses comprising restored native forest, degraded native forest, an oil palm estate and a eucalyptus plantation, these land uses varying in their vegetation types and structure. The main mosquito vector, *Anopheles balabacensis*, has adapted its habitat preference from closed canopy rainforest to more open logged forest and plantations. The eucalyptus plantations *(Eucalyptus pellit*a) assessed in this study contained significantly higher abundance of many mosquito species compared with the other land uses, whereas the restored dipterocarp forest had a low abundance of all mosquitos, in particular, *An. balabacensis*. No *P. knowlesi* were detected in any of the vectors collected during the study, however, *P. inui*, *P. fieldi* and *P. vivax* were found in *An. balabacensis*. These findings indicate that restoring degraded natural forests with native species to closed canopy conditions reduces abundance of this zoonotic malarial mosquito vector and thus reduces the human disease risk.It therefore should be incorporated into future restoration research and potentially contribute to the control strategies against simian malarias.

Abstract Reference: 20486
Mode of Presentation: Oral Presentation
Topic: Virology

Development of conditional replication system using Lassa virus-pseudotyped retroviral vector and its application to isolate a drug-resistant variant

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Abstract Content

Lassa virus is endemic in West Africa with 200,000 to 300,000 people infected annually. Due to its high mortality rate, handling replication-competent Lassa virus requires a biosafety level 4 (BSL-4) facility. This requirement significantly limits the number of scientists who can study the Lassa virus, thereby slowing the pace of drug development. So, we developed a conditional replication system using a Lassa virus-pseudotyped retroviral vector. This vector encoding the Lassa virus glycoprotein can only replicate in cells expressing the Gag-Pol gene of murine leukemia virus, allowing it to be manipulated in a BSL-2 laboratory. Previously our research group discovered that lamellarin alpha 20-sulfate inhibits infections by various viruses, including HIV-1, Ebola virus, and SARS-CoV-2. We found that this compound also inhibits Lassa virus glycoprotein-mediated infection. Using the conditional replication system, we isolated a glycoprotein variant capable of inducing replication in the presence of lamellarin, although the variant-mediated infection remained inhibited by the chemical. This glycoprotein variant contained two amino acid substitutions. We analyzed the impact of each substitution on viral entry and expression. One substitution reduced both expression and infection, while the other substitution dramatically enhanced infection by 50 times without affecting the expression. *In silico* analysis suggested that this substitution increases the affinity between the glycoprotein and its receptor, alpha-dystroglycan. This amino acid substitution can induce replication in the presence of lamellarin alpha 20-sulfate by mediating much more efficient viral replication.

Abstract Reference: 20487
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 1

Declining merozoite surface protein-1 polymorphism amidst increased *Plasmodium knowlesi* transmission in Thailand

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Abstract Content

Thailand show a substantial increase in *P. knowlesi* cases, with more than an eightfold rise by 2023 compared to 2018. This study investigates temporal changes in genetic polymorphisms associated with the increased transmission of knowlesi malaria in Thailand over the past two decades. Genomic DNA from 25 recent *P. knowlesi* samples (2018-2023) was sequenced for the 42-kDa region of *pkmsp1* and compared with 24 former samples (2000-2009). Seven unique haplotypes were identified in recent samples, compared to 15 in former samples. Nucleotide diversity and haplotype diversity were lower in the recent period ($\pi = 0.016$, Hd = 0.817) than in the former ($\pi = 0.018$, Hd = 0.942). A higher synonymous substitution rate was observed in both periods ($d_S - d_N = 2.77$ and 2.43, $p < 0.05$). The genetic diversity of *P. knowlesi* in Thailand has decreased, associated with higher transmission intensity and purifying selection. Eight out of 17 mutation points were located on B-cell epitopes and were shared between periods, indicating an adaptive response to evade immune recognition. Population differentiation based on Fst revealed high genetic differentiation between central and southern Thailand or Malaysia, while a lower Fst value between southern Thailand and Malaysia suggests closer genetic relationships. In conclusion, our findings highlight a decline in genetic diversity and purifying selection among the current *P. knowlesi* populations in Thailand, reflecting an adaptive response to increased transmission intensity. These insights contribute to understanding the evolutionary dynamics and movement of *P. knowlesi* and have implications for malaria control strategies.

Abstract Reference: 20489
Mode of Presentation: Oral Presentation
Topic: Veterinary Health

Prevalence of trypanosomes among camels (*Camelus dromedarius*) in Al Batinah governorates, Sultanate of Oman

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Abstract Content

Trypanosomes, which include *Trypanosoma evansi* and *Trypanosoma vivax*, are blood kinetoplastida that cause serious infections in camels, resulting in tremendous economic losses. This study aimed to investigate the prevalence of trypanosomes in camels utilizing molecular and sequencing techniques in Al Batinah governorates, Sultanate of Oman. A total of 425 blood samples were collected and examined using *T. evansi* primers (TBR1/2, ITS1, RoTat1.2 and non-RoTat1.2) and *T. vivax* primers (TviCatL). The highest prevalence was recorded in Al Batinah South at 19.3% (17/88), while the lowest was detected in Al Batinah North at 12.5% (42/337). The overall prevalence of *T. evansi* using TBR1/2 was 13.9% (59/425, CI: 17.5-10.9%). Out of them, only 15 (25.4%) samples were positive by the ITS1 and 55 (93.2%) samples were positive by RoTat1.2 primers. The four positive samples that tested negative by RoTat1.2 were found to be positive using non-RoTat1.2 primers. The TviCatL primers did not detect *Trypanosoma vivax* in any of the samples tested. The phylogenetic analysis of *Trypanosoma evansi* from Omani camels at the ITS rRNA locus demonstrated a high similarity of 97.8% with *T. evansi* isolated from Thailand cattle, and the RoTat1.2 sequences revealed a 99.2% similarity with *T. evansi* from Kenyan camels. The PCV in positive camels was significantly lower than negative camels. To the best of our knowledge, this is the first non-RoTat1.2 *T. evansi* identified in Oman. Further research is needed to determine the prevalence rates and types of *T. evansi* in other governorates and animal species.

Abstract Reference: 20490
Mode of Presentation: Oral Presentation
Topic: One Health – General 1

Assessment of automatic malaria microscopy with artificial intelligence in a non-endemic setting malaria reference laboratory

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Abstract Content

Gold standard for malaria diagnosis is the examination of thick blood smears by optical microscopy. However, this method is time-consuming and well-trained microscopists are needed. New techniques based on digital imaging analysis by deep learning and artificial intelligence methods are an alternative tool for the diagnosis of infectious diseases, including malaria parasites. This study aimed to assess the miLab^{TM} platform (Noul, Korea), a device with full sample preparation and artificial intelligence (AI) analysis of results, for malaria diagnosis. A total of 319 blood samples from patients with suspected malaria were sent to the Spanish Malaria Reference Laboratory for diagnosis by nested-multiplex malaria PCR (NM-PCR). In parallel, these samples were analyzed by thin blood smear microscopy and the miLab^{TM} platform. MiLab^{TM} platform provided suspected positive *P. falciparum* and *P. vivax* results. Comparison of the miLab^{TM} platform with thin blood smear microscopy provided 92% agreement, with sensitivity and specificity values of 93.65% and 89.19%, respectively. Among the 12 samples with a positive result in miLab^{TM} platform but negative with thin blood smear microscopy, 8 were true positive by PCR (sensitivity: 94.4% and specificity: 97.2%). The calculated parasitemia was relatively lower with the miLab^{TM} platform than with thin blood smear microscopy. The MiLab^{TM} Platform managed to detect malaria parasites with a performance similar to thin blood smear microscopy, but without the need for expert microscopists and with the automation of the entire process, including slide smear and staining, allowing it to act as a point of care.

Abstract Reference: 20496
Mode of Presentation: Oral Presentation
Topic: Malaria – Epidemiology 1

Outbreak investigation, including pvserotat and genomic analysis, for an unusual *Plasmodium vivax* malaria outbreak in a malaria-free district of Lao PDR

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Abstract Content

Nakai District in Khammuane Province, Lao PDR, has been considered malaria-free since 2016. Between 1 Jul-16 Aug 2023, 222 *P. vivax (*Pv*)* cases were detected in three villages (total population≈1,400, annual parasite incidence (API)=164) in Nakai District. The Center for Malariology, Parasitology and Entomology (CMPE) responded rapidly and comprehensively with a large-scale outbreak response within 4 days, and 2-rounds of mass drug administration using artesunate pyronaridine with single low-dose primaquine initiated within 2.5 months. Despite a dramatic reduction in transmission, cases continued to be detected. Molecular and serological surveys were undertaken to identify the origin of the outbreak using Pv genomic mapping to distinguish a recent point source from longstanding transmission and evaluate genomic diversity among the parasite population. The response also utilized a Pv serology test and treat strategy (PvSeroTAT) to address liver-stage parasite reservoirs. The serosurvey, in November 2023 enrolled 1,234 (98%) people aged >18 months. Of these, 47 (4%) were positive by PCR, 206 (17%) were positive by serology and 209 (17%) were positive by either PCR or serology. The following month, 205 (98%) people who were positive by PCR or serology were treated with Pv radical cure. Laboratory and data analysis for Pv genomic mapping and risk factors are ongoing, full results will be available before September. This outbreak was a stark warning of the potential for explosive outbreaks in post-elimination settings. These results will inform policy recommendations for the prevention of re-establishment of transmission in Lao PDR as well as the Greater Mekong Sub-region.

Abstract Reference: 20497
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 2

The impact of innovative strategies to accelerate malaria elimination in Lao PDR

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Abstract Content

Lao PDR has demonstrated remarkable progress towards malaria elimination. Malaria cases have fallen from 9,044 (53%=*P.f.*) in 2018 to 2,340 (21%=*P.f.*) in 2022. However, persistent localized transmission hotspots within high-risk populations remain a challenge. To address this, Lao PDR deployed an innovative set of interventions in the highest communities, including targeted drug administration (TDA) followed by monthly intermittent preventive treatment for forest and field goers (IPTf), intensified case detection, and vector control measures. These activities are bolstered by advocacy, early and ongoing community engagement, and census. The Accelerator Strategies were implemented annually between 2020-2023 among the highest-burden communities in Lao PDR. In 2020, a pilot project targeting 5 villages (1,300 people) was implemented and side effects from artesunate-mefloquine were noted. The national program switched antimalarial medicines to artesunate pyronaridine with single low-dose primaquine for the scale-up activities. In 2022-2023, activities were scaled out to 60 villages (23,000 people) and 40 villages (19,000 people), respectively. Strong community engagement, targeted outreach, and high-quality implementation yielded 80-90% coverage for TDA and IPTf. In 2022, the target districts reported 81% fewer cases for *P.f.* and 47% fewer cases for *P.f.*, compared to 2019-2020. A time series analysis to assess the impact of these strategies is underway and results will be available before September. The Accelerator Strategies were well accepted by the community and implemented to a high standard. A dramatic decline in malaria cases was observed when implemented as a complementary, time-limited intervention alongside strong surveillance and response, case management, and vector control measures.

Abstract Reference: 20501
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 2

Malaria imported to the Czech Republic

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Abstract Content

Malaria represents the most important infectious threat in the European travelers to the Sub-Saharan Africa. The objective of this study was to evaluate trends in epidemiology, clinical features and outcomes of imported malaria. The retrospective study analyzed all imported malaria cases recorded by the National Reference Laboratory for Tropical Parasitic Infections from 1992 to April 2024 and malaria cases treated at the University Hospital Bulovka in Prague from 2006 to April 2024. There were imported 742 malaria cases to the Czech Republic during 1992 and April 2024. Fifteen deaths (2.02%) were recorded (14 of *P. falciparum;* one of *P. vivax* imported from India). There were treated 259 patients with malaria at the University Hospital Bulovka during 2006 and April 2024 that represent 55.6% of all cases imported to the Czech Republic. *P. falciparum* was the predominant species (201/259) followed with *P. vivax* (43/259). Falciparum malaria was imported from Sub-Saharan Africa mainly (192/201; 95.5%). Malignant falciparum malaria developed in 43 patients (27% of *P. falciparum* cases). Forty one patients traveled without antimalarial prophylaxis. Four lethal outcomes were observed during the study period. Initial higher level of blood leukocytosis, hemoglobin, C reactive protein and lactate were associated with the risk of death. We observed an increase in imported *P. falciparum* malaria during recent years, which frequently resulted in severe disease, especially in older patients and those with delayed treatment. Described trends in the epidemiology of malaria may help to improve pre-travel consultation and post-travel diagnostics and management.

Abstract Reference: 20504
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 1

Discovering malaria's complexity via volume electron microscopy

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Abstract Content

Malaria, a life-threatening infectious disease caused by *Plasmodium* parasites, remains a significant global health burden. Understanding the intricate interactions between the parasite and its host is crucial for developing effective diagnostic methods and treatments. Volume Electron Microscopy (vEM), a cutting-edge imaging technique, offers unprecedented three-dimensional visualization capabilities, allowing for detailed examination of cellular structures and interactions. The vEM setup enables automated serial sectioning of samples, with the diamond knife removing ultra-thin layers (as fine as 20 nm), subsequently imaged using back-scattered electron detectors. Through this approach, a series of electron micrographs through the depth of a sample can be acquired to achieve high-resolution 3D reconstructions of biological structures. Here, we explore the application of vEM in studying malaria samples, focusing on two prominent species, *Plasmodium falciparum* and *Plasmodium knowlesi*. Different stages of the parasites have been processed to visualize their ultrastructural details, shedding light on the morphological changes induced during different stages of their lifecycle. By elucidating the spatial organization of parasite components and host cell organelles, vEM contributes to our understanding of parasite invasion mechanisms, intra-erythrocytic development, and host immune responses. Moreover, vEM could facilitate the study of drug effects at the subcellular level, aiding in the development of novel antimalarial therapies. This research underscores the potential of vEM as a powerful tool for malaria research, offering insights into the biology of *Plasmodium* parasites and their interaction with host cells, which advance our understanding of malaria pathogenesis and accelerate the development of targeted interventions for combating this devastating disease.

Abstract Reference: 20526
Mode of Presentation: Oral Presentation
Topic: Parasitology - Molecular Parasitology

Artificial intelligence for filariasis detection at the point of care

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Abstract Content

Filariasis presents substantial health burdens in endemic regions worldwide. The accurate detection and differentiation of filaria parasites are essential for providing timely access to treatment and effective disease management. Optical microscopy remains the gold standard method for filariasis diagnosis, however, it suffers from low sensitivity, time-consuming procedures, and the need for skilled analysts. We present a robotic AI system that automatically detects microfilariae in real time in blood smears, upgrading a conventional microscope and without the need for internet connection. The components of the system include a mobile phone securely attached to a microscope eyepiece through a 3D-printed adapter and a mechanical system controlled by the smartphone app, which moves the sample along the X and Y axes and automatically adjusts the focus along the Z axis. The app acquires images with the mobile camera and detects microfilariae species using an AI algorithm on the edge. The system can scan a whole blood smear with a 10x or 40x objective, digitize images, and run real-time AI analysis in under 3 or 15 minutes, respectively. The AI model showed a precision and recall of 94% and 92% for microfilariae detection, and 95% and 98% for species differentiation, including *Loa loa*, *Mansonella perstans*, *Wuchereria bancrofti*, and *Brugia malayi*. We envision a simple and robust device able to upgrade existing optical microscopes in low-resource settings and transform them into AI-driven diagnostic systems, scalable to other parasitic diseases and contributing to reducing the burden of neglected tropical diseases worldwide.

Abstract Reference: 20533
Mode of Presentation: Oral Presentation
Topic: One Health 1

Genetics and geography of lymnaeid vectors: Key aspects in a one health control strategy for fascioliasis

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Abstract Content

Fascioliasis is a snail-borne zoonotic trematodiasis emerging due to climate changes, anthropogenic environment modifications, and livestock movements. Highest prevalences and intensities were reported from four provinces of the northern Bolivian Altiplano, where preventive chemotherapy is ongoing. New strategies are now incorporated to decrease infection/re-infection risk, assessment of human infection sources to enable efficient prevention measures, and additionally a One Health initiative in a selected zone. 25 lymnaeid populations representative of the whole Altiplano, and 11 used for population dynamics studies, were analyzed by rDNA ITS2 and ITS1 and mtDNA cox1 and 16S sequencing. Comparisons of transmission foci data from the 1990’s with those of 2018 demonstrated an endemic area expansion. Altitudinal, northward and southward expansions suggest movements of livestock transporting *G. truncatula* snails, with increasing temperatures transforming previously unsuitable habitats into suitable transmission areas. Transmission foci appear to be stable when compared to past field observations, except for those modified by human activities. For a One Health initiative, the control of only one *Fasciola* species and snail vector species simplifies efforts because of the lower transmission complexity. Vector monomorphism suggests uniformity of vector population responses after control measure implementation. All populations outside previously known boundaries were close to villages, human dwellings and/or schools, and should therefore be considered during disease control planning.

Abstract Reference: 20538
Mode of Presentation: Oral Presentation
Topic: One Health 2

Assessing the prevalence of helminth parasites in urban *Achatina fulica* in Kota Samarahan, Sarawak

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Abstract Content

This study examines the prevalence of *Achatina fulica associated* with helminths in Kota Samarahan, an urban region, and explores the correlation between helminth load and snail weight. Diagnostic methods include wet mount, flotation, sedimentation, and Harada-Mori filter paper strip culture. The study's results indicated that the overall prevalence of the specimens examined was 44.9%. Of the 17 helminth species that have been identified, 15 are considered to be important for public health. *Strongyloides* spp. (16%) was the most prevalent, followed by hookworm (10%). The correlation between snail weight and helminth load was shown to be statistically insignificant through Spearman correlation analysis, with a correlation coefficient of -0.11264 and a p-value of 0.43613 ($p > 0.05$). These results emphasise the possible zoonotic health concerns linked to *Achatina fulica* and stress the need for community awareness, health education, and sanitation measures, particularly in urban areas such as Kota Samarahan and Sarawak, to reduce these risks.

Abstract Reference: 20543
Mode of Presentation: Oral Presentation
Topic: Parasitology

Glucose-6-phosphate dehydrogenase variants: analyzing in Indian *Plasmodium vivax* patients

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Abstract Content

The use of primaquine (PQ) in radical treatment of *Plasmodium vivax* (*Pv*) malaria is currently restricted in patients with glucose-6-phosphate dehydrogenase deficiency (G6PD-d) due to the substantial risk of developing severe hemolytic anemia. The correlation between G6PD and malaria has been extensively researched and investigated, yet it is poorly understood especially in India where the spectrum of mutation causing G6PD-d with context to *Pv* malaria is not well elucidated. This study assessed the different genotypic variants leading to G6PD-d in the Delhi and Goa regions of India and is the first study reported from these areas. A total of 46 retrospective samples (34 *Pv*-mono-infected samples and 12 *Pv*-uninfected samples) were included in the study. PCR amplification and DNA sequencing of eight targeted exons (3,4,6,8,9,10,11, and 12) of the *G6PD* gene were used to analyze various genetic variations that result in G6PD-d. Molecular analysis revealed the presence of four mutations in the study population: 1311C>T, 34.1% & IVSXI 93T>C, 45.5% and two novel mutations 1388G>T, 2.3% and 1398C>T, 2.3% (silent mutation). The bioinformatics and computational analysis demonstrated that R643L mutation in mutated protein causes slight conformational changes that are deleterious. While the role or association between G6PD-d and *Pv*-infected cases remains unclear in light of these mutations, further investigation is needed to fully comprehend and analyse the precise role of these mutations with context to malaria infections.

Abstract Reference: 20545
Mode of Presentation: Oral Presentation
Topic: Water & Food Borne Parasites

Impact of chronic human fascioliasis on protist/protozoan/helminth co-infections: High risk for individuals to acquire concomitant helminth infections in hyperendemic human areas

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Abstract Content

Coinfection and chronicity are the norm in human fascioliasis endemic areas. To assess the role of fascioliasis in multiparasitism, age-, gender- and geographically stratified data from an ongoing transversal study on the epidemiology of parasites and *Fasciola* infections in four rural areas of human hyperendemicity: the highland areas of the northern Bolivian Altiplano (1194 individuals), the Peruvian Altiplano (338 individuals) and the Cajamarca valley of Peru (362 individuals) as well as the lowland area of the Nile Delta in Egypt (679 individuals), is analyzed. Fascioliasis infection is present in all age groups. Only in the Egyptian population, is the prevalence of *Fasciola* higher in females than in males in all age groups. Considering protist/protozoa and helminth species detected, the homogeneity of the parasite spectrum is notable. The proportion of individuals who harbored mixed infections was 96.5 % in the Bolivian Altiplano, 100% in the Peruvian Altiplano, 98.7% in the Peruvian Cajamarca valley, and 84.1% in the Nile Delta. Considering the four areas together, the results of logistic regression analysis suggest that the fascioliasis risk increases as the total number of helminth species per individual increases, also indicating that both protozoan and helminth species present in the coinfection influence this process. Our analysis shows that numerous factors might have an influence on the presence of coinfection in human fascioliasis.

Abstract Reference: 20547
Mode of Presentation: Oral Presentation
Topic: Parasitology - Molecular Parasitology

Phenotypic characterisation of different morphs of helminth egg species applying a computer image analysis system (CIAS): Usefulness in the etiological diagnosis of helminthiasis

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Abstract Content

In helminthiasis, shape, and size of the fluke eggs from biological samples are crucial diagnostic features. The aim of the present study is to validate the identification of helminth species based on the shape and size of eggs, characterizing their morphometric traits using a computer image analysis system (CIAS). Eggs of three helminth species with three very different morphs were morphometrically characterized: a) *Calodium hepaticum* eggs from Sigmodontinae species (*Akodon azarae*, *Calomys callidus*, and *Oligoryzomys flavescens*) from Argentina; b) *Schistosoma haematobium* eggs from sub-Saharan migrants (from Mali, Mauritania and Senegal) in Spain, and c) *Fasciola hepatica* and *F. gigantica* eggs from humans and animals from fascioliasis human endemic areas (from Bolivia, Peru, Georgia, Egypt, and Vietnam). Each individual egg was photographed using a microscope connected to a digital camera, controlled by LAS software. Standardized measurements, depending on the morph of the egg species, using an image analysis software (Image Pro Plus), were calculated. Multivariate analysis and geometrical morphometrics were used. The results show the usefulness of CIAS, indicating morphological variations of eggs according to the parasite's geographical origin or the definitive host species. The morphological phenotyping of helminth eggs provides complementary information to that already obtained by existing molecular tools.

Abstract Reference: 20551
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 2

Active case detection and treatment of malaria in pregnancy using LAMP technology (LAMPREG): A pragmatic randomized diagnostic outcomes trial

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Abstract Content

Malaria infection during pregnancy (MiP) leads to low birthweight, a key risk factor for neonatal and childhood morbidity and mortality. Diagnosis of MiP is challenged by sub-clinical presentation and low parasitemia. This large scale study assessed the effectiveness of loop-mediated isothermal amplification (LAMP) in the detection of MiP during antenatal care (ANC) in Ethiopia. A pragmatic randomized diagnostic outcomes trial was conducted at eight rural health centres and hospitals from 2020-3. A total of 2425 pregnant women were enrolled and randomized to 855 in the standard of care (SOC) arm and 1570 in the LAMP arm. Malaria diagnosis relied on microscopy and rapid diagnostic tests (RDTs) in the SOC group and additional LAMP testing (LoopampTM, Human Diagnostica) of both symptomatic and asymptomatic women in the intervention arm. Artemether-lumefrantine (Co-artemTM) was given to patients positive by any method. LAMP was more sensitive (96.62%, n=3700) than microscopy (70.78%, n=3850) and RDTs (76.23%, n=3835) when compared to gold standard molecular testing. Newborns at day 1 in the LAMP group had higher average birthweights (3221.80 g vs. 3199.07 g, p=0.339) and at 28 days (4285.93 g vs 4165.64 g, p=0.003). LAMP was associated with improved birth weight gain (1060.65 g vs 974.89 g, p=0.013). In a multivariable model, being in a high transmission setting (OR 294.02, p<0.001), increased visits to the antenatal clinic (OR 48.03, p=0.02) were associated with improved weight gain at birth, while being in SOC arm was associated with reduced weight gain (OR -58.86, p=0.08).

Abstract Reference: 20557
Mode of Presentation: Oral Presentation
Topic: Virology

Spatiotemporal analysis of dengue cases in Bang Pong district of Thailand from 2013 to 2022: Spatiotemporal pattern, clusters detection, and spatial regression

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Abstract Content

Dengue has persisted in Thailand for almost 70 years. Certain areas, like Ban Pong district in Ratchaburi Province, have experienced disproportionately high disease burdens. To delve into this, we investigated case distribution and clustering in the area supplemented by spatial regression. After ethical approval, dengue case data from 2013 to 2022 in Ban Pong were obtained from the R506 reporting system. Environmental, population, and built area data were sourced. Built area percentage was derived from Sentinel-2 satellite imagery. We analyzed case numbers, incidence, age-stratified incidence, and seasonal trends. Clusters were identified using the local Moran's I index. Model fit was assessed using AIC for population density, built area percentage, and both predictors from 2017 to 2022. Dengue incidence varied annually from 0.6527 to 6.9443 per 1,000 population with a seasonal pattern. Children under 10 years had the highest incidence. Higher incidence and clusters were observed in the district's northern and northeastern parts. Spatial regression models yielded comparable AIC values. Elevated incidence among children likely stems from their lack of immunity. Clusters in the district's borders suggest possible case importation and/or spillover. Comparable AIC values indicate the interchangeability of population density and built area percentage in regression. In this hotspot, children under 10 were most affected, with clusters primarily at district borders. Population density and built area percentage showed similar predictive performance. Further research could explore these dynamics to inform targeted interventions.

Abstract Reference: 20560
Mode of Presentation: Oral Presentation
Topic: Veterinary Health

Current status of fish trypanosomiasis in China and the pathogens: A comprehensive review

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Abstract Content

China is the world's largest aquaculture producer, with fish farming in a vast scale, and providing a crucial source of dietary protein. However, with the expansion of fish farming, various farmed aquatic animals face threats from pathogens such as viruses, bacteria, and parasites, which severely impact the aquaculture's sustainability. Since 1997, fish trypanosomiasis has frequently broken out in both freshwater and marine fish farms in China. Regions such as Sichuan, Hong Kong, Hainan, Guangdong, and Fujian have reported outbreaks among species like southern catfish (*Silurus meridionalis*), areolate grouper (*Epinephelus areolatus*), Brown-marbled grouper (*Epinephelus fuscoguttatus*), humpback grouper (*Cromileptes altivelis*), barramundi (*Lates calcarifer*), largemouth bass (*Micropterus salmoides*), and large yellow croaker (*Larimichthys crocea*), with mortality rates ranging from 30% to 60%. These outbreaks highlight the widespread and severe impact of trypanosomiasis on China's aquaculture. However, despite its wide distribution and high mortality, the diseases are unclear in terms of their infection sources and transmission routes, and still lack effective treatment and control methods. Thus, research on fish trypanosomiasis and the improvement of prevention and treatment methods are urgently needed. To address this challenge, research teams in China, such as those from Fujian Agriculture and Forestry University, Sichuan Agricultural University, and Yantai University, are actively actively investigating these issues. Experts from Sun Yat-sen University, Qingdao Agricultural University, and the South China Sea Fisheries Research Institute are collaborating to identify *Trypanosoma epinepheli* and *Trypanosoma carassii* as the main pathogens. They have established corresponding research platforms, aiming to clarify the sources and transmission pathways of trypanosomiasis, and to develop effective prevention and treatment measures strategies.

Abstract Reference: 20561
Mode of Presentation: Oral Presentation
Topic: Parasitology and Microbiology

One health approach for protozoan parasites surveillance in the Republic of Korea

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Abstract Content

One health approach, involving collaboration between sectors with responsibility for human health, wild life and the environment, is necessary to prevent and control zoonotic diseases. Small mammals are natural reservoir hosts of zoonotic diseases including protozoan parasites. This study aimed to investigate the current status of protozoan parasites from small mammals in the Republic of Korea (ROK) and perform genetic comparisons with human infection case. Genomic DNA was extracted from 331 small mammal blood. The extracts were amplified for the 18S rRNA of Babesia and Theileria and the ITS1 of Trypanosoma spp. To confirm the genetic similarity and genotype of protozoan parasites, phylogenetic trees were constructed. We identified 23.9% for T. grosi and 10% for B. microti. However, we did not find any Theileria. All T. grosi are belong to be of the AKHA strain. B. microti US-type-infected small mammals were detected throughout the whole country, but the Kobe type was only detected in Jeju island. Two cases of locally transmitted babesia infection in human have been documented. Our study shows that different Babesia genus have been detected in human and wild small mammals. Our study is the first nationwide survey that confirmed T. grosi and B. microti infections at the species level from small mammals in the ROK. Also, we confirmed the Kobe type of B. microti from small mammals in the ROK for the first time. Following one health approach, these results provide valuable information for further molecular epidemiological studies on these zoonotic parasites.

Abstract Reference: 20564
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 3

Epidemiology and risk factors for malaria deaths in Sarawak over a 10 year period from 2014 to 2023

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Abstract Content

Malaria is a global health issue and public health threat in Sarawak. Most malaria cases in Sarawak are zoonotic in origin from *Plasmodium knowlesi* (*P.k*), followed by imported human malaria either *Plasmodium vivax (P.v)* or *falciparum (P.f)*. All malaria deaths were routinely reviewed at the state level. Cases from 2014 to 2023 were analysed. Patient's demographic and clinical data were collected. A total of 27 deaths were reported, 25 (92.6%) were infected by *P.k* and others by *P.f* . Most cases were female 17(63%), local natives 25(92.6%), median age of 63-year-old(IQR 22) and farmers 14(52%). 70% of cases had hypertension and diabetes mellitus. Cases first sought treatment at district hospitals 14(48%) and primary care clinics 10(37%). The mean duration from symptoms onset to healthcare presentation was 5.5 days. Fever was the commonest symptom. There were 22(81.5%) deaths occurring within 3 days of admission, in which 14(48%) deaths occurred within 24 hours. When compared with 5 deaths which occurred later (≥ 3 days of admission), mean duration from symptoms onset to presentation was not statistically significant between the two groups (p=0.063). All cases fulfilled at least one severe malaria criteria and mean parasite count on presentation was 151,905. Overall, 21 (78%) received intravenous artesunate, with 3 cases died prior to treatment due to missed diagnosis. *P.k* malaria was the main cause for malaria deaths in Sarawak. Late presentation with severe illness was the main contributing factor of death.

Abstract Reference: 20566
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 3

Malaria surveillance assessment in Lao PDR: a WHO tool to identify the system's strengths and weaknesses and inform the development of evidence-based, high-quality, and effective interventions to advance towards malaria elimination

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Abstract Content

Lao PDR aims to eliminate malaria by 2030. Strengthening malaria surveillance activities is key to meeting this target. In 2022, the Center for Malariology, Parasitology, and Medical Entomology (CMPE) conducted a comprehensive assessment of malaria surveillance to identify the system's strengths and weaknesses and inform interventions to strengthen surveillance activities. CMPE used the WHO Malaria Surveillance Assessment Toolkit and conducted quantitative surveys at the health facility (n=17) and community levels (n=14); a literature desk review supported by qualitative interviews with government (n=5) and implementing (n=3) partners; and a service delivery-level and a desk-level data quality assessment on core malaria variables. All levels and sectors of the health care system in Lao PDR are mandated to report malaria cases; 99% of reports recorded as complete and 88% of monthly reports submitted on time across all health facilities. 95% of confirmed malaria cases were correctly classified in the elimination districts, where case classification is mandated. Data are used to guide policy and surveillance and 78% of data review meetings occur when expected. Malaria staff reported some challenges with data use including village-level data not available in the dashboards. Additionally, data on care-seeking behavior and testing of symptomatic cases is not systematically collected. Priority recommendations included supply management strengthening, expansion of case investigation and classification nationwide, and surveillance activities enhancement beyond the village level. These recommendations were included in the Mid-term Review for the Malaria National Strategic Plan 2021-2025 and the Global Fund's RAI4E application to strengthen Lao PDR's progress toward malaria elimination.

Abstract Reference: 20569
Mode of Presentation: Oral Presentation
Topic: Entomology - Vector and Vector-Borne Diseases

Hybridization of Ixodes inopinatus and Ixodes ricinus in Southern Europe and its impact on transmission of tick-borne pathogens

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Abstract Content

In 2014, a new tick species *Ixodes inopinatus* was described from Spain based on morphology and the 16S rRNA gene sequence. However, several follow-up studies have shown that morphological differentiation of *I. ricinus* and *I. inopinatus* is difficult and that the 16S rRNA gene lacks the power to distinguish these two tick species. Previously, we used a combination of nuclear and mitochondrial markers to assess the differences between *I. inopinatus* from Algeria and *I. ricinus* from the Czech Republic and found signs of hybridization between them. This study aimed to identify Ixodid ticks from the Czech Republic, Italy, and Algeria and screen them for selected tick-borne pathogens. To identify *I. ricinus*, *I. inopinatus* and their hybrids, *TROSPA* and *COI* genes were sequenced. Ticks were then screened for the presence of *Borrelia burgdorferi* s.l., *Borrelia miyamotoi*, *Rickettsia* spp. and *Anaplasma phagocytophilum*. This study shows that *I. inopinatus* is a dominant tick species in Algeria, *I. ricinus* is the dominant tick species in the Czech Republic, and southern Italy likely serves as a hybridization zone between *I. inopinatus* and *I. ricinus*. Prevalence of *B. burgdorferi* s. l. and *Rickettsia* spp. was much higher in *I. inopinatus* than in *I. ricinus*, which might be attributed to geographical and ecological differences between the two species. The impact of a) transport of ticks by migratory birds between North Africa and Europe, b) tick hybridization, and c) climate change on transmission and spread of tick borne pathogens will be discussed.

Abstract Reference: 20574
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 3

Molecular epidemiology analysis of *Plasmodium vivax* in the Republic of Korea

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Abstract Content

Plasmodium vivax is the only indigenous species in the Republic of Korea (ROK). In this study, we performed a molecular analysis using four genes to determine patient cases and a mdr-1 gene to find drug resistance for vivax malaria patients in the ROK. Total 175 samples are tested, composed of recurrence (n=21), suspected clusters (33 cases, n=99), imported (n=4), and the ROK army (n=51) in 2023. Based on DNA sequences of four genes like as *PvMSP-1*, *PvAMA-1*, *PvCSP*, and *PvDBP*, subtypes of gene were compared between patients. Pvmdr-1 was only analyzed in recurrent, imported, and military patients. Among 21 recurrent patients, 14 patients could be defined recrudescence or relapse, and 7 patients were defined reinfection. Of the 33 suspected cluster cases, 13 cases were confirmed to have the same genotype between patients. In pvmdr-1 gene mutation analysis, 9 SNPs were identified. The Y976F, which is known to be clinically associated with resistance, has not been observed. Molecular epidemiological analysis of vivax malaria in recurrent cases were able to determine the cause of recurrent. Through cluster analysis identified with the same genotype, it could be identified areas where patients and mosquitoes should be intensively managed. Although no mutation in resistance gene to chloroquine has been observed in this study, it should be continuously monitored for the mutation on drug resistance genes. Molecular epidemiology analysis for malaria may helpful to control malaria including patient management and drug-resistant monitoring for malaria elimination in the ROK.

Abstract Reference: 20587
Mode of Presentation: Oral Presentation
Topic: Veterinary Health

Phylogenomic insights into the inter- and intraspecific relationships between trombiculid mites (chiggers) parasitising birds in Southeast Asia

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Abstract Content

Chiggers, the parasitic larval stage of trombiculid mites, are vectors of a bacterial zoonosis (scrub typhus) and can cause severe dermatitis (trombiculiasis) when feeding. In non-human hosts, including birds, trombiculiasis can be life-threatening and has impacts both in poultry production and conservation of rare species. However, bird chiggers have been neglected historically in the context of both scrub typhus epidemiology and as agents of dermal pathology, and lack molecular resources to aid identification and systematic studies. Here, chiggers were collected from 65 species of wild birds, as well as domestic chickens, across Malaysia and Thailand. In Thailand (Nan province), collection of free-living trombiculids was also performed in villages where chickens were heavily parasitized. A total of 23 chigger species were recorded, and approximately 60 pools of 10 species were successfully subjected to genome sequencing on an Illumina platform. Despite substantial host contamination in the genomic datasets, complete mitogenomes for *Neoschoengastia gallinarum* from Malaysia, a cause of avian trombiculiasis, were assembled successfully. Moreover, complete mitogenomes were obtained from *Eutrombicula wichmanni*, the primary cause of human trombiculiasis in Asia, using adult mites from Nan. However, since many samples did not produce complete mitogenomes, we applied the novel "Read2Tree" pipeline to unassembled sequence reads, enabling phylogenomic signals from chigger nuclear genes to be harvested. This generated a robust tree for all 10 sequenced species, which were placed into monophyletic groups without clear geographic segregation. This study emphasises the feasibility of short-read genome sequencing for generating phylogenomic resources for these minuscule and neglected ectoparasites.

Abstract Reference: 20589
Mode of Presentation: Oral Presentation
Topic: Parasitology - Molecular Parasitology

Liver transcriptomics and microbiome data revealed species-specific responses during infections with three food-borne liver flukes

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Abstract Content

Food-borne trematodes *Opisthorchis viverrini* and *Clonorchis sinensis* are classified as biological carcinogens to humans, while *O. felineus* is a non-carcinogen. The key precarcinogenic pathways of carcinogenesis by the liver flukes are studied fragmentarily, the role of microbiome is remained unexplored. In order to study differences in the activation of signaling pathways in the liver and to characterize the microbial communities, specific pathogen free hamsters were infected with metacercariae of *C. sinensis* (South Korea), *O. viverrini* (Thailand) and *O. felineus* (Russia). We performed high-throughput sequencing (MiSeq, Illumina) of microbiome and the liver transcriptomes at 1 and 3 months postinfection (HiSeq Illumina). Furthermore, *Helicobacter pylori* content was also assessed. Microbiome analysis revealed the significant phylogenetic diversity of the microbial communities among three liver flukes. The infection with any liver fluke significantly modified the bile and faecal microbiome, increasing the abundance of *H. pylori*. *C. sinensis* infection caused changes in the expression of 3148 genes in the liver; *O. viverrini* – 1464 genes, and *O. felineus* – 1408 genes. The responses of individual liver cells to transcriptomic response were also species-specific. Infections with *C. sinensis* and *O. felineus* are most characterized by the profibrotic changes, whereas *O. viverrini* – by proneoplastic abnormalities. The study provides first insights into comparative mechanisms of biological carcinogenesis of closely related foodborne trematodes. Mechanisms of host microbiome modification by the liver flukes are discussed. The study is supported by the Russian Science Foundation (№24-44-00048).

Abstract Reference: 20604
Mode of Presentation: Oral Presentation
Topic: Parasitology

Tick cell line contributions to mitochondrial genomics and phylogeny

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Abstract Content

Having accurate and available markers in which to distinguish between arthropod species is essential to deciphering species boundaries and monitoring vector surveillance amongst parasites of significant human and veterinary concern. Accurate tick taxonomic identification and phylogenetic inference is an ongoing challenge hampered by the scarcity of genomic data, suitable markers, and presence of cryptic species whose similar morphological features may lead to misidentification. The use of accurate and cost-effective sequencing platforms has enabled the accumulation of tick derived genomic data. Whilst complete nuclear genomes are the aspiring gold standard, their large genomic sizes (1-7Gb) present difficulties with assembly and annotation. Owing to their considerably smaller genomic sizes (14-17Kb), high copy number, and maternal inheritance, mitochondrial genomes (mitogenomes) are easily assembled and analysed for accurate and reliable taxonomic differentiation. In this study, we present the complete mitochondrial sequences of nine tick cell lines derived from *Amblyomma*, *Rhipicephalus*, *Hyalomma* and *Ixodes* spp., sourced from the Tick Cell Biobank, including the first mitogenome of *Amblyomma variegatum*. We investigated the phylogenetic relationship of these cell line-derived mitogenomes within the landscape of over 230 publicly available mitogenomes using the concatenation of 8 protein-coding genes. Our findings reliably place *A. variegatum* as sister to *Amblyomma hebraeum*and corroborate the taxonomic placement of these tick cell lines. Our findings underscore the importance of mitochondrial genomics in advancing our understanding of tick taxonomy and evolutionary relationships. This study contributes to stabilizing and improving the growing knowledge of tick phylogeny and taxonomic classification amongst vectors of significant concern.

Abstract Reference: 20606
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 2

Exploring the *in vitro* pharmacology of 8-aminoquinoline antimalarial compounds.

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Abstract Content

The 8-aminoquinolines are the only licensed class for the treatment of relapsing malaria. Key members of the class include currently licensed primaquine and tafenoquine; as well as legacy compounds: pamaquine and pentaquine. The hypothesised mode of action for primaquine comprises a 2-step biochemical relay: (1) Cytochrome P450 (CYP)-mediated (predominantly CYP 2D6) metabolism into reactive intermediates; and (2) redox cycling of metabolites with CYP reductase to form anti-parasitic levels of Reactive Oxygen Species (ROS). This work investigated whether this mechanism is class-wide; scrutinising CYP-mediated metabolism of, and ROS production from the 8-aminoquinolines. This study explored the physicochemical and pharmacological properties of 8-aminoquinolines and clinically relevant combination partners. Key analyses include hepatic metabolism with HμREL® co-culture clearance assay and CYP-specific metabolism, inhibition, and induction. Preliminary data into the pharmacodynamic mechanisms of 8-aminoquinoline action includes the measurement of CYP-mediated ROS using Pan-CYP and CYP-specific inhibitors and measures of oxidative stress including Haem Oxygenase-1, as well as interrogation of *in vitro* efficacy using a *Plasmodium cynomolgi* liver stage assay. Evidence is presented in support of a divergent bioactivation step (1), and convergent ROS-mediated step (2) in the mechanism of 8-aminoquinolines, with tafenoquine not showing hepatic metabolism or CYP-mediated ROS production. Tafenoquine licensing now requires compulsory co-administration with chloroquine due to treatment failure with alternative regimen, piperaquine-dihydroartemisinin. This study suggests that these drug-drug interactions are unlikely to be CYP-mediated for primaquine and tafenoquine. Ongoing research is underway to confirm the potentiating effect of chloroquine, and inhibitory effect of dihydroartemisinin on the redox-related efficacy of 8-aminoquinolines.

Abstract Reference: 20607
Mode of Presentation: Oral Presentation
Topic: One Health 2

The importance of FAIR data in vector research

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Abstract Content

To contribute to vector-borne disease mitigation, vector/health data availability is paramount. Therefore, compliance to FAIR principles helps remove blocks on how these data can be used for information flows to subsidise policies and decision making for vector control. FAIR principles (findable, accessible, interoperable and reusable) were created to support the use of the increasing volume and complexity of digital data. GBIF is an international network and data infrastructure funded by the world's governments and aimed at providing anyone, anywhere, open access to data about all types of life on Earth. GBIF has been engaged in increasing the representation of health data in its databases. Here, we show the results of a collaboration between GBIF, TDR/WHO and GigaScience Press to increase vector data content in the GBIF network. Two calls for data paper publication were released in 2022 and 2023, the calls mobilised 670,000 records published in GBIF and distributed in 19 data papers published in the Gigabyte journal. The datasets are ‘Findable’ by having being assigned a persistent identifier (DOI) when registered on GBIF; ‘Accessible’ by being available for download in GBIF; ‘Interoperable’ because data is mapped and formatted the widely used biodiversity standard (DwC); ‘Reusable’ as it is associated with detailed documentation on the data as well as released under a Creative Commons license. Publishing data to GBIF allows for open and FAIR sharing of data about vectors, increasing vector data relevance, exposure to wider audiences, compliance to FAIR principles and open science guidelines.

Abstract Reference: 20608
Mode of Presentation: Oral Presentation
Topic: One Health – General 1

Zoonotic malaria: Primate ecology as part of the solution

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Abstract Content

Monkey malaria, *Plasmodium knowlesi*, is a zoonotic form of malaria whose natural host is macaque monkeys (*Macaca fascicularis* and *Macaca nemestrina*). The infection of humans with *P.knowlesi* has been associated with changes in landuse, these landuse changes not only impact people and mosquitos, but also change the way primates use the landscape. The ZooMal project is a collaboration between Australian and Indonesian universities covering a range of disciplines including public health, parasitology, social science, entomology, geography and primate ecology. The project has used motion triggered cameras to map macaque and human occupancy across a variety of landscapes. Preliminary results show that Long-tail and Pig-tail macaques utilise the landscape (and landuses) in different ways. The results also highlighted high risk areas when humans and macaques overlap. Understanding how Long and Pig tail macaques utilise differing landuses, and how they respond to change will assist in landscape management to manipulate macaque populations. When combined with mosquito and human ecology, this knowledge of macaque ecology will assist in the control of *P.knowlesi* in humans.

Abstract Reference: 20628
Mode of Presentation: Oral Presentation
Topic: Entomology - Vector and Vector-Borne Diseases

Ticks and tick-borne pathogens in the United Arab Emirates

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Abstract Content

Ticks are hematophagous ectoparasites of domestic animals and wildlife, and tick-borne pathogens transmit a variety of diseases to humans and animals. Camels are a key part of UAE’s heritage as a source of milk and meat, a beast of burden and for sport. Ticks have been recorded throughout the year on camels in UAE with several tick-borne microbes detected including some pathogenic for animals as well as humans, e.g. Crimean-Congo Hemorrhagic Fever. This raises concern about camel ticks as potential vectors of disease with implications for public health and agricultural production. Continued research on ticks and tick-borne microbes in the UAE is needed to better understand this risk. Therefore, we collected ticks from various animal species including camels, cows, sheep, goats, horses, dogs and birds from the different Emirates of UAE. With over 600 tick samples collected, morphological and molecular identification reveal only 6 species occurring in UAE: *Hyaloma dromedarii* (by far the most prevalent), *Hyaloma anatolicum*, *Rhipicephalus sanguineus*, *Rhipicephalus evertsi*, *Rhipicephalus pulchellus*, and *Ornithodoros capensis*. *Hyaloma dromedarii*, and *H. anatolicum* screened for different pathogens and samples are in sequencing stage. We also assessed camel tick microbiome using 16S rRNA gene-based analysis that revealed genera *Francisella* with high relative abundance. We performed camel tick distribution mapping using MaxEnt modeling for surveillance strategies for ticks and tick-borne diseases and identified future priority areas. An overall aim is to build the necessary scientific knowledge helpful for public authorities to set the best tick management practices through a One Health approach in UAE.

Abstract Reference: 20653
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 2

Accelerating malaria elimination with an application of LAMP methods in Laos: Introduction of JICA/AMED Laos SATREPS project 2023-2028

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Abstract Content

In Laos, *Plasmodium falciparum* (*Pf*) and *P*. *vivax* (*Pv*) are the main species of human malaria. The Lao government adopted a goal of malaria elimination by 2030. The key interventions are distribution of long-lasting insecticide treated nets, early-diagnosis and early-treatment by artemisinin-based combination therapies, and introduction of the 1-3-7 approach. For monitoring the spread of drug resistance of *Pf*, integrated-drug-efficacy surveillance is implemented. Currently, targeted drug administration is also implemented in Savannakhet and Attapeu provinces for *Pf*, and Salavan and Sekong provinces for *Pv*. Thanks to those efforts, the number of malaria cases decreased from 39,589 in 2013 to 811 in 2023. In 2010, *Pf* was predominant species (98%), while in 2023, *Pv* was predominant species (89%). This result suggested that *Pf* is close to the elimination. In contrast, elimination of *Pv* remains difficult because of relapse due to hypnozoites and presence of low-density infections that cannot be detected by the standard diagnostic methods but can be a source of transmission in the endemic areas. To achieve malaria elimination by 2030, an effective strategy for *Pv* is urgently needed. Therefore, a high-sensitive diagnostic method, i.e. the loop-mediated isothermal amplification (LAMP) method will be implemented in the 25 healthcare facilities in the endemic areas under the scheme of the SATREPS project. Malaria LAMP induction trainings for researchers at IPL, CMPE and Savannakhet were conducted in 2023 and will be extended to other provinces in 2024. We expect that an introduction of malaria LAMP methods will accelerate malaria elimination, especially *Pv*.

Abstract Reference: 20654
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 2

Methylene blue treatment reveals biomarkers associated with cerebral malaria in coatneyi-infected macaque model

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Abstract Content

Plasmodium falciparum remains a major threat to the public health with its most common severe form of complication, cerebral malaria, which is fatal within 24 to 72 hours. *P. berghei* ANKA infection in CB57BL/6 mice has been widely used as the murine model for human cerebral malaria, but its relevance has been questioned due to their dissimilarity in histopathology. Hence, *P. coatneyi* – the malaria parasites of non-human primates – shares similar pathophysiological features with *P. falciparum* infection, and has been sporadically used as a model for severe malaria. With the emergence of drug resistance malaria, methylene blue has shown to be effective against chloroquine-resistant *P. falciparum*. Furthermore, methylene blue treatment has improved survival and ameliorated experimental cerebral malaria in murine model. Here, we compared the gene expression profiling in different organs (brain, heart, kidney and liver) of uninfected, untreated and methylene blue-treated Rhesus macaques infected with *P. coatneyi*. We were able to cluster the infected samples from uninfected and treated samples in brain stem based on their genetic profile. Differential gene expression analysis revealed the effectiveness of methylene blue treatment as it reversed the effect of infection on the brain tissues. By comparing the differential expressed genes in three datasets (human infected peripheral blood, *Macaca mulata* infected brain stem and *Macaca mulata* infected blood), we have successfully identified several genes that are associated with cerebral malaria. These biomarkers would accelerate the prediction and diagnosis for cerebral malaria or other complicated infections by *P. falciparum*.

Abstract Reference: 20660
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 3

Analysing natural environment risk factors of the last indigenous malaria cases in West Java, Indonesia using remote sensing and geographic information systems

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Abstract Content

Over the past two decades, malaria has become a major problem in many parts of the world. This is because host migration and cases from travel for work or tourism can potentially cause local transmission. The relationship between malaria and natural environmental risk factors (NERFs) was investigated in this study. The malaria information system (e-SISMAL) in West Java province provided malaria data per sub-district for 2019. Data from the Climate Hazards Group InfraRed Precipitation with Station (CHIRPS) were obtained for the monthly rainfall records. Landsat 8 Collection 2 Level 1 images covering the study area were used to determine normalised difference vegetation index (NDVI), normalised difference moisture index (NDMI), normalised difference wetness index (NDWI), normalised difference soil index (NDSI) and land surface temperature (LST). The distribution mapping of the estimated regression coefficients and the standard deviation of the residuals was then analysed using Ordinary Least Square (OLS) in ArcGIS Pro. The result of the Koenkers test (p-value 0.055620) showed stationarity ($p>0.05$), which implies stable relationships in the spatial context and good linear models for the predictions. The Jacque-Bera test result (p-value 0.000000) indicated a non-normal residual. Malaria was explained by 4.03% (R^2) of the NERFs. Almost all NERFs contributed significantly. Household and personal factors are suggested as the main parts of the prevention. Despite a larger area of NERFs in the province, malaria can be prevented through relevant efforts with household and personal factors.

Abstract Reference: 20661
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 2

A simple tool to kill malaria parasites in mosquitoes

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Abstract Content

A novel approach for malaria control is to kill the parasites in the mosquito with antimalarials rather than in the human [1]. This strategy targets a smaller population of parasites and reduces the chances of selecting for antimalarial resistance. It also brings into scope antimalarials otherwise unsuitable as drugs for people. We aimed to develop tools to deliver antimalarials directly to infected mosquitoes and quantitate how well compounds kill parasites in mosquitoes. We infected *Anopheles stephensi* mosquitoes with *Plasmodium falciparum*, then fed them sugar water laced with antimalarials. A single feed of sugar water laced with 100µm atovaquone—a potent antimalarial that specifically inhibits parasite mitochondrial electron transport—totally blocked oocyst and sporozoite production. Similarly, T-111, a lead compound that also inhibits parasite mitochondrial electron transport [2], also prevented oocyst and sporozoite development after one feed. We next explored simple ways to deploy such compounds in field settings. We freeze-dried T-111 and sucrose onto cotton wool, reconstituted with water, and fed to mosquitoes, which completely prevented oocyst and sporozoite development. Sugar baits laced with antimalarials are an attractive control strategy to reduce transmission by killing the parasites in the mosquito. Advantages include targeting a smaller population of parasites to reduce resistance, and vastly widening the array of useable antimalarials compared to human drug strategies. We discovered that antimalarials freeze-dried onto cotton wool, when later wetted and placed in the vicinity of mosquitoes, kill parasites thus offering a simple, inexpensive control strategy.

Abstract Reference: 20675
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 2

Harnessing cholesterol uptake of malaria parasites for therapeutic applications

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Abstract Content

Parasites, such as the malaria parasite *P. falciparum*, are critically dependent on host nutrients. Interference with nutrient uptake can lead to parasite death and, therefore, serve as a successful treatment strategy. *P. falciparum* parasites cannot synthesise cholesterol, and instead source this lipid from the host. Here, we tested whether cholesterol uptake pathways could be 'hijacked' for optimal drug delivery to the intracellular parasite. We found that fluorescent cholesterol analogues were delivered from the extracellular environment to the intracellular parasite. We investigated the uptake and inhibitory effects of conjugate compounds, where proven antimalarial drugs (primaquine and artesunate) were attached to steroids that mimic the structure of cholesterol. These conjugated antimalarial drugs improved the inhibitory effects against multiple parasite lifecycle stages, multiple parasite species, and drug-resistant parasites, whilst also lowering the toxicity to human host cells. Steroids with introduced peroxides also displayed antimalarial activity. These results provide a proof-of-concept that cholesterol mimics can be developed as a drug delivery system against apicomplexan parasites with the potential to improve drug efficacy, increase therapeutic index, and defeat drug resistance.

Abstract Reference: 20677
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 1

Perceptions surrounding urine color can hinder primaquine safety monitoring by community health workers (CHWs)

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Abstract Content

Primaquine use to eliminate liver stages of *P. vivax* is undermined by adherence issues due to the prolonged period of delivery, and the risk of haemolysis in individuals with low G6PD activity. In Indonesian Papua, community health workers (CHWs) were trained to encourage treatment adherence in patients taking 14-day low dose primaquine and monitor urine color changes as a drug safety measure. The training and activities of CHWs and community perceptions of CHW monitoring were investigated in Timika, Papua, Indonesia using qualitative methods, including 24 observations, 15 informal conversations, and 14 focus group discussions (FGDs) with CHWs, health workers, and community. CHWs and community members were not aware of the importance of primaquine safety monitoring, in contrast to their perceptions on treatment adherence. Urine color changes were often attributed to malaria and not to antimalarial treatment: "*...people say, if the urine is yellow, it means we have malaria.*" In addition, asking about urine color is seen as offensive, except in a clinical context. Most CHWs are therefore reluctant to ask patients about their urine color: "*...for us here in Papua you can't ask something like that.*" A few CHWs have found ways to address this issue indirectly using the Hillmen urine chart. In Indonesia the importance of safety monitoring following primaquine treatment has not been sufficiently emphasized. These findings revealed important perceptions on treatment monitoring that could inform community education and CHW training. Addressing community perceptions would optimize malaria case management.

Abstract Reference: 20679
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 2

Study on prescription audit to improve quality of prescription writing at tertiary hospital of Bhavnagar district, Gujarat, India

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Abstract Content

Inappropriate prescribing, a recognized worldwide problem in the healthcare delivery system, results in the wastage of economic resources and non-optimal patient treatments. In the last two decades, the World Health Organization (WHO) has promoted rational drug prescribing. WHO specifies drug use indicators for adoption in drug utilization studies. Detection of prescribing errors with their reasons, to assess and reduce the irrational usage of antibiotics, syrups, and injections. A cross-sectional study was carried out at a tertiary hospital in Bhavnagar district. A total of 100 prescriptions from the Dept. of Medicine, Surgery, ENT, Eye, and Skin were selected using simple random sampling. 100% of prescriptions are not duly signed, 95% of prescriptions don't mention allergic status, 84% of prescriptions don't have legible handwriting in capital letters, 66% of prescriptions don't mention follow-up advice and precautions, and 57% of prescriptions don't mention the date of the next visit. Efforts should be made to reduce the patient load at the hospital so that doctors and other staff can get sufficient time for prescription writing. Education and training are necessary for doctors.

Abstract Reference: 20687
Mode of Presentation: Oral Presentation
Topic: One Health 1

Morphology and molecular identification of *Chrysomya* fly species of forensic importance of wild animals in Southern India

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Abstract Content

Chrysomya flies are forensically important blow flies in vetro-legal cases because of its larvae found on dead wild animals. A total of 850 maggots were collected from 20 wild animals namely Elephant (*Elephas maximus indicus*), Leopard (*Panthera pardus*), Sloth Bear (*Melursus ursinus*), Indian gaur (*Bos gaurus*) and Wild boar (*Sus scrofa*) from 2019 to 2022 at Coimbatore, Kanniyakumari and the Nilgiris districts of Tamil Nadu and Nandyal district of Andhra Pradesh, India. The collected maggots were morphologically identified under the stereo zoom microscope and Scanning Electron Microscope as *Chrysomya megacephala*, *C. albiceps*, *C. rufifacies* and *C. villeneuvi*. Among the 4 species of maggots, *Chrysomya megacephala* (49.76%) was found with high prevalence followed by *C. albiceps* (40.70%), *C. rufifacies* (8.70%) and *C.villeneuvi* (0.82%). Among the 20 wild animals, highest prevalence of larval stages of *Chrysomya* was observed on Elephant (75.00%), followed by Wild boar (10.00%), Sloth bear (5.00%), Leopard (5.00%) and Indian gaur (5.00%). The PCR was employed for *Chrysomya megacephala* and *Chrysomya villeneuvi* which was collected from Wild boar and Elephant respectively by using both cox I and cox II primers and molecularly identified as *Chrysomya megacephala* and *C.villeneuvi* based on the base pairs of 631bpand 624bp for cox I respectively. Similarly, *Chrysomya megacephala* and *C.villeneuvi* were binded with 559bp and 605bp respectively by using cox II primers.

Keywords: Forensic Entomology, Wild animals, *Chrysomya megacephala*, *C. albiceps*, *C.rufifacies* and *C.villeneuvi*, Prevalence, Morphology, PCR

Abstract Reference: 20691
Mode of Presentation: Oral Presentation
Topic: One Health 1

Echinococcus ortleppi infection in humans: An emerging zoonosis in Asia

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Abstract Content

Echinococcus ortleppi is the genotype G5 belonging to *Echinococcus granulosus sensu lato* and is a zoonotic canine tape worm of which larvae causes cystic diseases in domestic animals and also humans. While this species is highly endemic and widely spread in domestic animals, especially in the livestock, in the southern hemisphere, human infection is extremely rare and only sporadic. Thus, entire picture of human cystic echinococcosis due to infection with *E. ortleppi* is unclear. We have made an extensive literature review on the human cases of *E. ortleppi* infection and found a total of 19 cases worldwide with recent emergence in Southeast to East Asian countries. Among 19 cases, 4 cases were from Vietnam (2 cases in 2017 and 2 cases in 2020) and 2 cases from China (1 case each in 2019 and 2021). Although 2 cases were recorded in Japan, they were from the endemic countries, one from Nepal and the other from Bolivia. In Vietnam, not only human cases, infections in non-human primates have been reported in the same endemic area. In Vietnam, China or other Southeast and East Asian countries, *E. ortleppi* infection in the definitive host dogs have not yet been reported. Establishment and the maintenance of the lifecycle of *E. ortleppi* in Southeast and East Asia should be urgently explored.

Abstract Reference: 20694
Mode of Presentation: Oral Presentation
Topic: Entomology - Vector and Vector-Borne Diseases

Molecular detection and genotypic profilling of *Orientia tsutsugamushi* in clinical samples of scrub typhus patients

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Abstract Content

Scrub typhus is a neglected tropical disease with an estimated 1 million cases annually globally. Scrub typhus is caused by *Orientia tsutsugamushi* and can result in severe multiorgan failure with a case fatality rate of up to 30% without appropriate treatment. The antigenic heterogeneity of *O. tsutsugamushi* precludes generic immunity and allows reinfection. As a neglected disease, there is still a large gap in our knowledge of the disease. Between August 2022 and April 2024, 514 clinical samples from patients with acute undifferentiated febrile illness (AUFI) were tested for *O.tsutsugamushi* PCR at the Rickettsial Laboratory of the Institute for Medical Research, Malaysia. Out of the 514 samples, 498 were buffy coat, 9 were eschar biopsy, 3 were cerebrospinal fluid, 2 were eschar swabs and 2 urine samples. DNA extracted from the samples were tested for 56kDa type-specific antigen (TSA) using nested PCR, 12.6 % (65/514) of buffy coat, 100% (9/9) eschar biopsy, 100% (2/2) eschar swabs in VTM and 50% (1/2) urine were confirmed positive for *O. tsutsugamushi*. Genetic analysis of the 560 bp partial 56kDa TSA gene demonstrated that most *O. tsutsugamushi* infections were with Karp, Gilliam, Taiwan, China and Bangladesh. This study demonstrates that eschar remains the most reliable biological sample for PCR diagnosis of scrub typhus and Malaysia has significant diversity of *O. tsutsugamushi* strains, which underlines the need for ongoing surveillance to increase our understanding of *O. tsutsugamushi* diversity and ensure accurate and timely diagnostics and treatment. Challenges in establishing clinical and laboratory diagnoses have made scrub typhus one of the most severely neglected tropical diseases in Malaysia.

Abstract Reference: 20701
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 2

Molecular identification and antibiotic resistance profile of clinical *Acinetobacter baumannii* isolates from Hospital Universiti Sains Malaysia

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Abstract Content

Acinetobacter baumannii, a Gram-negative bacterium, is a significant pathogen in healthcare settings, contributing to hospital-associated infections (HAIs) like ventilator-associated pneumonia. Its ability to survive in diverse environments and rapidly evolve into a multi-drug-resistant organism poses a severe public health threat. This study aimed to accurately identify the species and antibiotic susceptibility patterns of clinical strains. Eight non-duplicate clinical isolates of *A. baumannii* from 2011 to 2022 were collected from the Hospital Universiti Sains Malaysia biobank. Presumptive identification was done using Gram staining and conventional biochemical tests. Phenotypic identification and antibiotic sensitivity testing were performed using the VITEK®2 Compact System. Species verification was achieved through colony PCR and rpoB gene sequence analysis. The strains were identified as Gram-negative coccobacilli in pairs, and biochemical tests showed a 99% probability that the strains were *A. baumannii*. Antibiotic resistance patterns revealed strong resistance to current therapies, including carbapenems. Genotypic identification confirmed a high degree of conservation with known *A. baumannii* strains in the NCBI database. Phylogenetic analysis indicated all isolates shared a common ancestor with A. baumannii. This study confirmed that all clinical strains were *A. baumannii* through morphological, biochemical, phenotypic, and genotypic analyses. Extensive research is currently ongoing to explore potential preventive strategies, including vaccine development, to mitigate drug resistance infection in hospital settings.

Abstract Reference: 20706
Mode of Presentation: Oral Presentation
Topic: Virology

Facing future pandemics: Effect of a theory of planned behaviour-based preparedness module on intention to respond among health inspector students

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Abstract Content

Future pandemics, which are deemed unavoidable events, potentially spread more rapidly and major global catastrophe. Having well-prepared future staffs to public health law is a critical issue in managing future pandemics. Hence, unintentional responses towards future pandemics could lead to non-illness related absenteeism and worsen the shortage of workforce during past pandemics. This study is aimed to evaluate the effects of a theory of planned behaviour-based pandemic preparedness module (PPM) to improve the intention to respond towards pandemic. This quasi-experimental study was conducted with a control group encompassing Health Inspector students in selected government institution in Sungai Buloh, Selangor. A total of 48 participants who met the criteria were recruited into the intervention group, and 50 participants were in the control group. The intervention group received a 10-hour course of the module. The data were collected at baseline, post-intervention, and three months follow-up. Established validated questionnaire was the main instrument and analysed with SPSS (Version 27.0). The response rate was 100%. Both groups showed no difference in selected sociodemographic characteristics and history of attending pandemic training. Generalized Estimated Equation showed that a significant interaction for intention to respond, attitude, and knowledge ($\beta = 0.41$, $p < 0.05$, $\beta = 1.58$, $p = 0.00$, and $\beta = 0.31$ $p < 0.05$ respectively), with the intervention group scored higher. The PPM was effective in improving intention to respond, attitude, and knowledge towards future pandemics among participants. The results within the intervention group showed improvement in both constructs at immediate post-intervention.

Abstract Reference: 20708
Mode of Presentation: Oral Presentation
Topic: Virology

Estimating rabies post-exposure prophylaxis delivery capacity: A National survey among health staff in Cambodia

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Abstract Content

Rabies presents a significant public health challenge in Cambodia, characterized by limited surveillance and sparse data on post-exposure prophylaxis (PEP) availability across the country. Understanding the accessibility of PEP following potential exposure is crucial to estimating the disease burden. Between September 2023 and February 2024, we conducted an online national survey targeting a random sample of health facilities to determine the PEP availability and assess the types of facilities offering such services. The survey also explored health facility staff's knowledge, attitudes, and practices (KAP) towards rabies. The survey included 1,227 facilities across 25 provinces. Approximately 79.1% [75.2-82.5] reported receiving victims of animal bites, with 42.0% [33.8-50.8] of these facilities providing rabies post-exposure vaccination, equating to 33.2% [26.5-40.8] of all surveyed facilities. Only 0.6% [0.2-1.6] offered rabies immunoglobulin (RIG), spanning both public and private sectors. Among PEP providers, 94.0% [88.2-97.0] use a four-session intramuscular protocol, and 89.2% [82.3-93.6] received less than one patient per week. Additionally, 7.3% [4.9-10.7] reported encountering rabid patients, with 90 facilities recording 169 cases over the last year, suggesting an annual incidence of 848 [489; 1,207] rabid cases representing 5 cases/100,000 inhabitants. Rabies continues to be a significant public health concern in Cambodia. This study effectively detailed the availability of PEP across the country and estimated the annual number of rabies cases. By addressing the identified challenges and gaps through targeted training and enhanced surveillance, rabies prevention and control efforts could be significantly improved, leading to a reduction in disease burden and mortality.

Abstract Reference: 20711
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 3

Imported malaria cases in West Java, Indonesia: can we really sustain the elimination status?

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Abstract Content

Indonesia's malaria elimination program targets sub-national elimination by 2023 in the Java-Bali region, including West Java Province. This study focuses on analyzing malaria surveillance data from the region. Secondary data from malaria surveillance reports (2019–2023) and certification achievement data (2014–2022) were utilized. Data verification involved evaluating study documents and case analyses. Over the study period, West Java reported 2,013 malaria cases, six of which were indigenous (last reported in 2019 in Pangandaran Regency), with the rest being imported. Most cases were confirmed by microscopic examination (84.1% in 2021, 94.4% in 2022, and 90.0% in 2023) and rapid diagnostic tests (57% in 2019 and 58.1% in 2020). Men (over 93%) and individuals aged 15–64 (over 98%) were most affected. Military personnel (up to 75.7%) and police officers (40.5%) were disproportionately affected. Passive case detection was commonly used, and most cases required inpatient treatment. Plasmodium vivax was predominant, with high relapse rates. Four malaria-related deaths occurred (one in 2019 and three in 2023). West Java attained sub-national malaria elimination certification in 2023; however, imported cases persist. The predominance of Plasmodium vivax and high relapse rates pose challenges. Effective coordination among regions and inter-provincial efforts are crucial to prevent local transmission. Despite achieving sub-national elimination certification, imported cases remain a concern in West Java. Sustained efforts in surveillance, coordination, and prevention are essential to maintain progress toward malaria elimination goals.

Abstract Reference: 20721
Mode of Presentation: Oral Presentation
Topic: Water & Food Borne Parasites

Comparative renal and liver pathology during infections with three foodborne trematodes *Opisthorchis felineus*, *Opisthorchis viverrini* and *Clonorchis sinensis*

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Abstract Content

The food-borne trematodes Opisthorchis felineus, Opisthorchis viverrini, and Clonorchis sinensis are closely related liver flukes that infect approximately 40 million people in Eastern Europe and Asia. Despite their similar life cycles, these liver flukes have marked differences, particularly in their endemic areas, biology, and pathology. While O. viverrini and C. sinensis are recognized as biological carcinogens, O. felineus is not. The mechanisms of cholangiocarcinoma development are unknown. This study aimed to investigate species-specific liver and kidney responses in Syrian hamsters (Mesocricetus auratus) infected with O. felineus, O. viverrini, or C. sinensis in a specific pathogen-free (SPF) animal facility. Immunohistochemistry, histopathology, ELISA, and biochemistry were used to reveal species-specific peculiarities in the development of periductal fibrosis in O. felineus and C. sinensis-infected animals and more pronounced biliary epithelial neoplasia in the liver of O. viverrini-infected animals. Species-specific renal damage, including interstitial fibrosis development and immunoglobulin A (IgA) deposition in the glomeruli of O. felineus and C. sinensis-infected animals, was also detected. A direct association between the liver periductal fibrosis area and renal interstitial fibrosis area of all infected animals was revealed. Our study provides the first insight into the species-specific peculiarities of pathogenesis during infection with different trematode species. These findings might stimulate new comparative studies on the pathogenicity of liver flukes and help determine whether actual differences in carcinogenicity among these three liver fluke species exist. This study was supported by the Russian Science Foundation № 24-25-00080.

Abstract Reference: 20732
Mode of Presentation: Oral Presentation
Topic: Water & Food Borne Parasites

Liver fluke-derived exosomes mediated wound healing in type 1 diabetes mellitus

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Abstract Content

The search for novel therapies for diabetic ulcers is of great importance. Food-borne liver flukes, such as *Opisthorchis felineus*, have been shown to reduce acute inflammation and promote tissue repair. Additionally, *O. felineus*-derived extracellular vesicles (EVs) may stimulate angiogenesis, which is critical for wound healing. The aim of the study: to investigate the effects of EVs on wound healing in a type 1 diabetes mellitus model. The isolation of exosomes from worm incubation medium involved centrifugation, filtration, ultrafiltration and ultracentrifugation. Transmission electron microscopy confirmed the size of the vesicles to be within the exosome range of 50-150 nm. We utilized a streptozotocin-induced C57Bl/6j murine model of type 1 diabetes mellitus and inflicted superficial wounds. Specific treatment, vehicle, positive and non-specific controls were applied every three days for 14 days. Wound healing was assessed through histological and gene expression analysis, and exosome proteomic analysis was performed. EVs improved wound healing, as evidenced by: (i) reduced wound area, re-epithelialization; (ii) decreased inflammation and alleviated expression of inflammation-associated genes; (iii) reduced *Vegfa* expression and CD34+ vessel numbers; (iv) decreased expression of extracellular matrix remodeling genes. These results were comparable to the positive control and significantly different from the vehicle. The proteomic analysis of *O. felineus* exosomes identified 168 proteins. Apparently, the helminth exosomes contain factors that can be considered as potential agents for stimulating the regeneration of mammalian tissues (supported by the Russian Science Foundation #24-25-00082).

Abstract Reference: 20733
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 2

A novel, single-dose treatment for scabies

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Abstract Content

Scabies is a highly contagious dermatological condition caused by *Sarcoptes scabiei* var. *hominis*. The therapeutics, ivermectin and permethrin, mainly target parasite nervous system killing only the motile stages. Therefore, they require repeat treatments. Prolonged use of these drugs and patient incompliance to repeat treatments have led to parasite resistance. A single dose treatment which targets all stages of the *S. scabiei* life cycle is required. Two novel scabicides (FL01 and AB02) were tested as a combination *in vitro* and *pre-clinically*. Four groups of eight infected pigs each were treated with a single application of the combination treatment for 4h or 8h or with two-doses of ivermectin or kept untreated. LT100 for the combination was 2h for mites and young eggs, and 8h for late-stage eggs. Only the combination treatment groups were cured and free from parasites from day-1 post-treatment. Clinically, combination treatment groups showed significantly lower pruritus and much improved clinical scores compared the ivermectin and control groups. Maximum absorption of FL01 in the serum and skin was at 8h and 2h and at 2h and 8h for AB02 post-treatment. Efficacy of this combination treatment is significantly higher than available scabicides, indicating that our treatment is a promising novel scabicide.

Abstract Reference: 20738
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 3

Application of serological surveillance to assess malaria transmission in areas of differing endemicity in Indonesia

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Abstract Content

Serological-surveillance involves the detection of malaria species-specific antibodies as biomarkers for monitoring recent and historical malaria transmission at population-level. This study evaluates the potential applications of serological-surveillance to estimate malaria transmission intensity in three different endemic settings in Indonesia. Cross-sectional serological surveys were done in areas conducting malaria elimination, pre-elimination, and control programmes. Epidemiological data and blood samples were collected, and antibody responses to multiple *P. falciparum* and *P. vivax* antigens were measured using indirect enzyme-linked immunosorbent assay and beads-based assay. Seroprevalence for each of the multiple *P. falciparum* and *P. vivax* antigen was estimated. Seroconversion rates were estimated by fitting a simple reversible catalytic model to seroprevalence data. PfAMA1 and PvAMA-1 were identified as the most immunogenic antigens for *P. falciparum* and *P. vivax* in low transmission settings. The spatial analysis of antibody responses to PfAMA1, PfMSP-1-19, PvAMA-1 and PvMSP-1-19 were sensitive and useful to identify areas at risk for malaria outbreak in very low transmission setting. In the high transmission setting, the seropositivity to the most immunogenic *P. falciparum* antigen that reflect short-term exposure (Etramp5.Ag1) was sensitive and specific in predicting *P. falciparum* PCR positive infections in children, suggesting its potential use as a marker of recent exposure in children, which is important for surveillance and programme evaluation in elimination settings. This study highlights the potential applications of serological-surveillance as an alternative approach to estimate transmission intensity, predict parasite prevalence in children, and predict areas at risk of malaria outbreak.

Abstract Reference: 20741
Mode of Presentation: Oral Presentation
Topic: One Health – General 1

Immune response to *Eimeria* spp. of broilers fed different anticoccidials.

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Abstract Content

In the present study, 225 broiler birds were divided into five treatment groups: untreated challenged (PC), untreated unchallenged (NC), and challenged groups supplemented with salinomycin, monensin and thymol. On day 21, birds were challenged with sporulated oocysts, and data on body weights, feed consumption, FCR, and OPG were recorded. Immunological responses and histopathological changes were assessed on days 28 and 42. The PC group exhibited significant mortality and the highest OPG counts at 14th and 21st day post infection, while thymol supplementation initially increased OPG counts at 14th day post infection but significantly reduced them by 21st day post infection. Salinomycin and monensin treatment groups showed null OPG counts at both time points. Although the PC group had the lowest body weight gain, there was no significant difference compared to the NC group, while FCR and feed intake were significantly different between the PC and treatment groups. Salinomycin demonstrated superior FCR performance. Expression of pro-inflammatory cytokines IL-1β and IL-6 was significantly upregulated in the jejunum and spleen at 7-dpi, followed by downregulation at 21-dpi. These findings suggest that salinomycin, monensin, and thymol play critical roles in preventing economic losses and developing immunity against *Eimeria* spp. while reducing intestinal damage. Salinomycin emerges as a preferred coccidiostat option for inclusion in poultry feed. Thymol can also be used as an alternative coccidiostat in poultry feed.

Abstract Reference: 20747
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 2

Doxycycline inhibits translation in the apicoplast and mitochondrion of *Plasmodium falciparum*

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Abstract Content

The malaria parasite *Plasmodium falciparum* has two prokaryote-derived organelles: the mitochondrion and the apicoplast. Each organelle has its own reduced genome, and its own transcriptional and translational apparatus. Antibiotics that inhibit translation in the apicoplast are validated and useful antimalarials, but such inhibitors have a “delayed death” effect. These compounds have no immediate impact on growth after treatment, stopping parasite growth only one cycle after drug exposure. A notable exception is the prophylactic drug doxycycline, which has a delayed death effect, but also kills parasites quickly at higher concentrations. We characterised the impact of delayed death drugs on *Plasmodium* protein translation using quantitative proteomics, simultaneously assaying translation in the apicoplast, mitochondrion and cytosol. We applied mass spectrometry for label-free quantitation to measure protein abundance as well as stable isotope labelling by amino acids in cell culture (SILAC) to measure nascent protein translation. We find that delayed death drugs lead to a specific block of apicoplast translation, but doxycycline additionally inhibits translation in the *Plasmodium* mitochondrion. Seahorse metabolic assays also show that doxycycline decreases parasite oxygen consumption rate, consistent with a perturbation to mitochondrial metabolism consequent to mitochondrial translation inhibition. This provides a rational for doxycycline’s faster inhibition of parasite growth at higher doses. Importantly, these data reveal the first known inhibitor of *Plasmodium* mitochondrial protein synthesis, and support mitochondrial translation as a potential target for future drugs. The discovery of an additional target for a widely-used malaria prophylactic may also inform future drug combinations for malaria treatment or prevention.

Abstract Reference: 20772
Mode of Presentation: Oral Presentation
Topic: Parasitology and Microbiology

Waterborne protozoan pathogens in the Seven Maar Lakes of San Pablo, Laguna, The Philippines: Implications to public and ecosystem health

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Abstract Content

The vast ecosystem services and livelihood opportunities offered by the seven maar lakes of San Pablo City Laguna, Philippines have promoted the expansion of agricultural, aquacultural, residential, and ecotourism areas in the lakes' vicinities over the years. Realizing the effects of these anthropogenic activities, a comprehensive assessment should be in place to address the gaps in current monitoring efforts. Since the microbial water quality assessment of the lakes is limited to coliforms, this study aimed to determine the extent of contamination of waterborne protozoan parasites in the lakes that may be transmitted to the nearby communities through contaminated waters. A total of 105 surface water samples were collected from the lakes and were subjected to appropriate direct fluorescence microscopy, culture assay detection methods, and molecular identification using PCR. Results revealed that the lakes were contaminated with various protozoan parasites such as *Cryptosporidium* sp. (30.48%), *Blastocystis* sp. (20%), and *Giardia* sp. (14.29%). Moreover, free-living pathogenic amoeba, *Acanthamoeba* sp. (19.05%) was also detected. Interestingly, contamination was high in lakes near residential and agricultural areas where livestock and companion animals are present. Waterborne parasite contamination provides evidence of fecal pollution in the lakes as these organisms enter the aquatic ecosystems when passed in the feces of infected animal and human hosts. It is therefore recommended to improve sanitation and waste management in the lakes' vicinities, regulation of agricultural activities and residential establishments through land use plans, and to update the traditional monitoring of microbial water quality to include various waterborne parasites.

Abstract Reference: 20784
Mode of Presentation: Oral Presentation
Topic: Entomology - Mosquito Vectors

An updated checklist of the Anopheles of Indonesia

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Abstract Content

Anopheles is a genus of mosquitoes studied in Indonesia since the malaria outbreak in Batavia in 1733. Many studies have been conducted concerning Anopheles' role as various disease vectors in Indonesia, particularly malaria and lymphatic filariasis. Understanding the Anopheles systematics and their bionomic and biogeographic implications is essential for implementing appropriate vector control strategies. Historically, Indonesia's number of Anopheles species has been updated since the early 1900s. Swellengrebel in 1921 identified 29 Anopheles species. In 1932, Swellengrebel and Rodenwardt stated that at least 56 Anopheles species had been identified in the Indo-Australian region. Then, Stoker and Koesoemawinangoen reported an update on the Anopheles species situation in 1949, the list contained 66 species. O'Connor and Soepanto revised 1979. The list of Anopheles species in Indonesia has 66 species, with 1 sub-species and 4 varieties. In 1981, O'Connor and Sopa also updated Anopheles species in Indonesia, with a total of 80 Anopheles species having been identified. Currently, at least 101 formally named Anopheles species and at least 4 unnamed species have been listed in Indonesia.

Abstract Reference: 20785
Mode of Presentation: Oral Presentation
Topic: Parasitology

Falciparum malaria triggers circulating markers of extracellular matrix remodeling, with increasing levels associated with increasing disease severity and predicting mortality

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Abstract Content

With increasing anti-malarial drug resistance, exploring the immune response in malaria may be one of the first steps to approaching new treatment options. The extracellular matrix (ECM), “the intercellular space substance”, contributes to demodulation of biological processes with an important role in adhesion, migration, repair, development and survival of the cells. Integrins transmit signals through the plasma membrane into the cells where they control activation. Even small changes in ECM-structure or organization as in certain infections, may result in dysfunction or death of the present cell. We collected clinical data and blood samples from 205 adults with falciparum malaria in the Maputo Central Hospital Mozambique from 2017-2020. The malaria and HIV-diagnosis were based on PCR. Circulating levels of ECM remodeling mediators were quantified by enzyme immunoassay. Comparing uncomplicated and severe malaria, all examined components were significantly elevated, with increasing levels with increasing malaria disease severity. Exploring the different ECM-parameters versus the different severity criteria, only hyperparasitemia triggers all of them. Cerebral malaria and renal failure are also associated with elevated levels of all, except YKL 40, liver failure with ENRAGE and GAL 3, severe anemia with GDF 15 and bleeding disturbances/ hemolysis with GDF 15 and GAL 3. All markers, except YKL 40, were significantly elevated in patients who died during the hospital stay, compared to survivors, predicting mortality. Circulating markers of extracellular matrix remodeling have broad and significant elevated levels in severe compared to uncomplicated falciparum malaria, increasing with increasing disease severity and predicting death.

Abstract Reference: 20793
Mode of Presentation: Oral Presentation
Topic: Veterinary Health

Morphological and molecular identification of amphistomes of wild ruminants from selected game reserves of Zimbabwe

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Abstract Content

This study was conducted in wildlife conservancies and national parks located in Beitbridge, Nyamandlovu, and Hwange in the Matebeleland region of Zimbabwe during the 2019-2021 game hunting seasons. A total of 313 carcasses of wild ruminants were screened for amphistome infections in the gastrointestinal tracts, and specimen from 32 (10.22%) animals were infected. Prevalence of amphistomes per locality was 5.62% in Nyamandlovu, 35% in Hwange and 33.91% in Beitbridge. A high prevalence of 63% was recorded in *Kobus ellipsiprymnus* (waterbuck) from Beitbridge with a high parasitic burden of more than 10 000 parasites per animal. The lowest parasitic burden was observed in *Connochaetes taurinus taurinus* (blue wildebeest) and *Hippotragus niger* (sable) each with less than 10 amphistomes. Eighty-six amphistome specimens were harvested from *Syncerus caffer* (African buffalo) (n=27), *Aepyceros melampus* (impala) (n=17), *Tragelaphus strepsiceros* (kudu) (n=16), waterbuck (n=10), sable (n=7), *Redunca arundinum* (reedbuck) (n=7), and *Connochaetes taurinus taurinus* (blue wildebeest) (n=10) for morphological and molecular identification. Using a combination of histology to study morphological features and ITS-2 rDNA marker, seven amphistome species were identified as follows; *Leiperocotyle gretillati*, *Calicophoron microbothrium*, *C. raja*, *C. clavula*, *C. phillerouxi*, *Gigantocotyle symmeri*, and *Orthocoelium dicranocoelium*, and *Gastrothylax crumenifer* (pouched amphistome species). *Orthocoelium dicranocoelium*, *Ga. crumenifer and L. gretillati* are first records in wild ruminants in Zimbabwe. The large number of amphistome species reported in this study shows that wild ruminants of Zimbabwe have a rich fauna of this group of parasites and further studies are recommended.

Abstract Reference: 20810
Mode of Presentation: Oral Presentation
Topic: One Health – General 1

Web-based surveillance on vector mosquitoes, *Aedes albopictus* and *Culex quinquefasciatus*

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Abstract Content

The surveillance of vector mosquitoes is essential for prevention and control of mosquito-borne diseases. In this study, we developed an internet-based vector mosquito monitor, MS-300, and evaluated its efficiency for the capture of the important vector mosquitoes, *Aedes albopictus* and *Culex quinquefasciatus*. The linear sizes of adult *Ae. albopictus* and *Cx. quinquefasciatus* were measured and an infrared window was designed based on these data. A device to specifically attract these two species and automatically transmit the number of captured mosquitoes to the internet was developed. In mosquito-net laboratory cages, the efficiencies of MS-300 for catching and identifying *Ae. albopictus* were 98.5% and 99.3%, respectively, and 95.8% and 98.6%, respectively, for *Cx. quinquefasciatus*. In a wire-gauze screened house in semi-field trials, the efficiencies of MS-300 baited with a lure in catching *Ae. albopictus* and *Cx. quinquefasciatus* were 54.2% and 51.3%, respectively, which were significantly higher than 4% and 4.2% without the lure. The real-time monitoring data revealed two daily activity peaks for *Ae. albopictus* (8:00-10:00 and 17:00-19:00), and one peak for *Cx. quinquefasciatus* (20:00-24:00). During a 98-day surveillance trial in the field, totals of 1,118 *Ae. albopictus* and 2,302 *Cx. quinquefasciatus* were captured by MS-300. There is a a positive correlation in the species composition of the captured samples among the mosquitoes using MS-300, BGS traps and human landing catches. The data support the conclusion that MS-300 can specifically and efficiently capture *Ae. albopictus* and *Cx. quinquefasciatus*, and monitor their density automatically in real-time.

Abstract Reference: 20820
Mode of Presentation: Oral Presentation
Topic: Parasitology and Microbiology

Multi-dimensional variables related to stunting reduction in Semarang, Indonesia

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Abstract Content

Stunting is a serious public health problem globally, and it is associated with increased morbidity and mortality rates, reduced cognitive development, and lower economic productivity in adulthood. Therefore, understanding the factors contributing to stunting incidence is crucial in developing effective interventions to address this issue. This study involved 556 Children aged 0-59 months old. This study drew samples randomly from across sub-districts in Semarang. The outcome variable was the stunting status, while the latent variables were child characteristics, family characteristics, maternal factors, parenting, accessibility to health service, dietary habits, nutrition and food habits, specific intervention, Posyandu involvement, infectious diseases, and environmental factors. This study employed the structural equation modeling-partial least square to analyze the relationship between several latent variables. The results suggest that child characteristics, environmental factors leading to infectious disease, maternal factors, infectious disease itself, nutritional intake, specific intervention, and socioeconomic factors have a direct positive effect on stunting incidence. To overcome the stunting problem in Semarang, we present seven policy options that target the root causes and implement prevention and reduction of stunting incidents. The main principles for overcoming stunting in Semarang are "enhance child nutrition programs", "strengthen infectious disease prevention", "improve maternal and child healthcare", "enhance socioeconomic support", "strengthen sensitivity intervention", "foster collaboration and coordination", and “conduct targeted awareness campaigns”. By implementing policy recommendations that focus on improving nutrition, enhancing healthcare services, addressing environmental factors, and promoting socioeconomic development, it is possible to reduce stunting incidence rates and improve the overall well-being of children.

Abstract Reference: 20833
Mode of Presentation: Oral Presentation
Topic: One Health – General 1

Subclinical haemoparasite infections in canine population: implications for surveillance and intervention strategies

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Abstract Content

Canine haemoparasites hold global significance due to their impact on veterinary health, zoonotic potential, widespread distribution, vector-borne transmission, effects on working dogs, and economic implications. These parasites can cause a range of clinical manifestations, from mild subclinical infections to severe illness. Subclinical infections of canine haemoparasites can significantly impact both affected dogs by leading to secondary complications and the broader community, as they can serve as chronic carriers and pose zoonotic risk. A study was conducted on 39 dogs (19 service dogs, 20 retired dogs) housed at National Disaster Response Force (NDRF) as a part of routine health screenings. Despite being asymptomatic and actively engaged in training activities, the dogs were found to have normal complete blood count (CBC) and serum biochemical parameters, except few dogs with thrombocytopenia. Examination of blood smears under microscope also did not reveal any abnormalities or evidence of parasite presence. PCR analysis revealed the presence of haemoparasites in the samples. Most dogs tested positive for *Babesia gibsoni* (22/39), and a few for *Babesia vogeli* (4/39), *Ehrlichia canis* (1/39) and *Anaplasma platys* (9/39). This highlights the subclinical carrier status of the dogs, posing potential risk of transmission. Sub clinical infection with canine babesiosis leads to anaemia, immunosuppression, and organ damage, even in the absence of overt clinical disease. Prophylactic treatment with imidocarb and usage of supplements was recommended to prevent immunocompromised status, while environmental tick control measures were suggested to mitigate disease transmission.

Keywords: Canine haemoparasites, CBC, serum biochemistry, subclinical infections, *Babesia*.

Abstract Reference: 20855
Mode of Presentation: Oral Presentation
Topic: One Health 2

The hidden burden: Genetic and spatial dynamics of asymptomatic submicroscopic malaria in areas with high risk of malaria reintroduction in Malaysia

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Abstract Content

Malaria remains a significant health challenge, especially with asymptomatic submicroscopic infections hindering control and elimination efforts. In Malaysia, high-risk areas for malaria reintroduction harbour a hidden burden of these silent infections. Understanding the genetic and spatial dynamics of asymptomatic submicroscopic malaria is crucial for targeted intervention strategies. This study examines the prevalence of these infections in high-risk areas, aiming to assess spatial distribution and determine the population structure of malaria parasites. A cross-sectional study was conducted in identified high-risk reintroduction areas in Malaysia. Blood samples were collected from asymptomatic individuals and screened for submicroscopic malaria using polymerase chain reaction (PCR). Genes coding for msp-1 were genotyped by allele-specific nested PCR. Spatial analysis was performed using RStudio IDE software to map and analyze the distribution of malaria cases, incorporating socio-demographic data and geographical coordinates. Out of 3,322 blood samples from seven districts in Sabah, Perak, Johor, and Kelantan, all were microscopically negative, but 1.86% (62 samples) tested positive for malaria by PCR. The positive cases included 40.3% *Plasmodium malariae*, 29.1% *P. vivax*, 24.2% *P. knowlesi*, 1.6% *P. falciparum*, 1.6% *P. cynomolgi*, and 3.2% mixed species. Of these, 51 samples were from Kota Marudu, 3 from Keningau, and 8 from RPS Pos Kemar. Genetic polymorphism was analyzed in 24 *P. malariae*, 13 *P. vivax*, and 15 *P. knowlesi* isolates. Our findings highlight the hidden burden of asymptomatic submicroscopic malaria in high-risk reintroduction areas of Malaysia. Targeted interventions and enhanced surveillance are essential to address this challenge and prevent malaria resurgence.

Abstract Reference: 20858
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 2

Mechanistic analysis of artemisinin resistance: molecular modelling of kelch 13 protein interactions

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Abstract Content

Reduced clearance of parasite in artemisinin-treated malaria patients is a precursor to artemisinin resistance; yet, artemisinin-based treatments remain largely effective against malaria parasites. Artemisinin resistance development has been linked to several mutations in the Kelch 13 (K13) protein. Nonetheless, further research is required to understand the precise mechanisms underlying artemisinin resistance fully. Increased amounts of phosphatidylinositol 3-phosphate, decreased protein translation, altered DNA replication, inactivated unfolded protein response, increased cellular stress, and enhanced endocytosis have all been linked. This study uses computer-aided simulation to evaluate the interaction between artemisinin and the K13 protein. Artemisinin, K13 wild-type, and 27 non-synonymous K13 mutations were subjected to protein-protein interactions using 3D-structural validation and molecular docking simulation. Out of 27 non-synonymous K13 mutants that were examined, 18 mutants had diminished binding affinities towards artemisinin, hence suggesting a decline in susceptibility; meanwhile, 9 mutants with binding affinities equivalent to or even more potent than the wild type, indicating their ability to withstand the inhibitory actions of artemisinin, which may present challenges for malaria treatment. Through molecular docking simulation analysis, we have gained insights into the impact of K13 mutations on drug activity. Our findings suggest that a single non-synonymous mutation might be sufficient to alter the binding site of artemisinin in the malaria parasite, potentially initiating resistance. However, this hypothesis requires further investigation using complementary approaches such as Molecular Dynamics (MD) Simulations, Quantum Mechanics/Molecular Mechanics (QM/MM) Studies, Mutagenesis, in vivo and in vitro analyses, and Structural Biology techniques.

Abstract Reference: 20862
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 3

Application of alginate-gelatin hydrogel beads in controlling mosquito population within high-risk building areas

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Abstract Content

Control of mosquito is increasingly challenging due to the presence of insecticide resistance that caused by excess use of insecticide widely. An alternative strategy is the use of sugar baits, however it is limited due to short-term efficacy. Alginate-gelatin hydrogel beads (AGHBs) can be an effective alternative by providing longer periods of mosquito attraction and control by using 'attract-kill' mechanism. This study aimed todetermine the effectiveness of AGHBs in reducing population of mosquitoes within high-risk building areas. The AGHBs produced by biodegradable natural polymers were soaked in mixture of 3% of boric acid, banana essence and cordial mango solution overnight. Then, 30g of AGHBs were placed in standard ovitrap. This study was conducted at indoor and outdoor of two different hostels in USM, Gelugor, Penang. Fajar Hostel (FH) is near to Tasik Harapan which can be a strategic place for the mosquito colonization while Cahaya Gemilang Hostel (CGH) resembles the rural area since it is near to the forest and and highly vegetative. The data was collected based on number of mosquito larva trapped during pre-treatment, treatment and post-treatment period. Data analysis was carried out by using Kruskal-Wallis H test. The test indicated statistically significant difference for FH indoor and CGH outdoor, $p=0.013$ and $p=0.016$ respectively while FH and CGH outdoor shows, $p<0.01$. This field evaluation also justifies the applicability of AGHBs for outdoor and indoor applications in high-risk building areas is efficient. Thus, AGHBs are applicable as a baiting tool in combating mosquito population.

Abstract Reference: 20863
Mode of Presentation: Oral Presentation
Topic: Entomology - Vector and Vector-Borne Diseases

Vector-borne parasites in cats of different regions of Iran

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Abstract Content

This study aimed to provide a comprehensive overview of the prevalence of FVBDs in Iran. From 2018 to 2022, blood samples were collected from 772 cats (299 strays, 473 client-owned) of both sexes and different ages in six cities with different climates i.e. Tehran, Mashhad, Kermanshah, Hamedan, Yazd, and Kerman to assess the presence of pathogens' DNA (i.e., *Hepatozoon* spp., *Babesia* spp., *Cytauxzoon* spp., and filarioids). In total, 29 cats (21 stray, 8 owned) scored PCR-positive for *Hepatozoon* spp. Infected cats were found in Mashhad (8.4%), Hamedan (3.8%), Kermanshah (2.4%), and Tehran (1.7%). Sanger sequencing revealed *H. felis* (n = 25) and *H. canis* (n = 3). Hepatozoonosis was significantly higher in stray cats and in Mashhad. There was no statistically significant association between hepatozoonosis and age or sex. Other species were not detected. This largest epidemiological study on FVBDs in Iran demonstrates that cats in different regions of the country are at risk of FVBDs, particularly of feline hepatozoonosis. Further investigations on domestic and wild felids in other regions of the country, on the clinical impact of hepatozoonosis, and the possible presence of *H. silvestris* are suggested. Effective control strategies are advocated for minimizing the risk of infection in cats and the public.

Abstract Reference: 20867
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 2

In-house multiplex assay for identifying simian malaria *P. knowlesi* and *P. cynomolgi.*

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Abstract Content

The development, translation, and adoption of current, new, or evolving, are necessary for the development of new diagnostic tools that are more sensitive, robust, and selective for improving clinical cases. Malaysia has been free of human malaria for five consecutive years, but the incidence of simian malaria caused by *P. knowlesi* and *P. cynomolgi* infecting humans is on the rise. This will be extremely difficult with the few diagnostic tools available. Therefore, this study aims to develop a diagnostic tool for the identification of simian malaria using multiplex single-step qPCR assays. Using bioinformatic approaches, specific primers and TaqMan probes were constructed from genomes of *P. knowlesi* and *P. cynomolgi*. The multiplex technique was tested for the detection limit of DNA. The evaluation of sensitivity and specificity was performed using thirty confirmed cases of *P. knowlesi* in humans; twenty-two mixed infections and eighty-four negative macaque samples. The target gene was successfully amplified for both simian malaria, with the lowest detection limit for *P. knowlesi* and P. cynomolgi is 0.0038ng/µl and 0.012ng/µl, respectively. The duplex assay demonstrated 95% sensitivity and 100% specificity for detecting P. *knowlesi*, and 90% sensitivity and 100% specificity for detecting *P. cynomolgi*. No cross-reactivity with other plasmodium species was detected. Since *P. knowlesi* is the primary cause of malaria infections in Malaysia, our findings underscore the necessity of developing diagnostic methods to assist clinical investigations in identifying human cases of simian malaria infection. Additionally, infections from species other than *P. knowlesi* are starting to increase

Abstract Reference: 20873
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 3

Prevalence and risk factors of non-febrile malaria co-infection with hbv among pregnant women seeking antenatal care in Damaturu, northeast Nigeria

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Abstract Content

Malaria and Hepatitis B pose a serious risk to public health in all parts of the world. The aim of this study was to evaluate the prevalence and risk factors of HBV coinfection with malaria among pregnant women seeking antenatal care in Damaturu Metropolis. In this hospital based cross-sectional investigation, malaria rapid diagnostic test and microscopy were used to determine the malaria parasite while Hepatitis B surface antigen test kits using Micropoint. Hematological parameters such as WBC counts, PCV and liver function tests were performed on the blood samples from the 384 pregnant women participants. Demographic and socioeconomic information as well as KAP data were collected using a pre-tested questionnaire. The results revealed that 129 (33.6%) were positive for malaria while 25 (6.5%) were positive for HBV and 20 (5.2%) had co-infection. Pregnant women above 38 years showed highest malaria prevalence 10 (43.5%), HBV 3 (13.0%) and coinfection 3 (13,0%). A multivariate analysis showed that malaria was significantly associated with no IPTp taken and education below secondary, while HBV was significantly associated with low income and education below secondary level. Overall, 91.1% of the respondents had prior knowledge about malaria, and 7.3, 51.8 and 87.0% of them knew about the transmission, symptoms, and prevention of malaria, respectively. However, only 15.5% of the respondents had prior knowledge about HBV. Despite high knowledge about malaria in the study area, there is still significant gap in the use of IPTp as a preventive measure while there is need for more awareness about HBV.

Abstract Reference: 20877
Mode of Presentation: Oral Presentation
Topic: Entomology - Vector and Vector-Borne Diseases

Genotyping of Borrelia spirochetes in on-host ticks (Acari: Ixodidae) collected from recreational areas in Terengganu, West Malaysia

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Abstract Content

Ixodid ticks have been expanding their geographic range globally, creating their possibility of spreading pathogens, such as *Borrelia* species which cause Lyme borreliosis (LB) or relapsing fevers (RF) to humans. However, the presence and genotyping of *Borrelia* spirochetes in ticks have not extensively studied in Malaysia. This study aimed to detect and characterize the *Borrelia* species in various tick species collected from four recreational areas in Terengganu, West Malaysia. Nucleic acid extracts of ticks (4 genera; 7 species) were screened for the presence of borrelial DNA by nested PCR targeting partial sequence of the flagellin (*flab*) gene. Of the 118 ixodid ticks examined, 5.08% (n=6) were infected with *Borrelia* species. *Borrelia yangtzensis* (LB group) was found in four ticks (*Dermacentor steini* n=3; *Ixodes granulatus* n=1) and *B. miyamotoi* (RF group) spirochete was isolated in one female *I. granulatus*. In addition, a single female *Dermacentor auratus* was infected with *Borrelia* sp. and showed 98.9% similarity to *Borrelia* sp. isolated from *Haemaphysalis megaspinosa* in Japan (LC170031). Interestingly, a neighbor-joining tree revealed that this detected spirochete was clustered in a monophyletic clade of RF-like *Borrelia*, together with *B. theleri* or *B. lonestari*. To our knowledge, this is the first report of *B. yangtzensis* and *Borrelia* sp. RF-related being detected in local *D. steini* and *D. auratus* ticks. This study provides clear and convincing evidence for these two species of *Dermacentor* as a potential vector in transmitting *Borrelia*, emphasizing the necessity of continuous monitoring for circulation of *Borrelia* spirochetes in tick from this region.

Abstract Reference: 20878
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 2

Enzyme inhibition study of 3-Butylidenephthalide as a potential antimalarial targeting *Plasmodium falciparum* Lactate Dehydrogenase

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Abstract Content

Malaria mortality has decreased over the past few years, but malaria remains challenging due to the *Plasmodium* resistance to antimalarial drugs. Discovery of new, safe,and effective antimalarial drugs is vital by targeting *Plasmodium* lactate dehydrogenase (LDH) in *Plasmodium*'s glycolytic pathway. It is the only source of energy for the *Plasmodium* during intra-erythrocytic stage. Hence, this study aimed to assess the inhibition of recombinant *Plasmodium falciparum* lactate dehydrogenase (*Pf*LDH) by natural compounds, using computational method followed by enzyme inhibition studies. 3-Butylidenephthalide was virtually screened using combination of molecular docking and molecular dynamic (MD) simulation and analysed using Autodock 4 and GROMACS packages, respectively. Then, the compound was subsequently tested against recombinant *Pf*LDH that was purified to homogeneity by Immobilized Metal Ion Affinity Chromatography and Size Exclusion Chromatography, to observe the inhibition of *Pf*LDH compared to known inhibitor of *pf*LDH (BIH). Significant results showed by docking studies and MD simulation with minimum binding energy of -4.95 kcal/mol and -8.05 kcal/mol, respectively. The specific activity of recombinant *Pf*LDH was found to be 7368.42 U/mg, confirming the presence of active protein. 3-Butylidenephthalide showed that it could effectively inhibit the activity of *Pf*LDH by 6.0 % inhibition with concentration of 0.05 mM, which is higher than BIH (1.3 %). The IC_{50} value calculated 3-Butylidenephthalide is 0.13 mM. This study successfully yielded a promising antimalarial compound which can be utilized in the future drug development studies.

Abstract Reference: 20879
Mode of Presentation: Oral Presentation
Topic: Parasitology and Microbiology

Local cutaneous leishmaniasis in Penampang District, Sabah, Malaysia

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Abstract Content

Leishmaniasis caused by *Leishmania spp*. transmitted to humans through bite of infected female phlebotomine sandflies. WHO reported 99 countries were endemic for leishmaniasis. In Malaysia, it is considered a rare infection. In November 2023, dermal scraping from an external ear lesion of 55-year-old man living in District of Penampang, Sabah, east Malaysia was received by IMR, initially thought to be due to fungal infection that was confirmed as unlikely by PCR. DNA extracted from dermal scrap, tested by PCR and confirmed as *Leishmania spp*. DNA sequencing showed 99% similarity to *Leishmania infantum*. Giemsa-stained microscopic examination of his peripheral blood did not show presence of amastigote bodies. Immunoassay test showed IgG seropositivity to *Leishmania spp*. The patient never travelled outside the country, nor in contact with people from endemic countries. The Health District Office of Penampang then took blood samples from adults and dried blood spots from children presumed to be his close contacts. A total of 52 human samples, 2 dog blood and 3 cat blood domesticated within the house compound of the patient were subjected to microscopic examination, immunoassays and PCR. Five of 52 human samples (9.6%) were identified as *Leishmania infantum* by DNA sequencing and 15/52 (29%) human blood samples exhibit IgG antibodies to *Leishmania spp*. Animal blood samples were all negative for *Leishmania spp*. This finding indicates the need to establish the source of local infection, its transmission cycle, specific vector (s) and the risk factors of transmission.

Abstract Reference: 20880
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 2

Enhanced efficacy of vaccine formulations with new adjuvants for murine visceral leishmaniasis

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Abstract Content

Visceral Leishmaniasis (VL), caused by protozoan parasites of the genus *Leishmania*, transmitted by infected sandflies, primarily involves *Leishmania donovani* in Asia and Eastern Africa, with humans as the main reservoir. Current chemotherapy often results in severe side effects, resistance, prolonged treatment, and high cost. Despite trials with diverse antigens like whole-cell killed, live, live-attenuated, subunit proteins, and DNA, many have failed in phase II or III trials. Enhancing efficacy requires reconsidering these antigens with immunoenhancers. *L. donovani* strain (MHOM/IN/1983/AG83) was obtained from CSIR-IICB, Kolkata, and cultured in Medium 199 supplemented with 10% FBS. Formalin-killed and heat-killed antigens were used to immunize BALB/c mice alone or with adjuvants (Montanide ISA 201, AddaVax, Gardiquimod) thrice at 15-day intervals. Post-immunization, mice were challenged with 1×10^7 promastigotes. Controls included PBS-immunized groups with and without challenge. The animals (n = 6) were sacrificed at Pre-challenge, 4 weeks, 8 weeks and 12 weeks post-challenge. Adjuvanted vaccines significantly reduced parasite load in liver and spleen, enhanced delayed-type hypersensitivity response, shifted humoral immune response towards protective IgG2a, stimulated higher levels of Th1 cytokines, increased nitric oxide production as compared to antigen alone or infected controls. The absence of human vaccines against VL underscores the need for effective formulations. This study highlights promising efficacy, with Montanide ISA showing the highest effectiveness, followed by Gardiquimod and AddaVax. These findings highlight the potential of adjuvanted vaccines in enhancing protective immunity against visceral leishmaniasis.

Abstract Reference: 20881
Mode of Presentation: Oral Presentation
Topic: Virology

Establishment of dengue viruses global unified genotyping collaborative monitoring and tracing strategy

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Abstract Content

Dengue is the fastest spreading arboviral disease, posing great challenges on global public health. A reproduceable and comparable global genotyping framework for contextualizing spatiotemporal epidemiological data of dengue viruses (DENVs) and the Global Integrated Sequence Database for Dengue Viruses (GISDD) are essential for researches and effective collaborative surveillance. Using phylogenetics, phylogeography, phylodynamics, we have established a unified global high-resolution genotyping framework of DENVs with three hierarchical layers of genotype, subgenotype and clade with respective mean pairwise distances 2-6%, 0.8-2%, and≦0.8%, and characterized their epidemic patterns representing stratified spatial-genetic epidemic pairs of Continent-Genotype, Region-Subgenotype and Nation-Clade, thereby identifying 13 epidemic regions which prospectively facilitates the region-based coordination. Our framework can be utilized in an accurate stratified coordinated surveillance based on the defined viral population compositions, which is prospectively valuable for hampering the ongoing transition process of epidemic to endemic, addressing the issue of inadequate monitoring, and warning us to be concerned about the cross-national, cross-regional, and cross-continental diffusion of dengue, which potentially arouse large epidemics. We also established the GISDD. Our work has laid a foundation and re-unveiled the urgency for establishing a stratified coordinated surveillance platform for blocking global spreading of dengue.

Abstract Reference: 20882
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 2

Locked out and left behind: A study of organellar inheritance in P. *berghei*

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Abstract Content

Plasmodium parasites harbour a single mitochondrion and a single relic plastid (apicoplast) throughout their life cycle. Both organelles are essential and used as drug targets. Previous genetic cross studies indicated that both organelles are maternally inherited during sexual reproduction, but the mechanisms underpinning such uniparental inheritance were unknown. To investigate organellar inheritance in a sex-specific manner, we developed single sex *P. berghei* lines with fluorescently tagged apicoplasts and mitochondria. Using a combination of lattice light-sheet and expansion microscopy, we show that the mitochondrion and apicoplast are excluded from newly formed male microgametes during exflagellation. By contrast, female gametocytes possess an elongated, perinuclear positioned apicoplast and an expanded mesh-like mitochondrial network that encapsulates or cradles the nucleus throughout. In many organisms, organelle exclusion is preceded by degradation of the organellar genome. We used digital droplet PCR to show that there is a substantial decrease in the relative copy number of the apicoplast and mitochondrial genomes in male gametocytes that accompanies the exclusion of organelles from the microgamete. Maternal inheritance systems can sometimes fail. To test for paternal leakage in malaria parasites, we set up a forced cross with a selectable polymorphism in the mitochondrion of the male parent. Upon screening 1.9 million sporozoites across seven crosses, we identified a single male leakage event, thus demonstrating for the first time that drug resistance encoded by the mitochondrial genome of malaria parasites can, very infrequently, be inherited from the male parent. Overall, this work will better inform future therapeutic strategies targeting these organelles.

Abstract Reference: 20889
Mode of Presentation: Oral Presentation
Topic: Entomology - Mosquito Vectors

Intervention for Dengue Epidemiology in Malaysia (iDEM trial): Impact of integrated vector management on dengue incidence

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Abstract Content

Efficient vector control (VC) is the most effective preventive strategy to reduce the burden of dengue and other *Aedes* borne diseases. However, current VC rely primarily on reactive measures once a dengue case is identified. Malaysia is one of the Southeast Asian countries hardest hit by dengue. We implemented an Integrated Vector Management (IVM) approach in a large non-blinded cluster randomized controlled trial to derive high-quality evidence upon which to base future vector control programs in urban settings. 280 localities were randomized either to control, i.e., routine VC activities, or to an IVM strategy consisting of targeted outdoor residual spraying with deltamethrin based product K-Othrine Polyzone, auto-dissemination devices with active ingredients pyriproxyfen and *Beauveria bassiana*, and community engagement. The primary outcome was the comparison of the estimated dengue incidence between the two arms. Overall,1,434 and 1,663 dengue cases were recorded in the control and intervention arm respectively. A non-statistically significant decrease of 14% (RR: 0.86, 95%CI: 0.70-1.06, p=0.17) of dengue incidence was observed in the intervention arm compared to the control arm. However, we observed a reduction of 29% (p=0.04) and 43% ($p<0.001$) of dengue cases during outbreaks and in hotspots respectively in the intervention arm, compared to the control arm. Preventive and long-lasting approaches focused on high-risk transmission areas such as hotspots represent a new paradigm towards a more rational management of dengue prevention and control programs. Our study demonstrates the public health value of a proactive IVM compared to routine vector control activities.

Abstract Reference: 20892
Mode of Presentation: Oral Presentation
Topic: Entomology - Mosquito Vectors

Intervention for Dengue Epidemiology in Malaysia (iDEM Trial): Impact of integrated vector management on aedes population density

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Abstract Content

The iDEM, a cluster Randomized Control Trial, targeted 28% of the population in Kuala Lumpur and Putrajaya. This project aimed to assess the impact of a preventive vector control method on dengue cases and *Aedes* population density was run from February 2020 to September 2022 in 139 localities. All intervention localities received six cycles of targeted residual spray using K-othrine Polyzone (deltamethrin) and autodissemination devices, monitored and maintained every two months. Community engagement was conducted with local leaders. Entomological collections were conducted from 24 localities (12 in each intervention or control arm) using Ovitrap Index, Larval Index, and Adult Index endpoints. Wall deposit bioassays were conducted to monitor spray effectiveness, and resistance to deltamethrin (0.03%) was assessed following the WHO guidelines. Over the two-year trial, a small and not statistically significant relative decrease of 4% in mean adult *Aedes* density was observed in the intervention compared to the control (p=0.86). Species-specific analysis showed a 7% decrease (p=0.78) in *Ae. aegypti* adult density. Larvae density trends were decreasing but not significant for *Ae. aegypti* (8%, p=0.60). Wall deposit bioassays using adult *Ae. aegypti* showed lower knockdown (0.11 ; 95% CI: 0.07, 0.16) in wild strain compared to susceptible strain. Resistance levels remained stable (<40% for knockdown and mortality), with no significant increase due to the intervention. In conclusion, while we did not detect a reduction in the *Aedes* populations density, but we observe fewer dengue outbreaks in treatment arm compared to control

Abstract Reference: 20894
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 2

Proactive case detection of asymptomatic malaria infections in Nong District, Savannakhet Province, Lao People's Democratic Republic (Lao PDR)

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Abstract Content

Lao PDR nears malaria elimination. However, control measures solely focusing on symptomatic cases are not sufficient. Indeed, asymptomatic *Plasmodium* infections that remain often undetected by conventional diagnostic tools can be a source of transmission. Therefore, understanding the distribution of asymptomatic infections becomes paramount for designing interventions to eliminate malaria by 2030. This study aimed to assess the prevalence of asymptomatic infections with associated factors (age, gender, occupation, history of malaria episode, etc.) in malaria-endemic rural villages using a highly sensitive DNA diagnostic method: a loop-mediated isothermal amplification (LAMP). A cross-sectional survey was conducted in three malaria-endemic villages of Nong district in March 2024. Residents were invited to voluntarily join the survey. After obtaining written informed consents, finger-prick blood samples were collected from the participants (n=622). The malaria LAMP technique was used to detect any human *Plasmodium* DNA in the blood samples. 2.1% (13/622) of the samples tested positive by LAMP. The prevalence of asymptomatic *Plasmodium* infections was 1.8% (11/622) including 2 cases (15.4%) (2/13) of *P. vivax* while 84.6% of cases (11/13) were neither *P. vivax* nor *P. falciparum*. 63.6% (7/11) of the asymptomatic infections were observed in adults (mostly farmers, 81.1%). This study identified a 1.8% prevalence of asymptomatic *Plasmodium* infections in malaria-endemic areas, mostly in adults. These findings showed that malaria reservoirs are significant and could maintain malaria transmission. Therefore, to eliminate malaria in Lao PDR by 2030, interventions with advanced diagnostic tools targeting high-risk populations are necessary.

Abstract Reference: 20907
Mode of Presentation: Oral Presentation
Topic: Drugs and Drug Resistance 2

White gold (*Chlorophytum borivilianum*): Phytochemical screening, antioxidant, cytotoxicity assessment and evolution of in-vitro antimalarial activity

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Abstract Content

Resistance to artemisinin and its partner drugs poses a significant threat to global malaria control efforts, underscoring the need for new and safe therapies. This study evaluated the anti-plasmodial activity, cytotoxicity, and antioxidant properties of the medicinal plant *Chlorophytum borivilianum* (white gold), focusing on its roots as a potential antimalarial treatment. Methanol/water solvents were used to prepare extracts via Soxhlet and percolation extraction techniques. The anti-plasmodial activity was assessed using the WHO Mark III Schizont maturation inhibition assay and SYBR green assay. Along with this toxicity on human Red Blood Cells and MDBK cell lines was evaluated using hemolysis and MTT assays, while antioxidant potential was determined with DPPH and Ferric-reducing antioxidant power assays. Phytochemical analysis revealed the presence of secondary metabolites linked to antimalarial activity, validating traditional medicinal claims and highlighting the plant's role in reducing reactive oxygen and nitrogen species. *In vitro* toxicity experiments confirmed the plant extract's safety for MDBK kidney cells and demonstrated efficient compatibility with RBCs. Notably, this study is the first to investigate the effects of *Chlorophytum borivilianum* on the 3D7 malaria strain, indicating a need for further *in vivo* research to validate these promising findings.

Abstract Reference: 20908
Mode of Presentation: Oral Presentation
Topic: Water & Food Borne Parasites

Serodiagnostic antigens of *Clonorchis sinensis* identified and evaluated by high-throughput proteogenomics

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Abstract Content

Clonorchiasis caused by *Clonorchis sinensis* is endemic in East Asia; approximately 15 million people have been infected thus far. To diagnose the infection, serodiagnostic tests with excellent functionality should be performed. First, 607 expressed sequence tags encoding polypeptides with secretory signal and B-cell epitopes were expressed into recombinant proteins using an in vitro translation system. By protein array-based screening using *C. sinensis*-infected sera, 18 antigen candidate proteins were selected and assayed for cross-reactivity against *Opisthorchis viverrini*-infected sera. Of the six antigenic proteins selected, four were synthesized on large scale in vitro and evaluated for antigenicity against the flukes-infected human sera using ELISA. CsAg17 antigen showed the highest sensitivity (77.1%) and specificity (71.2%). The sensitivity and specificity of the bacterially produced CsAg17-28GST fusion antigen was similar to those of CsAg17 antigen. CsAg17 antigen can be used to develop point-of-care serodiagnostic tests for clonorchiasis.

Abstract Reference: 20910
Mode of Presentation: Oral Presentation
Topic: One Health 1

Double digest: exploring the gut microbiota of *Ascaris lumbricoides* and their human hosts

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Abstract Content

Soil-transmitted helminth (STH) infections are known to alter the gut microbiota of infected human hosts. However, few studies have focused on the gut microbiota within the STH parasites themselves. This study aims to explore the gut microbiota of the human nematode *Ascaris lumbricoides* and compare it with the gut microbiota of their human hosts. We profiled the gut microbiota from four adult *A. lumbricoides* worms recovered from a six-year-old indigenous Negrito boy living in an STH-endemic village in Perak, Peninsular Malaysia, using next-generation sequencing of the V3-V4 region of the 16S rRNA gene. We also compared them with the gut microbiota of their human host (four *Ascaris*-positive and three STH-negative individuals from the same tribe and village). The gut microbial community structure of *A. lumbricoides* was found to be significantly different from that of their human hosts. The worms exhibited lower bacterial abundance and diversity compared to humans. This disparity was highlighted by beta diversity analysis, which showed a clear separation between the two sample types. In humans, the predominant phyla were Firmicutes (52.3%) and Bacteroidetes (36.6%), followed by Proteobacteria (7.2%). In contrast, the microbiota within *Ascaris* guts was dominated by Firmicutes (84.2%, primarily from the genus *Clostridium*), with Proteobacteria (11.1%), Tenericutes (1.8%), and Bacteroidetes (1.5%) present in lower proportions. Our findings suggest a distinct gut microbiota composition in *A. lumbricoides* compared to their human hosts. Further studies with a larger sample size of *Ascaris* adults and human hosts are required to confirm these findings.

Abstract Reference: 20918
Mode of Presentation: Oral Presentation
Topic: One Health 2

One health field approach applied to leptospirosis: A systematic review and meta-analysis across humans, animals, and the environment.

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Abstract Content

Leptospirosis is a neglected bacterial zoonosis transmitted through urine of infected hosts or contaminated environments, affecting a broad range of mammalian hosts. The transmission of bacteria between humans, animals, and the environment underscores the necessity of a One Health (OH) approach to better identify risks. We conducted a systematic review to identify significant findings, challenges and gaps in OH research on leptospirosis, focusing on studies involving at least two of the three compartments: human, animal, and environment. We searched in PubMed, Web of Science, Medline, Scopus, and ScienceDirect from January 1, 1918 to March 30, 2023. We assessed the quality and risk of bias of these studies using Joanna Bings Institute (JBI) tools. We performed a meta-analysis to identify links between *Leptospira* seroprevalence or presence among humans, animals, and the environment. Of 1,140 leptospirosis studies including sample collections, 80 multicompartmental studies were included: 58 human/animal, 11 animal/environment, 4 human/environment, and 7 across all compartments. Among these, 70.0% of studies were prevalence surveys for which only 46.3% of JBI scores exceeded 0.5/1. We identified methodological shortcomings, affecting study design and statistical analysis. We found positive correlations between human and animal seroprevalences, including specific associations with domestic and livestock species such as bovine, pig, goat, and with rodents. The scope of our analysis was constrained by the limited number of OH studies, particularly those investigating the environment and the quality of research protocol. This highlights the critical need for more robust, well-supported OH research to clarify the transmission dynamics and identify risks.

Abstract Reference: 20920
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 3

Plasmodium falciparum in Bolivia: from imminent elimination to reintroduction and rapid spread

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Abstract Content

Bolivia is endemic for malaria due to *Plasmodium vivax* and *Plasmodium falciparum* (<10% of cases). Official malaria data were analyzed and the current situation was assessed with fieldworks. The highest reporting of malaria in 1998, with 74,350 cases, was followed by a sustained decline to the lowest reporting of 4424 cases in 2017. Regarding *P. falciparum*, autochthonous cases progressively decreased from 1200 in 2010, to seven in 2016 and zero in 2017 and 2018. Consequently, Bolivia decided to eliminate the transmission of *P. falciparum*. Unfortunately, *P. falciparum* was reintroduced in 2019 by an infected person from Brazil, followed by local transmission and the progressive increase in cases between 2019-2023 (43, 73, 230, 536 and 1140 cases, respectively), spreading in the departments of Pando, Beni and La Paz. The exclusion of the support of collaborators (volunteers) in the diagnosis and treatment of cases, socio-political conflicts related to the change of government in 2019 and the COVID-19 pandemic, could have harmed the achievements in malaria control. For example, the presence of *P. falciparum* gametocytes in patient blood samples, during our field evaluations, indicates that many cases were not rapidly detect and treated, despite the fact that Bolivia adopt the Diagnosis-Treatment-Detection strategy (DTD), prioritizing the process of "diagnosis, treatment, investigation and response" recommended to eliminate transmission. Currently, only nine Amazonian municipalities concentrate about 90% of malaria cases, however, the reintroduction and reestablishment of *P. falciparum* transmission reminds us that malaria surveillance requires great efforts when cases are sporadic or reporting remains at zero.

Abstract Reference: 20925
Mode of Presentation: Oral Presentation
Topic: Malaria - Epidemiology 2

Malaria in Southeast Asia and beyond - diagnostic options

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Abstract Content

Malaria is a major public health threat in tropical and subtropical countries. Rapid diagnostic in resource-limited settings remains a major obstacle to eliminate malaria, especially with the emergence of *Plasmodium knowlesi*. Microscopy is the gold standard but requires high competency. Molecular methods like PCR are sensitive but time-consuming and require a thermocycler. Isothermal amplification techniques like loop-mediated isothermal amplification (LAMP) have emerged as faster alternatives with high sensitivity, making them suitable for resource-limited settings. The present study aims to develop a method for rapid diagnosis of human malaria using loop-mediated isothermal amplification (LAMP) coupled with lateral flow (LF). To simplify the sample preparation process, a paper-based nucleic acid extraction method was utilized in this study. The entire procedure from sample preparation to diagnosis takes approximately 1 hour and 15 minutes to complete, LAMP-LF assay exhibited high sensitivity, as the detection limit was 5 parasite/uL for all five Plasmodium species. Clinical sensitivity was 100% using 42 malaria samples and specificity was 97.8% using 42 healthy samples. Combined with a simple nucleic acid extraction step, this optimized LAMP-LF method can be potentially developed as point-of-care diagnostic tool in future.

Abstract Reference: 20926
Mode of Presentation: Oral Presentation
Topic: Malaria - Diagnostics 2

Application of a low-cost, specific, and sensitive loop-mediated isothermal amplification (LAMP) assay to detect *Plasmodium falciparum* imported from Africa

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Abstract Content

Chinese citizens traveling abroad bring back imported malaria cases to China. Current malaria diagnostic tests, including microscopy and antigen-detecting rapid tests, cannot reliably detect low-density in factions. To complement existing diagnostic methods, we aimed to develop a new loop-mediated isothermal amplification (LAMP) assay to detect and identify Plasmodium falciparum in Chinese travelers returning from Africa. We developed a miniaturized LAMP assay to amplify the actin I gene of P. falciparum. Each reaction consumed only 25% of the reagents used in a conventional LAMP assay and the same amount of DNA templates used in nested PCR. We evaluated this LAMP assay's performance and compared it to microscopy and a nested PCR assay using 466 suspected malaria cases imported from Africa. We assessed the sensitivity of the new LAMP assay using cultured P. falciparum, clinical samples, and a plasmid construct, allowing unprecedented precision when quantifying the limit of detection. The new LAMP assay was highly sensitive and detected two more malaria cases than nested PCR. The LAMP assay detected 0.01 parasites/μL of blood (equal to 0.04 parasites/μL of DNA) using cultured P. falciparum and 1–7 parasites/μL of blood (4–28 parasites/μL of DNA) in clinical samples, which is as good as or better than previously reported and commercially licensed assays. The novel LAMP assay based on the P. falciparum actin I gene was specific, sensitive, and cost[1]effective, as it consumes 1/4 of the reagents in a typical LAMP reaction.

Abstract Reference: 20930
Mode of Presentation: Oral Presentation
Topic: Parasitology

Cerebral malaria model applying human brain organoids

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Abstract Content

Neural injuries in cerebral malaria patients are a significant cause of morbidity and mortality. Nevertheless, a comprehensive research approach to study this issue is lacking, so herein we propose an in vitro system to study human cerebral malaria using cellular approaches. Our first goal was to establish a cellular system to identify the molecular alterations in human brain vasculature cells that resemble the blood–brain barrier (BBB) in cerebral malaria (CM). Through transcriptomic analysis, we characterized specific gene expression profiles in human brain microvascular endothelial cells (HBMEC) activated by the *Plasmodium falciparum* parasites. We also suggest potential new genes related to parasitic activation. Then, we studied its impact at brain level after *Plasmodium falciparum* endothelial activation to gain a deeper understanding of the physiological mechanisms underlying CM. For that, the impact of HBMEC-*P. falciparum*-activated secretomes was evaluated in human brain organoids. Our results support the reliability of in vitro cellular models developed to mimic CM in several aspects. These systems can be of extreme importance to investigate the factors (parasitological and host) influencing CM, contributing to a molecular understanding of pathogenesis, brain injury, and dysfunction.

Abstract Reference: 20935
Mode of Presentation: Oral Presentation
Topic: One Health 1

Lymphatic Filariasis (LF) elimination in Malaysia: Challenges in addressing *Brugia malayi* transmission

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Abstract Content

Lymphatic Filariasis Elimination Program was launched in 2002 to reduce the prevalence of lymphatic filariasis (LF) to a level where it is no longer a public health concern. The primary objective was reducing the LF prevalence through mass drug administration (MDA). In 2003, more than 1 million people were found to be at risk of LF infection, with 127 endemic mukim (IUs). A once-yearly MDA of Diethylcarbamazine and Albendazole for 5 years was completed in the year 2008 and by the year 2021, 122 IUs has successfully reduced LF antibody prevalence (<2%), while 5 remaining IUs in Sarawak and Sabah were still on surveillance post-MDA. Triple drug therapy (Ivermectin + Diethylcarbamazine + Albendazole) was introduced in 2019 in 102 hotspot localities with antibody prevalence >2%. Post MDA IDA surveillance in Perak, Pahang, and Sarawak, had shown reduction of LF antibody prevalence to <2%. However, hotspot localities in Tangkarason and Pitas, Sabah showed LF antibody prevalence ranging from 2% to 25%. In 2016, operational research in Kg.Tangkarason conducted by the Disease Control Division, MOH, in collaboration with the Faculty of Veterinary University Putra Malaysia shown prevalence of *B. malayi* in cats (15.6%) and dogs (2.5%) suggesting cats and dogs may play an important role as reservoir hosts for human LF. The high prevalence of LF in humans suggests the potential role of zoonotic *B. malayi* transmission that led to the failure of MDA. Hence treating cats and dogs can have a positive impact on the reduction of LF in humans.

Abstract Reference: 20961
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Malaria characteristic at Prof Ngoerah hospital, Bali, Indonesia

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Abstract Content

Malaria is still a public health problem, currently the Indonesian Ministry of Health is making efforts to eliminate malaria by 2030. Bali has received malaria free certificate but as tourist destination is at risk of contracting malaria from traveler. Descriptive study from medical record of adult patients whom were treated for malaria infection in Prof Ngoerah Hospital since 2019 to 2023. Descriptive data regarding the patient characteristics, type of plasmodium, severity of infection and treatment outcome was reported. There were 37 cases of malaria treated. The mean age was 29.8 years old with majority gender was male (78,37%). All of malaria cases were import malaria. Malaria vivax were found to be the most frequent (51,35%), followed by plasmodium falciparum (45,94%) and one case plasmodium malariae infection was reported (2,7%). Severe malaria was diagnosed from 9 patients (24,3%) of which jaundice was the most common presentation (77,77%) followed by renal dysfunction (44,44%). All of the severe malaria cases were treated by artesunate intravena and primaquine and uncomplicated malaria were treated by dehydroartemycine (DHP) and primaquine. No death case was reported during hospitalization. All cases of malaria in Prof Ngoerah hospital were import malaria, most cases are malaria vivax followed by falciparum. There were severe malaria cases which jaundice as the common presentation. All malaria patients was delared cured.

Abstract Reference: 20974
Mode of Presentation: Oral Presentation
Topic: Veterinary Health

Cystic Echinococcosis – known and unknown facts in animals and human beings

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Abstract Content

Echinococcosis is a serious Zoonoses caused by *Echinococcus granulosus*, with rates of human cystic echinococcosis (CE) infection ranging from less than 1 per 100,000 to more than 200 per 100,000 in certain rural populations where there is close contact between human beings and domestic dogs. Cystic echinococcosis is often expensive and complicated to treat and may require extensive surgery and/or prolonged drug therapy particularly in human beings as compared to animal intermediate hosts that include herbivores such as sheep, goats, cattle, pigs, horses, camels etc., however sheep has been reported to be the major intermediate hosts. In the tissues of the affected intermediate hosts, the *E.granulosus* oncospheres in the eggs develop into hydatid cysts, usually over many years in the form of large, unilocular, fluid filled lesions. Prevention is by periodic deworming of dogs against the tapeworm, improved hygiene during slaughter of intermediate hosts as well as proper disposal of the infected offals and public awareness. Postmortem of the definitive host for the presence of the tapeworms or identification of eggs in the dog's faeces and in intermediate hosts, it involves postmortem, serology, imaging methods to identify the condition properly.

Abstract Reference: 20975
Mode of Presentation: Oral Presentation
Topic: One Health 2

Environmental and agricultural impact on the breeding habitat of zoonotic malaria vector *Anopheles* mosquitoes in Kapit, Sarawak

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Abstract Content

Plasmodium knowlesi, a simian parasite, has emerged as a significant cause of zoonotic malaria in humans, particularly in the Kapit division of Sarawak. The persistent cases in this region highlight the complexity of transmission dynamics, which are intricately linked to the environment, wild monkey populations, and human agricultural activities. This study aims to investigate the effects of human and agricultural activities on the breeding habitats of Anopheles mosquitoes, the primary vectors of P. knowlesi. Study was conducted across 12 months at three farm sites near longhouses of the Iban communities in Kapit. Molecular tools were employed to identify the mosquito larval species, revealing that most Anopheles mosquitoes in these areas were Anopheles donaldi and Anopheles latens. These mosquito breeding habitats were primarily found along river streams, ponds with vegetation, and shaded areas, all influenced by nearby agricultural practices. Observations suggest that paddy planting, clearing areas for small-scale plantations, and the use of fertilizers have significantly reduced mosquito breeding. Furthermore, the rainy season played a crucial role in washing out mosquito larvae, further disrupting breeding cycles. These findings are essential for developing targeted strategies to mitigate the risk of P. knowlesi transmission, considering the complex interplay between environmental management and vector control in high-risk regions.

RAPID ORAL PRESENTATION

RAPID ORAL PRESENTATION

Abstract Reference: 20028
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Exploring antimicrobial resistance profiles in dairy farm environments across Asian regions

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Abstract Content

Antimicrobial resistance (AMR) poses a significant “One Health” challenge, involving the transmission of resistant bacteria and resistance genes across humans, animals, and environment. Understanding the role of environment in facilitating the transmission of AMR is crucial in addressing this global health issues. Asia, a focal point of AMR, raised concerns due to its role in escalating AMR among major pathogens. This scoping review summarizes evidence of AMR prevalence and its resistance genes based on studies conducted by Asian countries between 2012 and 2022. An electronic literature search on PubMed, ScienceDirect, and Scopus, resulting in 37 studies that met the criteria and are discussed in this review. The geographical distribution revealed majority of the studies were in China, followed by India, and Bangladesh. Environmental samples predominantly included manure, soil, water, and wastewater. It was found with gentamicin being most frequently examined antibiotic, tetracycline and ampicillin exhibited highest resistance level in analyzed bacteria. In agreement with that, tetA gene was found predominant in the environment. In contrast, colistin demonstrated high susceptibility, partly due to its prohibition as feed additives in most countries. In view of these findings, it is essential to intensify studies on environment in relation to AMR and implementing proactive measures and preventive strategies to reduce the rising problems of AMR. Besides, embracing multidisciplinary collaboration among countries is vital to address AMR effectively. Failure to act may lead to a rise in morbidity and mortality rates, as well as an escalation of the economic burdens for the country.

Abstract Reference: 20036
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Post infectious basal ganglia encephalitis leading to parkinsonism –A rare CNS complication of dengue fever

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Abstract Content

A wide range of neurological manifestations including dengue encephalopathy, Guillain–Barre syndrome, acute disseminated encephalomyelitis, transverse myelitis, cranial nerve palsies, and myositis have been reported following dengue infection. But parkinsonism secondary to dengue virus infection is uncommon. We describe a 13-year-old adolescent boy, who presented with bradykinesia, bradyphonia and mask-like facies while recovering from uncomplicated dengue fever. Patient was brought with complaints of lethargy, decreased activity and staring look for past 3 days. After taking treatment on opd basis for 3 days and not much improvement they got hospitalized. Over next few days child got better and was diagnosed as a case of dengue fever. He got discharged after 4 days. After coming to home parents noticed that child was not interacting much and over next few days this behavior continued and then they brought him to our opd. Child was admitted and a possibility of functional disorder was kept for which psychological evaluation was done which showed some problem related to his studies. But inspite of intervention child didn’t show signs of improvement. At this point of time MRI head was done which showed bilateral basal ganglia opacities with possibility of para/postinfectious encephalitis. CSF analysis done was normal including NMO with MOG antibody profile. Patient was started on pulse methyl prednisolone for 5 days and Tab Syndopa plus. Child showed improvement in his Parkinson symptoms.Child was shifted to oral steroids. We believe that this case represents an acute post infectious (dengue fever) basal ganglia encephalitis, a disorder which is probably immune mediated with good neurological recovery.

Abstract Reference: 20037
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Leptospirosis and typhoid coinfection- a dual edge sword

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Abstract Content

Leptospirosis is an acute febrile illness of zoonotic origin caused by Leptospira species. Typhoid fever is another febrile illness which mainly affects gastro intestinal tract. Both the diseases are attributed to tropical regions and spread by infected water. The purpose of the present report was to look for potential coinfections of Leptospirosis and Typhoid among undifferentiated acute febrile illness patients. A 2.5 years boy was admitted with complaints of fever for 8 days, abdominal distension and pain for 6 days, loose stools for 4 days. On examination child had a HR=134,good volume pulses,BP=80/40,CFT=3 secs, RR=44 with 95% oxygen sat in room air. Patient was provisionally diagnosed as a case of tropical fever syndrome and started on inj Actamase, Inj Metrogyl and syp Azee. Per abdomen was distended with ascites and liver 5cm.Child's blood culture had grown salmonella sensitive to the antibiotics already started. Metro was stopped. In other tropical fever workup leptospira serology came positive so doxycycline was also started. On day 7 of hospitalisation child's fever intensified and he developed new onset cough. As there were many patients of Flu admitted in ward at that time Flu panel of the patient was also sent which came positive for H1N1. So Oseltamavir was added orally. Echocardiography done on day 2 was normal. Initial investigations revealed a platelet count of 27000/dl. In tropical fever workup leptospira came out to be positive. Child was discharged after16 days of hospitalisation. Conclusion: Coinfections (Leptospirosis with Typhoid) always leads to delay in appropriate intervention and prolonge hospital stay.

Abstract Reference: 20040
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Understanding of the abundance and distribution patterns of *Phlebotomus argentipes* (Diptera: Psychodidae) in Medawachchiya, North Central Province Sri Lanka

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Abstract Content

Phlebotamus argentipes (Diptera family Psychodidae) is well-known for its role in transmitting cutaneous leishmaniasis (CL) in Sri Lanka. However, there is still a lack of comprehensive understanding regarding its basic ecology. The present study evaluates the prevalence of *P.argentipes* using cattle-baited traps. The study was conducted in an endemic area Madawachchiya in North Central Province Sri Lanka which is one of the high-risk areas for CL. From February 2022 to September 2023, a total of two hundred forty-six *P.argentipes* sand flies were captured from 22 cattle traps placed monthly over 10 Grama Niladari divisions in the study site. The number of collected males (~69.9% / n=172) was higher than the females (~30.0% / n=74) which is a male-to-female ratio is 4:1. This explains the attractiveness of males to the bright surfaces containing the full spectrum of light and the courtship attraction of the females. The highest number of population densities were reported during the month of February while gradual increasing was observed from June to February in two consecutive years. The mean of the *P.argentipes* captured per trap per night was 7.82 (±15.045) for males, and 3.36 (±7.675) for females, 1.82 (±4.646) for blood-fed females. In this study, no correlation (r= -0.155) was found between the presence of blood-fed sand flies and the occurrence of CL. This indicates that CL transmission in the area is not solely dependent on the population densities but the combination of several risk factors that require more investigation soon.

Keywords: Leishmaniasis, *P.argentipes*, Prevalence, Sand flies

Abstract Reference: 20046
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Bibliometric analysis of neglected tropical diseases in Asia informing evidence-based approaches for disease control (2014-2024)

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Abstract Content

Neglected Tropical Diseases (NTDs) predominantly affect impoverished and marginalized populations in tropical and subtropical regions, particularly within specific Asian countries that are considered as economic powerhouses, nevertheless NTDs constitute a group of conditions intrinsically intertwined with poverty. The aim of this bibliometric study was to gather better cognizance to provide better policies combating NTDs. This study was essential to discerning domains characterized by research lacunae juxtaposed prevalence in Asia, which necessitated comprehensive investigation into its underlying mechanism and burden. We delved into several specific research areas, including trends related to research trends, research focus and years. This study incorporated an array of methods using Scopus database for data collection and VOSviewer software version 1.6.19 for data visualization and analysis. In this research, using bibliometric analysis between 2014-2024 there are 174 documents, it was found that Helminthiasis is commonly observed as one of NTDs. Moreover, China, which correlates with real time diseases prevalence in the country. Followed by Indonesia, Laos, and Malaysia led in Asia areas research regarding this topic. Approach through tracking the geographical distribution and prevalence of NTDs helps target interventions effectively and prioritize areas with the highest disease burden. This bibliometric analysis underscores the waning attention and research focus on NTDs publication trends in relation to prevalence in Asia. It underscores the value of consistent research to gain insights, formulate preventive measures, and enhance infection management on Asia and global scale.

Keywords: Bibliometric analysis, Neglected Tropical Diseases (NTDs), Asia, Prevalence.

Abstract Reference: 20051
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Water sources: Schistosomiasis transmission in Alitupu Village, North Loredistrict, Poso District, Central Sulawesi Province

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Abstract Content

Schistosomiasis continues to be reported in numerous East and Southeast Asian countries, which includes China, Japan, Indonesia, and the Philippines. Snail fever or schistosomiasis in Indonesia is found in the Lindu, Napu and Bada Highlands, Central Sulawesi Province in Poso and Sigi Districts, which spread in 28 villages. The objective of this study was to describe the habitat of the Oncomelania hupensis snail as a source of transmission and efforts to control it. Methods: Search for snails in areas suspected of being a suitable habitat for O.h lindoensis snails. If the snail was found, samples of the snail were taken at that location, and then it was examined whether the snail contained parasites using the "crushing" method. Result and discussion: There were 22 snail habitats in Alitupu Village. The snail habitat, in the shape of water seepage, is used by the community as a water source. Therefore, the control of snail habitats needs to be done by multisectors. Conclusion: Building water catchment tanks can decrease the density and contamination of snails in those habitats.

Keywords: Schistosomiasis, Oncomelania hupensis lindoensis, Poso Regency, Central Sulawesi

Abstract Reference: 20053
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Molecular biomarker identification in seasonal cardiovascular comorbid diseases (SCCD) using network metanalysis

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Abstract Content

The start of many illnesses is known to be significantly influenced by seasonal variations in the human cardiovascular system. Numerous clinical investigations, on the other hand, suggest that some groups of people are more seasonal sensitive, and that their maladaptation may contribute to a variety of disorders. As a result, evaluating the etiological and seasonal sensitive patterns of cardiovascular diseases (CVD), which affect the majority of the human population, is crucial. The study\'s premise was that cardiovascular and related disorders have significant links with seasonal and etiological fluctuations. Current study, data mining was used to find 852 disease association connections between cardiovascular and related illnesses from a systematic review of 4519 papers. To focus on only the most prevalent CVDs, a disease ontology-based semantic similarity network (DSN) study was carried out. Furthermore, topological analysis was employed that predicted the seven CVDs in three clusters. The seasonal sensitivity and temporal association of these seven CVDs were then investigated using Mann-Kendall and Cox-Stuart models and their temporal connections were validated using LOESS and TBATS. The study provides indirect evidence of an etiological relationship between three CVDs, including MI, atrial fibrillation, and atherosclerosis, all of which are seasonal. As a result, these three conditions qualify as seasonal cardiovascular comorbidities (SCCD). Following that, secondary network met analysis using GEO data from GSE2240 (atrial fibrillation) and GSE132651 (atherosclerosis) reveals a triad of NRF1-hsa-miR-124-3p-NRF2 is a significant module, and might trigger inhibition of GSK-3 phosphorylation which minimize the risk of myocardial infarction and improves heart pathology.

Abstract Reference: 20062
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

The one health research landscape in greater southeast Asia: A comprehensive bibliometric analysis

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Abstract Content

The proposed study is an initial analysis of the One Health (OH) research done in the dynamic Greater Southeast Asian (GSEA) region, comprising the countries of Southeast Asia, including Taiwan. Employing rigorous bibliometric methods, this research provides a panoramic view of scholarly endeavors, collaboration networks, and thematic trends within the OH domain. Publications from the opensource PubMed database will be collected and will extract data from abstracts of related studies beginning 2003, when the term “One Health” was coined following similar approaches in the past. Subsequent investigations will describe the trend of research directions from this point onwards, and will evaluate current advances in this field. The search strategy will include all potential OH publications, while identification and selection of data will follow the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines. Bibliometric data processing and analysis shall utilize R and R Studio for its extensive library and its ability to handle large and complex bibliographic datasets, while VOSviewer will be used for elaborate network visualizations. Tables and graphs are also expected to generate corresponding assessments for key bibliometric components, such as publication and citation, collaboration, keyword co-occurrence, and institutional impact analyses. By analyzing the research landscape, the study can identify key OH issues and knowledge gaps in GSEA, and results can guide public health policies, helping governments and organizations allocate resources effectively and ultimately address pressing health challenges in the region.

Abstract Reference: 20154
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Forest restoration and the zoonotic vector *Anopheles balabacensis* in Sabah, Malaysia

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Abstract Content

Anthropogenic changes to forest cover have been linked to an increase in zoonotic diseases. In many areas, natural forests are being replaced with monoculture plantations, such as oil palm, which reduce biodiversity and create a mosaic of landscapes with increased forest edge habitat and an altered microclimate. These altered conditions may be facilitating the spread of the zoonotic malaria parasite *Plasmodium knowlesi* in Sabah, on the island of Borneo, through changes to mosquito vector habitat. We conducted a study on mosquito abundance and diversity in four different land uses comprising restored native forest, degraded native forest, an oil palm estate and a eucalyptus plantation, these land uses varying in their vegetation types and structure. The main mosquito vector, *Anopheles balabacensis*, has adapted its habitat preference from closed canopy rainforest to more open logged forest and plantations. The eucalyptus plantations *(Eucalyptus pellit*a) assessed in this study contained significantly higher abundance of many mosquito species compared with the other land uses, whereas the restored dipterocarp forest had a low abundance of all mosquitos, in particular, *An. balabacensis*. No *P. knowlesi* were detected in any of the vectors collected during the study, however, *P. inui*, *P. fieldi* and *P. vivax* was found in *An. balabacensis*. These findings indicate that restoring degraded natural forests with native species to closed canopy conditions reduces abundance of this zoonotic malarial mosquito vector and therefore should be incorporated into future restoration research and potentially contribute to the control strategies against simian malaria.

Abstract Reference: 20161
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Mosquito abundance and its possible role of hemoplasma transmission in a pig farm in Loei Province, Thailand

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Abstract Content

Hemoplasma comprises a group of bacteria within the *Mollicutes* class inducing hemolytic anemia in various mammals, including pigs. Transmission often occurs through blood-sucking insects, although its dissemination via mosquitoes in pig farms remain relatively unexplored. In this investigation, between November 2021 - October 2022, mosquito surveillance was systematically conducted on a monthly basis at a pig farm in Loei province, Thailand. Mosquitoes were sorted under a stereomicroscope to distinguish between individually blood-fed specimens and pools of host-seeking individuals. A total of 5,797 female mosquitoes spanning five genera (*Aedes, Anopheles, Armigeres, Culex, and Mansonia*) were captured from this pig farm. Notably, *Culex* mosquitoes predominated in frequency, with peak abundance recorded in May. Subsequent nucleic acid extraction from these samples facilitated PCR testing targeting the 16S rRNA gene, revealing hemoplasma presence. Notably, 18.40% (85/462) of blood-fed mosquitoes and 2.17% (5/230) of mosquito pools tested positive for hemoplasma. Following the successful sequencing of 36 hemoplasma-positive mosquito samples based on the 23S rRNA gene, comprehensive analysis employing blastn, MEGA, and PopART elucidated the diversity of hemoplasma species encountered. Among these, the identified species included *Mycoplasma suis*, *Mycoplasma* sp. closely related to *Mycoplasma suis*, *Mycoplasma parvum*, *Mycoplasma wenyonii*, and *Candidatus* Mycoplasma haemobos. The collective findings of this inquiry strongly implicate mosquitoes as potential mechanical vectors for various hemoplasma species within the context of pig farming in Thailand. This underscores the importance of further research into the dynamics of hemoplasma transmission and the implementation of targeted control measures to mitigate associated risks within agricultural settings.

Abstract Reference: 20182
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Unravelling Streptococcus infections in paediatric populations: A clinical prediction rule approach

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Abstract Content

Streptococcus species infections, notably Group A *Streptococcus* (GAS), are a significant concern among children under 12 years globally. This retrospective study aimed to develop and validate a Clinical Prediction Rule (CPR) to predict *Streptococcus* species presence in throat swabs from children under 12 years old. Variables including gender, age, and ward of admission, clinical diagnosis, and antibiotic sensitivities/resistances were examined. Logistic regression modeling was employed to identify significant predictors associated with *Streptococcus* presence. In 233 children, mean age was 4 ± 0.25 years, with most under age 3 (62.7%). Tonsillitis was the primary diagnosis across all ages. Streptococcus species prevalence ranged from 69.3% to 56.7%. Antibiotic sensitivity varied: Chloramphenicol (64.1%), Erythromycin (100%), Gentamycin (61.6%), while resistance occurred in Amoxil (25.0%) and CTX (33.3%). Male gender exhibited a trend toward increased infection likelihood, albeit not statistically significant. Diagnoses such as Sepsis/Tonsilitis and ear discharge/tonsilitis were significantly associated with *Streptococcus* presence ($p < 0.001$). However, antibiotic resistance profiles showed inconclusive associations due to estimation issues and non-converging confidence intervals. While older age demonstrated a trend toward reduced infection likelihood ($p = 0.074$), the significance was marginal. The logistic regression model exhibited promising predictive performance, correctly identifying 95.4% of *Streptococcus* cases with a sensitivity of 95.4% and a specificity of 36.8%. In conclusion, this study contributes to our understanding of *Streptococcus* infection predictors in pediatric populations. The model's performance, alongside additional evaluation metrics, highlights its potential as a valuable tool for *Streptococcus* infection prediction and management in clinical practice.

Abstract Reference: 20198
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Microsporidiosis in children with diarrhea in Indonesia

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Abstract Content

Introduction: The disease caused by microsporidia infection is called microsporidiosis. Children have been identified as a population group at risk of developing microsporidiosis due to their immature immune system. Damage to the intestinal mucosa related to microsporidiosis causes chronic diarrhea, malabsorption and weight loss, especially in children. The reported age range for children with diarrhea with intestinal microsporidiosis is between < 1 year to 15 years. However, microsporidiosis is underdiagnosed because of the clinical symptoms are not specific, the size of the spores is very small which is easily missed during microscopic examination, and special staining for microsporidia is only done if there is a specific request. In Indonesia, microsporidia infection in children with diarrhea has not been investigated. This is a cross sectional study. The research samples consisted of stools from children (aged 0 to 18 years old) with diarrhea which were sent to the Parasitology Laboratory of Universitas Indonesia Medical Faculty. The sample size of this study was 105. Each sample was stained with microsporidia trichrome staining. To detect other intestinal parasites, direct microscopic examination, concentration, *Blastocystis* culture, modified acid-fast staining and coproantigen examination (for *Giardia* and *Cryptosporidium*) are carried out. The positive stool results for microsporidia were obtained from children with acute diarrhea, ongoing diarrhea and chronic diarrhea, respectively 20, 9 and 21. From those positive stools of microsporidia, no other intestinal parasites were found. Microsporidia can be found in children with acute diarrhea, ongoing diarrhea and chronic diarrhea.

Keywords: Intestinal microsporidia, diarrhea, child

Abstract Reference: 20200
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Lactococcus lactis strain plasma stimulation of PBMCs elicits interferon-alpha production and promotes broad-spectrum antiviral activity against tropical arboviruses

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Abstract Content

The growing risk of contracting viral infections due to high-density populations and disasters resulting in ecological changes such as climate change and increased population mobility has highlighted the need for effective treatment and preventive measures against these virus infections. Probiotics, particularly *Lactococcus lactis* strain Plasma (LC-Plasma), exhibit a broad immunomodulatory effect against several viruses. The present study aimed to assess LC-Plasma's immunomodulatory effects on peripheral blood mononuclear cells (PBMCs) derived from healthy volunteers and its subsequent antiviral response against Dengue virus (DENV), Chikungunya virus (CHIKV), and Zika virus (ZIKV) using an *ex vivo* infection model. LC-Plasma-stimulated PBMCs demonstrated elevated interferon-alpha (IFN-α) production and CD86 and HLA-DR upregulation, potentially linked to the activation of plasmacytoid dendritic cells (pDCs). The replication of DENV, CHIKV, and ZIKV was dose-dependently inhibited when Huh-7 cells were exposed to LC-Plasma-stimulated PBMC supernatant (LCP Sup). IFN-stimulated genes (ISGs) expression, including IFN-stimulated gene 15 (ISG15), IFN-stimulated exonuclease gene 20 (ISG20), IFN-induced transmembrane protein 1 (IFITM-1), Myxovirus resistance protein A (MxA), and Radical S-adenosyl methionine domain-containing protein 2 (RSAD2), was upregulated in LCP Sup-stimulated Huh-7. Findings from this study suggest that LC-Plasma has the potential to induce IFN-α production, leading to an enhancement in the expression of ISGs and contributing to a broad-spectrum antiviral response. LC-Plasma, hence, could be a rational adjunctive option for preventing viral diseases, warranting future clinical trials.

Abstract Reference: 20201
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Investigations into the genes involved in vascular leakage in severe dengue that are associated with diabetes

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Abstract Content

Dengue, an arboviral disease is a worldwide public health problem predicted to continue. There is an urgency to understand the mechanisms behind our immune responses that affects this balance between protection versus pathogenesis. However, both host and viral factors are yet to be clearly characterized. The hallmark of Severe Dengue is plasma leakage which is due to pro-inflammatory cytokines and dysregulation of endothelial barrier protein expression. Comorbidities such as diabetes have shown to worsen the clinical manifestation of Severe Dengue with endothelial dysfunction being the common biological mechanism. The underlying mechanisms regarding the association between this comorbidity and dengue are still lacking. The key factors of diabetes affecting the endothelium include junctional-related proteins expression and immune response causing increased viral replication and inflammation. To understand this, we performed electro-impedance assays (ECIS) to determine the effect of dengue and glucose on microvascular pulmonary endothelial cells. Based on ECIS measurement, the magnitude of vascular leakage observed was positively correlated with the concentration of glucose, whereby the loss of barrier function in HPMECs indicated an immediate junctional tightening happened, followed by a sudden loss of barrier function. Microarray analysis has been performed which intend to determine the genes affected. These genes in diabetic individuals could play pivotal role in the development of SD.

Abstract Reference: 20202
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Prevalence, and antimicrobial resistance of *Staphylococcus aureus* in dairy farms in Malaysia

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Abstract Content

Staphylococcus aureus (*S. aureus*) is an opportunistic pathogen that causes pneumonia, septicaemia, and endocarditis, mainly associated with multidrug resistance. The aim of this study was to determine the distribution of S. *aureus* and its resistance patterns in dairy farms in Klang Valley. Hand and nasal swabs of workers, raw milk, cow dung, and effluent were collected from dairy farms. The samples were platted on CHROMagar *Staph aureus*. The VITEX 2 system was used for the identification and determination of antimicrobial susceptibility. A total of 105 *S. aureus* were detected from dairy farms, with a high presence found among farm workers (75%), followed by raw milk (23%), effluent (1%), and cow dung (1%). About 56% of *S. aureus* were found to be susceptible to all antibiotics tested, while 15% were considered multidrug resistant bacteria (MDR). The highest resistance was to benzyl penicillin (56%). Methicillin-resistant *S. aureus* (MRSA) was detected in 5% of the isolates. Even though the presence of MRSA is still low, the occurrence of MDR- *S. aureus* shows possible antibiotic usage. Therefore, action should be taken to prevent the spread of MDR *S. aureus* in community settings. It is vital that farm owners and workers maintain good aseptic techniques when collecting milk and using personal protective equipment. It is imperative to halt cross-transmission from humans to milk or vice versa.

Abstract Reference: 20215
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Lipids in cercariae of the common trematodes and the method of their sampling

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Abstract Content

The role of lipids in the parasite's life is diverse: from suppressing the host's immune system to a structural function. Free-living stages of parasites can contain large stores of lipids and glycogen to survive in the external environment until encountering the host. Various aquatic animals consume free-living stages, such as trematode cercariae. Therefore, cercariae can serve as a source of essential lipids for the predators. However, research on lipidome of parasites is scarce due to complex methodology. For instance, a small size and an active movement of cercariae complicate the collection of sufficient material for lipid analysis. We compared different methods of collecting cercariae for lipid analysis to find the most effective one. In addition, we compared lipidome of cercariae of different trematode species (families Diplostomidae and Plagiorchidae). Cercariae were obtained from naturally infected snails *Lymnaea stagnalis*. Cercariae of one species and age from different mollusks were combined in one sample. Samples were concentrated either through a mesh or by cooling at −20 °C. Then, they were centrifuged, put in chloroform-methanol, and frozen. Gas-liquid and high-performance thin-layer chromatography were applied. It was shown that subzero temperature could be a more effective way of collecting cercariae than mesh-sieving or centrifugation for large-volume samples. Data on different species of cercariae showed similarity in composition of main lipid classes, and some specificity in proportion of fatty acids. The study was supported by Russian Science Foundation (grant 23-24-00418).

Abstract Reference: 20216
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Disentangling infracecological interactions of eye-dwelling fish parasites

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Abstract Content

In nature, hosts are usually infected with several species of parasites. Parasitic interactions within the infracommunity have important consequences for pathogens and their hosts. Within host bodies, parasites can either compete or facilitate the joint exploitation of their hosts. Either interaction type has important implications for evolution of virulence. However, interactions between parasite species are still rarely studied under controlled laboratory conditions. We experimentally infected fish with two closely related ubiquitous trematodes (*Diplostomum pseudospathaceum* and *Tylodelphys clavata*) to study how the presence of the potential competitor affects the infection success and growth rate of parasites. The first parasite is localized in the lens, the second – in the vitreous humor of fish. Lenses have priority access to nutrients compared with vitreous humor. Therefore, we hypothesized that *T. clavata* is a weak competitor and will suffer more from the presence of the rival parasitic species during the growth phase, whereas in the course of exposure, the competition is likely to be symmetric. Indeed, both parasitic species suppress the infection success of the counterpart when fish were infected simultaneously with both parasites. However, the vitreous humor parasite (*T. clavata*) grew slower in the presence of the competitor in the eye lens, while the growth of the lens parasite *D. pseudospathaceum* did not depend on the presence of *T. clavata*. Our study is a rare example of how the outcome of interactions between parasites could be predicted based on previous knowledge of within-host habitat (eye) structure. Funding: Russian Science Foundation (23-24-00419).

Abstract Reference: 20218
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Do trematode clones benefit from co-infections?

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Abstract Content

Hosts are often infected with several clones of a parasite in nature. Interactions between the parasite clones can determine the outcome of infections, thus, deserving special attention. Earlier studies of infection success in polyclonal infections provided evidence of competition, facilitation, and neutral interactions between clones. However, growth of parasite larvae in polyclonal infections has been rarely investigated, despite its importance for parasite fitness. Our aim was to compare infectivity and growth rates of parasites in single- and double-clone infections. We experimentally infected fish (*Salvelinus malma*) with clones and pairs of clones of the common trematode *D. pseudospathaceum,* which were identified by microsatellite analysis. Infectivity of most clones (3 of 4) was similar, while the growth rates were more variable. We found clone-specific relationships between these traits of parasites and fish mass. This means that different clones of *D. pseudospathaceum* could specialize on hosts of different sizes. Interclonal interactions differed among clone combinations. This result is consistent with the variety of relationships reported in the literature. We observed three scenarios of interclonal interactions in *D. pseudospathaceum*: a) neutral; b) facilitation during infection (higher infection success in pairs); c) competition during growth of metacercariae (lower growth rates in pairs). In addition, in co-infections we found positive density-dependent growth of metacercariae (Allee effect), rarely reported for parasites. Parasite infrapopulations usually demonstrate the opposite ‘crowding’ effect and it is an interesting question why the Allee effect existed only in the genetically diverse infections. The study was supported by Russian Science Foundation (grants 23-24-00419).

Abstract Reference: 20222
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Investigating dengue mosquito vector diversity, population dynamics across diverse agro-ecological zones in Khyber Pakhtunkhwa, Pakistan

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Abstract Content

Pakistan faces significant vulnerability to vector-borne diseases, with Dengue claiming hundreds of lives annually. Studies were conducted to assess the diversity, population dynamics, and potential plants extracts against larvae and pupae of Dengue mosquitoes. A total of 5000 samples were collected from different agro-ecological zones in Khyber Pakhtunkhwa. These mosquitoes were then reared in the laboratory for in-vitro research, resulting in the emergence of 4580 adult mosquitoes. The mosquito species identified include *Aedes albopictus*, *Aedes aegypti*, *Culex tritaeniorhynchus*, *Culex quinquefasciatus*, and *Anopheles stephensi*. Aedes species were predominantly found in urban areas, while Anopheles and Culex species were more prevalent in rural settings. Anopheles mosquitoes were also observed in urban environments, such as rainfed areas, wet mountains, and irrigated plains, whereas Aedes species were mainly confined to irrigated plains. Between November and April, collections did not yield *Ae. aegypti* and *Ae. albopictus* specimens, with their highest abundance reported in September and October. A negative correlation was observed between the pH and temperature of water, while a positive correlation was noted with salinity and electrical conductivity (EC) for larval development. The highest mosquito population was recorded in lower elevation areas such as Mardan, Peshawar, and Charsadda (<335m), while the lowest population was observed in higher elevated areas like Swat and Dir (980m above sea level). Various plant extracts were evaluated for their larvicidal potential against dengue mosquitoes in laboratory settings. Extracts from the leaves of *Artemisia scoparia*, *Justicia adhatoda*, and *Ailanthus altissima* exhibited notable larvicidal effects.

Abstract Reference: 20226
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Acute toxicity of the recombinant *Bacillus subtilis* spores expressing SARS-CoV-2 spike protein

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Abstract Content

The bacterial spore-display system has been used as a platform to express a number of heterologous proteins including viruses, as antigens. Anchor proteins are mostly used to display the target proteins on the spore surface. Here, we utilized the *Bacillus subtilis* spore for the expression of SARS-CoV-2 spike protein without the need of the bacterial fusion protein. A plasmid harboring the spike protein gene was introduced into competent *B. subtilis,* and successful expression was achieved upon induction of bacterial sporulation indicated by the immune- and fluorescence-based assay. A high number of purified spores was obtained following the removal of the vegetative bacterial cells and non-recombinant bacterial spores through rigorous purification. To demonstrate the safety profile of the recombinant *B. subtilis* spores, a single-dose acute oral toxicity study was undertaken using the specific-pathogen-free Balb/c mice. Our results showed that the recombinant *B. subtilis* spores expressing SARS-CoV-2 spike protein exert no adverse effects on the animal condition, behavior, clinical signs, food consumption, body weight, and other vital bodily functions in healthy mice indicating that it is safe and tolerable for oral administration.

Abstract Reference: 20231
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Phenotypic and genotypic characterization of antimicrobial resistance bacteria and their resistance genes among organic vegetables fertilized by dairy manure

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Abstract Content

Organic farming in Malaysia has seen a significant increase in demand. Examining past research on antimicrobial resistance (AMR) and resistance genes in animal manures, along with the increasing use of dairy manure as fertilizer, it is concerning how limited our knowledge is regarding the microbial risks it poses to organic vegetables in Malaysia. The study aims to assess the impact of using untreated dairy manure as fertilizer on the prevalence of AMR in soil and organic vegetables. Chillis and mint leaves were planted in experimental plots that received untreated dairy manure (test) and chemical fertilizer (control). The vegetables were then harvested once they reached maturity. We assessed the soils and vegetables for viable bacteria and identified them using 16S rRNA gene PCR. The isolates were evaluated for antibiotic resistance using the disc diffusion method, followed by PCR to detect resistance gene(s). The findings indicate that the application of dairy manure as fertilizer can lead to an increase in the bacterial population in the soil as compared to the control plot. In all sample types, *Staphylococcus* spp. was the most common presumptive bacteria, including dairy manure, soils, and vegetables. Results of genotypic characterization and susceptibility patterns are still pending. It could be hypothesized that *Staphylococcus* spp., present in dairy manure, could potentially colonize the soil microbiota and be transferred to vegetables. Additional research is needed to determine the most effective approach for managing animal manure to reduce the risk of antimicrobial resistance.

Abstract Reference: 20241
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Parasitic and antibiotic-resistant bacterial contamination of raw salad vegetables sold in local markets of Dhaka, Bangladesh

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Abstract Content

Salad vegetables are widely eaten raw in Bangladesh because of their high nutritional content and health benefits. But contamination with parasites and bacteria poses a significant health risk. The purpose of this study was to document the presence of parasites and antibiotic-resistant bacterial contamination of raw salad vegetables. 108 samples of raw salad vegetables: carrot, cucumber, tomato, coriander, mint, and lettuce were subjected to parasitological examination. After washing in saline water, sediments were centrifuged and analyzed using a microscope. 29.6% (32/108) of the vegetables were contaminated with parasites. *Ascaris lumbricoides* (20.4%), *Entamoeba* sp. (13.0%), *Hymenolepis nana* (9.3%), *Cystoisospora* sp. (5.6%), *Ancylostoma duodenale* (3.7%), *Trichuris trichiura* (3.7%), *Taenia* sp. (2.8%), and *Hymenolepis diminuta* (1.9%) were found. Leafy vegetables were most contaminated compared to non-leafy vegetables. Parasitic contamination was significantly related ($p < .05$) to the type of vegetable and the vendor's hygiene practices. 36 samples were subjected to bacteriological analyses and antibiotic susceptibility tests. 61.1% (22/36) of samples were contaminated. *Escherichia coli* O157 (19.4%), *Vibrio cholerae* (61.1%), and *Escherichia coli* (33.3%) were detected, but no *Salmonella* was detected. The highest bacterial contamination was recorded in coriander (83.3%) and lettuce (83.3%). No antibiotic was found to which all (100%) isolates were sensitive. All (100%) isolates were Penicillin and Amoxicillin resistant. This study demonstrated the presence of pathogenic parasites and antibiotic-resistant bacteria in raw salad vegetables which make the scenario very alarming. Unless adequately cleaned and disinfected, eating raw salad vegetables may spread food-borne diseases in Dhaka.

Abstract Reference: 20245
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Morphological and molecular comparison of *Phlebotomus argentipes* in India and Sri Lanka

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Abstract Content

Phlebotomus argentipes sand flies transmit leishmaniasis in the Indian subcontinent, causing cutaneous leishmaniasis (CL) from *Leishmania donovani*. This occurs in Sri Lanka and some parts of India with few visceral leishmaniasis cases. This study aimed to explore the molecular and morphological traits of *Ph. argentipes* populations related to atypical parasite species-phenotype associations. Sand flies were collected from Kerala, India, and Ambalantota, Sri Lanka, both recognized as endemic hotspots for CL infection, using CDC light traps. Morphological analysis involved examining the head, wing, and last three abdominal segments mounted in Hoyer's medium. A total of 32 Indian and 38 Sri Lankan *Ph. argentipes* sand flies were compared using standard taxonomic keys. DNA was extracted from 12 samples from each country. A variable region of the *cytochrome oxidase subunit I* gene was amplified by PCR and sequenced. Phylogeny trees were constructed using the neighbor-joining method. Morphological examination showed identity between Indian and Sri Lankan female *Ph. argentipes*, with consistent wing morphology and spermathecae shape. Sensilla chaetica lengths in females exceeded 0.5 relative to antennal flagellomere length in both countries. Male specimens exhibited parallel spines adjacent to the aedegus and a paramere with three unequal lobes. The resemblance of *Ph. argentipes* from both countries suggests the presence of *Ph. argentipes var. glaucus*. Phylogenetic analysis showed genetic divergence between *Ph. argentipes* from Kerala, India, and Sri Lanka, forming separate clades. Two lineages were identified within Indian clade, and three in Sri Lanka. The study emphasizes morphological similarity but genetic diversity among *Ph. argentipes* populations.

Abstract Reference: 20248
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Epidemiology of zoonotic *Toxoplasma gondii* and gastrointestinal nematode infections among household cats in Northern Mindanao, Philippines

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Abstract Content

This study focused on toxoplasmosis and gastrointestinal nematode (GIN) infections among household cats in Northern Mindanao, both significant veterinary and public health concerns. Recognizing domestic cats as hosts excreting oocysts, this research aimed to ascertain the prevalence of these parasites among 560 household cats through PCR and fecalysis and assess the associated risk factors, Knowledge, Attitudes, and Practices (KAP), and toxoplasmosis-related symptoms of cat owners. The findings offer pivotal insights into regional health concerns, aiding in gauging environmental contamination and public health implications and steering policy formulation in Northern Mindanao. Currently, the study found no *T. gondii* DNA, indicating the need for broader testing, like ELISA. The overall prevalence of GIN infection among household cats is 50%, with moderate parasite load. Parasites found were zoonotic hookworms and roundworms. Twenty-five significant risk factors for GIN infection include geographical variation and dietary choices, with raw food diets showing 100% infection rate. Cat owners showed *moderate* KAP, with evident gaps. Practices on self-diagnosis and local remedies, feeding raw food, and unrestricted outdoor cat access highlighted the need for targeted education and interventions. The non-specific nature of toxoplasmosis-related symptoms presented among owners suggests proper diagnosis. In conclusion, toxoplasmosis is negative, while GIN infection is prevalent among household cats, with 25 risk factors; owners have moderate KAP toward toxoplasmosis, and their identified symptoms can indicate toxoplasmosis but non-conclusive. The study necessitates coordinated, comprehensive, and easily-accessible public health initiatives and information to guarantee that people in Northern Mindanao are aware of these diseases and their prevention.

Abstract Reference: 20252
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Serological survey and risk factors of bovine anaplasmosis in a Mafriwal cattle population in Johor, Malaysia

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Abstract Content

Bovine anaplasmosis poses significant threats to ruminant industry globally. This study aimed to investigate the seroprevalence of bovine anaplasmosis among Mafriwal cattle in a government dairy farm using commercial cELISA test kits. A total of 242 blood samples were collected from calves of less than one-year-old, heifers, lactating cows and dry cows for packed cell volume (PCV) determination and serological testing. The association between seropositivity and risk factors were statistically analysed using Chi-square test. This study revealed a high seroprevalence of bovine anaplasmosis (79.75%) which was significantly associated with the age groups (χ^2(3,N=242)=9.98, P=0.02). Lactating group exhibited the highest seropositivity at 95.08%. Despite having no significant association between PCV and seropositivity (χ^2(1,N=242)=2.55, p=0.11), majority of seropositive cattle showed low PCV (82.73%). Additionally, cattle kept in semi-intensive housing had higher seropositivity (81.87%) than those kept in intensive housing (73.33%), but housing type did not significantly associated with seropositivity (χ^2(1,N=242)=2.04, P=0.15). Molecular analysis found no significant association between PCR results and seropositivity (χ^2(1,N=242)=1.18, P=0.28), yet PCR confirmed 82.14% of seropositive cases. The seropositivity was significantly associated with the year of sampling (χ^2(1,N=242)=18.10, P=0) and there was a rise in seroprevalence from 68.85% in 2021 to 90.83% in 2022, suggesting spreading of infection over time. In conclusion, bovine anaplasmosis was prevalent among the studied population based on the serological surveillance and it was associated with the age groups and year of sampling. Therefore, effective measures are needed, along with the exploration of other potential risk factors to control bovine anaplasmosis in the population.

Abstract Reference: 20259
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Molecular characterization and diversity analysis of prevailing *Theileria equi* genotype in equine from northern India

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Abstract Content

Blood samples were collected from 202 horses and subjected to microscopy and PCR to detect *T. equi*. The species-specific primers generated 435 bp amplicons uniquely specific to *T. equi*. *T. equi* was detected in 9.9% and 20.79% of horses screened by microscopy and PCR, respectively. The representative samples confirmed positive by PCR were sequenced, and submitted to NCBI. Employing Genetool and MEGA X software, the *T. equi* Indian isolates across the globe were compared, and the results demonstrated 99.52–100% and 95.89–100% homologies, respectively. All the *T. equi* Indian isolates belonging to genotype A. Phylogeny based on the EMA-1 gene of five isolates were also characterized by sequencing and support the previous findings. The median-joining network analysis based on the 18S rRNA gene sequence revealed 46 haplotypes across the globe with Hap_1 being the predominant one. Brazil exhibited the highest haplotypes (h=13) while India revealed three haplotypes. The haplotypes originating from a single country were predominantly located near each other, illustrating clear geographical clustering among *T. equi* haplotypes. Several individual haplotypes surrounding the predominant haplotypes (Hap_1, Hap_18, Hap_26, Hap_37) created a star-like pattern in the network, suggesting a rapid expansion of the *T. equi* population across the globe. AMOVA results revealed a significantly higher genetic variation among genotypes (78.61%) compared to within genotypic variations (21.39%). Pairwise genetic distance values (FST) exceeding 0.54 indicated considerable genetic differentiation (> 0.25) among different *T. equi* populations.

Abstract Reference: 20262
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Sampling strategies of wastewater surveillance in prison: Comparability of SARS-CoV-2 RNA concentration and its variants in composite and grab samples

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Abstract Content

Prisons pose a high risk for the transmission of infectious diseases, including COVID-19, due to their closed and semi-closed environment. Close contact between prisoners and prison staffs along with varied prison environments, makes non-pharmaceutical interventions such as social distancing and clinical testing less effective. Hence, alternative health surveillance methods, such as wastewater-based surveillance, are imperative to track SARS-CoV-2 and its variants. This study aimed to compare SARS-CoV-2 RNA detection and its variants in 24-hour composite and grab samples in prison settings. The wastewater samples were collected from February to May 2023 in a prison in Selangor. Total nucleic acid was extracted and SARS-CoV-2 RNA concentration was quantified using reverse transcription digital polymerase chain reaction. Samples were then sequenced using the Oxford Nanopore Technologies platform. SARS-CoV-2 RNA levels were consistent across the different sampling methods. There were no significant differences in RNA concentrations between grab and composite samples for the N1 and N2 genes. Moderate correlations were observed between composite and grab samples with Pearson's r values of 0.67 and 0.56 for the N1 and N2 genes, respectively. Freyja analysis showed that 67% of the samples had a sequence coverage of over 60%, with more SARS-CoV-2 variants found in the 24-hour composite samples. This study shows that grab sampling can effectively capture the overall trends in SARS-CoV-2 RNA concentrations and its variant over a 24 h period in a community. However composite sampling provides better insights into daily variant dynamics within the community.

Abstract Reference: 20268
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Evaluation of microscopic techniques, conventional PCR and real-time PCR for detection of *Ascaris lumbricoides* and its genetic characterization

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Abstract Content

The soil-transmitted helminth *Ascaris lumbricoides* is a parasite of great importance to humans. Diagnosis of helminthic infections is commonly based on microscopic detection of eggs, which has a poor sensitivity for light intensity infections. So molecular techniques have been developed in order to increase the sensitivity. To evaluate microscopic techniques, conventional PCR and real-time PCR for detection of *A. lumbricoides*. Second aim of this study is to analyze the mitochondrial DNA for genetic characterization. Six hundred fifty human stool samples were collected from North India and examined by microscopic methods. Conventional PCR and real-time-PCR was performed (ITS1 and COX1 gene). Limit of detection was also done. Positive samples were amplified with COX1 and NAD1 gene, sanger sequencing was done. Phylogeny FR web was used for phylogenetics. A Bayesian latent class analysis using Model103 was used for calculation of techniques sensitivity. *Ascaris* infection was detected in 30/650 (4.7%) stool samples. Eighteen samples were positive by microscopy (Kato-katz- 18, direct wet mount-7, concentration method- 12), 19 were positive by PCR and 30 by real-time PCR. Sensitivities was found 54.8% for microscopy and 80.0% for PCR, 99.4% for real-time PCR. Specificity was 100% for microscopy and conventional PCR, 98.7% for real-time PCR. Then positive samples were sequenced and analyzed for genetic variation, found *A. lumbricoides* spp. Phylogenetic tree was made. In our area we found only *A. lumbricoides* spp. Infecting humans and in molecular methods RT-PCR had best diagnostic performance for detection of *A. lumbricoides*.

Abstract Reference: 20285
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Antimicrobial susceptibility and molecular detection of chloramphenicol and beta-lactam resistance among Salmonella isolates from poultry farms in Kelantan

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Abstract Content

Antimicrobial Resistance (AMR) is listed among the top 10 threats to global health by the World Health Organization (WHO). The emergence of AMR in *Salmonella* among poultry contributes significantly to the epidemiology of salmonellosis and the challenges of antibiotic treatment. This study specifically investigates the resistance of *Salmonella* isolates to chloramphenicol and beta-lactam antibiotics. About 26 isolates were obtained from commercial poultry farms in Kelantan, Malaysia, between August to December 2023. Antimicrobial susceptibility testing was performed using the Kirby-Bauer Disc Diffusion method, and *Salmonella* resistance genes for chloramphenicol (cat-1 and cat-2) and beta-lactam resistance gene (blaTEM) were detected using Polymerase Chain Reaction (PCR). Of the 26 isolates tested, 88.5% showed resistance to at least one antibiotic. Specifically, 19.2% were resistant to amoxicillin/clavulanic acid, 80.7% to ampicillin, and 57.7% to cephalothin, respectively. Additionally, 88.5% of the isolates exhibited resistance to chloramphenicol. Furthermore, resistance genes were detected in most isolates, with blaTEM possessing the highest resistance (88.5%), followed by Cat-1 and Cat-2 (26.9%). The coexistence of resistance to beta-lactam and chloramphenicol, along with the presence of their respective resistance genes, raises significant public health concerns and poses economic challenges.

Keywords: AMR, Malaysia, Poultry, *salmonella*

Abstract Reference: 20287
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Multi drug resistance of *Vibrio vulnificus* and *Vibrio cholera* isolated from Asian seabass, *Lates calcarifer*: A public health concern

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Abstract Content

Vibrio vulnificus and *V. cholera* are the members of the Vibrionaceae family. They are Gram-negative rod-shaped bacteria of public health concern and a lethal opportunistic human pathogen and aquaculture. This study investigates multidrug (MDR) of *V. vulnificus* and *V. cholera* isolated from Asian sea bass in East Coast, Malaysia. In this study, 180 seabass were obtained from six different places. A loopful of kidney, spleen and liver of the fish were streaked separately onto thiosulphate-citrate-bile-sucrose (TCBS). Polymerase chain reaction (PCR) was used to detect Vibrio species using primer. Then, antibiotic resistance test was done according to Kirby-Bauer method and MDR value was calculated. As a result, 10 and 38 isolates of *V. vulnificus* and *V. cholera* were isolated from the diseased seabass, respectively. Most of the isolates were resistant to vancomycin and rifampicin. The MDR value ranging from 0.05 to 0.77. The present study showed that Laguna Tumpat, Kelantan has the highest MDR value and marked as high-risk sources, which may represent a potential human health risk.

Abstract Reference: 20291
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Geography and ecology of invasive *Pseudosuccinea columella* (Gastropoda: Lymnaeidae) and implications in the transmission of *Fasciola* species (Digenea: Fasciolidae) – A review

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Abstract Content

Pseudosuccinea columella is considered invasive and has become an important intermediate host of both *Fasciola* species worldwide. This systematic review assessed the geographical distribution of *P. columella*, and its implications in the transmission of *Fasciola hepatica* and *Fasciola gigantica*, globally. A literature search was conducted on Google Scholar, JSTOR and PubMed databases using Boolean operators in combination with predetermined search terms for thematic analysis. Results show that *P. columella* has been documented in 22 countries from Europe (3), Africa (8), Oceania (2), North America (3) and South America (6). Furthermore, this snail species has shown to adapt to and inhabit a vast array of freshwater bodies including thermal lakes and ditches with acidic soils. Studies showed that *P. columella* transmits *F. hepatica*, with natural and experimental infections documented in sub-Saharan Africa, Europe, South America and North America. Experimental infection studies in Cuba showed the presence of *P. columella* populations resistant to *F. hepatica* infection. Furthermore, some populations of this invasive snail collected from *F. hepatica* endemic locations in Brazil, Venezuela, Australia, South Africa, Colombia and Argentina were found without *Fasciola* infection. As a result, the role played by this snail in the transmission of *Fasciola* spp. in these endemic areas is still uncertain. Therefore, further studies to detect natural infections are needed in regions/countries where the snail is deemed invasive to better understand the veterinary and public health importance of this snail species in *Fasciola* endemic areas and determine the global dispersion of resistant populations of *P. columella*.

Abstract Reference: 20307
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Psychometric stress assessment of covid patients in emergency care helps in better equipping ICU for mood disturbance and fear patients

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Abstract Content

Infectious diseases pose health risks that harm physical as well as mental health. COVID-19 is a prime example of how it not only impacted the physical health of millions of people but also instilled fear in public. This is further exacerbated in scenario of hospital emergency treatment due to the large population, limited availability of primary and tertiary care centres, low doctor-to-patient ratio, &underequipped paramedic staff. As a result, we developed a psychometric test for COVID-19 patients in ICU wards to assess their stress levels, detect gaps, and target populations that require more mental health care than others. This psychometric exam assesses two key stress variables: Total Mood Disturbance (TMD) and coronavirus fear. The enrolled population of 104 people in this study has a diverse age distribution, 58% 40-60 (middle age), 21% 15-25 (younger age), and 9% aged 60 or more. TMD analysis reveals that students are more vulnerable to the psychological effects of lockdown than workers of greater age group. Further, analysis also shows females of younger age, regardless of profession, are more susceptible to the psychological effects of lockdown, with a significant Pvalue of 0.002719(n = 29). Hence our ICUs need to be better equipped for female patients, by having more female staff to attend to their special nursing requirements. Also for young patients, amenities like books, music &counseling can be of great help. This test can also be adapted to test stress levels in healthcare &field workers, and outreach patients to overall improve health care system.

Abstract Reference: 20314
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Unprecedented rabies outbreak in Nepal's Far-Western Region: A call for urgent action

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Abstract Content

Rabies, a highly lethal viral zoonotic disease, poses a significant threat in Nepal's Far Western Region. The disease primarily spreads through bites from rabid dogs, causing fatal encephalitis. In Nepal, underreporting masks the true extent of rabies cases, with 10-100 human deaths annually and thousands requiring post-exposure prophylaxis. Brain tissue samples from 91 suspected animals were obtained using the occipital foramen approach. Samples underwent field testing with the Antigen Rabies Ag Detection Rapid Test (RTD) and confirmatory diagnosis with the Fluorescent Antibody Test (FAT). A total of 84 samples (92.30%) were confirmed positive for rabies using FAT over nearly a one-year period. This included 41 cases in dogs, 26 in bovines (15 cattle and 11 buffalo), 12 in goats, three in jackals, one in a pig, and one in a cat. Tragically, a 13-year-old boy lost his life after being bitten by a suspected rabid dog. Efforts to manage the outbreak included vaccinating over 15,000 community dogs and sterilizing 2,107 of them, engaging more than 6,000 students in awareness programs, and training veterinarians. However, persistent gaps in diagnosis and control require comprehensive collaboration, increased surveillance, and healthcare infrastructure strengthening. The recent surge of outbreaks in a wide range of species raises significant concerns and necessitates immediate government intervention.

Abstract Reference: 20319
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Anti cryptosporidial activity of silver nanoparticles (AgNps) facilitated by *Uraria picta* extract

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Abstract Content

The unexpected onset along with the rapid spread of infections caused by *Cryptosporidium*, in addition to the regular development of resistance and ineffectiveness to typical drugs, emphasize the urgent requirement for alternative drugs to kill or inactivate this infectious pathogen. With the rapid development of nanomedicine, nanoparticles are considered an effective drug carrier for the treatment of parasitic diseases. Green silver nanoparticles generated using plant extracts as mediators demonstrate resilient antimicrobial properties and have great potential to be used as alternative anti-parasitic agents. So, we aim to synthesize plant extract-based silver nanoparticles and evaluate anti-cryptosporidia efficacy. The synthesis of silver nanoparticles was carried out by employing the extract of *Uraria picta*, along with 1 mM silver nitrate solution. These nanoparticles were characterized using TEM, FTIR, UV spectroscopy and Anti-cryptosporidial activity was carried out on *Cryptosporidium parvum* oocysts by treating them with nanoparticles for 24h and then allowing them to grow invitro for 48h. Morphologically, the nanoparticles were spherical with a molecule size of 20-40 nm. These nanoparticles have good antioxidant potential and are effective in inhibiting the viability (more than 70%) of *Cryptosporidium parvum* oocysts with very high potential. The present study suggested that these silver nanoparticles have great potential in the development of new anti- Cryptosporidial drugs. To the best of our knowledge, this has been the sole study to explore the effect of *Uraria picta* silver nanoparticles on *Cryptosporidium* spp., and more elaborated research is needed to further investigate its anti-cryptosporidia action in biological samples.

Abstract Reference: 20327
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Prevalence of amphistome species infections in intermediate snail hosts: A systematic review and meta-analysis

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Abstract Content

A systematic review and meta-analysis of peer-reviewed literature from 1984-2023 examined the prevalence of amphistome species infections in 167081 natural and 7659 experimental snails from 36 peer-reviewed articles that met the criteria. The overall pooled prevalence of amphistome infections from naturally infected snails was 2% (95% CI: 0 to 4), compared to 40% (95% CI: 18 to 64) on experimental infections. The highest pooled prevalence from natural infection was recorded in Europe 3% (95% CI: 1-7%). The highest overall prevalence of naturally infected amphistome was 6% (95% CI: 0-20%) for *Paramphistomum epiclitum*. The Americas had the highest pooled prevalence of experimental amphistome infection among freshwater snails (66%; 95% CI: 26-96%). The highest pooled prevalence of 65% (95% CI: 12-100%) was recorded for *P. cervi* in experimental infection. *Galba truncatula* was the only snail that qualified for meta-analysis for natural infection, with the pooled prevalence of 3% (95% CI: 1–8%). *Galba truncatula* and *Bulinus tropicus* in the experimental infection qualified for the meta-analysis, with the overall prevalence of amphistome infections of 66% (95% CI: 34-92%) and 30% (95% CI: 0-74%), respectively. The pooled prevalence of amphistome species among freshwater snails was lowest between 2011 and 2023, with PCR detection technique having the highest pooled prevalence in IH snails, compared to dissection and shedding of cercariae. The study revealed high heterogeneity and publication bias between studies. This meta-analysis provided valuable insights into the prevalence of amphistome infections in snail IH across different geographical regions.

Abstract Reference: 20328
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

A single-cell RNA-seq atlas of *Clonorchis sinensis* identifies the specific expression profile of reproductive and nutritive

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Abstract Content

Clonorchiasis is a neglected foodborne disease with an estimated 15 million sufferers in East Asia. The causative agent, *Clonorchis sinensis*, is parasitic in the host bile duct that lays approximately 4000 eggs per worm per day. However, there are few mechanisms and gene profiles of *C. sinensis* uncovered. More insights into *C. sinensis* are desired for identification of therapeutic targets and establishment of prevention measures. Using single cell RNA sequencing, we constructed a cell atlas across various tissues of adult *C. sinensis* and identified the classical cell types, such as gut and germline cells. Additionally, we conducted a comparative analysis between the hermaphroditic hepatic-parasitic trematode *C. sinensis* with the dioecious intravascular-parasitic trematode *Schistosoma mansoni*. This comparison revealed the differences in cellular components and expression profiling between the two organizations of body, particularly within the reproductive system and nutritive system. Collectively, these findings provide valuable molecular insights into the organ system of this significant parasite.

Abstract Reference: 20329
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Commercially available kit-based optimization and application of digital droplet PCR for the detection of SARS-CoV-2 in saliva specimens

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Abstract Content

The COVID-19 pandemic has been causing hundreds of millions of cases and fatalities. Although the infection has been declared endemic, it remains a substantial threat, particularly to those with compromised immune systems. This highlights the importance of an enhanced detection technique that possesses both heightened sensitivity and selectivity. In comparison to the gold standard, quantification by reverse transcription digital droplet polymerase chain reaction (RT-ddPCR) is both absolute and sensitive. Using a commercially available RT-qPCR reagent, we are the first to optimise RT-ddPCR for detecting SARS-CoV-2 in saliva specimens. Prior to optimising and validating RT-ddPCR, we used the RT-PCR method as a reference. The optimization procedure included evaluating the RT-ddPCR reaction mixture, adjusting the annealing temperature, and validating it using 40 stored saliva specimens. The ddPCR Supermix for Probes (no dUTP) was compatible with the annealing temperature of 57.6°C. The result revealed that the lower the Ct value of RT-PCR, the higher the concentration presented by the copy numbers of RT-ddPCR. The r^2 value significantly correlated with the N and E genes at 0.98 and 0.85, respectively. On the contrary, ORF1ab exhibited a weak correlation ($r^2 = 0.34$). The specificity of the targeted genes varied between 80.8% and 95.5%. All genes had 100% sensitivity (21/21). This research establishes the viability of implementing a modified approach within the ddPCR platform to detect comparable pathogens using saliva specimens.

Abstract Reference: 20335
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

What does monkey malaria means to you?: A photovoice study with rural communities in Sabah, Malaysia

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Abstract Content

Controlling Plasmodium knowlesi malaria in Sabah, Malaysia, poses challenges due to macaque monkeys, outdoor-biting Anopheles mosquitoes, and dynamic changes in the environment due to agricultural expansion. This study investigates perspectives and challenges to prevent zoonotic malaria among rural communities in Sabah using photovoice. As part of a larger study on women's empowerment to prevent malaria in Sabah, a photovoice study was conducted between 1 January and 15 2024. 20 female participants from three rural villages were purposively sampled. After photovoice workshop, participants used their smartphones to document photos based on the question ' What does monkey malaria means to you? After 20 days, the research team conducted Focus Group Discussions (FGDs) with each respective village. The FGDs were conducted in the Sabah Malay dialect and recorded, transcribed, and analyzed using reflexive thematic analysis. There are local beliefs among the participants, but the majority (>90%) were able to share knowledge on zoonotic malaria transmission. Challenges included individual factors such as occupation and living environment, livelihood activities, and environmental factors. Stakeholder support was emphasized for feasible control approaches. Findings from this study highlighted the critical need for community participation and engagement in zoonotic (monkey) malaria prevention in rural Sabah. Community participation was integral in identifying local obstacles and potential solutions. These findings can inform zoonotic malaria control strategies in Malaysia and other similar settings.

Abstract Reference: 20337
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Implementation of digital PCR for *Giardia intestinalis* and *Cryptosporidium* spp. detection in stool specimen

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Abstract Content

Giardia intestinalis and *Cryptosporidium* spp. are two re-emerging intestinal protozoa that are endemic to developing countries and responsible for public health problems, they have attracted worldwide attention as their infection rates rise in the past years. The detection of these protozoa mostly relies on microscopy and real-time PCR (rt-PCR). Lately, nano-plate digital PCR (dPCR), has been introduced as a new, highly promising molecular-based technology for DNA detection and quantification without a standard curve. This cross-sectional study utilized stored specimens collected from slum areas in North Jakarta, Indonesia and served as the first to be implemented on nano-plate dPCR. Detection of positive cases of *G. intestinalis* by rt-PCR compared to dPCR was 36.5% versus 21.4%, while detection of *Cryptosporidium* spp. by rt-PCR compared to dPCR was 6.3% versus 5%. However, the suspected false positive rate of *G. intestinalis* in rt-PCR was higher (24/58) than dPCR (13/58), as were the suspected false positive results in the detection of *Cryptosporidium* spp. with rt-PCR (2/10) and dPCR (0/10). The correlation between Cycle threshold (Ct) value of rt-PCR and concentration (copies/µL) of dPCR was measured, showing inverse correlation. The agreement of rt-PCR and dPCR methods were good for *G. intestinalis* and *Cryptosporidium* spp. Moreover, dPCR provided higher specificity than rt-PCR and allowed absolute quantification of DNA target concentration, which is beneficial for measurement of severity of intestinal parasitic infections. We concluded that dPCR is a highly accurate and reliable method for detection of *G. intestinalis* and *Cryptosporidium* spp.

Abstract Reference: 20355
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Comparative analysis of survival duration and egg production in partially engorged versus fully engorged sand flies

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Abstract Content

Vector-borne diseases remain a significant public health concern worldwide, with sand flies serving as important vector of leishmaniasis and several arboviruses. Understanding the reproductive behavior of sand flies is critical for developing effective insectary maintenance procedures and control strategies. This study compared the survival duration and egg production of partially and fully engorged sand flies following single and sequential blood meals, providing insights into blood-feeding behavior. *Phlebotomus papatasi* were reared under controlled conditions, fed on anesthetized mice, and categorized into engorgement groups based on blood intake. Survival duration and fecundity were assessed post-blood meals. Results revealed that partially engorged sand flies exhibited longer survival durations than fully engorged individuals across age groups. Additionally, fully engorged sand flies consistently laid more eggs per female than their partially engorged counterparts. Sequential blood meals led to varied responses, with different engorgement groups showing distinct patterns of survival and fecundity. These findings underscore the importance of engorgement status in shaping sand fly reproductive outcomes and highlight the complexity of interactions between blood feeding and reproduction.

Abstract Reference: 20357
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

The exosome proteome of *Trichomonas vaginalis* under iron stress

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Abstract Content

Trichomonas vaginalis is a parasitic protozoan of the human urogenital tract. Exosomes released by this parasite are vital in transmitting information and substances between cells during host-parasite interactions. In a prior investigation, we unraveled the core exosome proteome of *T. vaginalis* using liquid chromatography-tandem mass spectrometry (LC-MS/MS) on sucrose ultracentrifugation-enriched exosome and supernatant fractions from six isolates. Our proteomic analysis revealed 1207 exosomal-specific proteins after excluding 436 contaminant proteins. Among these, 72 common exosomal-specific proteins were expressed across all six isolates. Comparing our findings with three publicly available datasets, we identified 16 core exosomal-specific proteins, including tetraspanin (TvTSP1), and proteins primarily involved in catalytic activity and binding. Recently, we employed the same methodology to explore the exosomal proteome of *T. vaginalis* under iron stress conditions. Iron is indispensable for the organism's survival, energy metabolism, and redox homeostasis. We compared the exosomal proteomes of cells cultivated in iron-enriched medium to those in low-iron and iron-deficient media. Out of the 1066 proteins identified across all culture conditions, only 122 proteins (11%) were uniquely found in the low-iron culture, and only 54 proteins (5%) were uniquely found in the iron-deficient culture. In contrast, 177 proteins (17%) were present in cultures enriched with iron and in the other two iron-deficiency cultures. Our research underscores the significance of utilizing the supernatant fraction from exosomal extracts as a control to remove contaminating proteins. This study has established a foundation for comprehending exosome-mediated cell communication by delineating the core exosome proteome of *T. vaginalis*.

Abstract Reference: 20359
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Factors influencing mosquito oviposition behavior: A study on container size, water depth, and mating dynamics in *Toxorhynchites splendens*

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Abstract Content

Understanding mosquito oviposition preferences is vital for effective vector control. This study investigates *Toxorhynchites splendens*, a predatory mosquito species, focusing on how container size, water depth, and mating dynamics influence oviposition behavior. Mosquitoes were reared under controlled conditions, with two female groups established: "Mated Female" and "Mated Female Interrupted." Containers of varying sizes were created using eco-friendly rubber tire cups, and water depth ranged from 1.5 cm to 3.0 cm. The study was divided into 2 experiments including comparing surface area and depth of water between choice and no-choice tests. The results of surface area preference trials revealed that large containers generally yielded higher egg counts than small ones. Interruptions in mating processes notably affected oviposition behavior. Shallower water depths favored higher egg production, in comparison with deeper depths. This study explores the interactions among container size, water depth, and mating dynamics in shaping mosquito oviposition behavior. Understanding these interactions can inform mosquito-rearing practices in insectaries. Further research on interspecies interactions and environmental factors promises insights into managing mosquito populations and mitigating mosquito-borne diseases.

Abstract Reference: 20368
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

First molecular detection of microsporidiosis and its prevalence amongst refugee children in Selangor, Malaysia

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Abstract Content

Microsporidia are a group of obligate intracellular eukaryotic parasites and well recognized human pathogens such as *Enterocytozoon bieneusi* and *Encephalitozoon intestinalis*. August 2022 to January 2023, 91 stool samples have been successfully collected from 6 selected school of Rohingya children in Selangor. The overall prevalence of microsporidian infections by using microscopy was 56% (51/91: 95% Cl) and 60.44% (55/77; 95% CI) by using PCR approach. Interestingly, the prevalence of microsporidia infections was significantly higher among males (63.6%) compared to females (36.4%). The age range shows the infections occur between 5 to 15 years old. Nevertheless, highest prevalence of microsporidia infections were found at Rohingya school in Gombak, followed by REC Klang, REG Puchong, RISE Kajang, Al-Islamiyah Alternative Centre Kajang and the least one in Jenjarom School. It was confirmed that both *Enterocytozoon bieneusi* and *Encephalitozoon intestinalis* have been observed and identified via molecular works. *E. bieneusi* is the most common infection compared with *E.* intestinalis in this population. Among the selected schools, it showed that only Al-Islamiyah Alternative Centre, Kajang School and RISE Kajang were detected with positive *E. bieneusi* and no *E. intestinalis*. Only 2 out of 6 schools have been infected with multi-infection by both species which were REC Klang and Gombak. It revealed that refugee children could potentially have a high risk of microsporidia infections due to the poor sanitation and environmental factors. Hence, we could provide a basic insight towards diagnostic strategies for these pathogens that can be integrated towards treating or controlling microsporidiosis.

Abstract Reference: 20369
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Efficacy evaluation of Malaysia-isolated *Metarhizium anisopliae* towards *Rhipicephalus microplus*

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Abstract Content

Rhipicephalus microplus presents significant challenges to the livestock industry, traditionally managed with chemical acaricides, which have led to resistance and environmental concerns. In search of alternatives, this study evaluated the efficacy of *Metarhizium anisopliae* isolates from Malaysia against *R. microplus* using the Adult Immersion Test. Six *M. anisopliae* isolates, obtained from various localities in Malaysia, were applied at a concentration of 1 x 10^8 conidia/ml through tick immersion. Mortality rates were monitored daily for 14 days, with experiments conducted in triplicate. The results showed that the PR1 isolate exhibited the highest virulence, causing 83% mortality in adult *R. microplus*. Although no significant differences in mortality rates were observed among the isolates, PR1 demonstrated a faster kill rate with an LT_{50} of 10 days. Furthermore, PR1 significantly reduced the egg production of engorged female ticks compared to the control group. These findings highlight the potential of *M. anisopliae* isolates from Malaysia as an effective alternative to chemical acaricides for managing *R. microplus* under laboratory conditions.

Abstract Reference: 20371
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Non-classical *Bordetella* infection in a patient with extensive bronchiectasis

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Abstract Content

A growing body of literature has detailed the pathogenic potential of various non-classical *Bordetella* species. In both humans and animals, a wide range of respiratory-associated infections have been linked to *Bordetella hinzii* and *Bordetella pseudohinzii*. From the sputum of a woman in her early 60s who had severe bronchiectasis and presented with fever and brown-colored sputum, we report the isolation of a genetically close relative of *B. hinzii* and *B. pseudohinzii*. The non-enteric Gram-negative rod bacterium identification system, API 20NE, had originally identified the strain as *Bordetella avium*. The identification of this *Bordetella* isolate was not resolved by sequencing the 16S rDNA, *ompA*, *nrdA*, and genes utilised in the *Bordetella* multilocus sequence typing scheme. This isolate was placed in a separate cluster between *B. hinzii* and *B. pseudohinzii* in the phylogenetic tree according to whole-genome single nucleotide polymorphism analysis. In particular, whole genome sequencing should be taken into consideration for broader applications, such as the confirmation of rare microorganism identity in the clinical diagnostic microbiology laboratories, as it facilitated the subsequent identification of this uncommon microorganism.

Abstract Reference: 20372
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

The presence of *Plasmodium inui* in Bogor ’captive *Macaca fascicularis*

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Abstract Content

Indonesia has *Macaca fascicularis* (MF) that are spread across almost all the islands, including Sumatra, Java, and Kalimantan. *Macaca fascicularis* has a close relationship with humans in their search for food, which is supported by their rapidly increasing population and the decline of forest areas due to illegal logging. They are also a natural host for several zoonotic diseases, such as malaria caused by *Plasmodium inui*, *P. knowlesi*, *P. cynomolgi*, and *P. coatneyi*. The prevalence of *P. inui* in Bogor was 20% in 2016 and 13% in 2021. This study aims to confirm the presence of *P. inui* in Bogor's captive MF. DNA from blood samples of 57 MF was analyzed by PCR to amplify the small subunit ribosomal RNA target gene using consensus primers specific for Plasmodium species. The PCR-positive samples were then sequenced using commercial sequencing services. The sequences were analyzed with the BioEdit program and aligned with the Basic Local Alignment Search Tool from the National Center for Biotechnology Information. Phylogenetic trees were constructed using MEGA 11.0 and the neighbor-joining method to determine the relationships among Plasmodium species. Bootstrapping with 500 replicates was conducted to evaluate the robustness of the tree topologies. Results showed that 70.17% of the samples were PCR-positive, producing a 1640 bp amplicon. Nucleotide sequencing confirmed that these samples were *P. inui* with over 99% nucleotide identity compared to sequences in GenBank. Phylogenetic analysis of the SSU rRNA partial gene revealed that all isolates clustered closely with the *P. inui* EU 400387 sequence.

Abstract Reference: 20398
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

A rapid and sensitive eDNA-based method using NGS profiling for water borne pathogens as surveillance tool

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Abstract Content

Water is essential for all life activities, and river pollution is a potential health threat for both animals and the surrounding residents, especially as it contains pathogens that can bring about a range of waterborne diseases. Environmental DNA (eDNA), a new tool with the advantages of being fast, sensitive and non-invasive, has been widely used in ecological and pathogen monitoring in recent years. In this study, eDNA technology was combined with 18S rRNA and 16S rRNA barcodes to analyze water samples from the Perak River, the second longest river in Malaysia. The study summarizes the types, abundance, and distribution of pathogens in this watershed, discusses the potential threats of these pathogens to humans and animals, and explores the advantages of eDNA technology as a tool for pathogen monitoring in a river system. Moreover, this study shows the potential pathogens in Perak River in a more comprehensive way, which can help the relevant departments to assess the risk of diseases and take appropriate disease interventions, as well as provide a scientific basis for the future application of eDNA technology in public health management.

Keywords: eDNA, Waterborne diseases, Pathogen, Public health

Abstract Reference: 20408
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Investigating the difference in blood proteome profile to understand the mechanistic cues for malaria severity and heterogeneity in Indian population

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Abstract Content

To reduce the socio-economic burden of malaria, sensitivity and specificity of the diagnosis should be improved to reduce the unnecessary treatment and mortality rate. Currently, the gold standard of malaria assessment “light microscopic analysis of blood smear” has several limitations. Establishment of predictive blood serum biomarkers for effective diagnosis of the type and severity of the disease would be a better alternative. Present study carried out a comprehensive proteomic analysis of blood plasma samples from both falciparum and vivax malaria patients in Indian population with different severity levels. In-silico analysis predicted fibrinogen B-beta (Bβ) chain (FGB) as a potential biomarker to understand the progression of malaria from non-severe to severe infection irrespective of the plasmodial species infected. Serum proteins namely AMBP, SERPINA1, TF, AHSG, APOA1, HP and GC were predicted as potential biomarkers to differentiate between falciparum and vivax-induced blood serum alterations during the severe and non-severe phases of infection. The differentially expressed plasma proteins mapped in the pathways implied that platelet degranulation and complement cascade response were compromised in severe malarial patients resulting in augmenting the complications and pathogenesis of severe malaria. Loss of platelet integrity and RBC homeostasis in falciparum malaria would result in hemolysis and severe anemia intensifying the lethal complications associated with later as compared to vivax malaria. This is a novel study which proposed “Targeted Diagnostic strategy” based on blood serum protein biomarkers to increment the diagnostic accuracy of the type and severity of malarial parasitemia particularly for falciparum and vivax infections.

Abstract Reference: 20430
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Correlation between obesity, cholesterol levels, and blood pressure

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Abstract Content

Obesity is a non-communicable disease closely related to increased cholesterol and hypertension. According to the Ministry of Health, the prevalence of obesity in Indonesia increases by 1.6% to 23.4% in 2023. Obesity has become one of the risk factors for cardiovascular diseases. The aim of this research is to analyze the relationship between obesity, cholesterol, and blood pressure. The research method used is descriptive with a cross-sectional approach. The research sample consists of 285 respondents. The data samples are taken by using a purposive sampling method with a BMI ≥ 25. The data analysis uses the Chi-square test on categorical data and the Spearman test on numerical data. Based on the results of the categorical data research, there is no significant relationship between BMI, cholesterol (p=0.918), and blood pressure (p=0.139). Meanwhile, in the numerical data, it was found that there is a significant relationship between BMI and cholesterol levels (p=0.037) with a negative correlation. There is a good relationship between cholesterol levels and blood pressure categories (p=0.002) and between cholesterol levels and systolic pressure (p=0.001) with a positive correlation. There is a significant relationship between ages and BMI categories (p=0.019), cholesterol levels (p=0.028), and blood pressure (p=0.000), and there is a significant relationship between genders and cholesterol levels (p=0.000). Obesity can be harmful to young people, adults, and the elderly. Even though obesity is not significantly related, it is a risk factor causing increased cholesterol and hypertension should be concerned.

Keywords: Obesity, Hypercholesterol, Hypertension

Abstract Reference: 20436
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

The prevalence and distribution of gastrointestinal parasites in pigs in Korea

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Abstract Content

Gastrointestinal parasites significantly contribute to disease transmission in the pig farming industry, leading to reduced productivity. In this study, we aimed to investigate the distribution of gastrointestinal parasites in domestic pigs across Korea from May 2020 and February 2023. A total of 700 pig fecal samples were collected from 101 farms and examined for the presence of gastrointestinal parasites using both morphological and molecular methods. Fecal examinations revealed that 56.0% (392/700) of the pig fecal samples were infected with at least one gastrointestinal parasite. Using a fecal flotation technique with light microscopy, 294 *Balantioides coli* (42.0%), 50 strongyles (7.1%), 42 *Ascaris suum* (6.0%), 5 *Trichuris suis* (0.7%), and 19 coccidia (2.7%) were detected. In addition, PCR analysis identified apicomplexan parasites, specifically *Cryptosporidium* spp., *Eimeria* spp., and *Cystoisospora* spp. The prevalence of these parasites was found to be 7.0% (n=49), 3.4% (n=24), and 0.9% (n=6), respectively. This study provides crucial epidemiological data showing that gastrointestinal parasites are prevalent in pigs in Korea. Our findings highlight the necessity for continued surveillance and comprehensive parasite management programs to alleviate the impact on pig health and farm productivity.

Abstract Reference: 20449
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

The risk factors preeclampsia in multiparous women in red onion farming area

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Abstract Content

Onion farming areas with the highest use of pesticides are a risk factor for preeclampsia which causes 44% percent of maternal deaths. This study aims to determine the risk factors of preeclampsia in multiparous women in the Sitanggal Health Center working area. This research was a quantitative study and used an analytic observational design with a case control design. The population of this study were all cases of preeclampsia in multiparous women as many as 31 cases. The sample size was 75 multiparous women living in the Sitanggal Health Center working area consisting of 25 cases and 50 controls. Sampling was selected using purposive with inclusion criteria. The selection of case samples was randomized from the data of preeclampsia cases. The control samples was adjusted to the distance of the case sample's house location. The results showed a significant relationship between pesticide exposure, history of preeclampsia, Ante Natal Care, pregnancy distance, Haemoglobin level, and Body Mass Index with the incidence of preeclampsia in multiparous women. Multivariate analysis showed that nutritional status had the greatest influence on the incidence of preeclampsia. The number of factors associated is influenced by the lack of awareness of respondents to control their health regularly and due to genetic factors. It was hoped that mothers will routinely check their health and control their weight by regulating the consumption of sugar and fat and exercising regularly to prevent obesity which can cause preeclampsia.

Keyword: preeclampsia, red onion farm, pesticide, multiparous

Abstract Reference: 20465
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Potential for human-to-*Anopheles dirus* mosquito transmission of *Plasmodium knowlesi*

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Abstract Content

Plasmodium knowlesi, known as the fifth human malaria parasite, has rapidly spread throughout Southeast Asia. However, uncertainties remain about its transmission from human-mosquito-human transmission. This study investigates the transmission potential of *P. knowlesi* from human blood to mosquitoes. A direct membrane-feeding assay was conducted using laboratory-reared female *Anopheles dirus* mosquitoes fed with *P. knowlesi*-infected human blood. Seven days post-infection, mosquitoes were dissected and examined under a stereomicroscope for oocysts in the midgut, which were stained with mercurochrome. Fourteen days post-infection, sporozoites in the salivary glands were also examined. Malaria diagnosis was performed using microscopy by expert microscopists and nested PCR assays. Out of 1,439 blood-fed *An. dirus* mosquitoes dissected on day 7 post-infection, two mosquitoes (0.27%) had oocysts in their midguts. Additionally, out of 694 mosquitoes dissected on day 14 post-infection, three mosquitoes (0.43%) had sporozoites in their salivary glands. Nested-PCR assays confirmed these sporozoites as *P. knowlesi*. These findings highlight the potential for *P. knowlesi* transmission from humans to mosquitoes. The importance of these results requires further investigation, including controlled human malaria infection studies, for better understanding the transmission dynamics of *P. knowlesi* in Southeast Asia.

Abstract Reference: 20479
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Ownership and use of insecticide-treated nets in Myanmar: insights from a nationally representative demographic and health survey

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Abstract Content

Malaria poses a significant public health threat in Myanmar, necessitating rigorous efforts for elimination by 2030, with insecticide-treated nets (ITNs) being a key preventive measure. This study explored the ownership and use of ITNs in Myanmar and identified factors associated with non-use of ITNs. Household datasets from the 2015–2016 Myanmar Demographic and Health Survey, excluding children under five, were utilized. Descriptive and inferential statistics, including simple and multiple logistics regression and Pearson correlations, were employed. Among 46,507 participants, 22.3% (95% CI 20.0%, 24.5%) had access to ITNs, with only 15.3% (95% CI 13.7, 17.1%) sleeping under an ITN the night before survey. Factors associated with non-use of ITNs included age (15–34 years—aOR: 1.17, 95% CI 1.01, 1.30; 50+years—aOR: 1.19, 95% CI 1.06, 1.33), location (delta or lowland—aOR: 5.39, 95% CI 3.94, 7.38; hills—aOR: 1.80, 95% CI 1.20, 2.71; plains—aOR: 3.89, 95% CI 2.51, 6.03), urban (aOR: 1.63, 95% CI 1.22, 2.17), and wealth quintile (third—aOR: 1.38, 95% CI 1.08, 1.75; fourth—aOR: 1.65, 95% CI 1.23, 2.23; fifth—aOR: 1.47, 95% CI 1.02, 2.13). A coherent distribution of ITN ownership and use was seen across all states and regions, with a strong correlation between ownership and use (r: 0.9795, 95% CI 0.9377, 0.9933, alpha <0.001). This study reveals low ITN ownership and use, highlighting the need to increase distribution to achieve one ITN per two people. Strengthening ITN use requires targeted health promotion, especially in lowland, hill, and plain areas.

Abstract Reference: 20503
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Lessons learnt when digitising malaria entomological surveillance data in DHIS2 from Lao PDR

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Abstract Content

Establishing entomological surveillance is a necessary first step towards malaria elimination; but it is only useful when the information is readily accessible and used in a timely manner to drive decision making. Historically, CMPE has recorded entomological field data on paper-based forms to be transcribed and analysed across several spreadsheets. This process has been time-consuming, increased data quality issues, and delayed reporting-to-intervention processes. Digitising past and future data in a DHIS2 environment needed to consider the multitude of variables surveyed. Tracker Capture was the ideal DHIS2 data model for the reporting forms because of numerous surveillance visits that are made to specific locations based on collection type. Yet, the resulting configuration faced restrictions in visualising combined parameters, requiring the creation of an expansive set of indicators and charts to account for all reporting permutations. To overcome these limitations, the DHIS2 Standard Report application was utilised as it provided flexibility to create fit-for-purpose dashboards and specialised indicators. The applied solution, however, required advanced-level developer expertise that poses challenges for future updates and raises issues of sustainability. Nonetheless, the resulting product streamlined data-driven decision-making - a crucial factor in low-resourced elimination settings. CMPE can now instantaneously geolocate and examine entomological surveillance data for *Anopheles* density, composition, and biting rates and times. If changes in vector bionomics, coupled with information from human behaviour observations, are observed, CMPE can quickly mobilise and adjust program interventions. Moving forward, CMPE will continuously digitise their surveillance activities and advance DHIS2 datasets to support efforts towards malaria elimination.

Abstract Reference: 20507
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Initiation of primary cell cultures from embryonic *Rhipicephalus linnaei* ticks from Malaysia

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Abstract Content

Tick-borne zoonotic and neglected diseases pose a significant global public health challenge, necessitating innovative research strategies. One promising approach is the establishment of the Tick Cell Biobank (TCB) and its Outposts. The TCB Asia Outpost has been established at the Tropical Infectious Diseases Research and Education Centre (TIDREC), Universiti Malaya, serving as a hub for generating and distributing diverse tick cell lines to assist research on tick-borne diseases in the Asia-Pacific region. In this study, eight primary cell cultures were initiated from egg batches laid by 29 engorged female *Rhipicephalus* sp. ticks collected from dogs, and maintained at 28°C. After 14 months one culture, characterized by large, irregularly shaped clumps of heterogeneous cells, including fibroblast-like and spherical cells, with some forming floating clusters of multicellular vesicles, exhibited the potential to evolve into a cell line. The primary cell culture showed no microscopic evidence of contaminating microorganisms and was confirmed to be free of bacterial contamination through bacterial 16S rRNA and *Mycoplasma* screening. Amplification and sequencing of a fragment of 16S rRNA of the parent ticks revealed 99%-100% similarity to published sequences of *Rhipicephalus sanguineus* sensu lato "tropical lineage", recently reinstated as *Rhipicephalus linnaei*. This study marks the first successful initiation of embryo-derived cell cultures from *Rhipicephalus* ticks in Malaysia, where these ticks are prevalent and carry medically significant pathogens. The development of these tick cell cultures will facilitate future research into tick-borne diseases in the Asia-Pacific region, potentially leading to improved understanding and management of the associated health risks.

Abstract Reference: 20508
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Is there a role for birds in the epidemiology of scrub typhus in Malaysia?

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Abstract Content

Trombiculid larvae, or chiggers, are vectors of scrub typhus disease caused by the bacterium *Orientia tsutsugamushi*. The epidemiological role of birds in spreading chiggers in Malaysia has not been investigated. This study represents the first comprehensive investigation into the ecology and *Orientia* status of chiggers parasitizing birds in Malaysia. A total of 1141 birds were trapped using various methods and examined for chigger infestation across 22 sites in different habitats. Chiggers were identified at the species level and subjected to ecological analysis. Individuals from the same chigger species per host were pooled for genomic DNA extraction to detect *O. tsutsugamushi* via nested and quantitative PCR. The overall chigger infestation rate was 13.23%. Among the 11 chigger species collected, *Toritrombicula densipiliata* was predominant. Three species (*Leptotrombidium imphalum*, *Odontacarus audyi*, and *T. densipiliata*) infested migratory passerines. Bipartite network analysis confirmed the distinct and depauperate chigger fauna infesting five Galliformes species. One host species, *Pellorneum ruficeps*, had the highest incidence of polyspecific parasitism with three co-feeding chigger species. Unipartite analysis showed *Neoschoengastia gallinarum* and *Ascoschoengastia lorius* did not co-infest hosts, while *T. densipiliata* held central positions in the network, suggesting it is a generalist species. Natural forests were the most preferred habitat, whereas no chiggers were collected from shores or urban areas. *Orientia tsutsugamushi* was not detected in any of the 34 pooled chigger samples using both traD qPCR and TSA47 nPCR. Overall, this study suggests a low chigger diversity and found no evidence of *Orientia* infection in chiggers from birds in Malaysia.

Abstract Reference: 20509
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Molecular investigation of *Plasmodium* spp. from faecal samples of *Macaca fascicularis* in Indonesia

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Abstract Content

Threats to Malaria Elimination Program (MEP) are arising such as drug resistance parasites, insecticide resistance mosquitos, and zoonotic malaria. In Southeast Asia, zoonosis emergence of macaque malaria, *Plasmodium knowlesi*, has been a major concern to MEP. This parasite is presumably endemic, in wild populations of *Macaca fascicularis* (longtailed macaques) which are indigenous to South-East Asia. Besides *P. knowlesi* infection, the macaque is also infected by *P. inui* and *P. cynomolgi* which could be transmissible to human. However, the parasitology data from Indonesian macaque populations are sparse. Non-invasive sampling methods are the primary tool for primate infectious disease ecology. The present study aimed to investigate *Plasmodium spp* from faecal samples of long-tailed macaques in Indonesia. Faecal samples from semi-captive breeding sites and wild *M. fascicularis* have been collected. A total of 122 *M. fascicularis* faecal samples were collected from Java (West Java) and Sumatra (Lampung, Palembang, and Jambi). DNA samples were extracted and Nested Polymerase Chain Reactions (PCR) were used to detect *Plasmodium* genus using sets of mitochondria DNA (mtDNA) primers. There were 46 (37.7 %) samples positive of malaria and four species of *Plasmodium* parasites (*P. inui*, *P. cynomolgi*, *P. coatneyi* and *P. fieldi*) were detected in their natural host. None of the faecal samples identified as *P. Knowles* positive. This surveillance study contributed to determination of macaque malaria in distribution in Indonesia using non-invasive samples. The outcomes of this work are essential for understanding malaria prevalence in macaque hosts and controlling emergence of the pathogen in new human population.

Abstract Reference: 20515
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Controlling *Aedes albopictus* in a low rise apartment buildings park with Gravid *Aedes* Traps. An exploratory study in South-East France

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Abstract Content

The control of *Aedes albopictus* by Gravid Aedes Traps (GATs) has been evaluated for individual homes but not for collective housing areas. An exploratory study was conducted in a low-rise apartment buildings park in South-East France. The main objective was to assess the effectiveness of GAT trapping, with or without larval control, on reducing the abundance of adult female *Aedes albopictus*. Two areas were compared: an intervention area (three hectares, two buildings) with 19 BG-GATs^{Ò} and a similar control area without GATs. GATs were deployed from July to October in 2021, from July to November in 2022 and from April to November in 2023. Larval control was only carried out in the intervention area in 2021 and in both areas in 2022 and 2023. The abundance of female *Aedes albopictus* was measured fortnightly in both areas (four BG-Protector^{Ò} per area). Over the study, 98% of GATS were functional. No *Ae. albopictus* abundance reduction was observed in 2021. A significant reduction of *Aedes albopictus* abundance was observed in the intervention area in 2022 (-49%; p=0.009) and 2023 (-72%; p=0.005); compared to the control area. Larviciding and trapping cost was estimated at 320 euros per hectare/year. This study shows that installation of GATs in low-rise apartment buildings parks in the Mediterranean area can reduce the abundance of *Aedes albopictus* at low-cost, provided that: i/effective control of breeding sites is implemented; ii/early GATs deployment and late maintening during the vector activity season; iii/regular maintenance. Larger scale studies are needed to confirm these results.

Abstract Reference: 20519
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Indoor DENV transmission by *Aedes aegypti* in the French West Indies. Assessment by molecular xenomonitoring

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Abstract Content

In the French West Indies, *Aedes aegypti* is the vector of DENV. It is mainly endophagic and endophilic, and presents high resistance level to insecticides. During dengue fever outbreaks, controlling DENV indoor transmission remains an issue. Molecular Xenomonitoring (MX) is an easy and rapid method to detect the presence of pathogens in mosquito excreta collected on filter paper. To assess indoor DENV transmission, MX was used during the 2023 dengue outbreak in Martinique. *Ae. aegypti* were captured using by BG-Sentinel® or BG-Pro® traps with filter papers, and placed inside and outside homes of clinically suspected dengue fever cases. On average, 7.2 *Ae. aegypti* were captured outdoors and 2.6 indoors. The DENV was detected in 7/27 filter papers (26%): 6/23 were detected with BG-Sentinel® and 1/4 with BG-Pro®. None of the mosquitoes collected outdoors was infected by the DENV, even in households with one or more symptomatic individuals. Of the seven positive samples, two came from households with at least one case of dengue at the time of collection and five in households with at least one family member who had shown symptoms of dengue between eight to 31 days before sampling. This study confirms the predominant role of indoor DENV transmission by *Ae. aegypti* in the French West Indies. It also suggests a possible use of indoor trapping to prevent secondary DENV transmission in the home of a dengue case. These methods could be an additional tool for vector control, especially in areas where mosquito's resistance to insecticides is high.

Abstract Reference: 20573
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Serological exposure markers to detect the hidden burden of malaria in the spleen

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Abstract Content

Malaria elimination requires the detection and treatment of all reservoirs of infection, including the recently-discovered parasite biomass hidden in the spleen in chronic *Plasmodium vivax* and *P. falciparum* infections. Our prior studies in Timika, Indonesia, reported splenic infections that would remain undetected and untreated during routine practice, contributing to sustained transmission. Serological Exposure Markers (SEM) have been identified as a promising tool to detect hidden hepatic reservoirs of *P. vivax*. Here, we tested the diagnostic performance of SEM in individuals with a known splenic biomass of *P. vivax* and *P. falciparum* parasites. In Indonesia, plasma from 65 patients undergoing splenectomy in Timika (27 *P. vivax* and 33 *P. falciparum* infections) and 20 malaria-naïve volunteers from Jakarta were analyzed for IgG antibody responses against 14 *P. vivax* and 4 *P. falciparum* proteins using Luminex MAGPIX assays. Published algorithms were used to determine seropositivity, with splenic *Plasmodium* PCR positivity as the reference. SEM had a diagnostic sensitivity of 93% (25/27) for splenic *P. vivax* infections, compared to 44% and 96% by peripheral blood microscopy and PCR, respectively. Two individuals with known splenic *P. vivax* biomass were classified as seronegative despite low to medium antibody responses. Serological data from *P. falciparum* infections were recently collected and are currently being analysed. In conclusion, SEM is a promising diagnostic tool for the detection of splenic reservoirs of *P. vivax*. Future developments of SEM from a lab-based test to a lateral flow assay may embed its utility as a leading point-of-care diagnostic test in the field.

Abstract Reference: 20575
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Efficacy of a metofluthrin spatial emanator (SumiOne™) in coastal villages of Papua New Guinea

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Abstract Content

Malaria cases in Papua New Guinea (PNG) have increased since 2015 and incidence has doubled. The reasons may be multifactorial, including a weak healthcare system, lack of alternative vector control tools (VCTs), substandard bednets and high outdoor transmission rates. The NATNAT Project is exploring novel VCTs such as spatial emanators (SE) to complement existing control efforts in PNG. Passive SE are devices that emit volatile insecticides that may repel or kill mosquitoes, or inhibit biting, creating a protected space for the user, and potentially providing community protection. A small-scale field study of a metofluthrin (SumiOne™) SE was conducted in two PNG villages to evaluate the effect of SEs on mosquito-human contact. Mosquito landing, as measured by human landing catches, in selected study households where SEs had been deployed was compared to households without SEs. Protective efficacy (PE) was estimated as the reduction in number of mosquitoes landing on volunteer collectors in treatment households compared to untreated. The efficacy of the SE to reduce mosquito landing was also evaluated using a set of experimental huts. Furthermore, a community acceptability survey was conducted in parallel with the entomology field survey. Overall, SEs performed well indoors with an average initial PE of 60% (range 0-84%) and 45% (range 0-67%) 6 weeks post-deployment. The average initial outdoor PE was 43% (range 0-55%) but declined to 19% (range 0-52%) after 6 weeks, in line with product expectations. We will present a detailed performance analysis, with considerations regarding environmental, household and SE placement factors.

Abstract Reference: 20581
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Lessons from national dengue vector control programme approaches in the Asia Pacific region: A qualitative study of expert perspectives

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Abstract Content

Dengue poses a growing public health challenge globally. This qualitative study aimed to identify lessons for national dengue vector control programmes in the Asia-Pacific region by exploring the perspectives of global and national experts with experience in the region. We conducted semi-structured interviews with a purposive sample of 31 experts in dengue vector control, with a focus on the Asia-Pacific region. We analysed data thematically using abductive coding. Experts emphasised the importance of combining multiple control methods, such as source reduction, larviciding, and adult mosquito control, for effective dengue prevention. All highlighted the need for active community engagement, including community-based initiatives and communication campaigns, to enhance vector control efforts. Many described strategies informed by surveillance data, entomological research, and programme evaluation, as crucial for decision-making and resource allocation. Most acknowledged the influence of climate change on dengue transmission dynamics and stressed the importance of adapting vector control strategies to changing climatic conditions. This study provides insights into effective dengue vector control methods for high-income settings, highlighting the importance of integrated and evidence-informed approaches, community engagement, and climate adaptation. These perspectives underscore the need for proactive research-based strategies, learning from communities and other programmes globally, to provide effective dengue vector control and mitigate the evolving challenges posed by environmental changes.

Abstract Reference: 20588
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Laboratory rearing of the stable fly *Stomoxys calcitrans* and new protein source of larval diet

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Abstract Content

The stable fly, *Stomoxys calcitrans*, is an important pest that causes serious economic damage by sucking blood from herbivores, particularly cattle and goats. This study aimed to develop a laboratory-rearing technique and establish a laboratory strain of *Stomoxys calcitrans*. Insects were collected from NCHU animal farm and reared under laboratory conditions (25±1℃), fed on cotton pads soaked with commercial sheep blood. After the eggs are laid, transfer them into larva matrix for rearing and pupation. Pupae were then moved into the insect-rearing cage for adult emergence. Based on the above rearing method, ten generations of sub-breeding have already been completed and are continuing to establish a laboratory strain. The eggs hatch in approximately 1-2 days, followed by 10 days of larva development and 5 days of pupation time. The study evaluated three different protein sources, including fish meal, black soldier fly (*Hermetia illucens*) meal (BSFM), and peptone in the larval matrix to assess their effect on larval growth and development. 30 eggs were divided equally into three plastic cups containing the matrix for the observation of life cycle. Fish meal (FM) (as control group) in the matrix was replaced with the same amount of BSFM or peptone. The growth performance test was assessed by mixing different concentrations of BSFM or peptone with other materials to compare the impact of each concentration on the growth performance of the stable fly. The preliminary results suggest that compared to FM, using BSFM or peptone can enhance growth performance, and improve the rearing methods.

Abstract Reference: 20609
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Exploring the antifungal potential of andrographolide and its combined effect with conventional antifungal drug against *Aspergillus* species

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Abstract Content

Novel therapeutic techniques are necessary because of the rising antifungal resistance among fungal pathogens and the high occurrence of fungal diseases. This study evaluated the susceptibility of *Aspergillus fumigatus*, *Aspergillus terreus*, and *Aspergillus niger* to andrographolide and its synergistic effects with amphotericin B. A broth microdilution antifungal susceptibility testing using two-fold microdilution tests was employed. The MIC values of andrographolide against *A. fumigatus* and *A. niger* was found to be 400 µg/ml, while that of *A. terreus* was 800 µg/ml. The MFC values of the compound against *A. fumigatus* and *A. niger* was 800 µg/ml, while that of *A. terreus* was 1600 µg/ml. Amphotericin B generally exhibited superior activity compared to andrographolide against all the tested isolates, indicating higher potency and efficacy as evidenced by the susceptibility of *A. fumigatus*, *A. terreus* and *A. niger* with MIC values range from 50 to 100 µg/ml, and MFC values range from 200 to 400 µg/ml. The combination demonstrated synergistic activity against *A. fumigatus* and *A. niger* with FICI values of 0.3 (FICI ≤ 0.5), whereas an indifferent interaction with FICI value of 1.1 ($1 < \text{FICI} \leq 4$) was observed against *A. terreus*. The present study provides significant insights into the antifungal activity of andrographolide and its combination with amphotericin B. These findings may open new therapeutic avenues for the development of interventions against *Aspergillus* species infections; therefore, more research is necessary to clarify the underlying mechanisms of action of this compound and its interaction with traditional antifungal agents.

Abstract Reference: 20615
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Activity of *Etlingera elatior* rhizomes as anthelmintics against *Ascaridia galli* and *Raillietina* spp. in vitro

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Abstract Content

The research aimed to evaluate the effectiveness of kecombrang rhizomes as an anthelmintic against the worms Ascaridia galli and Reilietina spp in vitro. In this research, kecombrang rhizomes were grated and squeezed to extract the juice, and then tested at four concentrations, namely 100%, 50%, 25% and 12.5%. Five worms were placed in a petri dish, containing 25 ml of test solution. Observations were made every hour for 10 hours under a microscope. Albendazole 10% served as a positive control, and NaCl 0.9% as a negative control. Each treatment was repeated three times. Both treatment worms were collected from chicken intestines at the poultry slaughterhouse. The results showed significant differences in anthelmintic activity, with higher concentrations of kecombrang juice leading to faster worm death. For A. galli, the average times to death (mean ± SD) were 6.33 ± 1.29 hours at 100%, 5.93 ± 1.16 hours at 50%, 7.46 ± 0.92 hours at 25%, and 8.80 ± 1.66 hours at 12.5%, compared to 4.2 ± 0.44 hours for the positive control. Similar results were observed for Reilietina spp, with average times to death (mean ± SD) of 2.13 ± 0.36 hours at 100%, 3.2 ± 0.41 hours at 50%, 3.93 ± 0.59 hours at 25%, and 4.33 ± 0.62 hours at 12.5%, compared to 1.2 ± 0.45 hours for the positive control. In conclusion, E. elatior shows anthelmintic activity against Reilietina spp and A. galli, which has the potential to be developed as an anthelmintic.

Abstract Reference: 20639
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Discriminating lethal dose of chemical compounds in type II pyrethroid using the WHO bottle bioassay technique against *Culex quinquefasciatus* (Diptera: Culicidae)

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Abstract Content

Culex quinquefasciatus, a nocturnal and anthropophilic mosquito, serves as an important vector of lymphatic filariasis and arthropod-borne viruses, including St. Louis encephalitis virus and Japanese encephalitis virus. Synthetic pyrethroid insecticides are used to control the *Culex* population and reduce human-mosquito interactions in Thailand. The aim of this study was to establish the discriminating lethal dose of three type II pyrethroids—deltamethrin, alpha-cypermethrin, and cyfluthrin—against *Cx. quinquefasciatus.* At least five serial dilutions of each chemical were tested using three-to-five-day-old females, following the WHO bottle bioassay protocol. The observed data were subsequently analyzed using probit analysis with SPSS software. The results contributed to the investigation of pyrethroid resistance status and have the potential to aid in the development of more targeted and effective mosquito control methods for *Cx. quinquefasciatus.* In the future, we suggest that the evaluation of discriminating doses of other pyrethroid chemicals should be conducted, and field populations should be tested for resistance status.

Abstract Reference: 20662
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Retrospective cohort analysis of treatment and outcomes in patients treated for leptospirosis at University Malaya Medical Centre between 2011 – 2022

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Abstract Content

Leptospirosis is a neglected bacterial zoonotic disease of public health concern due to its global distribution, epidemic potential and relatively high mortality. The University Malaya Medical Centre (UMMC) infectious diseases unit is a tertiary referral centre in Kuala Lumpur, Malaysia managing leptospirosis cases. A 2011-2022 retrospective cohort of leptospirosis seen at UMMC was analysed. Those with a clinical and/or microbiological diagnosis of leptospirosis were included. Outcomes of interest were mortality, severe disease, and treatment strategies. The cohort included 777 patients, 18% (139/777) demonstrating positive initial/convalescent serology by the microscopic agglutination test (MAT; *Leptospira biflexa* serovar Patoc). The median age was 38 years (range 1-84) and 576 (74%) were male. A composite-outcome of severe disease was recorded for 536 (68%; requiring intensive care, manifesting systemic complications or organ dysfunction), comprising 72% (440/611) of those admitted to hospital. There were 28 deaths (4%), 621 successful medical discharges (80%), 51 discharged against medical advice (7%), 70 lost to follow up (9%), and 6 transferred to other facilities (1%) Steroids (dexamethasone, prednisolone or hydrocortisone) were administered to 54 patients (11 deaths). Antibiotics were given at first hospital contact to 585; 214 ceftriaxone (8 deaths), 304 doxycycline (6 deaths), 50 amoxicillin/clavulanic acid (1 death), 17 meropenem (4 deaths). We report treatment outcomes for a cohort of leptospirosis cases in Malaysia. Global distribution of disease and limited randomised trial data provide a strong case for a definitive randomised controlled trial to obtain unbiased treatment effects and harmonize treatment protocols for leptospirosis.

Abstract Reference: 20665
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Assessing the impact of insecticide resistance on dengue vector competences in *Aedes aegypti*

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Abstract Content

Aedes aegypti is a primary vector for numerous arboviruses, including dengue, which threatens over 3.9 billion individuals in 120 nations and affects over 390 million people annually, causing significant health and economic losses. The excessive use of insecticides has led to resistance, posing a major challenge for vector control programs. This study investigates the impact of insecticide resistance on vector competence (VC) for dengue virus (DENV-2) among three *Ae. aegypti* strains: NS (susceptible), Propoxur-resistant, and Permethrin-resistant. The study evaluates DENV-2 loads at intervals post-inoculation (1, 3, 5, 7, 10, 14, and 21 days) using semi-quantitative RT-PCR and survivability analysis by observing daily mortality. Significant differences in viral loads were observed at various intervals post-inoculation. In the early stages of infection (1 to 5 DPI), notable differences in DENV-2 loads were detected among the strains, particularly between NS and the resistant strains, and between the two resistant strains themselves. However, no significant differences were found at later stages (7, 14, and 21 DPI). Survivability analysis indicated no significant differences across strains, regardless of DENV-2 infection status. These findings suggest that insecticide resistance affects DENV-2 loads at early stages but does not impact mosquito survivability.

Abstract Reference: 20667
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Gonotrophic cycles in *Aedes albopictus*

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Abstract Content

Aedes albopictus is one of the primary vectors of arboviruses. The duration of the gonotrophic cycle can serve as an indicator of mosquito abundance, affecting the frequency of interactions between hosts and vectors, thereby influencing the risk of vector-borne virus transmission. This study aims to determine the gonotrophic cycle of *Ae. albopictus* between different environmental components. Blood-feeding experiments were conducted using 3-5-day-old female mosquitoes. After blood-feeding, mosquitoes were divided into two groups: individually reared and group reared. Oviposition papers were changed daily, and egg numbers were recorded to determine the duration of the gonotrophic cycle, egg production, and lifespan. The mosquitoes were allowed to undergo their first gonotrophic cycle after blood-feeding and lay eggs, continuing until the mosquitoes naturally died. Total egg production, and adult lifespan of *Ae. albopictus* were recorded throughout the study. Our observations revealed that oviposition rates reached a peak on the third day post-blood meal, followed by a subsequent decline. Notably, no female mosquitoes laid eggs on the first day after blood-feeding. Furthermore, in terms of total egg production, individually caged females laid more eggs on average compared to group-reared females. These results underscore the significance of considering both individual behaviors and social interactions in elucidating the reproductive biology of *Ae. albopictus* mosquitoes.

Abstract Reference: 20672
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Measuring patient satisfaction to improve quality of care at tertiary care public hospital of Bhavnagar, Gujarat, India

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Abstract Content

Introduction: Patient satisfaction has long been a concern for researchers, health professionals, and policymakers, and it has been extensively studied for some years. In our society, with a constant increase in health spending and budgetary constraints, it is important that the provision of care meet the subjective needs of patients. These days, measuring patient happiness is seen as adding value to other outcome metrics like life quality or health. To assess the satisfaction of patients visiting a tertiary care public hospital in Bhavnagar district. A cross-sectional study was carried out at a tertiary hospital in Bhavnagar district. A total of 100 patients from the Departments of Medicine, Surgery, Orthopedics, OBG, Pediatrics, ENT, Eye, and Skin were selected using simple random sampling. Most of the population selected this hospital because it is inexpensive. 45.5% of the of the population got information about hospitals from family members and 15.2% from neighbors. Only 17% of the population finds difficulty locating the hospital. Almost ¾ of the population facing overcrowding at the registration counter. The good behavior of registration clerks is seen toward most of the population. About 1/3 of patients are facing problems with sitting arrangements and cleanliness. Efforts should be made to reduce the patient load at the hospital so that doctors and other staff can give more attention and time to patients. Efforts are also needed to strengthen infrastructure and human resources at lower-level health facilities.

Abstract Reference: 20674
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Cecropin gene expression in *Aedes albopictus*

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Abstract Content

Aedes albopictus is one of the primary vectors of dengue virus. Antimicrobial peptides (AMPs) play a crucial role in the immune responses of insects, defending against pathogens and maintaining health. Some studies have shown that dengue virus infection triggers the expression of many AMP genes in mosquitoes, some of which may inhibit viral replication and dissemination, potentially reducing dengue transmission. This study aims to investigate *Ae. albopictus* cecropins (Aalcec) have antiviral activity against the dengue virus. The expression levels of the target genes were analyzed at 30 minutes, 6 hours, 24 hours, 48 hours, and 72 hours post-injection using RT-qPCR. In this experiment, we first examined the expression profiles of four Aalcecs in microbes-challenged *Ae. albopictus* adults, and found that the gene expression patterns of Aalcec A, B, D, and G were induced by Gram-positive bacteria, Gram-negative bacteria, and the dengue virus, respectively.

Abstract Reference: 20676
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Investigation of ectoparasites in feral pigeons in the park

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Abstract Content

Ectoparasites can be found in almost every bird, especially those living in urban, because of the feeding behavior and environmental composition of humans, the population of urban wild birds is large and dense, making it easier for urban wild birds to spread and contact humans, so it has become one of the important zoonotic pathogens. We caught wild pigeons (Columba livia Linnaeus, 1758) by bait and large walk-in traps in Taichung City, Taiwan, and fumigated them to collect ectoparasites, including chewing lices (Phthiraptera) and louse flies (Hippoboscidae). This is the first study of ectoparasites in urban wild birds in Taiwan, hoping to fill a gap in public health with this research.

Abstract Reference: 20692
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Long-read nanopore sequencing tool targeting the heat shock protein 70 gene for the identification of *Leishmania species*

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Abstract Content

Leishmaniases are caused by at least 21 species of *Leishmania* and significantly affect human and animal health in tropical and subtropical regions. Understanding their complex epidemiology has been hindered by traditional techniques' inability to capture the full diversity of *Leishmania* species. We developed a metabarcoding tool targeting the heat shock protein 70 gene using a portable Oxford Nanopore Technologies (ONT) MinION device to establish the diversity of *Leishmania* species infecting vertebrate hosts and vectors. We also created a new database and used it alongside the NanoCLUST analysis pipeline. This tool allowed the accurate classification of all 14 *Leishmania* species tested. Using this method, all *Leishmania* species were separated from each other, including those within the same complex, with percentage identity scores between 99.99 - 100% when compared to reference sequences. The species tested represented four *Leishmania* subgenera: *L. tropica*, *L. aethiopica*, *L. major*, *L. gerbilli*, *L. infantum*, *L. mexicana*, and *L. amazonensis* (subgenus *Leishmania*); *L. guyanensis* and *L. panamensis* (subgenus *Viannia*); *L. orientalis* (subgenus *Mundinia*); *L. tarentolae* (subgenus *Sauroleishmania*). This nanopore sequencing method provides a useful tool for the differentiation of *Leishmania* species to support epidemiological studies and the prevention and control of this disease in humans and animals.

Abstract Reference: 20722
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

The impact of global warming on hyperendemic fascioliasis region at high altitude

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Abstract Content

The high dependency of Fascioliasis transmission on climatic factors underlies the marked influences of climate change on this disease. In this scenario, the Northern Bolivian Altiplano (NBA) is a hyperendemic area for human Fascioliasis at very high altitude with extreme climatic conditions, where field surveys showed a geographical expansion of its lymnaeid snail vector. Our objective is to identify the main climatic characteristics that determine the expansion of the Fascioliasis transmission zone in the NBA. We utilized climatic data spanning at least a 30-year period and applied two climatic risk indices, the Wb-bs and Mt indices, to forecast fascioliasis transmission in this endemic area. Our results show that trends in maximum and mean temperatures demonstrate significant increases throughout the endemic area. Annual precipitation trends are negative in most localities. Climatic risk indices exhibit negative trends at lower altitudes. However, monthly and yearly values of climatic risk indices indicate a persistent transmission feasibility in nearly every location. The Wb-bs and Mt indices suggest that warmer temperatures have enabled lymnaeids to colonize higher altitudes beyond the previously observed endemic zone in the 1990s. Additionally, drier conditions may further promote fascioliasis transmission to higher altitudes by increasing exploitation of permanent water sources inhabited by lymnaeids. CIBER de Enfermedades Infecciosas (CB21/13/00056), ISCIII, Ministry of Science, Innovation and Universities, Madrid, Spain and European Union-NextGenerationEU; PROMETEO (2021/004), Generalitat Valenciana, Valencia, Spain; Marie Skłodowska-Curie Actions programme (RCN 242718, ID 101062347), European Commission, Brussels; APOSTD/2022 (CIAPOS/2021/134), Generalitat Valenciana and European Social Fund, Valencia, Spain.

Abstract Reference: 20723
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

High prevalence of hookworms and *Strongyloides stercoralis* in school-age children cohabiting with dogs in Cambodia, despite long-term, bi-annual mass drug administration

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Abstract Content

Diseases caused by soil-transmitted helminths (STHs) persist, despite efforts to control them in at-risk populations. The World Health Organization (WHO) aims to eliminate STH-associated morbidity by 2030. However, targeted deworming and inadequate monitoring can hinder the success of this goal. Moreover, dogs are recognised as possible reservoirs of zoonotic STHs, further complicating control efforts. In a Cambodian commune, we critically assessed the effectiveness of current control strategies by examining 706 children undergoing bi-annual mass-drug administration and 478 co-habiting dogs using qPCR. Genetic characterisation and regression models were employed to investigate the inter-host transmission dynamics of zoonotic STHs. Using qPCR, we recorded a high prevalence of select STH infections in children (46%) and dogs (84%), with hookworms predominating. There was a strong correlation ($p<0.001$) in the prevalence of *Strongyloides stercoralis* infections between children and dogs, suggesting inter-host transmission. Further molecular analyses revealed shared haplotypes of *A. ceylanicum* and *S. stercoralis* in both children and dogs. These results indicate that improved diagnostic tools are needed to achieve WHO's 2030 targets to control these STHs in a One Health context, which acknowledges the importance of animals as reservoirs for human infections.

Abstract Reference: 20729
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Inducible clindamycin resistance and genotypic characterisation of methicillin-resistance *Staphylococcus aureus* isolates in Terengganu, Malaysia

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Abstract Content

Methicillin-resistant *Staphylococcus aureus* (MRSA) is an important clinical pathogen commonly associated with multiple antibiotic resistances and virulence factors contributing towards its pathogenicity. The present study aims to detect the prevalence of macrolide-lincosamide-streptogramin B (MLSB) resistance phenotypes and their related genes, staphylococcal cassette chromosome *mec* (SCC*mec*) types, carriage of 19 virulence genes and to compare these characteristics between hospital-associated (HA) and community-associated (CA) MRSA isolates. A total of 197 MRSA isolates (HA=150; CA=16; unknown=31) were collected from Hospital Sultanah Nur Zahirah, the main tertiary hospital in Terengganu, Malaysia, from 2016 until 2020. A D-test was carried out to determine MLSB resistance phenotypes while PCR was performed to detect the presence of MLSB-related genes, SCC*mec* types and virulence genes. Inducible clindamycin resistance was common (52.3%, 103/197) among the MRSA isolates, with *ermC* being the most predominant MLSB-resistance gene (91.1%, 113/124). SCC*mec* type IV was the most prevalent and was significantly associated with HA-MRSA isolates (82.0%, 123/150, p = 0.003). Most of the MRSA isolates carried *hla* (80.2%, 158/197), *hld* (78.2%, 154/197), *sem* (75.1%, 148/197) and *seo* (73.6%, 145/197) virulence genes. The HA-MRSA isolates had a higher carriage of *hld* (82.0%, 123/150, p = 0.007), while *sec* (31.3%, 5/16, p = 0.004), *sel* (37.5%, 6/16, p <0.001), *lukED* (68.8%, 11/16, p <0.001) and *lukPV* (43.8%, 7/16, p <0.001) were greater among CA-MRSA isolates. The high prevalence of inducible clindamycin resistance highlights the importance of continuous monitoring of MRSA, and the presence of various virulence genes suggests that the MRSA isolates are highly virulent.

Abstract Reference: 20737
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Longitudinal antibodies and B-cell responses of SARS-COV-2 vaccination and infection against symptomatic SARS-COV-2 in Malaysia

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Abstract Content

Waning antibody against SARS-CoV-2 is a natural process of humoral responses. However, breakthrough infections (BTI) and reinfections incidence present the lack of COVID-19 immunity. This study explored the antibody and B-cells responses influenced by SARS-CoV-2 vaccinations and infections to assess the risk of symptomatic SARS-CoV-2. We analyzed serum IgM, IgA, IgG, and neutralizing antibodies levels in a prospective longitudinal cohort of 400 participants through ELISAs. We monitored antibody at baseline and up to nine timepoints over 12-months period. Incidence of SARS-CoV-2 infections during the study was recorded. A cross-sectional PBMCs analysis was conducted on 45 participants, randomly selected based on their COVID-19 vaccination to evaluate S and RBD-specific memory B-cells population. In serologically naive-SARS-CoV-2 group, the antibodies wanes starting 14 days post-second BNT162b2 dose. Antibody levels increased following a booster dose or BTI. However, in the boosted group without BTI, antibodies declined similarly as initial waning observed during post-second BNT162b2 dose. In BTI groups, participants which previously vaccinated with BNT162b2 had a higher antibody level than those with ChAdOx1 and CoronaVac. Despite this, the risks of BTI were similar in any vaccination platforms. PBMCs analysis showed BNT162b2 recipients had the highest percentage of S-specific memory B-cells, however, no significant difference in RBD-specific memory B-cells among vaccines. Our findings suggest that memory B-cells population during the waning antibody phase is similar for all vaccines which provide a comparable protective response against SARS-CoV-2. Therefore, COVID-19 vaccination is effective in reducing the risk of symptomatic SARS-CoV-2.

Abstract Reference: 20739
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Antibiotic resistance genes and bacteria in macaque faecal samples, Klang Valley, Malaysia

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Abstract Content

The challenge of antibiotic resistance transcends multiple domains, requiring integrated actions across humans, animals, and the environment. To assess the spread of antibiotic resistance and its zoonosis risk among wildlife in relation to human health, we examined the faecal sample of three macaque (*Macaca fascicularis*) individuals, each collected from three natural habitats in the Klang Valley of Malaysia. Samples were subjected to Oxford Nanopore Sequencing. Raw reads were then screened for the presence of antibiotic resistance genes (ARGs) using the ABRicate tool with the ResFinder database. 20, 42 and 39 reads were identified as harbouring ARGs from the 3,555,307; 5,419,388; and 3,823,287 total reads by the respective samples. Seventeen ARGs were found with an average of 95.3% coverage and 95.2% identity similarity to ARG references. Ant(6)-Ia, catP, tet(32), tet(40), tet(O), tet(Q) and tet(W) appeared in two out of the three samples. The identification of the ARG harbouring reads were performed through nucleotide blast in GenBank, yielding an average of 95.8% identity similarity with an average of 79.0% coverage to the reference bacteria. Among the total 101 reads from the three samples, only Enterobacter cloacae was identified as an ESKAPE bacteria. *Segatella copri*, *Bacteroides fragilis*, *Enterocloster clostridioformis*, *Flavonifractor plautii*, and *Eubacterium limosum* at species level; and *Lachnospiraceae* bacterium, *Proteiniclasticum sp.* and *Clostridiales* bacterium occurred in more than one site. The ARGs detection shows that streptomycin, chloramphenicol, doxycycline, tetracycline and minocycline resistance risks are also occurring among macaques, suggesting an enhanced stewardship steps on the usage of these antibiotics.

Abstract Reference: 20743
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Semi-field evaluation of transfluthrin-impregnated fabric against *Aedes albopictus* (Skuse) (Diptera: Culicidae) during morning and evening trials

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Abstract Content

Volatile pyrethroid spatial repellents cause repellency induced by airborne chemicals that result in human-vector contact, and provide personal protection to users. This study investigated the effect of a passive emanator on disarming, human landing and blood feeding behavior of *Aedes albopictus* in a semi-field system (SFS). A polyester fabric measuring 1,029 cm^2 impregnated with 0.25 mg/cm^2 TFT (6.8%, w/v) was attached on the black-screened vest to simulate insecticide-treated clothing for the SFS experiments. Two collectors wearing the treated and untreated clothing conducted human landing collections (HLC) from opposite test arenas during morning (06:00-08:00 h) and evening (18:00-20:00 h) trials for 12 days. Recaptured surviving mosquitoes were provided a blood meal for 60 min. Protective efficacy was estimated to be 55.9% (IRR: 0.44, CI: 0.37- 0.53; $p<0.05$) during morning trials compared to 20% (IRR: 0.71, CI: 0.64- 0.78; $p<0.05$) during the evening trials. Mortality and knockdown were not significantly different between morning: 34.7% t-test=-1.24, df=22; $p=0.23$), 7.64% (t-test=-0.87, df=22; $p=0.05$) and evening: 25.3% (t-test=-1.24, df=22; $p=0.23$), 5.54% (t-test=-0.87, df=22; $p=0.05$), respectively. Blood fed mosquitoes were significantly lower for treatment (37.51%) than control (67.00%) morning trials (t-test=-3.18, df=22; $p=0.0042$) during but not different for the evening trials (t-test=-1.63, df=22; $p=0.1164$). Transfluthrin-treated polyester fabric can offer personal protection against *Ae. albopictus* through disarming and blood feeding inhibition with significant effects on mosquito landing and blood feeing.

Keywords: Transfluthrin, Polyester fabric, Human landing collection, Protective efficacy, Time of intervention

Abstract Reference: 20751
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Plasmodium falciparum histidine-rich protein 2 and 3 deletions analysis among *P. falciparum* isolates from North Sumatra, Indonesia

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Abstract Content

Rapid diagnostic tests (RDTs) are essential tools for *Plasmodium* species detection. It is particularly important to ensure prompt access to diagnosis and treatment in malaria endemic areas, in order to improve malaria control. Nevertheless, there were increasing reports of RDTs failure due to Pfhrp2/3 deletion, leading to false-negative results. This study aims to evaluate the presence of Pfhrp2/3 deletions among *P. falciparum* isolates in North Sumatra. A passive case detection were conducted in four districts in North Sumatra from August 2019 – December 2020. Malaria diagnosis was made by microscopy, RDTs, and nested PCR. After confirming *P. falciparum* through nested PCR, the samples underwent further analysis using a multiplex real-time quantitative PCR (qPCR) assay to detect the presence of Pfhrp2 and Pfhrp3. Of 947 samples, 75 individuals were *P. falciparum* PCR-confirmed. Of these, 86.7% (65/75) and 83% (44/53) were detected by either microscopy and RDT, respectively. The median parasite density were 3000 parasites/μL. Four individuals were positive by microscopy but failed to be detected by RDT (Parasite densities of 741, 2191, 11869, and 160 parasites/μL). Analysis on the deletions in the Pfhrp2/3 will be conducted and presented in the meeting. Pfhrp2/3 deletions cause threats to malaria elimination programme. This is the first study to report an analysis of Pfhrp 2/3 deletion in North Sumatra, underscores the importance of the Pfhrp2/3 deletions status in the country to support malaria elimination programme.

Abstract Reference: 20756
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Detection of rodent-borne intestinal parasites infestation in North Sumatra, Indonesia: A potential public health concern

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Abstract Content

Around > 70 % of emerging human infections are derived from animals. Recent changes in environment increase risk of rodent-borne pathogens, including zoonotic intestinal parasites. This descriptive cross-sectional study aimed to identify zoonotic intestinal parasites in wild rodents from three areas in North Sumatra: Serdang Bedagai, Batu Bara, and Asahan. Using bait traps placed in houses, purposive sampling was done from July to August 2023. Rodent species were identified based on morphology. After being euthanized, intestines were dissected to extract the contents, proceeded with formalin-ether concentration technique (FECT). The sediments were microscopically examined for ova and parasites by direct lugol wet smear, and additional Kinyoun acid-fast stain to detect coccidian parasites. From 47 collected rodents, the main species captured were *Rattus tanezumi* (59.6%), followed by *Rattus norvegicus* (29.8%), and *Rattus tiomanicus* (4.3%). Other species found were *Rattus argentiventer*, *Rattus exulans*, and *Mus musculus* (2.1% of each). Twelve intestinal parasites species were detected in 38 (80.9 %) rodents, most were co-infections. The helminths found were *Nippostrongylus brasiliensis* (61.7 %), *Moniliformis moniliformis* (36.2 %), *Heligmosomoides polygyrus* (27.7 %), *Hymenolepis nana* (8.5 %), *Ascarids* (4.3 %), *Trichuris* spp. (4.3 %), and *Hymenolepis diminuta* (4.3 %). The protozoa identified were *Entamoeba* spp. (31.9 %), *Cryptosporidium* spp. (17 %), *Giardia* spp. (6.4 %), *Cyclospora* spp. (2.1 %), and *Blastocystis* spp. (2.1 %). We identified 12 intestinal parasite species in the rodents. The detected *Trichuris* spp., *H. nana*, *H. diminuta*, *Cryptosporidium* spp., *Entamoeba* spp., and *Giardia* spp. are zoonotic pathogens.

Abstract Reference: 20759
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Submicroscopic *P. malariae* infections threat the success to malaria elimination efforts in Indonesia

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Abstract Content

The strengthened malaria control and elimination strategies in Indonesia have resulted in the significant reduction of *P. falciparum* and *P. vivax* morbidity and mortality. Nevertheless, the impact on the other human *Plasmodium* infection, particularly *P. malariae*, seems to be negligible. Microscopy is insensitive to detect low-level parasitaemia In areas where malaria endemicity is low, control programmes need sensitive tools for identifying submicroscopic hidden malaria infections. This study aimed to assess the distribution of *P. malariae* infections, and its associated risk factors in four districts in North Sumatera, Indonesia. The study was conducted from January 2022 to March 2023, and *Plasmodium* infection was determined by nested PCR. A total of 4737 subjects was recruited, 27 (0.6%) individuals were diagnosed with *P. malariae*. None was detected by microscopic. The majority (92.5%) were symptomatic, and most infected individuals were female (62.9%) and adults (70.4%). Coconut plantation worker (OR=3.2 95% CI 1.06-5.4), living near palm oil plantation (OR=0.06 95% CI 0.0-0.4) and having bamboo-walled house (OR=13.6 95% CI 5.0-37.0) were associated significantly with *P. malariae* event (P<0.05). There is a shift in the trend of malaria infection to an increase of non-*P. falciparum* infection prevalence. Submicroscopic infection appears to be the source of transmission and creates further malaria elimination challenges in near malaria-eliminated regions.

Abstract Reference: 20765
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Phenotypic and genotypic characterization of antimicrobial resistance bacteria and their resistance genes among organic vegetables fertilized by poultry manure

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Abstract Content

The phenotypic and genotypic characterization of antimicrobial resistance (AMR) bacteria and their resistance genes among organic vegetables fertilized by poultry manure involves multiple causes and interrelationships. Poultry manure, used in organic vegetable production, can contain antimicrobial-resistant bacteria and resistance genes. These residues can persist in the manure and cause environmental contamination of soil, water, and crops. The objective of this study is to evaluate the impact of using untreated poultry manure in organic vegetable production systems. To do so, lettuce and chilies were sown in both test (untreated poultry manure) and control plot (chemical fertilizer) and harvested when mature. The climatic parameters were also recorded throughout the field operation, three timepoints of soil sampling were collected and tested. Both soils and vegetables were assessed for viable bacteria via colony count and bacteria species were identified by 16S rRNA gene PCR. The isolates were then evaluated for antibiotic resistance by disc diffusion method following by PCR for detection of resistance gene(s). From the data obtained the increased rainfall can lead to an increase in bacterial populations, due to the introduction of bacteria from the environment into water sources and the creation of ideal conditions for bacterial growth, such as increased humidity and temperature. The bacteria identification and AST test for microbe samples are still pending. In conclusion, Antimicrobial Resistance (AMR) requires a holistic approach that considers environmental, microbial, agricultural, and regulatory dimensions to minimize risks to human health and ecosystem integrity.

Abstract Reference: 20774
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology

Evaluation of control strategies based on a metapopulation transmission model of *Opisthorchis viverrini* infection: A data-driven modeling study

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Abstract Content

Existing transmission models of *O. viverrini* infection ignore the influence of population mobility and hydrological connections on transmission dynamics and intervention effectiveness. This study aims to construct a metapopulation transmission model at the provincial administrative level in Laos, incorporating population mobility and hydrological connections, to evaluate the control strategies. Based on the Susceptible-Infection transmission model, we incorporate inter-provincial population mobility and water connections to construct a metapopulation model. Using high-resolution prevalence estimates for Laos in 2018, Bayesian melding was used to estimate transmission rates. Intervention parameters were added to this model to evaluate control strategies. The observed prevalences all fell within the 95% credible interval (CI) of the estimated prevalences, with an EF score of 0.9947, indicating good accuracy and model structure. Among the 18 provinces, the highest transmission rate from fish to human was in Sekong Province of 6.66×10^{-13} (95% CI: 1.04×10^{-13}-8.39×10^{-13}), while the lowest was in Xiangkhouang Province of 6.14×10^{-14} (95% CI: 6.24×10^{-14}-3.58×10^{-13}). When chemotherapy, health education, and environmental modification were applied to Savannakhet Province and Vientiane Province with 100% coverage, the most significant declines were in Vientiane Capital and Saravane Province, with human prevalences dropping by 0.35% and 0.19%, respectively. The decline of prevalences in non-intervention provinces corresponded to the extent of contribution of water connections to transmission. This study is the first to establish a metapopulation transmission model of *O. viverrini* infection. Population mobility and hydrological connections influence the transmission dynamics and intervention effectiveness of *O. viverrini* infection in Laos.

Abstract Reference: 20780
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Comparison of four outdoor Anopheles vectors mosquito trapping methods as potential replacements for human landing catch targeting Southeast Asia

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Abstract Content

Monitoring malaria vector is increasingly important for understanding the dynamics of outdoor transmission. This study aims to compare four different trapping methods, namely Outdoor Human Landing Collection (OHLC), Human Double Net Trap (HDNT), Human Decoy Trap (HDT), and UV Light Trap (UVLT) in collecting outdoor mosquitoes.The evaluation of the trap methods was conducted across three seasons (winter, dry, and rainy). Four different traps (OHLC, HDNT, HDT, and UVLT) were utilized in a 4×4 replicated Latin square design over 48 nights in each season within a forest setting. Out of 3,721 specimens collected, 1,253 (33.7%) were *Anopheles* mosquitoes, representing three complex/groups. Molecular identification was employed to determine the species. Among the 123 Dirus complex, 49 (39.8%) were *An. baimaii*, 57 (46.3%) were *An. dirus*, and 17 (13.8%) were unidentified. For the 547 mosquitoes in the Minimus complex and related species, 473 (86.5%) were *An. harrisoni*, 58 (10.6%) were *An. minimus*, 10 (1.8%) were *An. aconitus*, and 6 (1.1%) were *An. varuna*. Among the 20 Maculatus group, all were confirmed as *An. sawadwongponi* (100%). The HDNT collected the most *Anopheles* mosquitoes (304, 44.1%) compared to OHLC (249, 36.1%), UVLT (124, 17.9%), and HDT (13, 1.9%). Therefore, HDNT is a potential replacement for outdoor sampling of *Anopheles* mosquitoes. The human double net trap (HDNT), which collected more *Anopheles* mosquitoes, is great in an outdoor sampling of *Anopheles* mosquitoes and has the potential for sampling outdoor host-seeking mosquitoes.

Keywords: Trap methods, *Anopheles* vectors, HDNT, Outdoor, Forest

Abstract Reference: 20782
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

The use of reverse transcription polymerase chain reaction to increase higher yields in detecting Plasmodium infections

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Abstract Content

PCR diagnosis is becoming more important to detect *Plasmodium* infections in near eliminated areas due to the predominantly high proportion of submicroscopic low-density parasites. These submicroscopic infections may contribute as a source of infection and threat the elimination progress. Reverse transcription PCR (RT-PCR) is a molecular technique and has a great potential in improving *Plasmodium* detection. This study aims to determine the potential of RT-PCR in improving the sensitivity of malaria detection. A total of 739 malaria clinical samples were initially screened for *Plasmodium* genus using qPCR targeting 18S rRNA described by Kamau *et al*. Positive *Plasmodium* genus isolates were further speciated for human Plasmodium infection using nested PCR with a similar target. Those who failed to be speciated had an RT step with one-step PCR added to increase the detection sensitivity. Repeat qPCR was subsequently performed to evaluate the changes in the average Ct values. Of the 739 samples tested, 289 (39.1%) had *Plasmodium* DNA detected by qPCR. However, only 164 (56.7%) were able to be identified to the species level (*Plasmodium vivax* 41.2% and *P. falciparum* 15.6%). 120 of 125 unidentified *Plasmodium* species underwent additional RT step, of these 60 (50%) showed lower average Ct values indicating that the DNA concentration has increased. The median difference of the Ct values was -6.415 (IQR -20.01 to -4.15). The use of additional step with reverse transcription in qPCR can increase the amount of DNA in *Plasmodium* thus enabling the detection of very small amounts of RNA.

Abstract Reference: 20803
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Epidemiological overview of dengue fever post Elnino phenomenon in Sidoarjo district East Java, Indonesia 2019-2024

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Abstract Content

Introduction: Dengue fever is a global health threat among 10 other diseases (WHO, 2021). The Case Fatality Rate (CFR) in Indonesia has increased in 2019-2021 and 2023-2024. Sidoarjo Regency is the district with the fourth highest CFR (1.9%) out of 38 regencies in East Java Province in 2023 under target of <1%. The larvae free rate 91.92% or under target (<95%). Methods: Descriptive study using a descriptive incident study design. Secondary data on dengue fever cases in Sidoarjo Regency for 2019-2024 consists of W2, K-DBD, DP-DBD, W1 reports, active surveillance report, KDRS. Results: Dengue fever cases in Sidoarjo Regency in 2019-2024 were mostly male (57%), aged 5-14 years (48%) who were school children, living in densely populated areas (Sidoarjo, Waru, Taman Districts). The increase in dengue fever cases mostly occurs in January-March each year, especially the impact of the El Nino phenomenon, dengue fever patients are treated at hospital health service facilities in Sidoarjo Regency (96%), Larval Free Rate <95%. Discussion: The dengue fever is influenced by the population's high mobility due to its strategic location supported by Juanda International Airport and Bungurasih Terminal, thereby increasing the risk of dengue virus transmission. Conclusion:Improving cross-sector collaboration all stakeholder, community health centers, regional and private hospitals, clinics and private doctors through memorandum of agreements for the prevention and control of dengue fever to be able to provide reporting dengue fever cases accurately and completely as a supporting document for accreditation to the health service.

Keywords: Dengue Fever, El Nino, Epidemiology

Abstract Reference: 20840
Mode of Presentation: Rapid Oral Presentation
Topic: Parasitology and Microbiology

Comparing sensitivity of saliva and oropharyngeal swabs for SARS-CoV-2 detection in acute infection

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Abstract Content

During the COVID-19 pandemic, saliva sampling emerged as a non-invasive alternative to nasopharyngeal (NPS) and oropharyngeal swabs (OPS) for detecting SARS-CoV-2. Although NPS is the gold standard, saliva sampling and OPS are preferred for ease of collection and patient comfort. This study aimed to compare the sensitivity of SARS-CoV-2 detection in saliva and OPS samples obtained simultaneously from individuals with acute infection. Viral RNA extraction was followed by SARS-CoV-2 real-time reverse transcription quantitative PCR (rt-qPCR) assay. ELISA was performed on saliva samples to detect and quantify SARS-CoV-2 specific salivary IgA (sIgA). The presence of SARS-CoV-2 specific sIgA, likely due to previous infection or vaccination, was used to assess its influence on viral load. Results indicated significantly higher viral loads in saliva compared to OPS samples (10.72 ± 4.30 vs. 4.66 ± 3.40, $P<0.001$) and lower Ct values (22.96 ± 6.55 vs. 29.37 ± 5.17, $P<0.001$). The positivity rate for saliva samples was 95.24% (n=40/42), with a 75.0% positive percent agreement between paired OPS samples. The mean difference in Ct values between saliva and OPS samples was 5.94. SARS-CoV-2 specific sIgA was detected in 81.0% (n=34/42) of cases, but no correlation was found between SARS-CoV-2 specific sIgA levels and Ct values. The lack of correlation suggests that the potential protective role of SARS-CoV-2 specific sIgA requires further validation. In conclusion, saliva sampling demonstrates higher sensitivity for SARS-CoV-2 diagnosis compared to OPS, potentially reducing false negatives and supporting better management of COVID-19 transmission.

Abstract Reference: 20848
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

25 years of rabies prophylaxis post-exposition in Cambodia (1998 - 2022)

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Abstract Content

Rabies remains a Cambodia’s public health challenge, prompting the opening of Rabies Prevention Centers (RPCs) in Phnom Penh (1995), Battambang (2018), and Kampong Cham (2019) to improve access and meet increasing demands for post-exposure prophylaxis (PEP). The study describes spatio-temporal evolution of PEP delivery (1998-2022) and identifies factors driving PEP completion. Patients’ socio-demographic characteristics, exposure type, animal characteristics, PEP timing and completion were collected through a standardized questionnaire. Statistical analyses included spacetime cluster analysis and logistic regression models for PEP completion. Overall, 607,129 patients sought PEP, with a strong increase over the years in all three RPCs. Average annual incidence of PEP displayed strong heterogeneity between provinces (3 to 468/100,000 inhabitants). 51% of patients were males and patients under 15yo were over-represented. 80% of exposures were caused by dogs and 19% by cats, with the proportion of the latter rising sharply after 2018. Based on WHO exposure categories, 60.5% were category III, 33.6% category II or III, 5.4% category II and 0.5% category I or undefined. For exposure categories II and III, overall completion was 88%. Completion increased from 76% in 1998 (one month 6-visits protocol) to 95% in 2019 (one week 3-visits protocol). PEP vaccination noncompletion was significantly higher in young adults, males, provoked attacks and increased with distance to RPCs. This study highlighted demographic and geographic disparities in access to rabies PEP and their role in protocol adherence. The increasing demand in newly opened RPCs suggests that demand for PEP exceeds the supply, some provinces remaining underserved.

Abstract Reference: 20850
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Public engagement for Wolbachia-based dengue control: the Singapore experience

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Abstract Content

Wolbachia technology is a novel vector control approach that can reduce mosquito populations and the associated dengue risk. In 2016, Singapore embarked on a multi-phased field study to assess the efficacy of *Wolbachia* technology in suppressing the *Aedes aegypti* mosquito population. The project involves the releases of male *Wolbachia*-carrying *Aedes aegypti (Wolbachia-Aedes)* mosquitoes into the study sites. Given the long-standing emphasis on the importance of keeping mosquito populations low, the unconventional strategy of releasing male *Wolbachia-Aedes* mosquitoes into the community may initially appear counterintuitive. Therefore, community engagement to educate the public on the project's objectives and goals is an integral component that cannot be overlooked. We developed a framework for engaging stakeholders including residents at the study sites and the general public, focusing on the key principles around which we have built our approach. The engagement process was designed to be inclusive, transparent, and collaborative, with a focus on garnering support, building trust and promoting understanding among the public. Notably, the project achieved high levels of awareness, trust, and acceptance across the population, underscoring the effectiveness of the public communication efforts. Furthermore, timely surveys were conducted to inform subsequent public communications and educational campaigns, enabling the targeted addressing of knowledge gaps among the population.

Abstract Reference: 20853
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Prevalence and genetic diversity of *Bartonella* spp. in wild small mammals from South Africa

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Abstract Content

Bartonella spp. are intracellular bacteria associated with several re-emerging human diseases. Small mammals play a significant role in the maintenance and spread of *Bartonella* spp. Despite the high small mammal biodiversity in South Africa, there is limited epidemiological information regarding *Bartonella* spp. in these mammals. The main aim of this study was to determine the prevalence and genetic diversity of *Bartonella* spp. from wild small mammals from fifteen localities in eight provinces of South Africa. Small mammals (n=183) were trapped in the Eastern Cape, Free State, Gauteng, Limpopo, Mpumalanga, Northern Cape, North West and Western Cape provinces of South Africa between 2010–2018. Heart, kidney, liver, lung and spleen were harvested for *Bartonella* DNA screening and prevalence was determined based on the PCR amplification of partial fragments of the 16S–23S rRNA intergenic spacer (ITS) region, *gltA* and *rpoB* genes. *Bartonella* DNA was detected in *Aethomys chrysophilus*, *Aethomys ineptus*, *Gerbillurus* spp., *Lemniscomys rosalia*, *Mastomys coucha*, *Micaelamys namaquensis*, *Rhabdomys pumilio* and *Thallomys paedulcus*. An overall prevalence of 16.9% (31/183, 95% CI: 12.2 – 23%) was observed. *Bartonella elizabethae*, *Bartonella grahamii* and *Bartonella tribocorum* were the zoonotic species identified, whilst the remaining sequences were aligned to uncultured *Bartonella* spp. with unknown zoonotic potential. Phylogenetic analyses confirmed five distinct *Bartonella* lineages (I-V), with lineage IV displaying strong *M. coucha* host specificity. Our results confirm that South African wild small mammals are natural reservoirs of a diverse assemblage of *Bartonella* spp., including some zoonotic species with high genetic diversity, although prevalence was relatively low.

Abstract Reference: 20857
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Towards developing a Lab-on-a-Chip device (Protein Array) for identifying the virulence-transmission prediction biomarkers of falciparum malaria based on comparative proteomics

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Abstract Content

Based on severity and fatality rate, *Plasmodium falciparum* is regarded as the deadliest species with high virulence. Due to lacuna in currently applied diagnostic and prognostic measures for falciparum malaria, need of the hour is to find reliable protein biomarkers that would effectively diagnose and predict the severity of the disease. Current study screened the comparative blood serum proteome profile from healthy community controls and non-severe and severe falciparum malaria patients of Indian population to identify the changes in serum proteins of patients with disease progression as compared to healthy persons. The in-silico analysis revealed that lipid metabolism particularly plasma lipoprotein assembly is mainly targeted by falciparum parasite to compromise the physiological health of an infected individual. Moreover, platelet-degranulation, acute phase response and complement cascade responses are also disturbed resulting in reduced immune response in falciparum infected malaria patients as compared to healthy controls. Fibrinogen factors (FGG, HP) and Apolipoproteins (APOA1/A2) were predicted to exacerbate the severity of complications and pathogenesis of severe falciparum malaria and can be regarded as potential biomarkers to understand the progression from non-severe to severe falciparum malaria. Complementing the existing technique of identification and classification of malarial disease severity, the current biomarkers would provide an additional insight into disease infection and progression. This is a novel study which aims to develop a Microfluidic "Lab-on a Chip device" (Protein array) for Fast and Sensitive Quantification of targeted serum proteins as Biomarkers, for timely and accurate diagnosis of malarial severity in patients infected with P. falciparum.

Abstract Reference: 20861
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Potency of lavender flower and mandarin orange peel essential oil to repel *Aedes* sp.

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Abstract Content

Mosquitoes could transmit many diseases which could be fatal or cause disabilities. To prevent mosquito borne diseases, repellent could be used. DEET is a standard repellent to be used until nowadays. Considering several study reports about the potentially negative effects about DEET application, it is wise to look for alternative way to repel the mosquitoes. In this seminar we would like to present the potency of lavender flower and mandarin orange peel essential oil against Aedes sp. The arm and cage method according to Fradin & Day to seek the duration of the repellent effect was conducted using these pure essential oils, soy bean oil, mixture of each essential oil with soybean oil in several ratios, and DEET as a positive control. It was analysed with ANOVA & HSD. It was concluded that all of these showed repellent effect, DEET was the most potent, mixture of the essential oil + soybean oil had longer duration than pure essential oil (p value < 0.05). The similar result was shown in a previous study against Culex sp, and soybean oil might protect the evaporation of these essential oils.

Keyword: lavender flower, orange peel, essential oil, Aedes sp. repellent

Abstract Reference: 20868
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Prevalence and clinical symptom comparison of COVID-19, influenza A, influenza B and DENV in Peninsular Malaysia

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Abstract Content

Dengue and influenza are globally concerning pathogens that cause feverish illnesses akin to COVID-19. Overlapping symptoms leading to potential diagnostic challenges and appropriate treatment delayed, thus urge in understanding the prevalence and symptoms of these infections. This study was carried out to determine the prevalence and compare clinical symptoms of COVID-19, Flu A, Flu B and DENV. Recruitment for this study took place between November 2022 and January 2024 in Kota Bharu, Klang, and Kelana Jaya, with a total of 1,046 participants enrolled. Oral swabs and serum samples were collected and analysed using RT-PCR assays to confirm pathogen's presence. Logistic regression was employed to calculate odds ratios (ORs) and 95% confidence intervals (CIs), comparing the association strength of clinical symptoms between COVID-19, Flu A, Flu B and DENV positive cases. The results revealed 61 patients were COVID-19, positive, accounting for a prevalence of 5.9%, 3.7% (n=39) of cases attributed to Flu A, 2.8% (n=29) to Flu B, and 2.6% (n=19) to DENV virus. Statistical analysis indicated DENV significantly associated with rashes, with higher OR (4.86) compared to COVID-19, Flu A, and Flu B infected individuals. Flu B specifically associated with runny nose (OR 2.89). Flu A was significantly associated with respiratory symptoms including wheezing (OR 6.06), sore throat (OR 2.48), sputum production (OR 2.18), loss of taste (OR 6.43), and loss of smell (OR 3.46). COVID-19 was linked with muscle and joint pain, specifically myalgia (OR 1.90) and arthralgia (OR 1.75). These findings may assist clinicians to enhance accurate diagnosis.

Abstract Reference: 20874
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Subsidization on pneumococcal vaccine uptake among older adults in Japan

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Abstract Content

Since 2014, the pneumococcal vaccine has been installed as a “routine vaccination (Class B disease)” by the Immunization Act for geriatrics in Japan. Eligibility is based on age and risk factors, with local government support. Municipality determine if individuals pay or receive the vaccine free, but uptake remains low. We collected data from an online survey (April 2022 to April 2023) targeting older adults. The survey included demographics, vaccine uptake rates, risk and time preferences, and cognitive reflection scores (CRT). Out-of-pocket expenses were calculated from subsidies collected from 1,726 cities in Japan through official websites and telephone inquiries with city offices. Descriptive statistics and Chi-squared tests were used to identify the associations. Pneumococcal vaccine uptake was 43.9% (428/975). Only 2.15% (21/975) received free, while most paid less than half. Tokyo residents reported lower payments than other prefectures. The subsidization did not significantly affect vaccine uptake (Chi2= 6.56, $p = 0.766$). Regarding time preference scores, the group with lower scores (L) had a higher uptake (46.39% (L) vs. 41.70%). For risk aversion, those with higher scores (H) showed slightly higher uptake (43.46% vs. 44.56% (H)). CRT identified people more likely to correctly answer questions correlated with higher vaccine uptake (47.11% vs. 43.9% (average)). Furthermore, lower risk aversion scores were associated with paying less out-of-pocket (Chi2= 79.64, $p < 0.05$). Pneumococcal vaccine subsidization varies in each prefecture, and behavioral factors may affect uptake among older adults in Japan—targeted strategies to improve future vaccination rates and public health outcomes.

Abstract Reference: 20887
Mode of Presentation: Rapid Oral Presentation
Topic: Entomology

Molecular detection of Rickettsia in on-host Laelapid mites (Acari: Mesostigmata) in Malaysia

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Abstract Content

Mites of the genus *Laelaps* (Mesostigmata: Laelapidae) are common ectoparasites of small animals and they have the potential to transmit certain disease agents. Although there have been some studies reporting on rickettsial detection in Laelapid mites, information on the circulation of *Rickettsia* between the animals and these mites remain very scarce. Therefore, there is a need to investigate the presence of rickettsial DNA in Laelapid mites and blood samples of their infested animal hosts. A total of 223 small animals were caught in 2022 from six locations in Sabah, in which, 1772 Laelapid mites were collected from 104 infested animal hosts. DNA extracted from these mites and animal blood were amplified using Nested PCR by targeting the outer membrane protein B (*ompB*) gene. From 71 pools of mite samples examined, 3 (4.2%) samples were detected with rickettsial DNA. However, only 1 (0.97%) animal blood was detected with rickettsial DNA. Sequence analyses of these 4 positive samples revealed the identity of *Rickettsia felis*, with 100% sequence similarity. To our knowledge, this is the first evidence of *R. felis* detection in Laelapid mites in Malaysia. It was also observed that the Laelapid mites infected with *R. felis* were not collected from the same animal host infected with *R. felis*. These mites could have been infected during previous feedings on another host. The presence of *Rickettsia* in hematophagous Laelapid mites may pose a potential health risk to humans, prompting the need for further investigation on the competence of Laelapid mites in rickettsial transmission.

Abstract Reference: 20891
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Demographic and clinical characteristics of COVID-19-related mortality among adults in Jakarta, Indonesia, during Delta and Omicron periods: a retrospective cohort study

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Abstract Content

Studies that comprehensively compare characteristics associated with COVID-19-related mortality between Delta and Omicron periods are limited. This study compared demographic and clinical characteristics associated with COVID-19-related mortality among the adult population between the Delta and Omicron periods in Indonesia. This retrospective cohort study analysed all adults >18 years old with PCR-confirmed COVID-19 recorded by the Jakarta Health Office, who either deceased or recovered between September 1, 2021, and July 24, 2023. We extracted demographic and clinical data, including symptoms and pre-existing comorbidities. Multivariable logistic regression models were used to assess factors associated with mortality during the Delta and Omicron periods. There were 23,167 (45.5%) and 27,790 (54.5%) PCR-confirmed COVID-19 cases recorded during the Delta and Omicron periods, respectively. The overall mortality rate was lower for Delta compared to Omicron periods (0.6% vs. 0.9%). Older age, having shortness of breath and malignancy were associated with an increased risk of death during both periods. Being males (aOR 1.41; 95% CI: 1.08 - 1.83), having pneumonia (aOR 4.29; 95%CI: 1.19 -15.40), hypertension (aOR 1.51; 95% CI: 1.08 - 2.10), diabetes (aOR 3.78; 95% CI: 1.89 - 7.52), and tuberculosis (aOR 5.00; 95% CI: 2.15 - 11.60) were associated with increased risk of death during Omicron, but not during Delta period. Our study found that COVID-19-related mortality occurred across periods, especially among older and comorbid individuals. This was especially true for people infected during the Omicron period, suggesting the extent of vulnerability of this group even after the primary dose vaccination reached 100% coverage.

Abstract Reference: 20895
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Cryptic absence and genetic variation of *Plasmodium falciparum* histidine-rich protein 2 and 3 in Papuan field isolates and their impact on malaria rapid diagnostic tests: A long-awaited update from Indonesia

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Abstract Content

The rising prevalence of histidine-rich protein 2 (*pfhrp2*) gene deletion poses a threat to false-negative results in *pfhrp2*-based rapid diagnostic tests (RDTs). Many countries have reported *pfhrp2* gene deletion (*pfhrp2*-) incidence, yet this information is scarce in Indonesia. Thus, we examined the prevalence of *pfhrp2* and its paralogue histidine-rich protein 3 (*pfhrp3*) gene deletion (*pfhrp3*-) from a study assessing three *pfhrp2*-RDTs between December 2022 and April 2023 in Timika, Papua. Of 2,157 symptomatic-enrolled patients, 566 *P.falciparum* mono-infection cases confirmed by microscopy and real-time PCR were included for *pfhrp2/3* exon 2 genotyping. Samples were defined as *pfhrp2*-RDT positive if all RDTs tested positive. We detected nine samples (1.59%) with *pfhrp2-/pfhrp3*-, eight having positive *pfhrp2*-RDTs results. Of three *pfhrp2*-/*pfhrp3+* samples (0.53%), one was *pfhrp2*-RDT positive. In contrast, 201 samples (35.51%) had *pfhrp3*-, five of which were *pfhrp2*+ but *pfhrp2*-RDT negative; however, four exhibited low parasitemia. To further investigate the genetic variation of *pfhrp2/3,* five *pfhrp2*-RDT negative samples with *pfhrp2+/pfhrp3+* were sequenced and aligned alongside two *pfhrp2*+ and *pfhrp2*-RDTs positive samples. We found more repeat-type variations in *pfhrp2* compared to *pfhrp3*. Type 2 (AHHAHHAAD) and 7 (AHHAAD) repeats were detected in *pfhrp2*, while only type 7 was found in *pfhrp3*. Seven unique repeat types in *pfhrp2* and one unique repeat type in *pfhrp3* amino acid sequences were characterized in single or multiple copies per sample. These results demonstrated the low prevalence of *pfhrp2-/pfhrp3+* (0.53%) suggesting *pfhrp2*-based RDT remains suitable for malaria diagnosis in Timika according to WHO.

Abstract Reference: 20896
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Demographic & clinical characteristics of COVID-19-associated hospitalization in children during Pre-Delta, Delta, and Omicron waves in Jakarta, Indonesia: A retrospective cohort study

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Abstract Content

Data on risk factors of COVID-19-associated hospitalization in children during pre-Delta, Delta, and Omicron waves from Southeast Asia are limited. This study investigated demographic and clinical characteristics associated with COVID-19 hospitalization in children in Jakarta, from May 5, 2020 until May 26, 2023. This retrospective cohort study included all children ≤18 years old diagnosed with COVID-19 in Jakarta, Indonesia. We extracted demographic and clinical data, including outcomes (hospitalization or self-isolation) from Jakarta Health Office surveillance records. We used logistic regression to assess risk factors associated with hospitalization. Of 37,525 cases, 2184 (5.8%) were hospitalized and 35,341 (99.5%) went to self-isolation. Age-specific hospitalization rate was 11% (106/954) for children <1 years old; 7% (360/5030) for 1-4 years; 6% (437/7842) for 5-9 years; and 5% (1281/23,699) for 10-18 years. The overall in-hospital mortality rate was 8.5% (16/2184), with the highest rate in children aged 1-4 years (5/360, 1.4%). Increased risk of hospitalization was significantly associated with younger age (aOR 2.51, 95%CI 1.94-3.24 for <1 year, aOR 1.44, 95%CI 1.23-1.68 for 1-4 years, aOR 1.21, 95%CI 1.05-1.40 for 5-9 years, compared to 10-18 years); being infected during pre-Delta (aOR 2.95, 95%CI 2.50-3.47) and Delta (aOR 1.44, 95%CI 1.26-1.64), compared to Omicron wave, and having multiple symptoms (aOR 1.22, 95% CI 1.13-1.32). Infections during Omicron wave resulted in lower hospitalization risk than during pre-Delta and Delta. However, the youngest children population suffered the most across the waves, underscoring the urgent need for targeted interventions to reduce hospitalization rates among younger children.

Abstract Reference: 20899
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

How much community engagement in health services research on three neglected tropical diseases occurs in LMICs?

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Abstract Content

This study aimed to summarize the evidence on the extent, nature, and quality of community engagement in health services research on three neglected tropical diseases: lymphatic filariasis (LF), dengue and soil-transmitted helminths (STH) in low-and-middle-income countries of Indo-Pacific Region. We performed a contextualization of the three systematic reviews on the three NTDs. Sixteen, 13, and 11 individual studies in a systematic review of community engagement in health services research on eliminating LF, dengue control, and STH control respectively were included. Various communities were included such as indigenous communities, school children/ parents, school teachers/schools, village heads. Overall, community engagement of in health services research was limited, with the majority (26/30) demonstrating a 'moderate level' of engagement mainly through 'collaboration' in 'developing methodology' " data collection" and in 'dissemination of findings". The five Consolidated Framework for Implementation Research domains of "intervention characteristics", "inner setting", "outer setting," individual characteristics", and "programme implementations" were used to identify/describe barriers/facilitators. The common barriers to the community engagement were lack of involvement of participating bodies and technology-related issues. The studies reviewed did not demonstrate/measure full community engagement. Future health services research on dengue, LF and STH control and elimination should be co-planned, co-designed methodologically, and fully aligned with community engagement principles at all stages of the research to facilitate sustainable accessible and acceptable services in line with universal health coverage.

Abstract Reference: 20903
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Melioidosis cases and its associated mortality risk factors in Sabah 2016-2020

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Abstract Content

Melioidosis is an opportunistic disease that affects humans and animals caused by *Burkholderia pseudomallei*. The disease is presented with various clinical vignettes and associated with a high mortality rate. The study aims to analyse the Melioidosis cases and risk factors associated with the mortality cases in Sabah from 2016 to 2020. The cases were extracted from Sabah Melioidosis cases registry. Data analysis involved conducting multiple logistic regression. A 95% confidence interval and a significance level of $p < 0.05$ were used to identify significant risk factors for mortality cases. A total of 646 confirmed Melioidosis cases were reported in Sabah from 2016 to 2020. The incidence varied annually, with the highest number of cases recorded in 2019 (175 cases). This study found that the case fatality rate (CFR) for melioidosis patients is 32.4% All clinically significant independent variables were included in the analysis for multiple logistic regression. In the analysis we found immunocompromised patients have 1.89 times increased odds (CI: 1.01-8.87, p-value = 0.004), as well as Gout patients who have 3.00 times increased odds (CI: 1.01-8.87, p-value =0.047). Patients who developed bacteraemia have the highest odds of dying of the disease, which is 20.77 higher than patients who are not bacteraemia. Melioidosis is a significant public health challenge in Sabah, with high morbidity and mortality rates. In conclusion, this study can validate the importance and understanding of melioidosis in Sabah state with its unique socio-demographical factors.

Abstract Reference: 20916
Mode of Presentation: Rapid Oral Presentation
Topic: One Health – Epidemiology

Epidemiology of *Trypanosoma cruzi* infection in cats in Brazil

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Abstract Content

Chagas disease is a Latin American zoonosis caused by *Trypanosoma cruzi* (*T. cruzi*). The objective of this research was to verify the prevalence of *T. cruzi* infection, the risk factors and distribution of the disease in cats in the municipality of Mãe d'Água, Paraíba, Brazil. The climate of the region is semi-arid with vegetation of the Caatinga type. Between 2021 and 2022, 89 blood samples were collected from cats and the parasite was identified by Nested-PCR. The geographic coordinates of the homes of infected cats were inserted into the municipality's digital cartographic database and maps were created using the Geographic Information Systems (GIS) and QGIS. Clusters and relative risk were identified with the SaTScan program. The prevalence of infected cats in urban areas was 59.55%. The risk factor identified by multiple logistic regression was the age of the animals, with emphasis on cats aged six to 24 months (OR= 0.32; CI= 95%) and those over six years old (OR= 0.67; CI= 95%) The risk factor identified by multiple logistic regression was the age of the animals between six and 24 months (OR= 0.32; CI= 95%) and over six years (OR= 0.67; CI= 95%). According to the Kernel density estimation, the central region of the municipality presented a relative risk of 2.09. It is likely that the high prevalence in cats in the municipality is due to the cat's eating habits and demonstrates the importance of this species as a sentinel host.

Abstract Reference: 20932
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Molecular screening of protozoa (Apicomplexa: Kineplastida, Piroplasmida) in ticks collected from selected ruminant farms in Peninsular Malaysia

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Abstract Content

Ticks are obligate hematophagous arachnids that feed on both humans and animals. While numerous bacterial studies have been conducted on ixodid ticks in Malaysia, there is limited knowledge regarding the detection of protozoa in these ectoparasites, particularly those feeding on farm ruminants. In this study, 1,241 ticks belonging to four species (*Rhipicephalus microplus*, *R. haemaphysaloides*, *Haemaphysalis bispinosa*, and *H. wellingtoni*) were collected from 674 farm ruminants in Peninsular Malaysia. The ticks were pooled and subjected to DNA extraction, followed by protozoal screening using Polymerase Chain Reaction (PCR). Amplification targeted the 18S rRNA gene fragment, and the resulting amplicons were sequenced and identified using BLAST. Out of 130 tick pools, 15 were positive for *Babesia* (11.54%), 10 for *Theileria* (7.69%), and nine for *Trypanosoma* (6.92%). No *Hepatozoon* protozoa were detected. All positive pools consisted solely of *R. microplus* ticks, with no protozoa detected from the other three tick species. BLAST analyses revealed that the *Babesia* sequences were identical to *Babesia bigemina*, while the *Theileria* sequences closely resembled *Theileria orientalis* and *Theileria sinensis*. The *Trypanosoma* strains showed close similarities to *Trypanosoma rhipicephalis* and other tick-associated trypanosomes. This paper documents the first nationwide screening of *Babesia*, *Hepatozoon*, and *Theileria* from cattle ticks and reports the first occurrence of tick-associated *Trypanosoma* in Malaysia.

Abstract Reference: 20933
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Detection of acaricide resistance against deltamethrin, cypermethrin and coumaphos in larval field tick isolates of *Hyalomma anatolicum* from Marathwada region of Maharashtra state, India

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Abstract Content

The present study investigated the status of resistance against deltamethrin, cypermethrin and coumaphos in larval population of *Hyalomma anatolicum* and confers the role of larval esterase's and glutathione-s-transferase (GST) metabolic enzymes in resistance. The larval immersion (LIT) and larval packet tests (LPT) were used for resistance characterisation. Among the eight isolates, Parbhani and Dharashiv isolates showed resistance to deltamethrin and cypermethrin acaricides. The estimated LC$_{50}$ values were 42.98 and 275.42 ppm using LIT and LPT, respectively against deltamethrin for Parbhani isolate. Against cypermethrin, the LC$_{50}$ values were found as 271.15 and 475.39 ppm using LIT and LPT, respectively. The LC$_{50}$ values against deltamethrin in Dharashiv isolate were determined as 51.78 and 56.72 ppm, respectively, using LIT. The Dharashiv isolate exhibited a significant level of resistance to cypermethrin. A 100% mortality of larvae was noted when exposed to a concentration of 49 ppm of coumaphos, implying that the compound has a potent effect on larval mortality, further reinforcing the efficacy and potential of coumaphos as an acaricide. The quantitative assessment of overall esterase activity measured by the metabolite naphthol, demonstrated a significant variation ranging from 124.306 to 201.419 nanomolar/min. μg of protein for α-esterase activity, and 59.991 to 102.083 nanomolar/min. μg of protein for β-esterase activity, across different field isolates of *H. anatolicum*. Whereas, GST enzyme activity levels ranged from 70.248 to 90.151 nanomolar/min. μg of protein in different field isolates. The elevated level of larval esterase's and GST was observed in resistant larval isolates than susceptible population of *H. anatolicum*.

Abstract Reference: 20941
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

Control of the invasive agricultural pest *Pomacea canaliculata* with a novel molluscicide: Efficacy and safety to nontarget species

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Abstract Content

The golden apple snail Pomacea canaliculata is an invasive pest that causes extensive damage to agricultural production. P. canaliculata is also an intermediate host of Angiostrongylus cantonensis, which causes human eosinophilic meningitis. In this study, the molluscicidal activity and safety profile of a novel molluscicide PBQ [1-(4-chlorophenyl)-3-(pyridin-3-yl)urea] were evaluated. PBQ exhibited strong molluscicidal potency against adult and juvenile snails (LC50 values of 0.39 and 0.07 mg/L, respectively). In field trials, PBQ killed 99.42% of the snails at 0.25 g a.i./m2 . An acute toxicity test in rats demonstrated that PBQ is a generally nonhazardous chemical. PBQ is also generally safe for nontarget organisms including Brachydanio rerio, Daphnia magna, and Apis mellifera L. Transcriptomics analysis revealed that PBQ had a significant impact on the carbohydrate and lipid metabolism pathways, which provided insights into its molluscicidal mechanism. These results suggest that PBQ could be developed as an effective and safe molluscicide for P. canaliculata control.

Abstract Reference: 20958
Mode of Presentation: Rapid Oral Presentation
Topic: One Health

The clinimetric profile of 11 generic quality indicators for appropriate antibiotic use in hospitalized patients in Indonesia

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Abstract Content

One of the efforts in antibiotic stewardship for limiting antibiotic resistance is the assessment of the quality of antibiotic use. To date, the quality and appropriateness of antibiotic use in Indonesia, a low-middle-income non-European country, have not yet been assessed using proven quality indicators (QIs). The aim of this study is to assess the clinimetric profile of 11 generic QIs based on van den Bosch et. al. in admitted adult patients receiving empiric antibiotics in Indonesian hospitals. This is an observational study with a cross-sectional design conducted at two government referral hospitals in Jakarta, Indonesia, from August 1, 2022, to February 2, 2023. In 500 inpatients from 2 hospitals, all QIs demonstrated good measurability with less than 10% of missing data. Ten QIs showed good applicability of >10%. Four QIs show good performance, while six QIs have significant potential for improvement (two blood cultures are obtained before empiric antibiotic treatment; culture sample is obtained from location suspected of infection; antibiotic is switched from intravenous to oral when clinically possible; antibiotics are stopped when there is no evidence of infection; a guideline is available and renewed every three years; and a guideline is adjusted to the local resistance pattern) making them priority targets for interventions to enhance the quality of antibiotic use in Indonesia. Of the 11 generic QIs, 10 demonstrated good reliability and applicability at two hospitals in Indonesia. Future intervention studies can utilize these generic QIs to measure improvement in the appropriateness of antibiotic use.

Abstract Reference: 20962
Mode of Presentation: Rapid Oral Presentation
Topic: One Health - Microbiology

Dengue virus serotypes among outpatients in public health centers in Samarinda city, Kalimantan

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Abstract Content

Dengue remain public health concern in endemic countries like Indonesia. Data showed that in the last two years there were significant increased numbers of dengue cases in many areas including Samarinda. There are four serotypes of dengue virus (DENV) circulating in this country. Identification of dengue virus serotypes is necessary to assess the potential epidemiological factors related to the virus of in a particular period. The objective of this research is to determine the distribution and frequency of dengue virus serotypes, and its clinical profiles. This is an observational study with a cross-sectional design, conducted at outpatient clinic of public health centers in Samarinda city from October 2023 to February 2024. Subjects age 1 year and older were recruited if they presented to public health centers with fever < 5 days and had been assessed as probable dengue. Dengue infection was confirmed by NS positive and or IgM positive. There were 155 subjects recruited for this study. Male contribute to 57.4% of total. Children are accounted for 76.1%. Most of subject live in urban areas. The presence of four serotypes: DENV-1 (9.1%), DENV-2 (31.8%), DENV-3 (36.4%), DENV-4 (19.3%), DENV-1&-4 (1.1%), and DENV-2&-4 (2.3%). There were no differences in the characteristics of DENV serotype infections based on age, gender, leukocyte count, platelet count, and hematocrit levels. Four serotypes of DENV were circulating in Samarinda city with DENV3 was predominant.

POSTER PRESENTATION

POSTER PRESENTATION

Abstract Reference: 20026
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

An alien intermediate snail host in Malawi - *Orientogalba viridis* (Quoy & Gaimard, 1832) - A new concern for schistosomiasis transmission in Africa?

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Abstract Content

The freshwater amphibious snail *Orientogalba viridis* (Quoy & Gaimard, 1832) commonly occurs in eastern Asia, on certain Pacific islands and more importantly has recently dispersed into Europe. Since this snail is now considered an invasive species, its distribution is of growing parasitological interest as an alien intermediate hosts for various trematodes, particularly liver fluke. As part of ongoing surveillance for snail-borne diseases in Malawi, a population of *O. viridis* was first observed May 2023, alongside the alarming presence of a human schistosome cercaria. This snail population later underwent detailed morphological characterisation with both snail and parasite identities confirmed upon DNA barcoding. This seminal observation triggered more extensive local snail surveys, finding 3 further separated rice paddies with numerous snails, where field-caught snails (n=465) were later screened for infections with schistosomiasis and fascioliasis. A selection was later used for repeated experimental challenges with miracidia from *Schistosoma haematobium* and *Schistosoma mattheei*. Although no field-caught (and experimentally exposed) snails were seen to shed schistosome cercariae, molecular xenomonitoring for schistosomiasis provided tangible DNA evidence of putative transmission potential, whilst that for fascioliasis did not. Our first report of *O. viridis* here in Malawi, and more broadly in Africa, flags the need for increased vigilance for this invasive species alongside local clarification(s) of its transmission potential for trematodiases of either medical and/or veterinary importance. A transcontinental dispersion such as this, from Asia to Africa, demonstrates the unexpected transmission biology of alien versus local snail-parasite relationships.

Abstract Reference: 20044
Mode of Presentation: Poster Presentation
Topic: Session 1 - Malaria

Low prevalence of antimalarial- resistance in 2014-15: Effect of combining primaquine with first-line therapy in India

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Abstract Content

Effective surveillance and containment of antimalarial drug resistance are critical for countries working towards malaria elimination. Evaluating resistance patterns before and after changes in treatment policies is essential for monitoring the evolution of drug resistance. We collected 939 *P. falciparum*-positive blood samples from ten sites in India between 2014 and 2015, categorized into four geographic clusters. Sequencing of PCR-amplified products was performed to identify point mutations in drug resistance-associated genes (*Pfdhfr*, *Pfdhps*, *Pfmdr1*, and *Pfk13*). Northeast India, bordering Myanmar, exhibited the presence of triple Pfdhfr mutants, contrasting with the dominance of wild types in central India. Pfdhps wildtypes were prevalent across all regions, with no double mutants identified. Pfmdr1 wildtype predominated in all clusters except Northwest India, where nonsynonymous double mutations were found. Pfk13 mutations were exclusively synonymous, occurring at low frequency in Central India. Linkage disequilibrium patterns and principal component analysis revealed low pressure for drug resistance and heterogeneity among the geographic clusters. The highest resistance levels were identified in Northeast India, particularly near the Myanmar border, aligning with the region's documented history of drug resistance. There is potential for it to spread to other parts of India. The widespread use of primaquine, serving as a gametocidal and schizonticidal drug, likely contributed to maintaining low drug resistance levels and preventing strong selection for resistance.

Abstract Reference: 20048
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Elucidating the immunogenicity and antigenicity of hookworm antigen, Glutathione-S-Transferase-1 (GST-1) as a vaccine candidate

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Abstract Content

The neglected tropical diseases (NTDs) comprise persistent parasitic and bacterial infections, like hookworm infections and schistosomiasis, prevalent in low- and middle-income countries (LMICs) affected by poverty. Although NTDs generally exhibit a low mortality rate compared to prominent severe and emerging diseases, they significantly impair susceptible populations, especially children and pregnant women. Despite early successes in mass drug administration (MDA) and NTDs control strategies, achieving widespread eradication remains improbable due to factors like cost and drug effectiveness in controlling reinfections. Vaccines offer additional or substitute controls by enhancing the host’s immune response against NTDs, either independently or in combination with specific drugs. Human hookworm infection, among the highest-burden NTDs caused by parasitic helminths (i.e. *Necator americanus*, *Ancylostoma duodenale*, and *Ancylostoma ceylanicum*), has gained gradual attention since the 21st century. Numerous studies have been conducted to investigate hookworm antigens as vaccine candidates. Glutathione-S-transferase 1 (GST-1) is one of the antigens produced by hookworms, vital for the blood-feeding and survival of the parasite. Studies have demonstrated that *Na*-GST-1 is a potential vaccine candidate, as vaccination with *Na*-GST-1 can stimulate an immune response. In this study, the *Na*-GST-1 sequence has been evaluated for its immunogenicity and antigenicity using bioinformatics tools. Five peptides from *Na*-GST-1 have been identified with varying immunogenicity and antigenicity scores. Each peptide elicits different immunogenicity and antigenicity scores, indicating peptides with high immunogenicity scores, and thus probable antigens, may be the major regions that induce an immune response in the host. Therefore, these peptides represent potential vaccine candidates for hookworm infection.

Abstract Reference: 20050
Mode of Presentation: Poster Presentation
Topic: Session 1 - Malaria

Evaluating the role of host microRNAs in modulating *Plasmodium falciparum* severe malaria

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Abstract Content

Severe *Plasmodium falciparum* malaria (SM) is a significant public health problem, and its high mortality remains prevalent in malaria-endemic countries despite the availability of effective antimalarial treatment. Early detection and case management are critical for a positive outcome in SM patients, but both are challenging, especially in its early phases. Thus, there is an urgent need to understand the pathogenesis of SM to develop novel interventions and diagnostic tools against life-threatening malaria. MicroRNAs (miRNAs) have been shown to be rapidly released from tissues into the circulation during the development of various pathologies. In this study, we are evaluating the potential of miR-21, miR-146a, miR-150, miR-181, and miR-187 as biomarkers of malaria severity in an Indian cohort of patients with strictly neurological cerebral malaria (CM, n=43), severe non-cerebral malaria (SNCM, n=50), uncomplicated malaria (UM, n=70), Asymptomatic malaria (AM, n=79), and non-malarial febrile illnesses (n=70). Reverse transcriptase quantitative PCRs (RT-qPCRs) are currently being performed using the TaqMan Advanced miRNA assays to determine the expression levels of target miRNAs and endogenous controls (hsa-miR-30d-5p and hsa-miR-191-5p). The results of this work have the potential to contribute to the development of diagnostic/prognostic tests based on miRNAs and their interacting gene targets, which could be useful in identifying patients at risk of developing life-threatening severe malaria.

Abstract Reference: 20052
Mode of Presentation: Poster Presentation
Topic: Session 1 - Entomology

The looming challenge of insecticide resistance: A systematic review of trends in DDT, deltamethrin and malathion efficacy against major malaria vectors in India from 2000-21

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Abstract Content

Vectoral resistance to common insecticides in major malaria vectors remains a significant concern and persistent threat in malaria control intervention in India. Our study aims to comprehensively identify and highlight the past and current trend in resistance pattern across various states and four major malaria vectors namely-*Anopheles culicifacies* , *Anopheles stephensi*, *Anopheles fluviatialis* and *Anopheles minimus*, from secondary literature. We compiled the data obtained from 54 studies, over 2000 data points spread across 27 different states in India reporting resistance status against a particular insecticide. Meta-analysis was conducted and results were represented in the form of box plots using R software. Q-GIS was used to map the pattern of resistance India from 2000 to 2021. Resistance to DDT was found to be widespread in the north, central, southern and western parts of India. In contrast north-eastern states shows susceptibility with some districts showing possible resistance to DDT in near future. Deltamethrin resistance is not as widespread as DDT but shows alarming resistance level in the central malarious states of Chhattisgarh and Madhya Pradesh. Malathion resistance was reported mostly across central, eastern and western India while north-eastern states show maximum susceptibility. Increasing resistance was observed across 4 major malaria vectors in the eastern states of Odisha, central states of Chhattisgarh and Madhya Pradesh. Overall our study identifies the hotspots of resistance across vector species and states thus giving a comprehensive map of the perpetual threat of insecticide resistance trend and need to monitor vector control intervention strategy in India.

Abstract Reference: 20058
Mode of Presentation: Poster Presentation
Topic: Session 1 - Malaria

Prevalence of *Plasmodium vivax* subtypes in Southwestern India

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Abstract Content

Goa state is endemic for both major *Plasmodium* species that infect humans: *Plasmodium vivax* and *Plasmodium falciparum*. Within *P. vivax*, genetic diversity is observed, with the presence of *VK210* and *VK247* subtypes. The present study aimed to investigate the prevalence of *P. vivax* subtypes circulating in Goa state. *P. vivax* infected blood samples were collected during 2016 to 2023 from Goa Medical College. The gene encoding *P. vivax* circumsporozoite surface protein (*Pvcsp*) was analyzed using PCR-RFLP and later Sequenced. Further, the patient gametocytaemia and parasitaemia were compared and Genetic diversity was determined using MEGA11 software. PCR-RFLP analysis of 110 *P. vivax* samples revealed that 93.6% were *VK210*, 3.6% were *VK247* and 2.7% exhibited mixed infections of *VK210* and *VK247*. Among *VK210*-infected patients, parasitaemia levels ranged from 0.039% to 1.7%, while *VK247*-infected patients showed parasitaemia levels between 0.545% to 1.346%. The study also noted fluctuations in VK210 case numbers, with a peak observed during the monsoon season. Furthermore, parasite metrics displayed seasonal variation, with elevated average parasitemia noted in March, April, and August, along with higher average gametocytemia levels in May and June. Several polymorphic characteristics of the *VK210* variant were observed. The predominant *P. vivax* subtype circulating in Goa is *VK210*. The Genetic diversity and seasonal dynamics of *P. vivax VK210* highlight the importance of targeted intervention strategies and surveillance efforts during the high transmission period.

Abstract Reference: 20063
Mode of Presentation: Poster Presentation
Topic: Session 1 - Bacteriology

Understanding the role of fliR gene in bacterial nanotube dynamics in *Escherichia coli* K12 sub strain CF1648 and observation of cell motility.

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Abstract Content

The study explores the adaptive mechanisms of pathogenic bacteria, highlighting the significance of previously undefined and overlooked bacterial nanotubes for bacterial survival and both intra and interspecific communication. Two coculturing isolates with distinct antibiotic resistance genes were shown to transfer resistance through nanotubes, forming a colony that had transiently acquired nonhereditary resistance to both drugs. In commensal non-pathogenic substrain *of E. coli* K-12, known as CF1648, there is a Type III Secretion Systems (T3SS) with conserved cores and >25 different proteins help with flagella formation. The ground breaking study by Bhattacharya et al. (2019) intriguingly demonstrates the dual functioning of a CORE complex, which is the export apparatus of flagella, in the creation of nanotubes and expansion of flagella in *Bacillus subtilis (Bs)*. Nonpolar deletion of five crucial CORE genes such as *fliP*, *fliQ*, *fliR*, *flhB*, *flhA*, and *fliO*, resulted in a nanotube deficient *Bs* mutant (ΔCORE), impacting in intercellular molecular trafficking and decrease cell density. Specifically, a *fliR* mutant displayed truncated bristle-like projections, suggesting disrupted nanotube elongation. Consequently, this study targets the *fliR* gene deletion to elucidate its role in nanotube formation, employing λ-Red recombination for allele replacement and Gibson assembly for constructing scarless deletion fragments. Overall, the research illuminates the intricate roles of the CORE complex and *fliR* gene in bacterial nanotube dynamics, providing insights into bacterial adaptation and communication mechanisms.

Abstract Reference: 20129
Mode of Presentation: Poster Presentation
Topic: Session 1 - Entomology

Factors related to compliance in implementing routine larval inspection (Pjr) programe by jumantik in Pudakpayung Sub District, Semarang City

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Abstract Content

The dengue hemorraghic fever (DHF) case in Pudakpayung Sub-District increased by more than threefold in 2022 with an IR of 61.45%. The participation of PJR programe to prevent DHF in Pudakpayung Sub-District was among the lowest three in 2022. This study aims to analyze the factors related to the compliance of Routine Larval Inspection (PJR) implementation by Jumantik in Pudakpayung Sub-District, Semarang City. The research employed analytical research with a cross-sectional study design. The population comprised all Jumantik RT with a sample size of 115 determined using simple random sampling technique. Data analysis utilized frequency distribution and Chi-square test. The results showed that the majority of respondents had a high level of education (74.8%), were unemployed (73%), had a long tenure (58.3%), had never received awards (88.7%), had no family history of dengue infection (78.3%), had never received training (54.8%), had attended health education (79.1%), had good knowledge (66.1%), supportive attitudes (60.9%), and compliance with PJR (73%). Factors showing associations were employment status (p=0.050), history of dengue infection (p=0.008), training history (p=0.020), knowledge (0.001), and attitude (p=0.006). Factors not associated were education level (p=1.000), tenure (p=1.000), history of awards (p=0.181), and history of health education (p=0.594). Thus, dissemination of information and cultivation of supportive attitudes toward DHF and PJR programe are needed both directly and through media channels

Abstract Reference: 20132
Mode of Presentation: Poster Presentation
Topic: Session 1 - Entomology

Mosquito vector studies in some selected regions of Bangladesh: A systemic microscopic morphological identification at 640x magnification

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Abstract Content

Mosquitoes are an increasing public health threat and spread deadly diseases (dengue, chikungunya, Japanese encephalitis, yellow fever, malaria, filariasis). Every year Bangladesh faces severe dengue outbreak situation and becomes deadly to places where they have never been found before. Mosquito control measures are hindered due to lacking of basic information on mosquito population available in Bangladesh. Present study deals with key identifying features of *Culex* and *Aedes* spp. Microscopic clear photographs (at 640x) of the key morphological elements were presented for the first time in Bangladeshi mosquito samples. Mosquitoes were collected from Savar, Satkhira, Darsana, Narshingdi, Gurudaspur upazila, Bogura and Old Dhaka regions of Bangladesh from indoor and outdoor habitats. *Cu. quinquefasciatus* showed swift jerking movement and fascinated to stay mostly in surface water while *Aedes spp.* comparatively slow and followed snake-like movement. *Cu. quinquefasciatus*, *Ae. albopictus* and *Ae. aegypti* were different in antenna, head size, thoracic hooks, comb scales, pecten and saddle. *Cu. quinquefasciatus* had no dorso-lateral thoracic hook at base of its bristles, comparatively small hook found in *Ae. albopictus* and *Ae. aegypti* had strong black hooks. *Cu. quinquefasciatus* contained a patch of comb scales, *Ae. albopictus* had a single line of thorn like comb scale while *Ae. aegypti* retained a line of distinct denticles comb scales at the 8th abdominal segment. Length of siphon and pecten are different in these species. Results obtained from this study would help for the exact identification of mosquitoes and facilitates the accuracy of mosquito control activities, simultaneously to prevent mosquito-borne diseases.

Abstract Reference: 20137
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

A murine malaria parasite suppressed collagen-induced arthritis via IL-10-independent immunosuppressive mechanism

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Abstract Content

Collagen-induced arthritis (CIA) is a type of Th17-dependent arthritis and serves as an animal model of human rheumatoid arthritis. Previously, we reported that the murine malaria parasite *Plasmodium yoelii* 17X (Py) suppressed CIA and increased IL-10 production by Tr1 cells. Therefore, the requirement of IL-10 in the suppression of CIA by Py was investigated. IL-10KO DBA/1J mice were immunized with bovine type II collagen (CII) and 1 week later infected with Py-infected erythrocytes. Three weeks after immunization, serum, spleens, and paws were harvested. Splenocytes were cultured under anti-CD3 antibody stimulation for 48 h, and culture supernatants were collected. Various cytokines in the culture supernatant and serum anti-CII IgG were analyzed by ELISA. In the non-infected group, CIA developed from 2 weeks after immunization and the arthritis score peaked at 4-5 weeks. In contrast, the Py-infected group did not develop CIA until after 3 weeks of immunization, and the arthritis score increased after 4 weeks of immunization when the Py parasitemia disappeared and became comparable to the non-infected group after 5 weeks of immunization. In splenocyte cultures, significant suppression of both pro-arthritic IL-17, TNF-α, and anti-arthritic IFN-γ, IL-4 was observed in the Py-infected group. No difference in anti-CII IgG was observed between the Py-infected and non-infected groups. Py infection suppressed the development of CIA in IL-10KO mice during the parasitemia, suggesting that Py may have an IL-10-independent immunosuppressive mechanism.

Abstract Reference: 20152
Mode of Presentation: Poster Presentation
Topic: Session 1 - Virology

The influence of communicable diseases before, during, and post-COVID-19 in Taiwan from 2017 to 2023: A descriptive analysis

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Abstract Content

The COVID-19 pandemic persisted for over three years, and by 2023, the world had transitioned into the post-COVID-19 era. During this crucial period, the impact of the COVID-19 pandemic on other communicable diseases in Taiwan was assessed. The data of this study was collected from the Taiwan Centers for Disease Control (CDC) Statistics of Communicable Diseases and Surveillance System open database. The study period was divided into three groups: before COVID-19 (January 2017 to December 2019), after COVID-19 (January 2020 to December 2022), and post COVID-19 (January 2023 to December 2023). The Mann-Kendall test examined the p-value for the trend of communicable diseases over the seven-years span. The percentage different in communicable diseases with various transmission pathways was calculated, and the p-value was tested for two proportions. A total of 239,072 cases of communicable diseases (71 communicable diseases), including 3,560 imported cases, occurred over the seven-year period. Notably, sexually transmitted and blood-borne diseases showed a continue increase in 2020 (4.37%), 2021 (7.89%), 2022 (11.45%), and 2023 (4.68%), compared to the before COVID-19 per years. Conversely, airborne or droplet diseases, food and water-borne diseases, contact diseases, and vector-borne diseases decreased from 2019 to 2023. Among the imported cases of communicable diseases, the majority were attributed to dengue fever, amoebiasis, shigellosis, acute hepatitis A, and chikungunya fever. In conclusion, the dynamic of communicable diseases after and post-COVID-19 pandemic with a significantly increase in sexually transmitted, constrasting with a decline in other transmission pathways, emphasizing the necessary of the public health interventions.

Abstract Reference: 20156
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

From dish to danger: Unveiling foodborne zoonotic nematode infections risks in Malaysia through knowledge, attitude, and practice surveys

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Abstract Content

Food-borne zoonotic nematode infections are common human diseases caused by incidental exposure of the nematode through infected hosts, cultural practices related to the consumption of host animals containing the nematode and poor hygienic practices lead to ingestion of infective stages of the nematode. The current study aimed to assess the knowledge, attitude, and practices (KAP) related to food-borne zoonotic nematode infection transmission among Malaysian citizens. A cross-sectional study was conducted through an online Google Form survey for five months from 1st June to 31st October 2022, which involved 385 respondents who are residents of Malaysia with an age range of 18 to 70. Questions were divided into four sections, including demographic data, awareness and knowledge, attitude toward prevention and management, and individual food preparation practices. The results demonstrate that respondents have a positive attitude and good practices but low knowledge levels on food-borne zoonotic nematode infections. The results demonstrated that the risk factors of human angiostrongyliasis were poor attitude, food handling and personal hygiene practices. Culinary habits of consuming raw or undercooked vegetables, fruits and meat contaminated with parasite larvae might increase the risk of infections. This study revealed the need to improve knowledge, awareness, and practices of food-borne nematode infections among Malaysian residents through media campaigns on radio and television as well as health education programmes.

Abstract Reference: 20172
Mode of Presentation: Poster Presentation
Topic: Session 1 - Bacteriology

Epidemiology: Recent outbreak of leptospirosis in central Java, Indonesia

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Abstract Content

Leptospirosis is an infectious disease caused by the direct zoonotic agent *Leptospira spp*. It is transmitted through direct contact with urine and body fluids of infected animals or indirect contact with *Leptospira*-contaminated water and soil. The province of Central Java is one of five provinces in Indonesia that still has a high number of leptospirosis cases. Based on data from Purworejo District Health Office, the leptospirosis cases increased from 2021 to January 2024. The highest leptospirosis case occurred in 2023. There were 19 mortalities out of 130 cases including 28 female and 102 male patients in Purworejo District. Dadirejo Health Center had the highest number of leptospirosis cases of all health centers in 2023. The aim of this study was to determine the distribution of leptospirosis in Dadirejo Health Center. A quantitative study with descriptive analysis. The variables are people, place, and time. Data analysis using secondary data from Purworejo Health Office and geographic information systems. Leptospirosis morbidity at the Dadirejo Health Center was 18 cases with 3 mortalities. Morbidity and mortality of leptospirosis spread in Dadirejo, Tlogokotes, Semono, Karang Jambu, Semagung, Hargorojo, Bapangsari, Krajan, and Karangnongko villages.

Keywords: Epidemiology, leptospirosis, mapping

Abstract Reference: 20175
Mode of Presentation: Poster Presentation
Topic: Session 1 - One Health

Transforming partnerships through cross-cultural transboundary research

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Abstract Content

Research partnerships are about relationships between people to increase the quality and efficiency of research. Transnational research in partnership between institutions and researchers from different cultural and economic backgrounds is part of a complex and dynamic research for development system that requires a continuous process of sound knowledge generation, building mutual trust and learning, and shared ownership. Despite good intentions, inequalities in existing capacities and access to resources can lead to disempowering imbalances that constrain the performance of these partnerships. Reducing inequalities remains a nebulous and sometimes elusive goal because it is not clear what actually needs to be reformed to bring about meaningful change. Transformative partnerships, where participating organisations are willing to be influenced by each other to improve their individual ways of working, are key to achieve equative relationships. In contrast to transactional partnerships, a transformative collaboration identifies a set of goals that the partnership wants to work towards and agrees on the process to achieve these goals. Critical thinking about how and why the desired changes are expected to occur will therefore guide the planning of "who will do what and how" in a participatory way. Transformative partnerships are achieved through a two-way exchange based on complementarity and clear roles for partners, engaging in activities with good communication and mutual benefit to develop trust and respect, and monitoring the partnership's performance to ensure consolidation of results. This transformative framework has the potential to guide specific actions to reduce imbalances within research partnerships and strengthen the institutions involved.

Abstract Reference: 20176
Mode of Presentation: Poster Presentation
Topic: Session 1 - Vector-Borne Diseases

Integration of vector-borne parasites diagnosis, prevention and control of vector-borne parasitic diseases in small scale livestock farms in North-eastern part of Thailand

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Abstract Content

Theileriosis, babesiosis, anaplasmosis, and trypanosomosis are vector-borne parasitic diseases (VBPDs) in cattle, significantly impacting animal health, production, and the livelihoods of farmers. Early recognition is challenging. Integrating VBPDs diagnosis, prevention, and control in small-scale livestock farms is crucial for rapid diagnosis and improved disease control measures. Project announcement, collaboration to regional veterinarians to generate sample collecting teams in North-eastern region department of livestock (DLD). Conventional and nested PCR services for four pathogens (*Theileria*, *Babesia*, *Anaplasma*, *Trypanosoma*) and guidelines for treatment and control of VBPDs were provided to the veterinarians and farmers within 14 days. Satisfactory evaluation was conducted. There were 41 small scale farms in which 239 samples were collected from Nong Khai (50), Sakon Nakhon (56), Ubon Ratchathani (34), Sri Sa Ket (50) and Surin (50) provinces in November to December, 2023. Samples were submitted for DNA extraction and pathogen detection by PCR. The PCR results and suggestions were successfully reported. Ten farmers rated the approach 4.90 out of 5. 1.They recommend it should be provided once per year, to benefit bovine health. 2.The project's free-of-charge service brings them significant satisfaction. There were 228 (95.40%), 3 (1.26%), 33 (13.81%) and 0 (0%) of *Theileria* spp., *Babesia* spp., *Anaplasma* spp. and *T. evansi* infected animals, respectively. Implementing molecular diagnostic services and treatment guidelines for VBPDs has challenges but benefits farmers. It aids in detecting and treating infected animals, preventing disease spread. Strengthening collaboration between researchers and local veterinarians is vital for sustainable VBPDs control across Thailand.

Abstract Reference: 20197
Mode of Presentation: Poster Presentation
Topic: Session 1 - Vector-Borne Diseases

Prevalence of rickettsia Africae in tick vectors collected from mammalian hosts in sub-Saharan Africa: A systematic review and meta-analysis

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Abstract Content

African tick bite fever (ATBF), a significant rickettsial infection for international travellers to sub-Saharan Africa, showcases the diverse infection rates of *Rickettsia africae* among tick species. This systematic review and meta-analysis draws from studies reported between 2005 and 2020 in PubMed, Web of Knowledge, Google Scholar, and SCOPUS, focusing on *R. africae* infection rates in adult ticks, nymphs, and larvae across sub-Saharan Africa. Utilizing a quality effects model to address observed heterogeneity and assess publication bias, our analysis integrates data from 32 studies, examining 12,301 ticks (adults, nymphs, larvae) and 1,214 pooled samples. Results indicate a significantly higher prevalence of *R. africae* in *Amblyomma* spp. (48%) compared to *Rhipicephalus* spp. (1%), *Hyalomma* spp. (1%), and other tick genera, with notable regional disparities. *Amblyomma* spp. exhibited the highest prevalence in Western Africa (53%), underscoring the necessity of understanding tick vector species' roles in *R. africae* transmission to humans. This research highlights the marked heterogeneity between species and regions, providing crucial insights into the epidemiology of ATBF and emphasizing the importance of tick vector monitoring in sub-Saharan Africa.

Abstract Reference: 20199
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Identification of helminths and protozoa in feces using metabarcoding of leopard cats, raccoon dogs, water deer, and wild boars in Korea

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Abstract Content

Four species of dominant wild animals, namely, *Prionailurus bengalensis euptilurus*, *Nyctereutes procyonoides koreensis*, *Hydropotes inermis argyropus*, and *Sus scrofa coreanus*, are hosts of potential infectious agents, including helminths and protozoa. Therefore, it is necessary to analyze the infectious agents present in these wild animals to monitor and control the spread of pathogens. In the present study, fecal samples from 51 wild animals were collected from the mountains of Yangpyeong, Hoengseong, and Cheongyang in South Korea and metabarcoding of the V9 region of the 18S rRNA gene was performed to identify various parasite species that infect these wild animals. Genes from nematodes, such as *Metastrongylus* sp., *Strongyloides* spp., *Ancylostoma* sp., and *Toxocara* sp., were detected in the fecal samples from wild animals. In addition, platyhelminthes, including *Spirometra* sp., Echinostomatidae gen. sp., *Alaria* sp., *Neodiplostomum* sp., and *Clonorchis* sp., and protozoa, including *Entamoeba* sp., *Blastocystis* sp., *Isospora* sp., *Tritrichomonas* sp., *Pentatrichomonas* sp., and *Cryptosporidium* sp., were detected. In the present study, various parasites infecting wild animals were successfully identified using metabarcoding. Our technique may play a crucial role in monitoring parasites within wild animals, especially those causing zoonoses.

Abstract Reference: 20204
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Alteration of sensitized antigens of *Anisakis* spp. by gut microbiome change in mice

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Abstract Content

The gut microbiome plays an essential role in host immune responses, including allergic responses. However, commensal gut microbiota are extremely sensitive to antibiotics, and their excessive usage can lead to microbial dysbiosis. In this study, we investigated how ampicillin-induced gut microbiome changes affect the production of IgG1 and IgG2a antibodies in mice exposed to *Anisakis* spp. antigens. Ampicillin treatment led to a notable change in the gut microbiome, as evidenced by both alpha and beta diversity indexes. In a one-dimensional immunoblot using *Anisakis*-specific anti-mouse IgG1, a 56 kDa band corresponding to an unnamed *Anisakis* protein was detected by mass spectrometry analysis only in the ampicillin-treated group. In the *Anisakis*-specific anti-mouse IgG2a-probed immunoblot, the band for heat shock protein 70 kDa detected in the *Anisakis*-immunized without ampicillin group but it was disappeared in the ampicillin-treated group. For better resolution, we performed a two-dimensional immunoblot against *Anisakis* extract with immunized mouse sera and observed altered spot patterns in both groups. In conclusion, ampicillin altered gut microbiome composition in mice, resulting in altered immunization of antigens from *Anisakis* spp. This research could serve as a basis for the development of vaccines or allergy immunotherapies against parasitic infections.

Abstract Reference: 20205
Mode of Presentation: Poster Presentation
Topic: Session 1 - Entomology

Metabarcoding of the microbiome, parasites and blood-meal hosts in three *Ae. albopictus* and *Cx. pipiens* populations in Korea

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Abstract Content

Mosquitoes are vectors of important infectious diseases and pose a heavy public health burden. The composition of the bacteria and parasites consortium associated with mosquitoes can modulate their fitness. Therefore, vector control measures will require extensive information of the microbiome and eukaryome of different mosquito species from various geographic regions. We used 16S, 18S and mit-12S rRNA gene metabarcoding through the iSeq100 sequencing platform to characterize the bacterial and eukaryotic consortium and blood-meal hosts of three populations of *Aedes albopictus* and *Culex pipiens* from two urban areas (Seoul and Asan) in the Republic of Korea. We identified 19 bacteria phyla and 111 families in total and found that bacterial alpha and beta diversity varied by population. Proteobacteria was the dominant phylum in both species. At the genus level *Wolbachia* was the most enriched taxon in a *Cx. pipiens* population (Seoul), while the other (Asan) was dominated by *Aeromonas.* In *Ae. albopictus* the most enriched group was *Enterococcus*. ASVs of the kinetoplastid *Crithidia fasciculata* were found in *Cx. pipiens*. The gregarine parasite *Ascogregarina taiwanensis* was highly prevalent in *Ae. albopictus* and its absence was marked by the presence of seven bacteria taxa. Metabarcoding of the 12S rRNA gene showed blood-meal host ASVs from *Homo sapiens* and *Mus musculus*. This is the first characterization of the microbiome in *Ae. albopictus* and *Cx. pipiens* in the ROK and contributes to the current information of the microbiome of mosquito species that can be used in further studies to assess pathogen-microbiome and microbiome-microbiome interactions.

Abstract Reference: 20206
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Optimization of 18S rDNA metabarcoding for the diagnosis of intestinal parasitic infections

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Abstract Content

This study aims to detect various intestinal parasites simultaneously using a metabarcoding methodology. It also optimizes library preparation protocols for next-generation sequencing (NGS) and to analyze the impact of various factors on NGS results. Using TA-cloned 18S rDNA V9 regions from 11 parasite species, we pooled equal amounts and concentrations of 11 plasmids into a single tube to prepare a metabarcoding library. Subsequently, an amplicon NGS experiment targeting the 18S rDNA V9 region was performed using Illumina iSeq 100 platform. Metabarcoding identified 434,849 reads, detecting all 11 parasite species. Initially using the same plasmid amounts and concentrations, the number of reads for each parasite was different. The read count ratio ranked as: *Clonorchis sinensis* (17.2%); *Entamoeba histolytica* (16.7%); *Dibothriocephalus latus* (14.4%); *Trichuris trichiura* (10.8%); *Fasciola hepatica* (8.7%); *Necator americanus* (8.5%); *Paragonimus westermani* (8.5%); *Taenia saginata* (7.1%); *Giardia intestinalis* (5.0%); *Ascaris lumbricoides* (1.7%); and *Enterobius vermicularis* (0.9%). Additionally, DNA sequence of the 18S V9 region formed a specific DNA secondary structure (hairpin structure) in which the number of GC base pairs had a negative association with the number of NGS reads ($p = 0.004$). Moreover, read counts increased with the amplicon PCR annealing temperature, especially for *A. lumbricoides*, *E. vermularis*, and *T. saginata*. This study successfully detected 11 species of intestinal parasites using metabarcoding. The GC pairs in DNA secondary structures show a negative association with the number of NGS reads, and increasing the amplicon PCR annealing temperature can mitigate the effects of these GC base pairs.

Abstract Reference: 20207
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Fecal eukaryotic profiles of domestic pigeons in Seoul, Korea

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Abstract Content

This study aimed to investigate potential zoonotic risks associated with pathogens found in the feces of pigeons in Seoul, Korea, using a metabarcoding method. The goal was to enhance understanding of the zoonotic risks associated with pigeons, which frequently come into close proximity with people in public areas. For sample collection, we gathered 149 fresh pigeon fecal samples from in and around the Seoul area. Amplicon sequencing targeting the V9 region of 18S rRNA gene was targeted to assess eukaryotes. Bioinformatic analysis was performed using Quantitative Insights Into Microbial Ecology version 2 (QIIME 2). At the genus level, *Torulaspora* was the predominant eukaryotic composition, with a relative abundance of 36.7%, followed by *Eimeria* (24.8%), *Isospora* (3.5%), and *Tetrameres* (2.5%). In total, five protozoa and four helminths were identified. The five detected protozoa taxa were *Eimeria*, *Isospora*, *Cyclospora*, *Acanthamoeba*, and *Cryptosporidium*. The four detected helminth taxa were *Tetrameres*, *Strongylidae*, *Baruscapillaria*, and *Brachylaima*. The PERMANOVA test, using the Bray-Curtis index, confirmed that eukaryotic composition differed significantly depending on ecological factors such as the presence of homeless individuals. However, the eukaryotic composition did not differ significantly based on urbanization levels in the area. In this study, we unveiled distinct eukaryotic profiles within pigeon feces. These findings emphasize the significant impact of environmental factors on eukaryotic components, which can affect both pigeon health and human public health. This research highlights the importance of assessing zoonotic risks of pigeons for the public residing in highly populated cities like Seoul, South Korea.

Abstract Reference: 20209
Mode of Presentation: Poster Presentation
Topic: Session 1 - Vector-Borne Diseases

The association between obesity and dengue severity through the investigation of the genes involved in vascular leakage

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Abstract Content

Dengue virus (DENV) infections, have gained notoriety as one of the most important mosquito-borne viral infections in the world. Transmitted predominantly by the Aedes aegypti mosquito, dengue has emerged as a major public health threat in the tropical and subtropical regions of the world. Obesity on the other hand is also a growing public health concern that have far-ranging socioeconomic effects, especially in developing countries. Past clinical studies have shown comorbidity such as obesity worsen the clinical manifestation of dengue infection causing severe dengue. However, discussion regarding the underlying mechanisms and the association between this comorbidity and dengue are lacking. Dengue patients progress into severe dengue due to acute plasma leakage which is caused by several factors including the expression of pro-inflammatory cytokines and dysregulation of endothelial barrier protein expression. The key factors of obesity affecting the endothelium include altered lipid metabolism and immune response causing increased viral replication and inflammation. In this study, microvascular endothelial cells (MECs) are treated with DENV as well as varying amounts of neurotensins which is a putative obesity biomarker to assess the possible outcomes. Evidence of leakage of MECs was identified by using electro-impedance assays (ECIS). Based on ECIS measurement, the magnitude of vascular leakage observed was positively correlated with the concentration of neurotensin, whereby the loss of barrier function in HPMECs showed junctional tightening followed by a sudden loss of barrier function. Gene expression study was done to identify the dysregulated genes and pathways association as a risk factor contributing to SD.

Abstract Reference: 20210
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Unlocking relief: The role of parasite identification in managing delusional parasitosis

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Abstract Content

The Parasite Excellence Clinic is part of the Tropical Medicine Excellence Clinic at the Hospital for Tropical Diseases, Faculty of Tropical Medicine, Mahidol University. This clinic receives various specimens from patients, including fecal specimens, worms, parts of worms, and objects resembling worms, which are submitted to the Department of Helminthology. Additionally, specimens are sent from external laboratories, including fecal specimens that tested negative for helminth eggs or larvae, as well as foreign objects reported in these samples. The negative fecal samples sent from external laboratories were submitted for confirmation. Under the microscope, using the Kato-Katz technique, both truly negative samples and some artifacts resembling helminth eggs or larvae were observed. These artifacts included white blood cells, mushrooms and fungal spores, pollen grains, plant hairs, and fat. Although the morphology of these artifacts is similar to that of helminth eggs and larvae, their sizes vary, being either larger or smaller than the usual size. The study showed the importance of positive identification, which is helpful for a definite diagnosis of parasitic infection. Moreover, delusional parasitosis was also discussed. The data collected from our laboratory would be beneficial not only for inexperienced laboratory personnel but also for physicians in assisting with disease diagnosis.

Abstract Reference: 20214
Mode of Presentation: Poster Presentation
Topic: Session 3 - Bacteriology

Reassessment of typhoidal fever among patients admitted at the national infectious disease referral hospital, the Philippines using an in-house PCR assay

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Abstract Content

In developing countries, typhoidal *Salmonella* infections are major causes of community-acquired bacteremia (CAB) yet estimating their true disease burden is challenging due to diagnostic and surveillance limitations. Assessing the role of a multiplex PCR assay as complementary diagnostic test for detecting *Salmonella* infection among CAB patients at an Infectious Disease Hospital in the Philippines. Utilizing specific primers, the developed multiplex PCR assay was applied to DNA samples from CAB patients. Descriptive statistics were used for analysis. Of 1,924 tested CAB samples, PCR identified 21 cases(1.1%) including 8 *S*.Typhi cases missed by blood cultures and clinical assessment. With PCR application,laboratory confirmed cases increased from 21 cases(blood culture) to 31(47.6%). Adding to initial 92 typhoid fever cases in the CAB study, total number of cases increased to 100(8.7%). PCR positive and blood culture negative patients had higher antibiotic pretreatment compared to only blood culture positive patients (60% vs 16.7%, p value of 0.021). Cases identified solely with PCR were younger with shorter duration of illness before admission. The study highlighted the need for complementary diagnostics to enhance typhoid fever diagnosis and disease surveillance. The findings suggested a potential underestimation of disease burden using current methods.

Abstract Reference: 20217
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Does common eye fluke *Tylodelphys* sp. manipulate behavior of the fish host?

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Abstract Content

Parasites can manipulate host behavior to increase their probability of transmission to the next host. In trophically transmitted parasites, these changes often manifest themselves in worsening host defensive behavior, thus, predisposing the host to the predator (parasite's next host). One classic example of a manipulative parasite is the eye fluke, *Diplostomum pseudospathaceum*, which interferes with their second host (fish) defensive behavior and predisposes fish to the piscivorous bird (final host). It is widely believed that closely related eye fluke (*Tylodelphys* sp.) localizing in the fish vitreous humor has similar effects on host behavior. However, this hypothesis has never been checked under controlled laboratory conditions. We experimentally infected fish (*Salvelinus malma*) with *Tylodelphys* sp. and tested whether this parasite affects host activity, depth preference, and avoidance of simulated predator attack. We expected that, as with *D. pseudospathaceum* infection, fish infected with *Tylodelphys* sp. would be more active, swim closer to the surface and avoid simulated predation less successfully. Contrary to our expectations, no evidence of parasitic manipulations was found in this host-parasite study system. Infected fish did not differ from control ones in the expression of any aforementioned behavioral trait. Interestingly, parasites influenced the size-dependent activity of fish. Larger infected fish were more active, while larger control fish were less active. Our results suggest that even closely related parasites occupying similar ecological niches can drastically differ in their ability to manipulate the behavior of their hosts. The study was supported by the Russian Science Foundation (grants 23-24-00418).

Abstract Reference: 20220
Mode of Presentation: Poster Presentation
Topic: Session 1 - One Health

Rapid field diagnosis of buffalo calf scours in buffalo bathans in coastal area of Bangladesh

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Abstract Content

Diarrhea is one of the most important diseases that threaten the health of calves causing the highest economic losses. This study aimed to rapid diagnosis of diarrheal calves for the immediate treatment in the remote coastal buffalo farms. During September to December 2023, calves aged between 0 to 105 days reported with diarrhea (100) were tested by Rapid Test Kit for major pathogens of calf diarrhea (Corona virus, Rota virus, *Giardia* and *Cryptosporidium)*. Pathogens detected were Bovine rotavirus (BRV) (42.5 %), Bovine corona virus (BCoV) (8.7%) and *Cryptosporidium* and *Giardia* mixed infections (17.3%). The overall prevalence of microorganisms was 57.5%. The analysis showed that *Cryptosporidium* and BRV being the most important pathogens responsible for diarrhea in buffalo calves. The test kit was found very promising for the rapid diagnosis and was able to save the lives of hundreds of calves in the remote coastal area where veterinary support and services are limited. Thus, the in-depth investigation of the above calf diarrhea pathogens is the basis for the prevention and treatment of calf diarrhea and avoiding the mixed infection caused by multiple pathogens is of clinical significance. The coastal region is a high-frequency area for parasite reproduction and transmission and many parasites, bacteria and viruses can be transmitted through water associated with geographical and environmental factors. Therefore, a cost-effective raid diagnostic kit should be developed to help the farmers to diagnose and save the calves suffering from diarrhea.

Keywords: Rapid test kit, buffalo calves, diarrhea pathogen, coastal area, Bangladesh

Abstract Reference: 20224
Mode of Presentation: Poster Presentation
Topic: Session 1 - Vector-Borne Diseases

A bat scientist gambit – A first reported Lyme disease in Malaysia

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Abstract Content

Lyme disease, previously unreported in Malaysia and considered non-endemic, has manifested in our case study featuring a prominent Malaysian bat scientist with an extensive global travel history and diverse animal exposures. The scientist presented with multiple circular rashes on the distal forearm and bilateral lower limbs, leading to a consultation with a general practitioner who prescribed a series of antibiotics. However, her condition did not improve. Subsequently, she developed debilitating bilateral knee joint pain, prompting a clinical suspicion of Lyme disease based on a detailed clinical history that included travel history, animal exposure, and a thorough examination. Sequential serology testing confirmed the late-stage diagnosis of Lyme disease. Treatment with Doxycycline over a month resulted in a remarkable recovery, enabling the scientist to resume professional activities. This case underscores the necessity of maintaining a high index of clinical suspicion, particularly in patients with significant travel histories, and emphasizes potential epidemiological correlations. Our findings contribute valuable insights into the clinical manifestation and management of Lyme disease in non-endemic regions, highlighting the importance of global scientific collaboration and vigilance in the face of emerging infectious challenges.

Abstract Reference: 20225
Mode of Presentation: Poster Presentation
Topic: Session 1 - Bacteriology

A survey of colistin-resistant *E. coli* isolated from pigs, farmers, and environments on colistin withdrawn pig farms in Songkhla Province, Thailand

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Abstract Content

Colistin resistance is an important concern for public health, particularly in agriculture. This study aimed to investigate the prevalence of colistin-resistant *Escherichia coli* (*E. coli*) among colistin-withdrawn pig farms in Songkhla Province, Thailand. A total of 101 samples were collected from pig feces (77), farmer feces (4), and environments including soil (4), drinking water (3), wastewater (3), and pen floor (10) from three different pig farms. Isolation and identification of colistin-resistant *E. coli* were conducted using microbiological and molecular techniques on selective media agar with MacConkey agar and supplemented with 2 mg/L of colistin. Then, two small pink or red colonies were collected to identify the isolates of *E. coli* by biochemical tests and confirmation with the multiplex-polymerase chain reaction (M-PCR) method with *uidA* genes and 16s rRNA genes. The antimicrobial susceptibility testing used the broth microdilution method with colistin to determine the minimum inhibition concentration value (MIC). All screening of colistin-resistant *E. coli* isolates has identified 210 isolates and confirmed biochemical tests have identified 87 colistin-resistant *E. coli* isolates. Finally, a total of 85 colistin-resistant *E. coli* isolates were confirmed with M-PCR. The results of the MIC values showed that all colistin-resistant *E. coli* isolates (n = 85) were resistant to colistin (10.59%), intermediate (71.76%), and susceptible (17.65%), and the MIC_{50} was 2 mg/L of colistin. In conclusion, a low percentage of colistin-resistant *E. coli* isolates was detected in healthy pigs, farmers, and environments on pig farms following cessation of colistin use.

Abstract Reference: 20239
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Neuronal determinants of Toxoplasma infection

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Abstract Content

Toxoplasma gondii is an intracellular neurotropic pathogen of the phylum Apicomplexa. In healthy individuals, the parasite infection remains asymptomatic. In immunocompromised patients or neonates, it can be life-threatening with severe neurologic manifestations. Several studies have revealed the pathogenesis of *T. gondii* in mature neurons but *T. gondii* infection in undifferentiated neuronal cells and its effect on neuronal maturation is poorly understood. The parasite can impair the maturation of undifferentiated neural progenitor cells, potentially leading to neurological disorders. The molecular mechanism is not known, however. To better understand infection-induced neuronal pathogenesis, development and mechanisms, we have established an infection model in murine neural progenitor N2a cells. Morphometric analysis showed significant reduction in neurogenesis in infected progenitor cells. Besides, a meta-analysis of transcriptomics data of parasite-infected brains and neuronal stem cells revealed differentially-expressed miRNAs, some of which are known to control neurogenesis. Our extended *in-silico* analysis narrowed down to target mRNAs of the selected miRNAs that have a known role in neuronal development and physiology. Some of these were verified by expression analysis, suggesting an important role of host miRNA during infection. Currently, we are deploying CRISPR tools to alter the expression of these genes and thereby determine their physiological relevance in differentiation of parasitized neurons.

Abstract Reference: 20254
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

Improving sporulation of *Eimeria tenella* oocysts purified from chicken feces

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Abstract Content

Coccidiosis is a major and recurring intestinal disease in the chicken industry caused by an infection of *Eimeria* species *E. tenella* is among the best studied and economically important of these coccidians. Oocyst purification is a common method that is critically important for the study of this coccidian species. Various methods have been used for the purification of coccidia oocysts, however, no study has outlined the most effective method for increasing the sporulation of *Eimeria tenella* oocysts. Thus, the study aims to compare and validate the applications of three common oocysts sporulation methods: (i) forced aeration without a shaker and (ii) forced aeration in combination with a shaker, and (iii) magneto based without forced aeration. A total of 9 individual 21-day-old broiler chickens were inoculated individually with a single 1 mL dose containing 2000 *Eimeria tenella* oocysts via oral gavage. Water and food were provided *ad libitum* throughout the experiment period. Pooled group faecal samples were collected during post-mortem. The average (range) of sporulated oocysts counts for the forced aeration without shaker was 2250 (1000-2000), forced aeration in combination with shaker was 2000 (1000-1500), and the magneto base without forced aeration was 5500 (2000-3500). The results from the study indicated that the magneto base without forced aeration was the most effective method for increasing the sporulation of *Eimeria tenella* oocysts.

Abstract Reference: 20260
Mode of Presentation: Poster Presentation
Topic: Session 1 - Vector-Borne Diseases

Molecular investigation of vector borne haemoparasites in small ruminants from northern India: A comprehensive report

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Abstract Content

This study explored the prevalence and risk factors associated with haemoparasitic infection among small ruminants. Microscopy of 402 sheep blood samples revealed a prevalence of 47.26%, 0.24%, and 33.08% for *Theileria*, *Babesia*, and *Anaplasma* spp., respectively. Microscopy examination of 405 goat blood samples unveiled a prevalence of 18.27%, 0%, and 35.33% for *Theileria*, *Babesia*, and *Anaplasma* spp. Notably, co-infection of *Theileria* spp. and *Anaplasma* spp. was observed in 16.66% of sheep and 6.66% of goats. However, in PCR analysis, the overall prevalence of ovine haemoprotozoan, *Theileria*, *Anaplasma*, and *Babesia* was determined to be 60.94%, 51.24%, and 1.24%, respectively. For goat samples, these figures were 33.58%, 53.82%, and 0.49%, respectively. Utilizing PCR-RFLP facilitated species differentiation of *Theileria*, revealing *T. ovis* and *T. lestoquardi* as the primary causative agents of ovine and caprine theileriosis in the region, with a few instances of *T. luwenshuni* reported. Additionally, *T. annulata* infections were documented in sheep for the first time. Mixed infections with different *Theileria* spp. were also documented in both sheep and goats. Nested PCR specific to species confirmed *B. ovis* as the prevalent *Babesia* species. Among sheep blood samples, 35.82% and 5.97% tested positive for *A. ovis* and *A. marginale*, respectively, with mixed infections detected in 9.45% of cases. Similarly, among goat blood samples, 38.77% were positive for *A. ovis* and 4.69% for *A. marginale*, with mixed infections observed in 10.37% of cases. The ticks collected from small ruminants were identified as *Rhipicephalus* spp., *Hyalomma* spp., *Rhipicephalus* (*Boophilus*) *microplus*, and *Haemaphysalis* spp.

Abstract Reference: 20261
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

The relationship between work environmental factors and work behavioral factors and the incident of malaria in the lowland area of pt freeport Indonesia

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Abstract Content

Malaria is caused by a protozoan parasite that is spread via the Anopheles mosquito. The parasite causes malaria in humans and this disease often occurs in tropical and subtropical regions. The problem studied is whether there is a relationship between work environment factors and work behavior factors with the incidence of malaria. This research is a cross sectional methodology conducted on 170 regional respondents in the PTFI lowland area. Investigating information uses univariate examination, bivariate examination using the chi square test with the SPSS program. The results of bivariate analysis showed that age (p=0.323), gender (p=0.001), education (p=1.000), length of work (p=0.498), work outside at night (p=0.012), having activities in at night (p=0.022), going to work often (p=<0.001), routine activities (p=0.006), wearing long clothes (p=0.506), often leaving the house at night (p=0.002), having to go home from work at night (p=0.329), hanging clothes (p=0.182), using lotion (p=0.022), using mosquito repellent (p=0.053), having a mosquito net (p=0.047), using a mosquito net (p=0.212), often close doors and windows (p=0.497), office ventilation (p=0.286), house ventilation (0.167), house has a river (p=0.021), house has a forest (p=1.000), house has puddles (p=0.128), the workplace has (p=0.741), the workplace has puddles (p=1.000), the workplace has forests (0.077), the workplace has swamps (p=0.016). Variables related to the incidence of malaria are sex, work going out at night, having activities at night, going to work often, often going out at night, using lotion, the house has a river, and the workplace has a swamp.

Abstract Reference: 20263
Mode of Presentation: Poster Presentation
Topic: Session 1 - Malaria

Mass cytometric immunological profiling of malaria phenotypes in endemic areas of Kenya: A longitudinal cohort study

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Abstract Content

Malaria is a life-threatening disease caused by *Plasmodium* parasites and transmitted via infected *Anopheles* mosquitoes. In 2022, an estimated 249 million cases were registered worldwide, with the WHO African Region accounting for more than 90% of cases and deaths. Almost 80% of all deaths in this region were among children under the age of 5. Children, as well as unexposed individuals, are more susceptible to malaria due to a lack of acquired functional immunity, which is developed through multiple exposures to malaria. Clinical manifestations of malaria can be categorized as asymptomatic, uncomplicated, or severe, and the outcome depends on a dynamic interplay between host, parasite, and environmental factors. The host immune response to *Plasmodium* shapes the course of the infection. *Plasmodium*-specific T and B cells determine the progression from asymptomatic to severe malaria and the development of immunological memory. However, the dynamics underlying the anti-*plasmodium* immune reaction remain poorly understood. To define the immunological profile of individual reactions to malaria, we interrogated a heterogeneous population with a full spectrum of clinical phenotypes from a highly malaria-endemic area of Kenya. Baseline surveys indicate a prevalence by RDT of 40.7% and the presence of both asymptomatic and symptomatic cases. By analysing PBMCs from a longitudinal cohort of 300 individuals aged 5 to 65 via high-throughput mass cytometry (CyTOF), we aim to profile specific antimalarial immunity and stratify the population into distinct infection groups. This will give us insights into specific immunological signatures of the host antimalarial immune response and potential immunotherapeutic strategies.

Abstract Reference: 20264
Mode of Presentation: Poster Presentation
Topic: Session 1 - Bacteriology

A 15-year retrospective study of cholera in Sabah, Malaysia reveals recurrent outbreaks in coastal areas

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Abstract Content

Cholera is a major public health challenge in the Malaysian state of Sabah. Sabah reports cholera outbreaks every year, highlighting the need for comprehensive epidemiological analysis to identify factors driving risk. Therefore, this study aimed to characterize environmental risk factors and dynamics of cholera outbreaks by analyzing the trend of cholera outbreaks during the past 15 years. Data of the notified cases and asymptomatic carriers from 2005 through 2020 were collected from the database of Sabah State Health Department. There were wide variations of outbreaks throughout the study period, with a mean incidence rate of 5.6/100,000 (95% CI: 3.4–7.9). Cholera cases occurred throughout the year, peaking in July. Similar numbers of symptomatic and asymptomatic cases (705 vs 727) were identified. The male:female ratio was similar in cases (1:0.99) and asymptomatic carriers (1:1.04). Average population density in case-affected villages was 19.4 person/km^2. The study detected significantly more cases occurring near coastal areas and at low elevation on average (19.45 m). Moreover, there was an increased risk of contracting cholera within 0–5 days after a cholera case was notified at a health facility. Those within 0–500 m of the primary case had a 9.74-fold increase in risk of contracting cholera (95% CI: 7.51–12.41), suggesting local transmission. Children and adolescents were the most vulnerable, with 49.4% of symptomatic cases under 15 years old (348/705). This study provides valuable insights into the dynamics of cholera outbreaks in Sabah, aiming to contribute to policymaking decisions on cholera prevention and control.

Abstract Reference: 20269
Mode of Presentation: Poster Presentation
Topic: Session 1 - Malaria

The histological effect of *Canarium odontophyllum* (dabai) on ICR mice host infected by *P. berghei* NK65

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Abstract Content

Malaria is still a threat to human, especially when drug-resistant Plasmodium variations occurred. Thus, the aim of this study was to evaluate the effectiveness of Canarium odontophyllum leaf extracts on organs of Plasmodium berghei NK65 infected ICR mice. Following a four-day suppressive test, liver, renal and brain were harvested, processed, and observed under 40 x magnification light microscope. Hemozoin pigments were detected in mice' s livers at all dosages when treated with methanol extracts. Immune cell infiltration seen in 100 mg/kg and 300 mg/kg dosage. The renal had minimal hemozoin pigmentation and early indications of proximal tubule necrosis at all dosage treatments; parasitized red blood cells (PRBC) at 100 mg/kg and 500 mg/kg dosage treatment. No hemozoin pigments found in brain tissue, but inflammation presence at 500 mg/kg dosage. For hexane extracts, PRBC were prominent in liver tissue of all dosage treatment. Abundant of hemozoin pigments found in 100 mg/kg treatment extracts, few hemozoin pigments and immune cell infiltration seen in 300 mg/kg and 500 mg/kg dosage. During all dosage treatments, the renal displayed early indications of proximal tubule necrosis, with inflammation at 100 mg/kg treatment dosage and PRBC at 500 mg/kg dosage, but very few hemozoin pigments across all dosage treatments. No hemozoin found in the brain tissue on all dosage treatment, with inflammation at 100 mg/kg and 300 mg/kg dosage of hexane extracts. In conclusion, methanol and hexane leaf extracts, at 300 mg/kg and 500 mg/kg dosage respectively demonstrated effective antimalarial properties against Plasmodium berghei NK65.

Abstract Reference: 20276
Mode of Presentation: Poster Presentation
Topic: Session 1 - One Health

Improving biological training in rural schools: Prioritizing the focus on child health and the complexity of zoonotic and vector-borne infectious diseases

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Abstract Content

The «One Health» program provides a promising strategy for understanding, preventing and mitigating the impact of pediatric diseases by encouraging interdisciplinary science-to-practice-to-school connection. The schools in rural areas often face limited resources and insufficient conditions for children's education, which can negatively affect their health. Indicators of parasitic incidence of children in Kazakhstan per 100 thousand population in 2023 were: enterobiasis - 75.2; ascariasis – 10.6; echinococcosis – 3.1; trichocephalosis, strongyloidiasis, opisthorchiasis, taeniasis, trematodosis - from 0.02 to 0.53. We have developed a program of activities to improve biology education in rural schools, while prioritizing the health of children and the control of zoonotic and vector-borne infectious diseases. Secondary school of Michurino village, Pavlodar region, Kazakhstan has been selected as a pilot site, where experimental work was carried out. This program combines the active educational organization, taking into account priority attention to the children health and the prevention of parasitic diseases and includes the outdoor learn activities, the student project activities, the involving experts of epidemiology and hygiene into conducting extracurricular activities, the usage of digital technologies, the creation of a virtual laboratory to illustrate the life cycles of parasite and the measures to prevent zoonotic and vector-borne infectious diseases.

Abstract Reference: 20278
Mode of Presentation: Poster Presentation
Topic: Session 1 - Vector-Borne Diseases

The intrigue of bartonella: Unmasking and managing deep seated abscess in HIV infection

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Abstract Content

Bartonella is intracellular, fastidious gram-negative bacilli and is a rare disease in HIV infected patients. It has diverse clinical manifestations in late-stage HIV disease hence elusive to diagnose *Bartonella* disease. The clinical presentations may include skin lesions, fever, weight loss, headache, and deep organ abscess. We present here a case of 30-year-old man with newly diagnosed Retroviral Disease (RVD) and severely low CD4 count. He was commenced on antiretroviral therapy for a month before presenting with fever, cough, runny nose and diagnosed as COVID category 2 however at the same time developed multiple red, purple flesh- colored skin lesions. Skin biopsy exhibited a typical characteristic of dome shaped expansion of upper dermis with proliferation of vessels lined by prominent endothelial cells and presence of peripheral collarette, in keeping with angiomatosis lesions. Ultrasound imaging revealed liver and splenic micro abscesses. Confirmation of *Bartonella henselae* infection via PCR test prompted the addition of rifampicin in combination with doxycycline due to deep-seated infection. The skin lesions, liver, and splenic micro abscesses completely resolved after three months of combination therapy. *Bartonellosis* affects HIV patients mostly in advanced stage of HIV infection. This case underscores the important of early recognition and treatment of *Bartonellosis* in severely immunosuppressed HIV patients to achieve favorable outcomes.

Abstract Reference: 20282
Mode of Presentation: Poster Presentation
Topic: Session 1 - Bacteriology

Clinical features of leptospirosis in the Yaeyama Islands, Okinawa, Japan.

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Abstract Content

Leptospirosis, a zoonotic infectious disease, is notifiable in Japan, yet its annual incidence remains low, with only a few dozen cases reported, making it rare. The Yaeyama Islands, where our hospital is located, are the most endemic region for leptospirosis in Japan, warranting clarification of its clinical features in this area. Patient data and outcomes were extracted from electronic medical records of individuals diagnosed with leptospirosis at our hospital between April 2020 and March 2022. A total of 20 cases were analyzed, with a median age of 35.4 years and 90% being male. While 19 patients showed improvement, one patient died. Diagnosed cases were concentrated between July and October, with tourism being the predominant occupation (50%). Ishigaki Island (8 cases) and Iriomote Island (12 cases) were presumed infection locales. All three Weil's disease cases exhibited Jarisch-Herxheimer reaction (JHR) upon admission, and 76% of non-Weil's disease cases experienced JHR during treatment. Third generation cephalosporins were the initial treatment in 19 cases. Approximately 25% of all documented leptospirosis cases in Japan during the study period were from our hospital, with many patients working in tourism, exposing them to freshwater. Notably, all three Weil's disease cases experienced JHR, with two requiring catecholamine administration. The higher incidence of JHR suggests that it may be the notable feature of leptospirosis in this region.

Abstract Reference: 20296
Mode of Presentation: Poster Presentation
Topic: Session 1 - Bacteriology

Descriptive study of patients with leprosy admitted in Fontilles: 1909-2020

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Abstract Content

The study aimed to characterize leprosy patients admitted to Fontilles throughout the 20th and 21st centuries, focusing on differences across three significant periods. It also explored variables linked to patient survival.; A retrospective descriptive-analytical study analyzing the medical records of Fontilles patients from 1909 to 2020. It assessed 27 clinical, sociodemographic, and temporal variables (n=2652) using SPSS 27.00.; Over time, patients received more treatments, increasing their age of onset, admission, and death. In the third period, most patients came from foreign countries, exhibiting greater skin symptoms and having more infected relatives. As time passed, neurological symptoms were more commonly diagnosed. Leprosy patient survival relied on the period and age of leprosy onset, with no significant association with clinical form, gender, or country of origin. The findings may be explained by the absence of an effective treatment until 1980, a thorough self-examination, and the realization that leprosy is not inherited. Most leprosy patients are foreign-born, which coincides with a lower prevalence of leprosy in Spain. More specific symptoms may be diagnosed due to diagnostic advancements. Despite reducing the prevalence of leprosy, rifampicin may be able to help avoid impairments. Improved living conditions have resulted in the majority of leprosy patients being foreign-born; nonetheless, leprosy remains neglected due to the increase in the length of symptoms before admission over time. Rifampicin was not the primary driver of the mortality decrease; rather, improvements in cleanliness, antibiotics, surgery, and general healthcare were.

Abstract Reference: 20301
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Giardia infection is associated with altered community structure of murine gut microbiome post antibiotic and probiotic treatment

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Abstract Content

The intestinal microbiota plays critical role in gut homeostasis and overall health and its alteration by enteropathogens is associated with gastrointestinal diseases. Dietary interventions contribute to microbial diversity and influence *Giardia* pathogenesis. Therefore, intestinal microbiota could help in exploring new treatment options and monitoring therapies like fecal microbial transplant. To evaluate shifts in commensal diversity associated with giardiasis in Non-treated and Treated (Probiotic and Antibiotic) mice model. Study included six cohorts of BALB/c mice (N=168) of Antibiotic and *Lactobacillus*-treated and Non-treated groups with Giardiasis along with respective controls at different time points. DNA was extracted and V3-V4 of 16sRNA was amplified and paired-end sequencing was performed with Illumina platform. Further,parasite quantification was performed using Real-Time PCR. Giardiasis in untreated cohorts disrupts commensals homeostasis with *Proteobacteria* expansion and *Firmicutes* reduction PI. In Antibiotic-treated cohort, significant 80-fold microbial disruption relative to that in untreated mice was observed. *Lactobacillus*-treated cohort results in normalisation of gut flora PI with *Proteobacteria* decrease and *Firmicutes* increase. Alpha diversity measure: *Giardia* alone resulted in highest microbial shift at 7thday PI. Antibiotic and *Lactobacillus*-treated cohort with giardiasis exhibited highest and lowest community richness/diversity respectively. PCoA revealed that during giardiasis, Antibiotic-treated cohort resulted in microbial disruption at all time points in contrast to *Lactobacillus*-treated group where microbial shifts were normalised PI. The study highlights importance of intestinal microbiome against *Giardia*. The assessment of shifts in gut microbiome and parasite burden during giardiasis in post antibiotic and probiotic-treated mice could lead to both preventative and therapeutic strategies for treatment.

Abstract Reference: 20303
Mode of Presentation: Poster Presentation
Topic: Session 1 - Malaria

Low genetic diversity of *Plasmodium vivax* circumsporozoite surface protein in clinical isolates from southern Thailand

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Abstract Content

The Genetic diversity within the circumsporozoite surface protein (PvCSP) of *Plasmodium vivax*, the predominant malaria species in Thailand, is primarily observed in the northwestern region along the Thailand-Myanmar border. However, as *P. vivax* cases shift to southern provinces, particularly Yala Province near the Thailand-Malaysia border, PvCSP diversity remains understudied. Between 2018 and 2020, 89 *P. vivax* isolates were collected in Yala Province, a significant malaria hotspot. Employing polymerase chain reaction amplification, restriction fragment length polymorphism (PCR-RFLP), and DNA sequencing, the gene encoding PvCSP (*Pvcsp*) was analyzed. All Yala *P. vivax* isolates belonged to the VK210 type, distinct from strains in the western region near the Myanmar border. The central repeat region of *Pvcsp* revealed two common peptide repeat motifs—GDRADGQPA and GDRAAGQPA—across all southern isolates. Sequence analysis identified two subtypes, with S1 more prevalent (92%) than S2 (8%). This study underscores the limited diversity of VK210 variants of *P. vivax* populations in southern Thailand. These baseline findings facilitate monitoring for potential new parasite variants, aiding in the future control and management of *P. vivax* in the region.

Abstract Reference: 20306
Mode of Presentation: Poster Presentation
Topic: Session 1 - Entomology

Molecular responses of sugar metabolism-associated genes in the male reproductive physiology of *Anopheles stephensi*

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Abstract Content

Sugar metabolism is vital for fueling mating behaviors in mosquitoes. This study delves into the molecular responses of sugar metabolism-related genes, particularly the trehalose transporter (TreT) and trehalase (TreH) genes, within the male reproductive physiology of Anopheles stephensi. Understanding the connection between sugar-metabolism and mating offers valuable insights into mosquito population dynamics and presents opportunities for innovative vector control strategies. The research involved mosquito rearing, sample collection from different physiological mating-stages, RNA isolation cDNA synthesis, and real-time-PCR analysis to measure the expression levels of sugar metabolism-associated genes finally we will attempt functional analysis via ds RNAi-mediated gene-silencing of selected genes. We found Increased expression of both TreH and TreT during the in-copula phase, indicating their crucial role in providing energy for mating behaviors in mosquitoes. Additionally, preliminary functional genomic analysis suggested that disrupting the TreT gene could impact sugar-metabolism and decrease mating success, emphasizing the significance of this gene in mosquito reproductive physiology. Mosquitoes depend on sugars for energy, with TreH and TreT working together in trehalose metabolism to convert trehalose to glucose for energy. Silencing TreT disrupts this process, impacting energy balance and reproductive success in mosquitoes. Understanding the molecular responses of sugar metabolism-associated genes in mosquitoes offers potential for improved vector-control strategies. This study sheds light on energy requirements during various mating stages, the significance of trehalose metabolism in crucial physiological events like mating, and the impact of silencing the TreT gene on mosquito reproductive physiology, a key focus for effective vector-control measures.

Abstract Reference: 20308
Mode of Presentation: Poster Presentation
Topic: Session 1 - Malaria

Tackling malaria in Indonesia’s new capital: Results from pilot study on mobile migrant populations

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Abstract Content

Massive deforestation in the establishment of Indonesia's new capital city in East Kalimantan increases the risk of malaria transmission, particularly among Mobile Migrant Populations (MMPs) employed as forest workers. The study aimed to reduce malaria transmission among MMPs using the malaria intervention package. The operational study was conducted in three malaria-endemic districts in East Kalimantan Province, deploying two rounds of Targeted Drug Administration (TDA) and Intermittent Preventive Treatment for forest-goers (IPTf). TDA, using Dihydroartemisinin-Piperaquine (DHP) and Primaquine, targeted MMPs aged 15 to 60 at risk of malaria. IPTf was given to people of all ages entering or leaving forested areas, with similar treatments as TDA. Distribution of Long-Lasting Insecticidal Nets (LLINs) was also included at the study sites. A total of 391 participants were involved in the TDA and 306 participants in IPTf. Coverage rates for TDA were 83% in the first round and 84% in the second round. IPTf coverage reached 84.1% in the first round and 85.3% in the second round. The LLINs distribution achieved 100% coverage by the second round, a significant increase from the initial 57.7%. The antimalarials were tolerable, with minimal adverse events reported. The incidence of malaria demonstrated a significant reduction during and after the interventions compared to the baseline period. The pilot program achieved substantial coverage and was effective in reducing malaria transmission among MMPs. This demonstrates the potential for sustainability and applicability in similar endemic settings.

Abstract Reference: 20309
Mode of Presentation: Poster Presentation
Topic: Session 1 - Malaria

A high-throughput screening of Thai natural products reveals Cleistanthin A with dual activity against gametocyte and asexual blood stage parasites of *Plasmodium falciparum*

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Abstract Content

Nature’s pivotal role in discovering malaria treatments, such as quinine and artemisinin, have saved countless lives. However, the rising resistance of *Plasmodium falciparum* to artemisinin and its partner drugs is a significant challenge. Exploring Thailand’s diverse natural products highlights the region’s rich biodiversity and its drug discovery potential. Our goal is to employ high-throughput screening to uncover new antimalarial compounds. A library of 1,094 Thai natural compounds were screened against asexual blood stages and gametocytes of *P. falciparum* 3D7 strain using high throughput viability assays in 384-well format. Specifically, a SYBR Green-based assay was employed for the asexual parasites, while an AlamarBlue assay was used for the gametocytes. The active hits identified in the screening were subjected to dose-response assay (EC_{50}) in a 96-well format. An exflagellation assay was conducted to validate the gametocytocidal activity of the hits. Their cytotoxicity was assessed against human kidney HK-2 cells. A set of 41 compounds was identified and further confirmed for their antimalarial activity. Among them, only two compounds, ECDD-N86 and ECDD-N93, exhibited dual-activities against both gametocytes, responsible for human-to-mosquito transmission, and asexual parasites that cause the clinical symptoms. ECDD-N86 and ECDD-N93 were identified as Cleistanthin A, extracted from *Phyllanthus taxodiifolius* Beille (Euphorbiaceae) and *Cleistanthus collinus* plants, respectively. Cleistanthin A showed no toxicity towards HK-2 cells, with selective indices of >426 and >52 against blood-stage parasites and gametocytes, respectively. This study revealed important new natural chemical scaffold that can be used as starting points for dual-activity antimalarial drug development.

Abstract Reference: 20310
Mode of Presentation: Poster Presentation
Topic: Session 1 - Entomology

Diversity and identification of Anopheles mosquitoes with Plasmodium circumsporozoite protein in malaria-endemic Western Thailand

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Abstract Content

Malaria is an infectious disease caused by Plasmodium spp. parasites and transmitted by Anopheles mosquitoes. Vector control is one strategy to accelerate towards malaria elimination. This requires a better understanding of the Anopheles mosquitoes, including the importance of various strains, behaviors and feeding patterns, and their capacity for Plasmodium transmission. For the latter, detection of the Plasmodium protein CSP in mosquitoes has served as a surrogate tool to assess malaria transmission intensity. CSP plays an important role in sporozoite formation and hepatocyte invasion during the pre-erythrocytic infection. This project aimed to investigate Anopheline abundance and vectorial capacity, and the correlation between these vector measurements and Plasmodium prevalence (via CSP of P. falciparum and two distinct strains of P. vivax: Pv-210 and Pv-247) in an endemic area. We collected Anopheles (n=246 pools) in Tak Province; Tha Song Yang, Phop Phra, and Umphang district during November 2023 to February 2024. The survey demonstrated that January showed the highest abundance and species diversity of Anopheles mosquitoes, with An. minimus emerging as the main species. 607 Anopheles mosquitoes collected from traps located around infected patient houses were utilized to detect CSP via Sandwich-Enzyme-linked Immunosorbent Assay (ELISA). Using a pooling strategy, we detected Plasmodium CSP in 1.29% of dissected mosquitoes, with positivity only in Tha Song Yang and Umphang and only in November and December. Interestingly, we did not detect CSP from a main malaria vector, An. minimus. The findings suggested An. barbirostris might be a relevant vector for spreading P. vivax western Thailand.

Abstract Reference: 20313
Mode of Presentation: Poster Presentation
Topic: Session 1 - One Health

Ethical issues from the co-creation process of engagement activities that promote the integration of community-based malaria activities

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Abstract Content

In remote communities in Thailand, maintaining human and financial resources for community-based malaria diagnosis and treatment is vital to improving health care accessibility and achieving elimination goal. Co-creation process offers one approach to implementing this sustainably. This project aims to collaborate with local stakeholders to co-design and promote the integration of malaria care that best fit the local context. Here, we highlight the ethical challenges arising from the preliminary result analysis. Qualitative content analysis was conducted with two data sources. Data from engagement logs and participation evaluation were collected throughout 23 engagement activities (2023-ongoing) ranging from consultation and brainstorm meetings to public awareness campaigns with 270 individuals. Data was also extracted from observational journals and team debriefs from previous research projects (2019-2023) in endemic communities along the Thai-Lao-Cambodian border. Based on our engagement activities, four interconnected ethical issues were identified: (1) willingness to participate, which noticeably differed between community members and policy makers and between research and engagement participation; (2) power dynamics and their effects on the ability to contribute in a participatory activity, particularly when engaging with health volunteers and their supervisors; (3) balancing the project's agenda of malaria elimination while also being responsive to local health priorities; and (4) sharing local ownership throughout the process to ensure sustainable impacts and mitigate unintended consequences from project exit. Co-creation process has strong potential for ensuring the sustainability of community-based health care in the context of declining awareness and advocacy of vertical disease programs, such as in the case of malaria.

Abstract Reference: 20318
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Rata-Too-Ill: Foodborne rat lungworm in rats from selected rural and urban communities in the Philippines

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Abstract Content

Angiostrongylus spp. (rat lungworm) is a zoonotic foodborne parasite causing meningoencephalitis among humans and animals. Angiostrongyliasis is a globally emerging public health concern with several reported outbreaks; however, it remains to be neglected in the Philippines. The lack of information on this parasite in the country leads to underreporting and misdiagnosis. Accurate diagnosis through correct identification is essential for treatment and control of parasitic diseases. In support to the Sustainable Development Goals, this study investigated *Angiostrongylus* in selected communities in the Philippines. Rats were collected from selected communities in Laguna, Davao del Sur, Agusan del Sur, and Surigao del Norte. Lungs were harvested after dissection and artificially digested to isolate the parasite. DNA was extracted from the parasite and SSU-rRNA and COI genes were amplified and sequenced. Results showed a prevalence of 37.30% with significantly higher prevalence in rural and sub-urban communities. Molecular data showed two species: *A. cantonensis* and *A. malaysiensis*. These species differ in infectivity and pathogenicity, thus requiring different management. This is the first report of co-endemic *Angiostrongylus* spp. in Mindanao. Evidence of *Angiostrongylus* spp. in rats together with its role as agricultural pest and known habit of eating raw or improperly prepared food may imply unseen transmission of *Angiostrongylus* to humans. This highlights the need for developing a surveillance scheme for the neglected foodborne disease – angiostrongyliasis – and establish its public health importance in the country. Further, a unified and interdisciplinary action is necessary for the control and prevention of angiostrongyliasis.

Abstract Reference: 20323
Mode of Presentation: Poster Presentation
Topic: Session 1 - Bacteriology

First case report of fatal *Francisella tularensis* subspecies *novicida* bacteremia in Malaysia

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Abstract Content

Francisella tularensis subspecies novicida (FTSN) is a non-sporing, non-motile Gram-negative coccobacillus and a rare cause of human infection. It is very closely related to *Francisella tularensis* subspecies holartica, the main causative agent of tick-born disease tularaemia. We describe the first case of fatal FTSN bacteraemia reported in Malaysia. A 68-year-old woman presented with history of fever, cough, generalised body weakness, vomiting, and diarrhoea for five days. She has underlying diabetes mellitus type II, hypertension, and dyslipidaemia. Initially treated for infective acute gastroenteritis, she became tachypnoeic and required intubation for respiratory collapsed. Despite intravenous meropenem, she continued to deteriorate and died on day seven of admission. Blood culture taken during admission flagged positive after two days of incubation, revealing gram-negative coccobacilli on microscopy. The bacteria grew on blood agar after 48 hours of incubation under ambient condition and at 37℃ as tiny, translucent, non-lysis colonies. The urease test was negative. Identification using matrix assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF) were unsuccessful. 16s rRNA sequencing done at reference laboratory identified the isolates as FTSN. Unlike other subspecies, FTSN has no obvious transmission route or reservoir. Since FTSN is currently not available on the standard MALDI-TOF database, suspicion should be raised when gram-negative coccobacillus with negative urease test is unable to be identified by MALDI-TOF. Although FTSN is considered opportunistic, early identification and appropriate treatment may prevent severe infection and death.

Abstract Reference: 20326
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Differential expression of mitochondrial processing peptidase (Metallopeptidase M16) is linked to miltefosine drug resistance in *Leishmania donovani*

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Abstract Content

Leishmaniasis is a spectrum of diseases, from mild cutaneous to life-threatening visceral disease. Visceral leishmaniasis is referred to as the most severe and fatal type of leishmaniasis caused by *Leishmania donovani* and *L. infantum*. Miltefosine (MIL) is the only oral drug available to treat Leishmaniasis. Our proteomics study of MIL-sensitive and MIL-resistant *L. donovani* (clinical isolate) shows a two-fold increase in the expression of Mitochondrial Processing Peptidase (MPP) protein in MIL-resistant *L. donovani* in comparison to the MIL-sensitive *L. donovani* strains. MPP cleaves the N-terminal mitochondrial targeting sequences and delivers pre-proteins to the mitochondria. In this study, we validated the upregulation of MPP protein in MIL-resistant *L. donovani* clinical isolates in comparison to MIL-sensitive *L. donovani* strains. Interestingly, the enzyme activity of MPP was also found high in MIL-resistant clinical isolates in comparison to MIL-sensitive *L. donovani* strains. Episomal overexpression of MPP protein in MIL-sensitive parasites was found to increase MIL resistance in sensitive parasites, and knockout of the MPP gene in resistant and sensitive parasites makes them more susceptible to MIL drug and slow growth pattern with abnormal parasitic morphology. Hence, MPP is vital for cell viability and will be a better drug target to treat the drug resistant *Leishmania* parasite infection.

Keywords: Visceral Leishmaniasis, *Leishmania donovani*, Miltefosine, Drug Resistance, Mitochondrial Processing Peptidase (MPP)

Abstract Reference: 20339
Mode of Presentation: Poster Presentation
Topic: Session 1 - Bacteriology

Molecular epidemiology and virulence characteristics of *Helicobacter* spp. in companion dogs/cats and owners

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Abstract Content

Helicobacter spp., including gastric and enterohepatic types, are getting attention. They could cause not just gastroenteritis but also cancers. Besides *H. pylori*, little is known about other *non-H. pylori species* spread and how they make people sick. Recent research found that 75.8% of stray or pet dogs in Taipei City had gastric or enterohepatic *Helicobacters*. Worryingly, 26.4% of these dogs carried *H. pylori*, meaning owners could catch it from their pets. Therefore this study aims to see the importance of knowing about zoonotic transmission between pets and people and to further compare the differences between rural and urban districts in Taiwan. The questionnaire survey was carried out in the community to see the knowledge, attitudes, and practices of pet-ship. Two hundred pet feces samples were gathered from seven western Taiwanese animal hospitals. To detect *Helicobacter* species, we used semi-nested PCR, total DNA was extracted. For additional phylogenetic and comparative database investigations, the PCR products were sequenced. So far given a prevalence of 95% (19/20) of *Helicobacter* infections of pets, after blasting against the NCBI database, we mostly got *H. Canis* (9/12). These latest preliminary findings suggest that there may be a risk of cross-transmission between humans and pets, therefore more research should be done to develop and monitor these bacteria from pets' stomachs.

Abstract Reference: 20340
Mode of Presentation: Poster Presentation
Topic: Session 1 - Entomology

Bionomics studies on *Anopheles subpictus* sibling species complex and its potential role in malaria transmission

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Abstract Content

Secondary vectors have enormous importance for sustaining malaria transmission during both peak and dry seasons. In India, *Anopheles subpictus* carries plasmodium parasites mostly found in coastal regions. Goa state is located in the western coastal part of India and has been endemic to malaria. A thorough investigation into the bionomics of *An. subpictus* in this coastal region of India has not been conducted. To comprehend its bionomics and transmission dynamics, the study was conducted. Mosquito collections were carried out for one year using standard entomological methods in selected urban and rural areas of North and South Goa districts. Vector incrimination, sibling species identification and host blood feeding behavior were investigated through dissection and PCR. A total of 56,290 mosquitoes were collected. *An. subpictus* was 14.13% of the total Anophelines and its per trap density (PTD) was found to be higher in the North Goa study areas as compared to the South Goa study areas. *An. subpictus* human bait landing collection (HBLC) rate of indoor collection was higher in North Goa study areas. The man hour density (MHD) of outdoor resting collection (ORC) of this species was found to be greater or equivalent to the MHD of indoor resting collection (IRC). The change in the biting behaviour of *An. subpictus* is observed. The species was found positive for Plasmodium infection throughout the study period. This study shows the potential role of *An. subpictus* to be an emerging secondary malaria vector in the western coastal part of India

Abstract Reference: 20343
Mode of Presentation: Poster Presentation
Topic: Session 1 - Virology

Assessment of signal transducer and activator of transcription-1 (STAT1) expression and level of phosphorylation in human metapneumovirus infected cells

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Abstract Content

Human metapneumovirus (HMPV) is a leading cause of respiratory infections in infants, the elderly and immunosuppressed people. Type I interferon is one of the first lines of defense against viral infection. Thus, it is a target for vaccines design and therapeutic drugs. Our lab has demonstrated that infection with an HMPV A2 genotype strain could lower STAT1 expression and impaired STAT 1 activation in response to type I Interferon treatment compared to mock infected cells. However, the question remains whether this feature of HMPV is conserved throughout all lineages. This project aims to assess the ability of infection with other HMPV genotypes (A1, B1, B2) to downregulate type I interferon signaling through inhibition of STAT 1 phosphorylation and for potential impairment variability among the genotypes. Infection of rhesus monkey kidney epithelial cells was conducted with all 4 HPMV genotypes and treatment with type I IFN after 24 h at an MOI of 0.5. Quantification of STAT 1 expression and phosphorylation level were assessed through western Blot and prism software. Results suggest that STAT 1 phosphorylation level is significantly lower in all infected IFN treated cells except for A1; for which, we will conduct infectivity assay at different MOI to determine possible reasons. For future steps, we will look into HMPV small hydrophobic protein’s role in downregulating type I IFN and its variability across the genotypes. HMPV is a leading cause of acute respiratory illness. This might bring new insight for vaccines design and drug development.

Abstract Reference: 20361
Mode of Presentation: Poster Presentation
Topic: Session 1 - Malaria

Efficacy of artemether 20 mg-lumefantrine 120 mg for the treatment of uncomplicated *Plasmodium falciparum* malaria in Guinea-Bissau in 2021

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Abstract Content

Artemether-lumefantrine has been the recommended first-line medication for uncomplicated malaria by Plasmodium falciparum in Guinea-Bissau since 2006. The present study evaluated the efficacy and safety of artemether-lumefantrine for the treatment of uncomplicated malaria to inform policy. A single-arm prospective cohort study with follow-up until day 28 after treatment was carried out at the health centers: Buba, Bairro Militar, Gabú, and Cantchungo located in four regions, from September to November 2021. Children aged 6 months to 11 years with uncomplicated malaria were included, treated under supervision, and followed up weekly on clinical and parasite clearance through microscopy. Therapeutic efficacy assessed through adequate clinical and parasitological response (ACPR) was 96.3% (95%CI: 92.2-98.6) on day 28 of follow-up. After PCR Correction, efficacy was 97%; two cases (2.2%; 95%CI: 0.3-7.7) with early treatment failure; one (1.1%; 95%CI: 0.0-6.0) with late clinical failure and zero cases with late parasitological failure. On day 1 after treatment 13% had a fever and on day 2 only 2.7%. Children with parasitemia on day 2 were 25%, on day 3 only 3.6%, and 1.8% on day 7. No serious adverse events were recorded during the study. These results corroborate other studies in West Africa, which showed the effectiveness of Coartem® from around 100% in Benin to 93% in Ivory Coast. The efficacy observed is considered adequate by the WHO (≥ 90%) so it is recommended that the drug continues to be used as the first line for treating uncomplicated malaria in the country.

Abstract Reference: 20362
Mode of Presentation: Poster Presentation
Topic: Session 1 - One Health

Community-based intervention in vector control strategy: A systematic review

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Abstract Content

As part of WHO's One Health initiative, vector-borne disease control requires multidisciplinary and community involvement. This review examined community vector control intervention methods, their efficacy, and their drawbacks. The study was conducted following PRISMA guidelines and extracted data from four medical databases, i.e. PubMed, Clinical Key, ProQuest, and ScienceDirect, within 2014 and 2023. The search used keywords "community intervention", "vector control", and "mosquito". Filter was set for full text, article source, scholarly journal, and publication date within the last ten years. Review papers and papers that lacked a study on community intervention were omitted. A total of 1,035 articles were retrieved during the initial search. Thirty-two full-text articles were selected after screening and assessed for eligibility. Fifteen papers were finally included in the qualitative analysis. Studies focused on arbovirus or malaria vectors, designed in RCT, pre- and post-intervention surveys, community-based implementation surveys, or qualitative research. The interventions most commonly applied were community-driven vector population control and community education. Overall, there was improvement in outcome measures, e.g. entomological indices, community knowledge and practice, cost, and disease incidence. Some studies posed low perception and acceptance. There were several modes of intervention that could be applied in the community. The evidence from this study will be beneficial, particularly in resource-limited settings. This review consistently demonstrated a positive trend in favor of community intervention for managing mosquito vectors.

Keywords: integrated vector management, vector-borne diseases, One Health

Abstract Reference: 20364
Mode of Presentation: Poster Presentation
Topic: Session 1 - Bacteriology

Distinguishing *Chlamydia psittaci* from community-acquired pneumonia by using Taqman hydrolysis probe PCR assay incorporating a synthetic double-stranded gene fragment as control

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Abstract Content

C. psittaci is an obligatory intracellular Gram-negative microorganism responsible for psittacosis. Birds act as an important reservoir and excrete the infectious spore-like form into environment that can persist for 15 days to 2 months. Infection in humans occur through inhalation. Early detection is key to better clinical outcomes and outbreak management. In this study, we described a novel real-time PCR for the detection of *C. psittaci* DNA in clinical respiratory specimens. The developed primer and probe amplify *C. psittaci ompA* gene that encodes for an antigenic major outer membrane protein. The assay was evaluated 29 microorganisms and 30 symptomatic human DNAs, and as well as a synthetic double-stranded gene fragment that serve as positive control. Upon testing, no undesired amplification was observed in both non-*C. psittaci* microorganisms and the human DNAs. In conclusion, the developed real time PCR assay was specific for the detection of *C. psittaci* DNA and warrant further analytical and clinical evaluation for clinical and veterinary fields.

Abstract Reference: 20386
Mode of Presentation: Poster Presentation
Topic: Session 1 - Malaria

Prevalence and epidemiological risk factors associated with *Plasmodium inui* infection among *Macaca fascicularis* in Peninsular Malaysia

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Abstract Content

Simian malaria caused by parasites of the genus *Plasmodium* is endemic in Malaysia, with many zoonotic infections reported in Malaysia yearly. *Plasmodium inui* is among the species which naturally infects Long-tailed macaques (*Macaca fascicularis*) and has been demonstrated to be able to infect humans experimentally. In spite of its zoonotic potential, there remains a dearth of published information on the epidemiology of *P. inui* in Malaysia, and little is known about its zoogeographical distribution and transmission dynamics. The present study was therefore undertaken to determine the prevalence and epidemiological risk factors associated with *P. inui* infection among *M. fascicularis* in Peninsular Malaysia. A total of 1587 *M. fascicularis* blood samples were collected from 122 locations throughout the country, and nested PCR was performed to detect *P. inui* infection. The prevalence of *P. inui* was 22.9%. Multivariate regression analysis revealed that host age, spatial sampling zones, habitat type, and elevation of the sampling areas were significant ($p<0.05$) risk factors for *P. inui* infection among the macaques examined. The adult macaques had the highest prevalence (60.0%) and twice the odds of infection (OR=2.002, 95%CI=1.253, 3.197) compared to the conspecifics in the other age groups. Macaques inhabiting the Midwest region of the country had the highest parasite prevalence (OR=3.907, 95% CI=2.410, 6.352), with numerous infection hotspots having >75% infection rates. The macaques sampled from the forest recorded the highest infection rate (28.4%) followed by those sampled in the sub-urban (26.7%) and urban (25.2%) areas. Higher prevalence of infection was also noted for the macaques sampled in habitats further away from the coast (>60km) and those inhabiting the inland at higher elevations (>80m above sea level). The present study constitutes the first attempt in Southeast Asia to screen a large number of macaques and to determine the epidemiological risk factors for *P. inui* infection among the sylvatic macaque hosts. The data obtained from this study is envisaged to provide a better understanding on the epidemiology and spatial distribution of this potentially zoonotic parasite in this country, and to facilitate further surveillance and control programs to be initiated both locally and in the Southeast Asian region.

Abstract Reference: 20391
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Case report: Discovery of *Paragonimus westermani* lung flukes in tiger (*Panthera Tigris*)

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Abstract Content

Paragonimiasis is a typical food-borne parasitic zoonosis caused by lung fluke's trematodes of the genus *Paragonimus*. The first and second intermediate hosts of these flukes are typically freshwater snails, crabs, and crayfish. Recently, the National Wildlife Rescue Centre, Sungkai, Perak conducted a postmortem examination of two adult male wild tigers (*Panthera tigris jacksoni*) that had died. The lung samples of the tigers were hemorrhaged with general multifocal nodules in the ventral part, which were sent to the laboratory for identification. Upon examination, flukes were discovered inside the nodules. The flukes were stained using Aceto Alum Carmine stain and mounted for identification. The flukes were identified as *Paragonimus westermani* based on their morphology, with oral and ventral suckers of similar size placed on the anterior side of the body. It is important because various carnivorous species including felids, canids, viverrids, mustelids, some rodents, and pigs can serve as reservoir hosts for *Paragonimus* spp. Humans can become infected after eating raw freshwater crabs or crayfish that have been encysted with the metacercaria of *Paragonimus* spp.

Abstract Reference: 20393
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Helminthiasis in ruminants diagnosed by the Veterinary Research Institute (VRI) from 2021 to 2023

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Abstract Content

Helminthiasis is a serious problem caused by parasitic worms that can have a significant impact on livestock production. It can lead to a range of health problems for animals including anaemia, nutrient deficiency, low immunity, and even death. This study aims to assess helminth infestation in ruminants specifically sheep, goats, and cattle from 2021 to 2023, using samples received at the Veterinary Institute in Ipoh, Perak. The diagnostic methods used included floatation, sedimentation, and McMaster technique. Out of 1,036 faecal samples, 743 (71.72%) were positive for helminthiasis. Among ruminants, goats were highly infested followed by cattle and sheep with 73.61% (357 out of 485), 72.24% (203 out of 281), and 67.78% (183 out of 270), respectively. Helminth ova detected in goats mostly were strongyle (63.71%), followed by *Strongyloides* spp. (8.25%) and *Moniezia* spp. (1.65%). For cattle, 60.5% were infested by fluke, followed by strongyle and *Moniezia* spp. at 11.03% and 0.71%, respectively. In sheep, strongyle (61.85%), *Strongyloides* spp. (3.70%), and *Moniezia* spp. ova (2.22%) were detected. Based on the helminth categories, most of the infestations were nematodes (53.76%), followed by trematodes (16.41%) and cestodes (1.54%). This study revealed that small ruminants were mainly infested by nematodes, while large ruminants were more likely to be infested by trematodes. To minimise the economic losses in ruminant livestock, it is recommended that routine monitoring of helminthiasis in the farm should be performed, in order to provide advisory services on deworming and health management.

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Mode of Presentation: Poster Presentation
Topic: Session 1 - Entomology

A survey on potential disease vectors in cattle and sheep barn facilities in Veterinary Research Institute, Ipoh, Perak

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Abstract Content

This study aims to survey the potential disease vectors for cattle and sheep in animal facilities at the Veterinary Research Institute (VRI), Ipoh. Six commercial insect traps were placed within 50 meters of the animal facilities. Three traps per facility were set up in three different locations, labelled as indoor (I), outdoor (O), and environment (E). The traps were placed for three consecutive weeks, from week 1 to week 3 for 12 hours, overnight prior to collection. From this study, a total of 4,147 insects were trapped, including 1,946 and 2,201 insects from cattle and sheep barn, respectively. Among the insects, 176 (4.24%) were biting insects, with 90 (4.62%) from cattle facilities and 86 (3.91%) from sheep facilities. For cattle, 18 (20.00%) biting mosquitoes and 72 (80.00%) biting midges were detected. These were identified as *Aedes* spp. (7.78%), *Culex* spp. (12.22%) and *Culicoides* spp. (80.00%). Whereas, for sheep, 23 (26.74%) biting mosquitoes and 63 (73.26) biting midges were detected, with *Aedes* spp. (17.44%), *Culex* spp. (9.30%) and *Culicoides* spp. (73.26%) were identified. No biting flies were found during the study. Based on locations, most biting insects were trapped indoors (I), with 67 (38.07%) biting insects, followed by outdoor (O) and environment (E), with 64 (36.36%) and 45 (25.57%) biting insects, respectively. This study showed the importance of vector control to limit the population of biting insects, as these potential vectors were discovered in the observed animal facilities.

Abstract Reference: 20395
Mode of Presentation: Poster Presentation
Topic: Session 1 - Vector-Borne Diseases

Retrospective study of trypanosomosis cases in cattle and deer in Perak

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Abstract Content

Trypanosomosis is a disease caused by a flagellated blood protozoan namely *Trypanosoma* spp. This parasite is transmitted by tsetse, tabanid, or other biting flies. The objective of this study is to determine the status of trypanosomosis in cattle and deer in Perak, Malaysia by retrospective assessment of the cases submitted to the Veterinary Research Institute (VRI). A total of 3,434 fresh blood samples (291 cases) including 1,761 cattle (186 cases) and 1,673 deer (105 cases) were screen for blood protozoa from 2017 to 2022. The samples were stored and transported at 4°C to the Parasitology Laboratory, VRI and underwent thin blood smear, buffy coat, and haematocrit concentration technique for screening. The results showed that 21 out of 291 cases (7.21%) detected positive for trypanosomosis, with 5 cases (2.69%) in cattle and 16 cases (15.24%) in deer. In terms of the total number of samples, 68 (1.98%) out of 3,434 were positive for trypanosomosis, with 10 (0.57%) from cattle and 58 (3.47%) from deer. Among positive cases, 68 (18.84%) out of 361 blood samples were detected with *Trypanosoma* spp., with 10 (13.33%) from cattle and 58 (20.28%) from deer. The PCV values for samples positive with *Trypanosoma* spp. were 19.50±6.84 for cattle and 36.59±5.83 for deer. The study revealed a low occurrence of trypanosomosis in Perak for cattle and deer over six years. Understanding the current disease status is important for developing future mitigating strategies. Controlling the biting flies is one of the efforts to minimise the transmission of the disease.

Abstract Reference: 20399
Mode of Presentation: Poster Presentation
Topic: Session 1 - Entomology

Diversity of sand flies and molecular identification of sand fly-borne pathogens from different regions in Thailand and Southern Vietnam.

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Abstract Content

Sand flies, belonging to the Psychodidae family, represent small, hairy insects that serve as significant vectors in various medical and veterinary diseases. Despite being recognized by the World Health Organization as a Leishmaniasis- endemic area, Southeast Asia lacks comprehensive information on the diversity and biology of sand flies. This knowledge gap poses challenges in sand flies identification and vector incrimination. To address this, our study aimed to survey sand fly biodiversity and screen for sand fly-borne pathogens in both Thailand and Southern Vietnam. Sand flies were collected using CDC light traps, morphologically identified, and molecularly confirmed using mitochondrial *cytochrome oxidase c subunit* I (*COI*) and mitochondrial DNA *cytochrome b* (*cytb*). A total of 3539 sand flies were collected, with 78.8% (2786 specimens) from Thailand and 21.2% (753 specimens) from Vietnam. After removing damaged specimens, fourteen sand fly species belonging to the genera *Phlebotomus*, *Sergentomyia*, *Idiophlebotomus*, *Chinius*, and *Grassomyia* were identified. While no *Leishmania* DNA was detected, in Thailand, *Trypanosoma* spp. was found in five pools of *Id. asperulus* sand flies, and in one pool each of *Ph. stantoni* and *Ph. betisi* sand flies. In Southern Vietnam, one pool of *Se. silvatica* from An Giang was positive for anuran *Trypanosoma* spp. This study provides the first morphological and molecular characterization of sand flies in Southern Vietnam and offers a comparative analysis with Thailand's sand flies and pathogens. The acquired knowledge on sand fly diversity and the pathogens they harbor is essential for mitigating and controlling sand fly-borne diseases in endemic areas.

Abstract Reference: 20401
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Nutritional and health status of school-aged children in Sangthong district, Vientiane capital, Laos: A focus on parasitic infections and anemia

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Abstract Content

The study aimed to assess the nutritional and health status of school-aged children in Sangthong district, Vientiane Capital, Laos, with a focus on intestinal parasitic infections and iron-deficiency anemia. A cross-sectional study was conducted on 323 primary school children. Height and weight were measured. Stool samples and hemoglobin levels were analyzed using kato-katz methods and HemoCue, respectively. Hygiene and dietary practices were assessed using structured questionnaires. Harada-Mori cultures and molecular diagnostic methods characterized hookworm species. The overall parasitic infection rate was 10.04% (28/279). The most common infections were hookworm (5.38%), *Enterobius vermicularis* (1.79%), *Opisthorchis viverrini* (1.43%), and *Trichuris trichiura* (1.08%). Hookworm infection intensity was low (average EPG 204.8 ± 359.5845). Molecular analysis identified *Necator americanus* and *Ancylostoma ceylanicum*. No significant risk factor differences were found between hookworm-positive and negative individuals. Anemia prevalence was 19.25% (62/322). Frequent consumption of iron-rich animal products significantly reduced anemia risk (aOR: 0.18; 95% CI: 0.04-0.76; p=0.020). The average BMI was 15.55 ± 2.729 and with 8.36% of students classified as thin (BMI<-2SD) and 2.17% as severely thin (BMI<-3SD). Stunted growth (HAZ<-2SD) was observed in 5.57% of students. The low prevalence of parasitic infection may result from proper sanitation practices, footwear usage, and deworming programs. The study highlights the importance of healthy eating habits in addressing malnutrition and improving hemoglobin levels. These findings provide valuable insights into the status of parasitic infections and emphasize the critical role of dietary intake in enhancing the nutritional well-being of primary school children in Laos.

Abstract Reference: 20403
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Exercise reduces parasitic infection: A possibility?

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Abstract Content

According to the WHO, one-third of all deaths worldwide are due to infectious and parasitic diseases, and approximately two million deaths annually are attributed to physical inactivity. It is reported that 60 – 85% of the world's population lives a sedentary lifestyle; many do not exercise as part of their lifestyle. The study aims to determine the effect of exercise on parasitic infection in humans. Among all the searched databases from 2010 to 2023, six articles were eligible to be included in this systematic review. It is noted that children were exposed to high-intensity exercise as opposed to adults, medium-intensity exercise. The causal agents include blood protozoan (*Trypanosoma cruzi*), blood helminths (*Schistosoma haematobium* and *Schistosoma mansoni*) and intestinal helminths (*Trichuris trichiura*, *Enterobius vermicularis*, and *Ascaris lumbricoides*). Children in Africa and South America were infected with *Schistosoma* spp., blood protozoa, while children in China were infected with *Trichuris trichiura*, an intestinal parasite. The adults in the American continent were infected with *Trypanosoma cruzi*, which is typical in that region. In general, these studies showed various associations between exercise and parasitic infections. Overall, exercise may have a more positive impact on the health status of parasitic-infected adults than children. This study concluded that while exercise may improve the health status of parasitic-infected adults, it is the opposite for children. Nonetheless, future studies could focus on carefully selected exercises suitable for children to achieve a similar outcome as adults. Nevertheless, exercise may be considered a non-pharmacological intervention to improve adults' health status.

Abstract Reference: 20410
Mode of Presentation: Poster Presentation
Topic: Session 1 - Vector-Borne Diseases

Comparative analysis of duck tembusu virus cluster 1 and cluster 2.1 in *Culex tritaeniorhynchus*

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Abstract Content

Duck Tembusu virus (DTMUV) is an emerging mosquito-borne flavivirus that causes agents of newly emerging duck egg-drop syndrome and severe neurological disorders. The viral RNA genome consists of a single open reading frame (ORF) that is translated into three structural (envelope (E), membrane precursor (prM), and capsid (C)) and seven nonstructural (NS1, NS2A, NS2B, NS3, NS4A, NS4B, and NS5) proteins. NS5 is the largest and most conserved flaviviral protein, which is comprised of an RNA-dependent RNA polymerase domain. The virulence of DTMUV in ducks is potentially associated with the virus genotype. Currently, DTMUV is classified into three distinct clusters based on significant genetic divergence: cluster 1, cluster 2 (subdivided into 2.1 and 2.2), and cluster 3. In this study, we explore the infectivity patterns of DTMUV cluster 1 (DTMUV1) and cluster 2.1 (DTMUV2.1), which are detected through various surveys across Southeast and East Asia in the primary mosquito vector, *Culex* (*Cx*.) *tritaeniorhynchus*. Our objective was to explore the relationship between the mosquito vector and DTMUV genotype, intending to determine whether the mosquito vector alters the virus and influences the infectivity characteristics in vertebrate cells. We found that DTMUV1 underwent higher replication than DTMUV2.1 in mosquito salivary glands and saliva. Furthermore, DTMUV1 from mosquito saliva produced larger plaque sizes in baby hamster kidney-21 (BHK-21) cell culture than DTMUV2.1 derived from either cell culture or mosquito saliva. Our findings collectively suggest that the amino acid composition of DTMUV1 and DTMUV2.1 can be modified within *Cx. tritaeniorhynchus* in a manner that can augment viral virulence and potentially worsen virus transmission.

Abstract Reference: 20411
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

Diversity and seasonal abundant of questing ticks collected in wildlife habitat in Eastern Thailand

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Abstract Content

Ixodid ticks, crucial vectors for tick-borne diseases (TBDs), pose a public health concern worldwide, including in Thailand. Recreation areas in wildlife habitats are deemed high-risk zones for tick exposure and the emergence of TBDs in humans. Although much work has been done in foreign countries, only a few data about questing ticks in wildlife habitats in Thailand have been reported. This study aimed to determine the seasonal diversity of ticks in Khao Kheow-Khao Chomphu Wildlife Sanctuary, Chon Buri, Thailand. A total of 1,331 immature questing ticks were collected from dragging from November 2021 to March 2023. The proportion of collected larvae was highest in February 2022, while the number of nymphs peaked in December 2021. Of 80 tick pools, 45 pool samples were selected for molecular identification. *Haemaphysalis* (*H.*) *lagrangei* (27/45; 60.0%) is the predominant tick inhabiting this area, followed by *H. wellingtoni* (3/45; 6.67%), *H. shimoga* (3/45; 6.67%), *H. obesa* (2/45; 4.44%), *Dermacentor auratus* (5/45; 11.11%), *Rhipicephalus microplus* (2/45; 4.44%), and *Amblyomma integrum* (3/45; 6.67%). Notably, *A. integrum* has recently been recorded at the molecular level in Thailand. *H. lagrangei* is primarily parasitized on wild ungulates as well as small mammals and occasionally humans. Given that the cool season typically spans from November to February each year in Thailand, the highest number of ticks found during this period highlights the higher potential risk of tick exposure. Visitors should be advised to take more precautions during these times.

Abstract Reference: 20418
Mode of Presentation: Poster Presentation
Topic: Session 1 - Vector-Borne Diseases

Serological and molecular epidemiological features of dengue virus in Sabah, Malaysia

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Abstract Content

Dengue, a *mosquito-borne tropical disease caused by dengue viruses (DENVs),* is endemic in more than 128 countries including Malaysia (a hyperendemic country for dengue). Since most of the studies conducted in Peninsular Malaysia, there are limited data on DENV serotype and genotype distribution from Malaysia, specifically Sabah. We determined the serological and molecular epidemiological characteristics of DENVs in patients from Sabah during 2019-2020, serum samples were collected from febrile patients attending a district hospital. They were subjected to virus isolation, serological tests, viremia level measurements, and whole-genome sequencing. Among the 188 serum samples, 89 have DENVs (20 DENV-1, 46 DENV-2, 20 DENV-3 and 1 DENV-4) as detected by quantitative real-time PCR. There were 38 DENV isolates (13 DENV-1, 11 DENV-2 and 14 DENV-3). About 68% of samples with isolates were NS-1 positive and 20% were IgM positive. Primary DENV infection was mostly observed in 1–30-year-old patients; secondary infection was mostly in those with >40 years of age. The predominant serotype was DENV-2; the highest viral load was in DENV-3. Isolates belonged to DENV-1 (genotype I), DENV-2 (cosmopolitan genotype), and DENV-3 (genotypes I and III) and were phylogenetically related to the reported genotypes from Malaysia, Indonesia, and the Philippines. Continuous molecular surveillance of DENV will help improve in the general understanding of dengue dynamics in this region, and thus, will contribute to disease prevention and management.

Abstract Reference: 20419
Mode of Presentation: Poster Presentation
Topic: Session 3 - Bacteriology

A case report of *Empedobacter falsenii* bacteremia in Malaysia

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Abstract Content

Empedobacter falsenii, previously known as *Wautersiella falsenii*, is a rare cause of infection, with a few cases described in immunocompromised and hospitalised patients. It is an aerobic, non-motile, non-fastidious and non-fermenting gram-negative rod bacterium. It has been isolated from various samples, including both clinical and non-clinical samples. We present the case of a 70-year-old man with underlying dyslipidemia who presented to the emergency department with painful swelling of the right leg, accompanied by fever, nausea, vomiting, loose stools and lethargy. He was admitted with an initial diagnosis of right leg cellulitis. Blood cultures taken upon admission identified *Empedobacter falsenii* using matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF) and 16s rRNA sequencing. Antimicrobial sensitivity testing revealed multiple drug resistances, and the bacteria were susceptible to ciprofloxacin, cefoperazone, co-trimoxazole and vancomycin. The patient was initially treated with intravenous cefuroxime 1.5mg three times daily, which was later switched to intravenous ciprofloxacin 500mg twice daily for five days. A repeated blood culture one week after admission showed no growth. The patient was discharged in good condition with oral ciprofloxacin 500mg twice daily for two weeks. Bacteremia caused by *Empedobacter falsenii* is extremely rare. There was only one other case reported recently in 2023 involving a man with liver cirrhosis and chronic leg ulcer. The significance of *Empedobacter falsenii* in clinical practice warrants further study, particularly concerning its epidemiology and the mechanisms underlying its multidrug resistance.

Abstract Reference: 20428
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Study of prevalence of blood parasitosis in humans and non-human primates in an animal rehabilitation center in The Democratic Republic of The Congo

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Abstract Content

Many tropical diseases, such as Malaria, and several Neglected Tropical Diseases are due to parasites transmitted by blood-sucking vectors with a wide variety of animal reservoirs. Highly sensitive and specific molecular diagnostic tests, such as PCR, are vital for the early detection, control and eradication of these diseases which should be conducted under a multidisciplinary approach including their possible reservoirs. This work aims to study the prevalence of blood parasitic infections in humans and non-human primates (NHP) from an animal rehabilitation center in Lwiro in the Democratic Republique of Congo using a real-time PCR for blood parasites (multiplex RT-PCR-sp) for screening *Plasmodium* spp., Trypanosomatidae and filariae. Blood from humans and NHP were analysed by Multiplex RT-PCR-sp and results were confirmed by microscopy, by specific RT-PCRs and by Sanger sequencing. Infection with *Plasmodium* was detected in 43% of cases and filariae in 30%, with a 13% of coinfections. No cases of trypanosomatids were characterized. Specific PCR and sequencing confirmed results showing the presence of *P. falciparum* only in humans and *P. gaboni* in chimpanzees. Filariae (*Mansonella* spp. and *M. perstans*) were found only in NHP. The RT-PCR-sp has confirmed its usefulness, showing excellent sensitivity. Furthermore, due to the similarities between *P. falciparum* and *P. gaboni* by microscopy, including the banana-shaped gametocytes, the method plus sequencing may be a good way to avoid possible misidentification of *P. falciparum* in NHP. The presence of *Mansonella perstans* in NHP confirmed its role as reservoirs for human mansonellosis.

Abstract Reference: 20429
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

Assessment of pfdhfr, pfdhps, pfmdr1 and pfcrt *P. falciparum* molecular markers associated with resistance in Ogbosmoso, Southwestern Nigeria

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Abstract Content

Nigeria is the world's leading country in number of malaria cases. To control malaria disease a proper diagnosis and effective antimalarial treatment are required. The aim of this study was to determine SNPs in *pfdhfr*, *pfdhps*, *pfmdr1* and *pfcrt P. falciparum* genes and its relationship with resistance to anti-malarial drugs in southwestern Nigeria samples. Dried blood samples from schoolchildren were transferred to the National Centre of Tropical Medicine, Spain. *P. falciparum* positive samples were selected to screen resistance markers using a specific nested-PCR and Sanger sequencing. 105 samples were analyzed. Prevalence of triple *pfdhfr* mutation (S108N-N51I-C59R) was 96.19%, whereas the I164L mutation was absent. The new emerged I431V *pfdhps* SNP was detected in 20% of the samples, mostly in *pfdhfr/pfdhp*s irnI/vagKgs (6.67%) and irnI/vagKgA (6.67%) haplotypes. While K540E *pfdhps* mutation was absent, the prevalence of A613S and A581G was 24.73% and 58.10%, respectively. Findings showed that *pfdhfr/pfdhps* irnI/ISgKAA and irnI/IagKAA haplotypes (partially resistant) were present in 20.95% of samples, while fully and super resistant haplotypes were absent. The *pfdhfr* irnI haplotype and SNP A437G in *pfdhps* reached a prevalence of 92.38%. Prevalence of the Ciet *pfcrt* haplotype was 8.57%, and the 86Y allele of *pfmdr1* was absent. High resistance levels were found in *pfdhfr* and *pfdhps* markers, with the triple *pfdhfr* mutation almost fixed, as was the A437G *pfdhps* allele. The absence of K540E agrees on its geographical distribution, opposite to the I431V mutation. Surveillance of resistance markers is essential to malaria treatment strategies.

Abstract Reference: 20432
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Dynamic changes of liver macrophage polarization induced by *Clonorchis sinensis* infection in mice

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Abstract Content

Clonorchis sinensis infection can cause diseases such as cholangitis and liver fibrosis. Liver macrophages are important factors of innate and acquired immunity, and play important immunomodulatory roles in helminth infection. In this study, the mRNA levels of M1-related markers iNOS, CD86 and IL-1β and M2 related markers Arg1, CD206 and Ym1 in primary liver macrophages of mice at 0, 1, 2, 3, 4, 6, 8 and 10 weeks after infection with *Clonoris sinensis* were detected by qRT-PCR. The objective is to analyze the dynamic changes of liver macrophage polarization during *Clonorchis sinensis* infection. The results showed that mRNA levels of M1-type related markers were significantly increased at 1 to 2 weeks of infection, significantly decreased at 3 to 4 weeks of infection, polarization was significantly increased again at 6, 8 and 10 weeks of infection, and mRNA levels of M2-type related markers were significantly increased throughout the infection stage. In summary, the polarization of M1-type liver macrophages increased significantly in the early stage of infection (weeks 1 and 2), decreased in the stage of egg discharge (weeks 3 and 4), increased again in the middle and later stages of infection (weeks 6, 8 and 10), and significantly increased in the entire stage of infection. Therefore, by analyzing the mRNA expression of polarization markers of M1/M2 type liver macrophages in mice at different stages of *Clonorchis sinensis* infection, the dynamic change of polarization was analyzed, which would provide insights for better control of Clonorchiasis.

Abstract Reference: 20433
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Mitochondrial genome characterization and genetic evolution of *Rhabdias bufonis*

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Abstract Content

Rhabdias bufonis is an important parasitic nematode in the intestinal tract of frogs, and severe infection can lead to host death. At present, the taxonomic status of *R. bufonis* is still controversial. Mitochondrial (mt) genome is a powerful tool for parasite taxonomy, population genetics and systematics. Then it is meaningful to enrich the mitogenomic data and investigate the phylogenetic relationships of the family. In this study, the *R. bufonis* were collected from intestinal tract of wood frogs in Heilongjiang Province, and the complete mt genome sequence was amplified by polymerase chain reaction and sequenced in the NCBI database. The characteristics of mt genome and the phylogenetic analysis were performed to clarify the classification of Rhabditida nematode. As a result, the complete circular mt genome of *R. bufonis* was 14,939 bp in length. It contained 12 protein-coding genes, 22 tRNA genes, two ribosomal RNA genes and one non-coding region. In the complete genome of *R. bufonis*, there were 18 gene spacer regions ranging from 2 to 55 bp, with an AT content of 75.27%. The phylogenetic analysis showed that *R. bufonis* and *R. kafunata* branched a sister clade, which had more closely relation. This study provides molecular basis for further research on the genetic and evolutionary relationship of Rhabditida nematode, and lay a foundation for the prevention and control of *R. bufonis* disease.

Abstract Reference: 20435
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

Susceptibility of malaria vectors to insecticides in Guinea Bissau, 2022

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Abstract Content

Malaria stands as one of the top ten causes of death in Guinea-Bissau. The use of Pyrethroid long-lasting insecticidal nets as a vector control method of anophelines has contributed to the emergence and increase in resistance. This study aimed to assess the susceptibility of malaria vectors to insecticides and explore molecular mechanisms associated with resistance phenotypes. A cross-sectional entomological study was conducted from September to October 2022 with mosquitoes from four regions of Guinea-Bissau: Bissau, Gabú, Buba, and Cacheu. They were monitored for species ID and insecticide resistance, using diagnostic and intensity WHO bioassays and molecular assays. Molecular analysis identified An. arabiensis as the most prevalent species (35%), with mutations associated with kdr-West more prevalent than kdr-East. Resistance to Permethrin and Deltamethrin (sensitivity 13.8%-58.0%) was observed at discriminatory concentrations in all regions. Tests to determine resistance intensity (5x) revealed suspected (89.3%-96.0% sensitivity) resistance to pyrethroids in all regions. The synergistic PBO-permethrin indicated resistance in SAB (76%) and suspected resistance in other regions. PBO- deltamethrin was sensitive (100%) in Bissau but tolerant in other regions. There were a few exceptions in Cacheu (100% sensitivity to deltamethrin) and SAB (98.7% sensitivity to deltamethrin 5x). The results highlight widespread resistance, even at concentrations of 5x, across all regions. Compared to previous studies (2018 and 2021), resistance has increased, even in regions where malaria prevalence was historically low. Regular assessment of malaria vector susceptibility should be integral to malaria prevalence reduction programs to inform policy.

Abstract Reference: 20442
Mode of Presentation: Poster Presentation
Topic: Session 1 - Malaria

Diagnosing aspects of severe malaria and bacterial sepsis: A case report

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Abstract Content

In daily clinical practice, malaria sometimes become challenging. We present a malaria case with the possibility of sepsis due to soft tissue infection. Point of discussion is about deciding whether the patient suffered from severe malaria or sepsis due to bacterial infection which had implication for choosing anti-malarial regimen. A 32-year-old male was consulted by orthopedist because of acute onset fever. Seven days before, he undergoned surgery procedure for crush injury on his right cruris due to gunshot in highly endemic malaria region. He had stable vital signs. Wound base was granulation tissue and some necrotic with pus. Laboratory revealed thrombocytopenia, leucopenia, hyperbilirubinemia, slightly increase serum creatinine, and very high procalcitonin. Malaria microscopic revealed *Plasmodium vivax* in trophozoite and gametocyte stages. He got artesunate injection continued by dihydroartemisinine-piperaquine and primaquine. His condition and laboratory parameters were improved and malaria microscopic became negative after anti-malarial regimen. Severe malaria has similarity with bacterial sepsis. In this case the patient fulfilled sepsis SOFA criteria. On the other hand, hyperbilirubinemia and increasing creatinine also can be found in severe malaria. Procalcitonin itself can be a clue as systemic bacterial infection and also as a prognostic factor in malaria. The consideration for giving artesunate injection was based on the risk if we delayed for treating severe malaria, although it was a vivax malaria which rarely progress as severe malaria. Diagnosing severe malaria concomitance with other condition needs careful consideration about the risk and benefit for early start of anti-malarial regimen.

Abstract Reference: 20447
Mode of Presentation: Poster Presentation
Topic: Session 1 - Malaria

The C-terminal region of the *Plasmodium berghei* gamete surface 184-kDa protein Pb184 contributes to fertilization and male gamete binding to the residual body

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Abstract Content

Malaria is a global health concern, caused by parasites of the *Plasmodium* genus, which undergo gametogenesis in the midgut of mosquitoes after ingestion of an infected blood meal. The resulting male and female gametes fuse to form a zygote, which differentiates into a motile ookinete. After traversing the midgut epithelium, the ookinete differentiates into an oocyst on the epithelial basal side. We investigated membrane proteins with increased gene expression levels from gametes to oocysts in *P. berghei*, utilizing the PlasmoDB. As a result, 184 kDa membrane protein, Pb184 was selected. After confirming the expression of Pb184 through immunofluorescence staining, we examined whether Pb184 is involved in the fertilization using antibodies targeting the C-terminal region of Pb184 and biotin-labeled C-terminal region peptides of Pb184. We found that Pb184 is expressed on the surface of both male and female gametes. The antibody inhibited zygote and ookinete formation in vitro. When mosquitoes fed on parasite-infected blood containing the antibody, oocyst formation decreased on the second day after feeding. Synthesized a biotin-labeled peptides matching the C-terminal region of Pb184 bound to the female gamete and the residual body of male gametes, and inhibiting differentiation into ookinetes in the in vitro culture system. These finding may be useful for the further studying in the fertilization mechanism of Plasmodium protozoa. In addition, there is a potential for their application as future tools to prevent malaria transmission.

Abstract Reference: 20452
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

Comparison study of the eukaryome of three laboratory reared cockroach species

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Abstract Content

Cockroaches, commonly regarded as pests, have been identified as potential reservoirs for an array of fungi and parasites. However, the comprehensive analysis of this biodiversity within cockroaches remains underexplored. Total DNA was extracted from the gut of 13 individual laboratory-reared cockroaches (*Blattella germanica*, *Periplaneta fuliginosa*, and *Periplaneta japonica*), followed by metabarcoding of the 18S rDNA V9 region using iSeq 100 platform. In the metabarcoding analysis, the protozoan *Nyctotherus* sp. was predominantly observed in most cockroach specimens, and its ciliary motility was confirmed via microscopy. In *B. germanica* samples, the nematode *Blatticola* sp. was identified, while *Leidynema* sp. was identified in *P. fuliginosa*, and *P. japonica*. Furthermore, *B. germanica* showed a higher prevalence of the fungus *Nephridiophaga* sp. compared to other species. *Entamoeba* sp. was detected in *P. fuliginosa* and *P. japonica* samples. This study investigated the eukaryotic community in the gut of three cockroach species and detected various parasites (e.g., *Blatticola* sp., *Leidynema* sp., *Entamoeba* sp., *Nyctotherus* sp.) and fungi (e.g., *Nephridiophaga* sp.). These findings highlight the cockroaches' capacity as reservoirs of various parasites and fungi and shed light on their interactions with the hosts.

Abstract Reference: 20457
Mode of Presentation: Poster Presentation
Topic: Session 1 - Vector-Borne Diseases

Rickettsia in soft ticks from bats in Thailand: A preliminary study

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Abstract Content

Rickettsia species are small, Gram-negative coccobacilli that are obligate intracellular parasites of eukaryotic cells. This genus comprises three pathogenic clades: the spotted fever group, the typhus group and transitional group. Soft ticks are recognized as vectors of several zoonotic pathogens, including *Rickettsia*. Recent studies have reported the presence of *Rickettsia* in bat ticks across various regions. However, there has been no documentation of *Rickettsia* in bat ticks in Thailand. Therefore, this study aimed to investigate the prevalence of *Rickettsia* in bat ticks within Thailand. Bats were captured between February 2018 and February 2023 across ten provinces of Thailand. Each bat underwent morphological identification and was examined for tick infestation. All ticks were identified through both morphological and molecular analysis using morphological keys and conventional PCR targeting the mitochondrial 16S rRNA gene fragment. Subsequently, *Rickettsia* spp. were screened using conventional PCR targeting the *gltA* gene fragment. Among 1,031 bats belonging to 7 bat families, 11 genera, and 28 species, 34 bats harbored 95 soft ticks in the larval stage. These soft ticks were exclusively discovered on two bat species: *Craseonycteris thonglongyai* (33/139, 23.74%) and *Eonycteris spelaea* (1/2, 50%). All soft ticks were identified as *Reticulinasus faini* based on mitochondrial 16S rRNA sequence BLASTn results. Out of the 48 pools, 41 (85.41%) tested positive for *Rickettsia*. The *gltA* sequences showed the highest percent identity with *Rickettsia lusitaniae* from Zambia (GenBank accession no. MN388795). This study reveals the presence of *Rickettsia* in bat ticks in Thailand for the first time.

Abstract Reference: 20459
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Molecular characterization of gastrointestinal protozoa of pigs from southern region Karnataka and its zoonotic significance

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Abstract Content

Intestinal protozoa an apicomplexan parasite distributed worldwide responsible for neonatal diarrhea and poor growth in pigs. So far, no report on intestinal protozoa of pigs from Karnataka state. Hence, work was taken to study the molecular characterization of intestinal protozoan of pigs and zoonotic significance. A total of 336 faecal samples collected from pigs of different age groups and rearing system were screened by sedimentation, flotation and formal ether methods. Sixty samples were subjected to nested-PCR by targeting 18S rRNA gene for *Cryptosporidium* spp., *Entamoeba* sp. and *Cystoisospora* sp. and β-giardin gene for *Giardia* spp. The sequence and phylogenetic analysis of n-PCR product was carried out by NCBI BLAST. *Cryptosporidium* spp. (19), *Entamoeba* spp. (10), *Cystisospora* spp. (1) and *Giardia* spp. (3) were detected by faecal analysis. The n-PCR targeting 18s SSU rRNA gene revealed positive for *Cryptosporidium* spp. (19) by yielding a single amplicon of 834bp, *Entamoeba* sp. (10) with a single amplicon of 600 bp and *Cystoisospora* sp. (01) with an amplicon of 1500 bp. Whereas, 3 isolates of *Giardia* sp. at an amplicon of 300-400 bp targeting β-giardin gene. However, the sequence and phylogenetic analysis confirms *Cryptosporidium scrofarum* (pig genotype-II), *Entamoeba poleki* and *Cystoisospora suis* in pigs from southern region of Karnataka. The species are identified for the first time in pigs from Karnataka state are of zoonotic significance. The people who are closely associated with infected pigs are under higher risk of infection and the present report serves as surveillance and baseline data for control programs.

Abstract Reference: 20473
Mode of Presentation: Poster Presentation
Topic: Session 3 - Vector-Borne Diseases

Serological study of rickettsial exposure in Papua New Guinea Defence Force personnel

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Abstract Content

Malaria is a known health threat to both Papua New Guinea Defence Force (PNGDF) and Australian Defence Force (ADF) personnel within Papua New Guinea (PNG). However, surveillance on PNG military bases of non-malaria febrile infections is limited. To address this knowledge gap we conducted collaborative epidemiological surveys of PNGDF personnel, as well as family members, to test for key vector-borne and other diseases that may affect military capability. Serological testing against rickettsial diseases was included as part of the survey disease test panel. Cross-sectional surveys involving venous blood collection from PNGDF participants from military establishments at Manus Island and Wewak, East Sepik Province (2019, n=201), Lae, Morobe Province (2023, n=184), and Port Moresby, Central Province (2024, n=400) were conducted. Participant sera were tested by immuno-fluorescence assay (IFA) against a panel of strains from the three rickettsia groups, Spotted Fever Group (SFG), Typhus Group (TG) and the Scrub Typhus Group (STG). The seroprevalence rate to SFG was 5.5% in Wewak/Manus compared with 16.3% in Lae survey participants. For STG, the seroprevalence rate was 12.4% in Wewak/Manus compared with 1.6% in Lae survey participants. The predominant determined seroprevalence rates amongst PNGDF were to the SFG and the STG. However, seroprevalence to these different groups differed quite markedly between survey sites. Rickettsial diseases pose a threat and may account for a proportion of fever-like illness amongst personnel at military bases in PNG. Findings highlight the value in disease risk awareness, and associated mitigation against infection, by military personnel.

Abstract Reference: 20478
Mode of Presentation: Poster Presentation
Topic: Session 1 - Vector-Borne Diseases

Diversity of ticks infested wild boars (*Sus cristatus*) and molecular detection of tick-borne bacteria in Indonesia

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Abstract Content

Ticks are one of the major vectors for several pathogens of zoonotic diseases. To clarify the risk of tick-borne diseases, we investigated ticks infesting wild boar in Indonesia. A total of 116 ticks were collected from 13 wild boars in South Sumatra Province, Indonesia. After dissection to salivary gland and midgut, DNA were extracted from them, followed by detection of partial DNA fragments of rickettsial 17kDa antigen gene, *gltA* gene, ehrlichial *groEL* gene and borrelial *flaB* gene by PCR. In addition, 38 samples of salivary glands were examined for cultivation using BSK medium. *Rickettsia* sp. was detected from a *Dermacentor astrosignatus* and was related with *Rickettsia* sp. (U76907) by 17kDa antigen gene and ticks on Sambar deer, respectively. An ehrlichial DNA fragment was detected from *Haemaphysalis hystricis*. This *Ehrlichia* sp. was closely related with that detected from mosquitoes in China. The DNA fragments of *Borrelia* sp. were detected from *D. astrosignatus* and *D. steini*. This *Borrelia* sp. was closely related with Candidatus *B. ivorensis* that was detected from *Amblyomma variegatum* infesting cattle in Africa. These bacteria detected from ticks on wild boar in Indonesia might become a risk factor of unknown diseases for livestock.

Keywords: Borrelia, ehrlichia, Indonesia, rickettsia, tick, wild boar

Abstract Reference: 20488
Mode of Presentation: Poster Presentation
Topic: Session 2 - Bacteriology

The potential of phthalide compounds against leptospirosis

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Abstract Content

Leptospirosis is one of the re-emerging zoonotic diseases that the number of cases had been increasing continuously in Malaysia. The disease caused by pathogenic bacteria from genus Leptospira by direct contact with the urine of infected animals. Numerous attempts have been made to control the disease especially by chemoprophylaxis but only showed limited success. Therefore, the present study investigates the anti-leptospiral potential of phthalide compounds comprise of Px, Px-Br, Py and Py-Br. The phthalide compound is an organic material that has a basic chemical structure known as isobenzofuranone. The compounds were assayed for anti-leptospiral activity at different concentration ranged from 1 mg/ml to 1 x 10^{-5} µg/ml using broth microdilution method towards *Leptospira interrogans* (serovar Bataviae) and *Leptospira borgpetersenii* (serovar Javanica). On the other hand, DNA damaging properties of phthalide compounds towards DNA of *Leptospira* sp. was done by incubating the bacteria with the presence or absence of phthalide compounds and analyzed by electrophoresis. Among all these four compounds, activity of compound PxBr shows a potential anti-leptospiral agent with an IC_{50} value of 1 x 10^{-2} mg/ml towards L.*interrogans* serovar Bataviae and with IC_{50} value of 1 x 10^{-6} mg/ml towards L.*borgpetersenii* serovar Javanica. In conclusion, among all phthalide compounds, PxBr has the most potential of anti-leptospiral activity by inhibiting the growth of both serovar of *Leptospira* sp.

Keywords: Leptospira, Leptospirosis, Phthalide compound

Abstract Reference: 20500
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Filarial infections imported to the Czech Republic

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Abstract Content

Filarial infections are rarely imported to Central Europe. We present a clinical case series of human filarial infections imported to the University Hospital Bulovka in Prague, Czech Republic, between 2003 and 2023. A 47-year-old man traveled to Cameroon in 2002. In October 2003, a subcutaneous nodule in the sacral region was palpated. He had eosinophilia (2,000/µl) and positive serology for filariasis. The nodule was excised, but antiparasitic treatment was not initiated. In October 2008, he detected three new subcutaneous nodules. Ultrasound revealed the movement of threadlike worms, and onchocerciasis was confirmed through histology of the excised nodule. Treatment with doxycycline and ivermectin was administered. A 54-year-old man visited West Irian (Indonesia) in November 2007. He developed a febrile illness with high eosinophilia (13,860/µl) and seroconversion for filariasis. Although lymphatic filariasis was suspected, thick blood films were negative. The patient was treated with diethylcarbamazine (DEC) or ivermectin regularly from 2007 to 2014. Eosinophilia resolved in 2016, and serology for filariasis is borderline. Two cases of Loa loa infection were imported from the Central African Republic in 2011 and 2020, respectively. Both patients presented with fever, migratory subcutaneous nodules, and high eosinophilia. Diagnosis was confirmed using PCR on the worm removed from the nodule. Treatment with DEC and prednisolone was successful. Filarial infections should be suspected in travelers presenting with fever, subcutaneous nodules, and eosinophilia. As microfilariae detection in blood or skin can be negative, molecular methods should be incorporated into diagnostic procedures.

Abstract Reference: 20502
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Involvement of a pseudokinase pPK4 in the exflagellation center formation in *Plasmodium yoelii*

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Abstract Content

Human malaria is a global health burden that significantly affects pregnant women and young children in Sub-Saharan Africa. Pseudokinases are a class of proteins that resemble typical kinases but cannot catalyze phosphorylation reactions. Several *Plasmodium* pseudokinases are highly transcribed at both the schizont stage and the sexual stage and may have critical roles at both stages. Previously, we reported that one pseudokinase, pPK1, was involved in the invasion into red blood cells (RBCs) and exflagellation center formation using a rodent malaria parasite, *Plasmodium yoelii*. This study characterized another pseudokinase, pPK4, in *P. yoelii*, which is highly transcribed at schizont and male gametocyte stages. An immunofluorescence assay of transgenic parasites expressing Myc-tagged pPK4 revealed that the protein is expressed in the cytosol of the schizont and sexual stages. pPK4 knockout (KO) lines showed significant growth defects, decreased virulence in mice, and a significant reduction in the number of oocysts. *In vivo* RBC invasion assay revealed that invasion, but not egress, was affected. There were no significant differences in gametocytemia and gametocyte egress in either male or female gametocytes; however, there was a significant reduction in the number of exflagellation centers. Thus, we concluded that pPK4 plays an important role in RBC invasion and exflagellation center formation. These phenotypes were similar to those observed in the pPK1-KO lines.

Abstract Reference: 20510
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Fascioliasis in Kazakhstan and Uzbekistan: Millenia-long human-guided pack animal movements throughout the Silk Road underlie the present distributional outline

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Abstract Content

In Kazakhstan and Uzbekistan, *F. hepatica* infects livestock in areas with harsh climates throughout, but with higher prevalences along the southern and western parts of both countries, mainly in sheep but also in goats, cattle, camels, and horses. In its turn, *F. gigantica* appears to be restricted to floodplains of the southern desert zones, in the southwestern Kazakh flat landscape with dry, hot climate, as in the lowlands near the Syrdarya River. A 10-11% infection rate by *F. hepatica* has been reported in sheep from the easternmost Tian Shan, and up to 21% from the Karatau mountains and the foothills in the southernmost central Shymkent Province, including sporadic infection by *F. gigantica*. This distributional frame of fasciolids is the consequence of seasonal movements of sheep and other livestock as a crucial animal husbandry from the earliest times of the Silk Road, including traditional herd migration routes following a pattern with a northward movement of several hundred km in spring, grazing of the northern steppe zone in summer, and a return to the milder south for winter grazing. Such a livestock management adapts to the extreme continental climate of this wide region, with long and very cold winters in the north, and milder temperatures in the south. Rainfall is low, except in the mountains, and decreases from north to south.

Abstract Reference: 20511
Mode of Presentation: Poster Presentation
Topic: Session 1 - One Health

Demographic and socioeconomic barriers to accessing malaria services for Myanmar migrants in Thailand

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Abstract Content

Migrants, often mobile and vulnerable, face significant barriers to accessing routine malaria prevention, diagnostics, and treatment, leading to unchecked malaria transmission. This study aimed to explore the demographic and socioeconomic obstacles to malaria service access for Myanmar migrants residing in Thailand. A cross-sectional study was conducted in early 2024 across three districts near the Thailand-Myanmar border. Quantitative data were collected from Myanmar migrants using standardized questionnaires through face-to-face interviews. Of the 300 participants, only about a quarter (27.3%) had adequate access to malaria services, including prevention, diagnostics, treatment measures, and malaria-related health information. In multiple logistic regression models, factors associated with inadequate access included: i) age over 60 years (aOR:7.63, 95% CI:1.74, 20.58), ii) being accompanied by one to three family members (aOR:3.33, 95% CI:1.06, 8.45), iii) having monthly incomes below 3,000THB (aOR:5.13, 95% CI:1.38, 19.09) and 3,000 to 6,000THB (aOR:3.64, 95% CI:1.06, 12.51), iv) being of Karen ethnicity (aOR:2.13, 95% CI:1.02, 3.84), v) able to speak and understand Thai (aOR:15.18, 95% CI:1.91, 12.41), and vi) having low attitudes (aOR:2.03, 95% CI:1.03, 4.01), and poor preventive and health-seeking practices (aOR:5.83, 95% CI:2.71, 9.55). Meanwhile, having poor malaria knowledge showed a negative association (aOR:0.32, 95% CI:0.15, 0.69). A significant proportion of Myanmar migrants face demographic and socioeconomic barriers to accessing malaria services in Thailand. Tailored interventions are urgently needed to expand access, including recruiting more worksite health volunteers, fostering private sector collaboration with local farm and company owners, and strengthening the roles of ethnic health organizations, alongside continued cross-border collaboration.

Abstract Reference: 20513
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

Species diversity and prevalence of chewing lice (Pthirapthera: Mallophaga) in a poultry farm in Laladon, Bogor

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Abstract Content

Poultry lice are notorious ectoparasites that pose significant challenges to the health and productivity of poultry, thereby affecting their economic value. This study aimed to investigate the diversity, prevalence, and degree of infestation of chewing lice in five different bird species: domestic chicken (*Gallus gallus*), turkey (*Meleagris gallapavo*), fantail pigeon (*Columba livia domestica*), swan geese (*Anser cygnoides*), and Muscovy duck (*Cairina moschata*). Specimens were collected from various body regions and identified using established identification keys. The results revealed the presence of *Menacanthus* and *Menopon* genera in chickens and turkeys, exclusive presence of *Lipeurus* in chickens, *Anaticola* in Muscovy ducks and swan geese, *Colpocephalum* in fantail pigeons and swan geese, *Columbicola* and *Campanulotes* exclusively in fantail pigeons, and *Holomenopon* exclusively in swan geese. The prevalence of lice infestation was determined, with all bird species exhibiting a 100% prevalence, except for Muscovy ducks, which showed a prevalence of 40%. This data on Mallophaga lice in poultry were first fully reported in Indonesia. Moreover, farmers need to be aware of the detrimental effects of chronic lice infestations on poultry health and productivity.

Keywords: Chewing lice, diversity, Indonesia, infestation, poultry

Abstract Reference: 20514
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

Vectors of human and simian Plasmodium parasites in Phatthalung and Songkla provinces of Thailand

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Abstract Content

In the past five years, significant progress has been made in controlling malaria in Southern Thailand. While *Plasmodium* falciparum has nearly disappeared in many areas, the incidence of *Plasmodium knowlesi* malaria cases has risen. We conducted a study to identify malaria vectors in hotspots within the Tamot district, Phatthalung province, and the Saba-Yoi district, Songkla province. A total of 309 *Anopheles* mosquitoes were captured using human landing catches over three nights in February, March, and July 2023. *An. dirus* was the major vector in the Tamot district (91.67%), while the Saba-Yoi district had a species composition of *An. maculatus* (63.7%), *An. minimus* (35.9%), and *An. dirus* (0.4%). *Plasmodium* sporozoite infection was analysed using 18s nested PCR. In the Tamot district, 6 out of 72 *An. dirus* specimens were positive for Plasmodium, with two confirmed as *P. knowlesi.* The species of the other five specimens remain to be confirmed but presumably represent non-human malaria parasites. In the Saba Yoi district, 24 out of 237 *Anopheles* mosquitoes were *Plasmodium* positive. Among these, one *An. maculatus* and one *An. minimus* were infected with *P. malariae*, and one *An. maculatus* carried *P. falciparum*. The remaining 21 positive specimens were negative for human malaria and may represent non-human malaria.This research confirms the presence of *P. falciparum* and *P. malariae* in the Saba Yoi district in 2023, despite the last reported clinical cases in 2019 (*P. malariae*) and 2020 (*P. falciparum*). *An. dirus* is likely the primary vector for *P. knowlesi* in the Tamot district.

Abstract Reference: 20516
Mode of Presentation: Poster Presentation
Topic: Session 2 - Vector-Borne Diseases

Serological evidence of the possible presence of severe fever with thrombocytopenia syndrome virus in Sabah, Malaysia

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Abstract Content

Severe fever with thrombocytopenia syndrome (SFTS) is an emerging tick-borne viral infection endemic in China, Japan and Korea. It is caused by *Dabie bandavirus,* SFTS can develop into hemorrhagic fever and can be turned into fatal. It has been reported from Vietnam and Thailand but not from other Southeast Asian countries including Malaysia. Rich biodiversity and frequent human-animal exposure make this country conducive for SFTS. Therefore, this study was undertaken to assess whether there is serological evidence of possible presence of SFTS virus among the rural population of Sabah. Serum samples were collected from healthy individuals residing in the rural areas of Kudat district of Sabah state, in Malaysian Borneo. Serum samples were subjected to enzyme-link immunosorbent assay and the cutoff value was set at the mean plus three times the standard deviation, 2.5% (53/2089) of the serum samples were positive for SFTS virus-specific IgG antibody. Their age ranges from 1 to 90 years, with equal proportions of males and females. This is the first report of possible presence of SFTS virus in Malaysia and suggest a wide range of exposure to this virus from very young to old. Neutralization assay is underway to confirm SFTS virus exposure. Further studies are needed to understand the epidemiology of SFTS in humans and the presence of this virus in ticks including tick’s distribution for early detection and control of outbreaks.

Abstract Reference: 20518
Mode of Presentation: Poster Presentation
Topic: Session 2 - Vector-Borne Diseases

Association of severe fever with thrombocytopenia syndrome virus between ticks and human host

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Abstract Content

Severe fever with thrombocytopenia syndrome (SFTS) is a tick-borne infectious disease caused by *Dabie Bandavirus* (previously, SFTS virus) characterized by a high fatality rate of approximately 18.2% in Korea. Ticks were collected using tick traps with dry ice in Gangwon Province, Korea in 2022 and 2023, and SFTSV were detected using real-time PCR. A total of 32,452 ticks were collected and *Heamaphysalis longicornis* (*H.longicornis*) accounted for 99.12%, the most dominant tick species, followed by *H. flava* (0.77%), and *Ixodes niponensis* (0.11%). The infection rate (number of positive tick pools / number of tested tick pools x 100) of SFTSV was 15.2%. Of the positive ticks, male and female adult ticks accounted for 5.4% and 35.1%, respectively, and lymph and larvae occupied 13.5% and 45.9%, respectively. SFTSV from ticks belonged to B2 type and A type, and in the phylogenetic analysis, the sequences of SFTSV from ticks were very close to those of patients from the same region. Infection rates of SFTS in ticks peaked in June and October, and this pattern was similar to that of human SFTS. These support the strong association between vector and human in the outbreak of SFTS cases.

Abstract Reference: 20520
Mode of Presentation: Poster Presentation
Topic: Session 2 - Vector-Borne Diseases

Distribution of arthropod vectors and detection of Lumpy Skin Disease (LSD) virus transmission in Indonesia

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Abstract Content

Lumpy Skin Disease (LSD) poses a significant threat to the cattle industry in Indonesia. The primary mode of transmission is through the bites of blood-sucking arthropod vectors, including flies, mosquitoes, gnats, and ticks. Despite its low mortality rate, the high morbidity associated with LSD have a major impact on livestock health. This research aims to elucidate the diversity of arthropod vectors and their role in LSD transmission in Indonesia. Blood-sucking flies were collected using sweep nets around cattle bodies between 09:00 am and 13:00 pm. In addition, mosquito vectors were collected using light traps placed in cowshed and ticks were collected manually. All samples were examined the presence of LSD virus by RT-PCR. Several arthropod vectors were collected in cowshed, included flies (*Stomoxys*, *Haematobia*, *Tabanus*), mosquitoes (*Aedes*, *Anopheles*, *Culex*), *Culicoides*, and ticks (*Rhipicephalus*). Two dominant fly species were *Stomoxys calcitrans* (75,6%) and *Stomoxys sitiens* (10%). Based on RT-PCR of whole body and/or proboscis of vectors, there was no LSD virus detected. This findings provide fundamental insights into the prevention and control of LSD vectors in Indonesia.

Keywords: Blood-sucking vectors, cattle, lumpy skin diseases, vectors

Abstract Reference: 20521
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

The phylogenetic diversity of *Haemaphysalis Longicornis* (Acari: *Ixodidae)* based on sequence of mitochondrial Cox1 gene

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Abstract Content

Ticks are an important vector of human and animal diseases, including Severe fever thrombocytopenia syndrome (SFTS), Rocky mountain spotted fever, Lyme disease, and babesia. *Haemaphysalis longicornis* (*H. longicornis*) is a predominant tick in Korea, a vector of SFTS in Asia, including Korea, China, and Japan. In this study, we analyzed the phylogenetic diversity of *H. longicornis* using the cytochrome c oxidase 1 (Cox 1) sequence (1,600-bp full length), a mitochondrial DNA gene. A total of 11,862 ticks were collected using a flagging method from 17 sites in 9 provinces in Republic of Korea and *H. longicornis* accounted for 99.4%. Based on Cox1 sequence, 71 haplotypes were identified from the *H. longicornis* in Korea and 42 novel haplotypes were found. There were diverse haplotypes in each region, but in particular, Juju province and Gangwon province each had one haplotype. In the phylogenetic analysis, *H. longicornis* were segregated into six distinct clusters, and clade A contains from Gyenggi Kwangju, Gokseong, and Ulju area, as well as sequence from USA, China, New Zealand and Austria. The clade B is predominant and distributed nationwide in Korea. This study shed light on the genetic diversity and population structure of ticks in the Republic of Korea and could contribute to provide a genetic marker for molecular epidemiology of *H. longicornis* and to control of tick and tick-borne diseases.

Abstract Reference: 20524
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Molecular profiles of antifolate drug resistance genes in *Plasmodium vivax* in Pakistan

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Abstract Content

Emergence and spreading of antimalarial drug resistance are a great hurdle to combat malaria. The dihydrofolate reductase (DHFR) and dihydropteroate synthetase (DHPS) of *Plasmodium vivax* are known to be associated with sulfadoxine-pyrimethamine (SP) drug resistance. The present study aimed to analyze the polymorphism of *dhfr* and *dhps* genes in *P. vivax* isolates collected in Pakistan. Blood samples of patients infected with *P. vivax* were collected in Khyber Pakhtunkhwa province, Pakistan in 2021–2022. The *pvdhfr* and *pvdhps* genes were amplified, cloned into TA vector, and sequenced. Mutations associated with SP resistance in *pvdhfr* and *pvdhps* were analyzed. A total 116 *pvdhfr* and 94 *pvdhps* were successfully amplified in Pakistan *P. vivax* isolates. In *pvdhfr*, prevalence of mutations at codons F57L, S58R, and S117N were 1.7%, 31.9% and 46.6%, respectively. The wild-type haplotype $F_{57}S_{58}T_{61}S_{117}$ was the most common (50.4%), followed by the double mutant haplotype $F_{57}\mathbf{R}_{58}T_{61}\mathbf{N}_{117}$ (29.3%). In *pvdhps*, only a single mutation A383G was detected in a low frequency of 2.1%. The wild-type haplotype $S_{382}A_{383}K_{512}A_{553}V_{585}$ was predominated, accounting for 97.9%, followed by $S_{382}\mathbf{G}_{383}K_{512}A_{553}V_{585}$ in 2.1%. Combination analysis of *pvdhfr* and *pvdhps* haplotypes revealed that the most prevalent haplotype was wild type (46.5%), followed by $F_{57}\mathbf{R}_{58}T_{61}\mathbf{N}_{117}$/ $S_{382}A_{383}K_{512}A_{553}V_{585}$ (31.4%). The majority of Pakistan *P. vivax* isolates harbored a wild-type allele of *pvdhfr* and *pvdhps*, suggesting Pakistan *P. vivax* may still be susceptible to SP. However, continuous monitoring of mutations linked to SP resistance is necessary to surveil the evolution of SP resistance in Pakistan *P. vivax* population.

Abstract Reference: 20525
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

A study on *Wolbachia*-dengue-carrying Aedes mosquitoes (Diptera: Culicidae) focuses on the sustainability and frequency of *Wolbachia* in high-rise buildings in Selangor, Malaysia

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Abstract Content

The challenge of dengue control due to the unavailability of a specific medication stresses the importance of releasing *Wolbachia*-carrying mosquitoes through vector control programs. This study investigated the sustainability and frequency of *Wolbachia* in *Wolbachia*-dengue-carrying mosquitoes in two dengue hotspot localities in Selangor. A modified sticky ovitrap was used to collect adult mosquitoes in two *Wolbachia*-releasing areas in Selangor, Kelana Puteri and Kelana D'Putera condominiums. All mosquito samples were subjected to PCR using *wsp*-specific primers for *Wolbachia* detection. Dengue virus was detected using RT-PCR, followed by multiplex-PCR. Out of the 80 *Aedes* spp. collected, *Ae. aegypti* was the most predominant species. More than one-third of *Ae. aegypti* were positive for *Wolbachia*, with 22.9% being superinfected with both *Wolbachia A* and *B* strains. About 61.4% of the species were uninfected with *Wolbachia*. *Ae. aegypti* carrying the *Wolbachia A* strain was also identified, which has previously never been reported. This strain was similar to the one found naturally in *Ae. albopictus*. None of the *Ae. aegypti* and *Ae. albopictus* were positive for dengue virus. This study could serve as a model for local researchers or health authorities to design and plan an effective field release and monitoring of *Wolbachia*-infected mosquitoes.

Abstract Reference: 20528
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Neglected tropical parasitic diseases and malaria: Revealing their actual incidence in the Peruvian Amazon through a new multiplex qPCR.

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Abstract Content

Neglected tropical parasitic diseases and malaria pose a global health burden, with low-income countries being the most affected. In our study, we aimed to evaluate the incidence of malaria and other blood parasites employing a new multiplex real-time PCR (MqPCR) for simultaneous detection of *Plasmodium spp.*, *Filariae* and *Trypanosomatidae* in asymptomatic population from Iquitos (Peruvian Amazon). During May 2022, asymptomatic individuals from different rural areas of Iquitos were serologically screened for Chagas disease. Additionally, DBS samples were collected and subsequently analysed through a new MqPCR. Positive samples were then confirmed by specific qPCR for the detected microorganisms and Sanger sequencing. All individuals serologically screened for Chagas resulted in negative. Nevertheless, MqPCR showed 26 (10.2%) of the screened individuals being infected with one or more different parasites. *Plasmodium* was the most common parasite found, being present in 16 (7.1%) of the individuals, with all the cases characterised as *P. vivax* when sequencing was performed. Filariae were detected in five (2%) of the individuals, all cases identified as *Mansonella ozzardi* by sequencing. Finally, MqPCR tested positive for trypanosomatids in three of the individuals. Specific *T. cruzi*, *T. rangeli*, and *Leishmania* qPCR tested all negative, but sequencing showed two of them to be *Trypanosoma evansii*. The Peruvian Amazon constitutes a highly complex area, with many different parasites circulating without causing clinical symptoms in the native population. Molecular screening programs provide new data about the real incidence of these diseases in this area, contributing to their best knowledge and control.

Abstract Reference: 20530
Mode of Presentation: Poster Presentation
Topic: Session 1 - Virology

A bibliometric analysis of schistosomiasis research during the COVID-19 pandemic

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Abstract Content

In 2020, during the COVID-19 pandemic, many diseases were affected by the health policies implemented by governments to prevent the transmission of the coronavirus. This impact could be particularly severe for neglected tropical diseases (NTDs), especially considering that prevention and control efforts for schistosomiasis rely heavily on community health interventions. As research is a crucial aspect of combating any disease, we aimed to assess the pandemic's impact on schistosomiasis research. To achieve this goal, we conducted a thorough bibliometric analysis using the Scopus electronic database for the period between 1 January 2020 and 26 March 2022. The study included a total of 1988 articles. Although the year-wise distribution of publications suggests no impact on schistosomiasis research, it is important to note that many resources have been diverted to research on COVID-19. As a result, the Global Schistosomiasis Alliance has reported that the main activities for eradicating schistosomiasis have been affected. The United States of America was found to be the most productive country, with the majority of articles being published in PLoS Neglected Tropical Diseases. The National Natural Science Foundation of China was the most prolific funding institution. The total number of publications per country showed a significant correlation with population, GERD, and researchers per million inhabitants, but not with GDP per capita and MPM.

Abstract Reference: 20531
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Antiparasitic plants can improve the health of domestic animals

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Abstract Content

Maintaining pasture biotopes in a natural state, researching their vegetation cover, and preserving plant biodiversity are the best ways to protect livestock against parasite infections. Wild plants, notably those are fed livestock, have strong antiparasitic (anthelminthic and antiprotozoal) qualities, and insectoacaricidal herbs can repel blood-sucking parasites. In 2023–2024, we collected current data on the species composition of Bayanaul National Natural Park higher plants and identified economically important species. The research discovered 97 anthelmintic, 48 antiprotozoal and 51 insecticidal and acaricidal species. Of the listed species of plants with an antiparasitic effect the most important ones are *Achillea millefolium*, *A. nobilis*, *A. asiatica*, *Ptarmica carthilaginea*, *Chelidonium majus*, *Tanacetum vulgare*, *Equisetum arvense*, various types of wild onions and garlic.We recommend feeding each adult head of cattle or horses a grass mixture of several meadow landscape plants with anthelmintic properties in the following ratio, in %: *Rumex confertus* (roots and fruits) -21; *Gratiola officinalis* (herb) – 5; *Geum urbanum* (grass or whole plant) – 30; *Filipendula ulmaria* (whole plant) – 10. It is necessary to expand the development and use of herbal premixes with anthelmintic effects. The natural plants contain the health components (improving digestion, stimulating appetite, regulating the amount of opportunistic microflora in the intestine).

Abstract Reference: 20534
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

Species composition and seasonal dynamics of the blood-sucking midges in the Irtysh valley in Kazakhstan

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Abstract Content

Midges (Simuliidae) are small dipterous insects belonging to the suborder of long-whiskered dipterans. They can mechanically transmit pathogens of tularemia, anthrax and a number of other infectious diseases. In addition, midges are specific carriers of pathogens of a number of diseases of domestic animals, as onchocerciasis of cattle, and a number of diseases of poultry caused by protozoa (species of the genus *Leucocytozoon*). In the Irtysh valley in Kazakhstan, we identified 5 species of midges: *Wilhelmia equina*, *Boophthora erythrocephala*, *Byssodon maculata*, *Simulium galeratum*, *Schoenbaueria pusilla*. During the study of the seasonal dynamics of the number of midge larvae in the middle reaches of the river Irtysh in 2023, we have recorded several peaks. The first peak was observed in the third decade of April, when the density of larvae was 68.5 lich/dm^2 of substrate. From the second decade of May, an increase in the number of larvae was observed to 165.3 lich/dm^2 of substrate. In the third decade of May 2023, the maximum peak in the number of larvae was noted, amounting to 697.7 specimens/dm^2 of substrate. In the third decade of June, the maximum peak in abundance was observed - 214.7 individuals/dm^2 of substrate. The next increase was recorded in the third decade of July - 47.7 lich/dm^2 of substrate. The larvae of *B. erythrocephala* were dominant during this period – 79.8%.

Abstract Reference: 20536
Mode of Presentation: Poster Presentation
Topic: Session 2 - One Health

Pig and donkey, important livestock reservoir species in human fascioliasis endemic areas: Their physiological features linked to disease transmission

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Abstract Content

Domestic pigs are closely related to humans in terms of anatomy, genetics and physiology. In the pig, the liver has five lobes including a right lateral, right central, left central, left lateral, and caudate lobes, thus differing from humans. Thegenetic and *physiological* traits of pigs are similar to humans and their immune system closely resembles humans in more than 80% of the parameters. Moreover, the gut barrier functions have revealed conserved defense mechanisms between pigs and humans, particularly in functional permeability, which may affect fluke juvenile infectivity mainly in pig adult specimens. The donkey, as equines in general, lacks a gallbladder. This means that the bile produced by the liver goes directly to the small intestine, and it is not stored. Animals lacking a gallbladder tend to eat small amounts of food several times a day. Furthermore, the natural diet of grasses that donkeys ingest while grazing is not particularly high in fat, and consequently they digest and absorb it well. Thus, from the point of view of the liver fluke transmission, the eggs cannot be stored in the gallbladder and their faecal excretion should be more regular and constant than in animals having a gallbladder.

Abstract Reference: 20544
Mode of Presentation: Poster Presentation
Topic: Session 2 - One Health

Malnutrition and human fascioliasis in schoolchildren from Atlixco, Mexico

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Abstract Content

This study aims to evaluate the relationship between nutritional status and the presence of fascioliasis in children.A cross-sectional study was performed based on clinical and analytical data from 865 schoolchildren, 6 and 14 years of age, from Atlixco (Mexico), including 488 schoolchildren without enteric parasitosis (WEP), 50 with fascioliasis (F) and 327 with enteric parasitosis other than fascioliasis (EP). The nutritional status of these 3 groups was determined using gender-specific anthropometric z-scores for height/age, weight/age, and weight/height, following the WHO child growth standards. A logistic regression analysis was performed to calculate the Odds Ratio (OR). The proportion of cases of low height/age (stunting) is highest in F (16.6% WEP, 19.8% EP and 28% F). The OR of stunting increases as the number of helminth species present increases. The proportion of cases of low weight/age (underweight) is lowest in F (1.2% WEP, 0.9% EP and 0.0% F). The proportion of cases of wasting (low weight/height) is highest in WEP (0.6% WEP, 0.0% EP and 0.0% F). The proportion of cases of severe malnutrition is highest in F (0.2% WEP, 1.5% EP and 4.0% F). The OR of severe malnutrition increases as the presence of the number of helminth species increases. The harmful effect of fascioliasis on the nutritional status of schoolchildren is demonstrated for the first time. CIBER de Enfermedades Infecciosas (CB21/13/00056), ISCIII, Ministry of Science, Innovation and Universities, Madrid, Spain and European Union—NextGenerationEU; and PROMETEO (2021/004), Generalitat Valenciana, Valencia, Spain.

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Topic: Session 2 - One Health

Time-to-event (= time lag) relation between climate and monthly number of infected subjects in human fascioliasis: Usefulness for prevention and control

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Abstract Content

Fascioliasis is caused by *Fasciola hepatica* and *F. gigantica*. To assess the correlation between climate changes and number of fascioliasis infected subjects, two climate-based fascioliasis risk indices were used: the Wet Day (Mt) forecast index and the Water-Budget-Based System (Wb-bs) forecast index. Generalized linear models (GLM) were applied to analyse the correspondence between monthly values of fascioliasis risk indices and monthly number of human fascioliasis cases in endemic areas of different climatic zones. The analysis revealed that human fascioliasis cases appear related with previous fascioliasis risk indices. When analysed according to areas, all GLM were significant with time-to-events (= time lags) between 7-12 months (average of 9 months). Key aspects to consider are time elapsed between symptom onset and diagnostic, coprological or serological technique used, and detection capacity from infection. This time-to-event range becomes a very useful tool because of defining the time for reaction available, and consequently for prevention and control in areas:
(i) suffering abnormal extreme climate situations (i.e., catastrophic climate events, drastic rainfall changes, heat/cold waves, inundations); (ii) where climate factors follow a regular mono- or bi-seasonality pattern; (iii) suffering from multi-year cycling climate changes such as the ENSO phenomena (El Niño-Southern Oscillation). Southern Asia and Andean countries are well-known extreme examples.

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Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Schistosoma hybrids detected in sub-Saharan migrants diagnosed in Southern Spain

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Abstract Content

In recent years, the number of patients diagnosed with urogenital schistosomiasis in Europe has increased due to significant migration from sub-Saharan Africa. Hybridization within the *Schistosoma* genus is becoming more common in Africa, raising concerns about transmission, epidemiology, and morbidity. However, *Schistosoma* hybrids have been poorly studied in patients diagnosed in Europe. In this study, *Schistosoma* eggs from the urine of 31 sub-Saharan migrant patients diagnosed in Southern Spain were genetically characterized. To determine species and identify hybrids, individual eggs were analyzed using mitochondrial *cox*1 and nuclear ITS-2 and 18S rDNA regions. The results confirmed that 38.7% of the patients carried *Schistosoma* hybrids, in all cases coexisting with terminal-spined eggs belonging to genetically pure *S. haematobium*. The most common observed hybrid was *S. haematobium x S. bovis* (detected in the 50% of the patients carrying hybrids), followed by *S. haematobium x S. mansoni* (33.3%) and *S. haematobium x S. curassoni* (16.6%). This study indicates that *S. haematobium* hybridization with other human intestinal (*S. mansoni*) and zoonotic (*S. bovis, S. curassoni*) species is common in sub-Saharan migrants with urogenital schistosomiasis. Diagnosis and treatment of patients with schistosomiasis are essential not only to prevent serious complications, but also to prevent possible future autochthonous transmission in areas of the European continent where competent intermediate hosts are present.

Abstract Reference: 20555
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Genetic polymorphism and molecular evolution of Duffy binding protein of Pakistan *Plasmodium vivax* isolates

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Abstract Content

Plasmodium vivax merozoites invade reticulocytes via interaction between Duffy binding protein (PvDBP) and the Duffy Antigen Receptor for Chemokines (DARC) on the hosts' reticulocyte surface. The amino-terminal cystine-rich region II of PvDBP (PvDBPII) is a potential vaccine candidate, but the genetic polymorphism has been reported in global isolates, suggesting allelic variations may affect vaccine efficacy. The PvDBPII was amplified from 118 *P. vivax* isolates from Khyber Pakhtunkhwa, Pakistan. The cloned PvDBPII genes were sequenced, and their genetic diversity, neutrality, recombination, and linkage disequilibrium were analyzed using MEGA and DnaSP programs. A haplotype network plot of global PvDBPII was generated with PopART. A total of 28 single nucleotide polymorphisms (SNPs) were identified in Pakistan PvDBPII. Twenty-two SNPs were non-synonymous, resulting in thirty-eight distinct haplotypes. Most amino acid substitutions occurred in subdomain II, among which 6 were commonly found in the global PvDBPII population. Overall amino acid change patterns in Pakistan PvDBPII resembled global PvDBPII, but the frequency of amino acid changes differed by country. The nucleotide diversity of Pakistani PvDBPII was comparable with global PvBDPII. Evidence of natural selection and recombination was observed in Pakistan PvDBPII. Haplotype network analysis of global PvDBPII revealed a complicated network of 179 haplotypes, but no geographical clustering was detected. The findings from this study have significant implications for understanding the genetic nature of Pakistani PvDBPII. Comprehensive analysis of nucleotide diversity and evolutionary force in the global PvDBPII population provides useful information for the development of malaria vaccines based on this antigen.

Abstract Reference: 20558
Mode of Presentation: Poster Presentation
Topic: Session 2 - One Health

Bacterial and protozoal communities in severe asthma patients in South Korea

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Abstract Content

This study involved 41 severe asthma patients and conducted metagenomics analysis using their sputum samples. Sputum samples were obtained from outpatients with moderate to severe asthma at the Allergy and Asthma Clinic at Severance Hospital. The patients were differentiated into eosinophilic (30 patients) and neutrophilic asthma (11 patients) based on the cellular profile of the sputum. Using targeted gene amplicon next-generation sequencing with Illumina’s iSeq100, the study performed metagenomics analysis. For bacterial microbiome analysis, the 16S rRNA gene V4 region was utilized, and for eukaryotic microbiome analysis, including parasites, the 18S rRNA gene V9 region was used. The bacterial microbiome results identified *Veillonella* sp., *Haemophilus* sp., *Neisseria* sp., and *Streptococcus* sp. as the most dominant species. *Lautropia* sp. was more abundant in those with neutrophilic asthma. In the eukaryotic microbiome analysis, dominant species included fungi such as *Candida* sp., *Malassezia* sp., and *Aspergillus* sp., as well as protozoa such as *Trichomonas* sp. and *Tetratrichomonas* sp. Subsequent experiments using specific primers and Sanger sequencing identified these protozoa as *Trichomonas tenax* (n=7) and *Tetratrichomonas buttreyi* (n=2). No significant difference in infection rates of these protozoa was observed between the eosinophilic and neutrophilic asthma groups. These findings suggest that an approach exploring bacteria, fungi, and protozoa simultaneously could be crucial for identifying biomarkers to determine the type of non-eosinophilic asthma in severe asthma patients.

Abstract Reference: 20559
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

The diversity and species composition of Anopheles mosquitoes, zoonotic malaria vectors, in different land categories in Kalabakan, Sabah, Malaysia.

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Abstract Content

Between 2011 and 2021, there were 23,143 cases of *Plasmodium knowlesi* malaria recorded in East Malaysia. Understanding the distribution of the mosquito vectors driving transmission is crucial for accelerating malaria elimination. This study aims to investigate the distribution, diversity, and composition of *Anopheles* mosquitoes, malaria vectors, across a land-use gradient in Kalabakan, Sabah, Malaysia. Between May and October of 2023, sampling took place five times (150 catch nights), and adult mosquitoes were collected using the Mosquito Magnet traps in five different land categories: built, oil palm, log plantations, primary forests, and secondary forests. *Anopheles* species were identified morphologically using morphological keys. In total, 2,459 *Anopheles* of twenty species were captured in this study. The most prominent species was *Anopheles balabacensis*, accounting for 34.6% (n = 853), followed by *An. donaldi* at 28% (n= 691). The land category with the highest total captures (n = 848), plantations, has the highest Shannon Diversity Index of 1.63 and also has the highest evenness (Evar evenness index) (0.892). Oil palm has the lowest species diversity of 1.24. Secondary forest has the highest species richness (n = 15), whereas built and primary forests have the lowest species richness (n = 10). In conclusion, six important malaria vectors (*An. balabacensis, An. latens, An. maculatus, An. donaldi, An. letifer*, and *An. epiroticus*) were recorded in Kalabakan, especially the first four species, which were found throughout the sampling period. Thus, this study indicates the spatial heterogeneity of malaria transmission and the importance of on-going surveillance in the area.

Abstract Reference: 20567
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Detection of Acanthamoeba antigens using Acanthamoeba-specific monoclonal antibodies

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Abstract Content

Acanthamoeba keratitis (AK) is a painful infectious eye disease which can inflict permanent visual damage. AK is often accompanied by bacteria or fungi, which hampers correct diagnosis. Therefore, a rapid and accurate *Acanthamoeba*-specific diagnosis is necessary to differentiate AK from keratitis of other microbial origins. Here, we produced a monoclonal peptide antibody targeting the chorismate mutase (CM) of *A. castellanii* and evaluated its potential as an AK diagnostic tool in mice. To evaulate the *A. castellanii*-specific antibody production against the CM antigen, enzyme-linked immunosorbent assays (ELISA) was performed using sera of immunized rabbits. The ELISA results demonstrated high antibody titers which specifically interacted with the *Acanthamoeba* trophozoites and cysts in a dose-dependent manner. CM antibody specificity against *Acanthamoeba* trophozoites and cysts was confirmed by immunocytochemistry after co-culturing *Acanthamoeba* with human corneal epithelial (HCE) cells, *Fusarium solani*, *Staphylococcus aureus*, and *Pseudomonas aeruginosa*. Immunocytochemistry results revealed that CM antibody specifically detected *A. castellanii*. AK mouse models were produced by corneally inoculating *A. castellanii* trophozoites for 7 and 21 days. *Acanthamoeba* antigens present in the tear wash samples and eyeball homogenates of AK mice were detected using CM antibody via ELISA. Our findings demonstrated that the CM antibody reported here can specifically detect *A. castellanii* in both *in vitro* and *in vivo* models. These results indicate important data which could support further development of the CM antibody for rapid and accurate AK diagnosis.

Abstract Reference: 20571
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Exploring the incidence of *Plasmodium knowlesi* human infections in Malinau, North Kalimantan and Sabang, Aceh, Indonesia

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Abstract Content

Plasmodium knowlesi, a malaria parasite primarily found in monkeys, has increasingly been identified as a cause of human malaria infections in Indonesia, raising public health concerns. Studying *Plasmodium knowlesi* infection in Malinau and Sabang is crucial for developing more effective strategies to control malaria in Indonesia, especially zoonotic malaria. The aim of this study is to establish molecular epidemiological surveillance for zoonotic Plasmodium species in Malinau and Sabang, Indonesia, to determine the prevalence of *P. knowlesi* infection and assess the public health implications. The cross-sectional study was conducted at four healthcare centers in Sabang and a regional general hospital, Malinau between December 2019 and September 2020. A total of 429 blood samples were collected from individuals presenting with malaria-like symptoms. Reverse transcriptase polymerase chain reaction (RT-PCR) was used to increase sensitivity and specificity in identifying the presence of Plasmodium species including *P. knowlesi.* There were 19 Plasmodium positive samples by PCR, 5 cases of human malaria caused by *Plasmodium vivax* and 14 cases of *P. knowlesi* infections. Specifically, 3,3% (14/429) of the samples tested positive for *P. knowlesi* with four positive cases identified in Sabang and ten positive cases in Malinau. All *P. knowlesi* positive cases were observed in adult males over the age of 20, suggesting an association with demographic patterns in infection susceptibility. These findings highlight the need for improved diagnostic methods and emphasize the importance of continuous surveillance and public health interventions to mitigate the impact of this emerging malaria threat in Malinau and Sabang.

Abstract Reference: 20576
Mode of Presentation: Poster Presentation
Topic: Session 2 - Parasitology

Discovery of new lead compounds against amoebiasis by high throughput screening of drug discovery initiative compound library

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Abstract Content

Amoebiasis is an infection caused by the parasitic protozoan *Entamoeba histolytica*, and one of the most common diarrheal diseases in low and middle income countries. Metronidazole (MTZ) is the first-line drug, but occasional treatment failure with MTZ, emergence of MTZ resistance in metabolically similar protists and bacteria and the adverse side effects of MTZ have been reported. Thus, drug discovery efforts of the new compounds with preferably a new scaffold and a non-overlapping mechanism of action are always necessary. We conducted the phenotypic cell-based screening of approximately 220,000 structurally elucidated compounds of the Drug Discovery Initiative library, The University of Tokyo, against the trophozoite stage of *E. histolytica* HM-1: IMSS reference strain using a 384-well plate platform. One hundred eighty-four compounds showed cidal effects after 24 hours at 10 µM and among them, twenty-five compounds showed the IC$_{50}$ values of < 5 µM and no cytotoxicity against human cell lines. We classified these hits and finally selected four major classes of compounds, which contain quinoxaline, purine, pyrazine or nitrobenzene. We reconfirmed their activity with repurchased and resynthesized compounds. We further focused on the quinoxaline series and investigated the structure-activity relationship of the series using commercially available analogs. Furthermore, to better understand the mode of action and the mechanism of resistance of quinoxalines, we generated resistant strains using an *E. histolytica* strain that expresses error-prone (proofreading-deficient) DNA polymerase delta mutant and show >60 fold higher mutation frequency, followed by whole genome sequencing of resistant lines.

Abstract Reference: 20577
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Cellular pathways involved in *Plasmodium falciparum* adaptation in rodent erythrocytic environments

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Abstract Content

Malaria is a life-threatening disease that affects millions of people worldwide and is caused by parasites of the *Plasmodium species*. Of the five known human-infecting species, *Plasmodium falciparum* has been the most studied due to its widespread distribution and severity of the disease outcome. Despite being well researched *in vitro*, there is a lack of a suitable mouse model to study *P. falciparum in vivo*, with most mouse models utilizing humanized mice with intraperitoneal injection of human red blood cells (hRBCs), often presenting issues due to poor erythroid engraftment and host immune response. We aimed to overcome the species barrier by adapting *P. falciparum* into mouse RBCs (mRBCs). We reconfirmed that *P. falciparum* was able to invade mRBCs but attempts to adapt *P. falciparum* into mRBCs through a long-term *in vitro* culture of six months, containing a mixture of mRBCs and hRBCs, were unsuccessful. With this, we proceeded to perform microarray hybridisation and downstream microarray analysis, including differential gene expression analysis and weighted gene co-expression analysis. The functions of the key differentially-expressed genes provides insight of the impaired development at the ring stage that was observed, and serves as a stepping stone to the understanding of *P. falciparum* in a murine erythrocytic environment.

Abstract Reference: 20578
Mode of Presentation: Poster Presentation
Topic: Session 2 - One Health

Trend and pattern of diseases under the IHIP (Integrated Health Information Platform) at a tertiary care hospital: An observational study from the western part of India

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Abstract Content

Pandemics put the public health system under strain, causing disruptions in healthcare, the economy, society, and politics. Notification of all the infectious diseases or diseases which have the potential to create epidemics or pandemics is vital for prompt response. Given this, India implemented an information technology-based decentralized surveillance method known as the Integrated Disease Surveillance Programme to notify infectious diseases via an effective surveillance system. The Integrated Health Information Platform (IHIP) is the next-generation, enhanced version of Integrated Disease Surveillance Programme (IDSP). To investigate the trend and pattern of diseases under IHIP at a tertiary care hospital in the Western Region of India. It was an observational study in a tertiary care hospital in the western region of India. Quantitative data was collected from the IHIP unit between January 2021 and March 2024. Data was collected from syndromic, presumptive, and laboratory-confirmed cases and analyzed. We await the results. According to reports from last year, typhoid, dengue, and chikungunya were the most prevalent diseases. Major syndromic cases were fevers lasting less than seven days, coughs with or without fever, and animal bites—specifically, dog bites—reported in the previous year. In the previous year, labs at a tertiary care hospital in the Western Region of India confirmed more cases of typhoid, dengue, and hepatitis A. I'm currently attempting to look into trend and pattern from the previous three years. It would depend on the result.

Abstract Reference: 20582
Mode of Presentation: Poster Presentation
Topic: Session 2 - Bacteriology

Advancing atypical bacterial pneumonia diagnosis in Malaysian hospitals using a multiplex Taqman qPCR

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Abstract Content

Severe atypical pneumonia is linked to high mortality and could involve extrapulmonary sequelae, especially in patients with co-morbidities, such as diabetes, elderly, and immunocompromised individuals. Aetiologic agents of atypical pneumonia includes *Mycoplasma pneumoniae* and *Chlamydophila pneumoniae*, which are challenging to detect as they are difficult to culture and poorly stained. As a result, this study explores to potential of molecular assay to detect these organisms. Briefly, 200 lower respiratory samples were collected from Hospital Shah Alam and Hospital Raja Perempuan Zainab II, Kota Bharu. Next, total DNA was extracted and subjected to a multiplex Taqman qPCR against *M. pneumoniae*, *C. pneumoniae* and human RNAse that serve as amplification control. From the study, 7% samples (n = 14) were positive with *M. pneumoniae* and none for *C. pneumoniae.* The age distribution indicates that 62% of the samples were collected from patients aged between 18 – 64 years and 14% were from older than 65-year-old. In conclusion, the multiplex Taqman qPCR was able to detect substantial cases of atypical pneumonia caused by *M. pneumoniae*, which otherwise, were undetectable via conventional methods.

Abstract Reference: 20583
Mode of Presentation: Poster Presentation
Topic: Session 3 - One Health

Development of an automated processing framework for remote sensing imagery: The Ecology and Health Sustainable Platform (EHSP)

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Abstract Content

Climate and landscape changes can significantly impact the emergence or re-emergence of various infectious diseases, particularly vector-borne diseases. Understanding the effects of climate and land cover/use changes on transmission dynamics is crucial for developing early warning systems and control strategies. Diverse environmental parameters derived from satellite images enable scientists to evaluate transmission risk and develop prediction models on both global and regional scales. However, the complexity of image processing often limits public health researchers' ability to efficiently access and process these satellite images. Our project aims to establish the Ecology and Health Sustainable Platform (EHSP) to automatically generate diverse environmental variables from various satellite image sources (e.g., MODIS, ERA5, CHIRPS, Sentinel-1, Sentinel-2, Landsat, and WorldCover). The EHSP enables users to acquire environmental indices from earth observations without requiring coding skills. The EHSP is a web-based graphical user interface that leverages the powerful cloud-based computational capabilities of Google Earth Engine (GEE). It allows users to calculate a range of customized environmental parameters, including land surface temperature, air temperature, NDVI, NDWI, precipitation, or land cover/land use types, for any region on Earth. We also demonstrated various risk assessment or prediction models for dengue fever in Taiwan, *Plasmodium knowlesi* in Malaysia, and avian influenza in the Philippines using parameters generated by the EHSP.

Abstract Reference: 20586
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Evaluating the efficacy of the automated hematology analyzer XN-31 for monitoring parasitemia in malaria treatment.

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Abstract Content

Automated Hematology Analyzer XN-31, developed by Sysmex Corporation, measures complete blood count (CBC) and the number and ratio of malaria parasite-infected red blood cells (MI-RBC#/%). It also suggests *Plasmodium* species using flow cytometry in approximately one minute. This study evaluated the efficacy of the XN-31 in monitoring parasitemia during malaria treatment. Between December 2020 and February 2024, 74 patients suspected of malaria at NCGM hospital were studied. Both microscopic observation of Giemsa-stained blood smears and XN-31 measurements were performed. For those testing positive for malaria, parasite clearance was monitored following antimalarial treatment using both methods. The XN-31 showed strong correlation with microscopy in detecting % parasitemia from the first day of treatment onward. Its scattergrams provided visual evidence of decreasing malaria parasites. Moreover, these scattergrams allowed for the qualitative assessment and determination of *Plasmodium* species, unaffected by antimalarial treatment throughout the monitoring period. Remarkably, the XN-31 detected parasites on the final monitoring day when microscopy did not, highlighting its potential superior sensitivity. The XN-31 facilitated both quantitative and qualitative monitoring of parasite clearance during malarial treatment. These findings supported the potential of the XN-31 not only for initial parasite detection, but also for ongoing treatment monitoring.

Keywords: Automated Hematology Analyzer XN-31, Flow cytometry, Parasite clearance, Parasitemia monitoring, *Plasmodium* species

Abstract Reference: 20592
Mode of Presentation: Poster Presentation
Topic: Session 2 - Vector-Borne Diseases

The tick cell biobank: Tick and insect cell lines for research into control of tropical diseases

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Abstract Content

Many of the most widespread and deadly tropical diseases are transmitted between their human hosts by arthropod vectors such as ticks, mosquitoes, sandflies, tsetse flies and biting midges. Continuous cell lines derived from these vectors have an important role to play in many aspects of research into transmission and control of the causative agents, which include viruses, bacteria and protozoa. The Tick Cell Biobank (TCB) at the University of Liverpool, the world's only dedicated culture collection for cell lines derived from ticks and other arthropods, has been storing and supplying arthropod cell lines and training in their maintenance to scientists since 2009. Between them, the TCB and its Outposts in Malaysia (TIDREC, Universiti Malaya) and Brazil (Fiocruz and Federal Rural University of Rio de Janeiro) have distributed tick and insect cell lines to over 100 laboratories in 38 countries, and trained over 160 young scientists. The TCB and TCB Outposts also generate new cell lines from tick and insect vectors not already represented in the collection, with a focus on regionally-important species such as malaria-transmitting mosquitoes and tick vectors of highly pathogenic viruses. The TCB houses a small collection of obligate intracellular arthropod-borne bacteria including several strains of *Wolbachia*, an insect symbiont with applications in control of dengue, other arboviruses, and potentially malaria. Through their activities, the TCB and TCB Outposts underpin many aspects of international cell-based research into control of tropical vector-borne diseases. For further information about the cell lines visit the TCB website at https://www.liverpool.ac.uk/research/facilities/tick-cell-biobank/.

Abstract Reference: 20595
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

Small non-coding RNAs of extracellular vesicles of parasitic worms as regulators of human target genes

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Abstract Content

Small non-coding RNAs regulate gene expression. Parasitic organisms also secrete microRNAs in extracellular vesicles (EVs). The human liver fluke *Opisthorchis felineus* infection leads to biliary epithelial neoplasia. The role of parasitic extracellular vesicles and non-coding RNAs has not been studied. Identification of small non-coding RNAs that enable bioregulatory activities in relation to human cholangiocytes. Small RNA of *O. felineus* EVs were sequenced on BGISEQ-500. Transcriptome of human H69 cholangiocytes after exposure to extracellular vesicles of *Opisthorchis felineus* were sequenced on DNBseq. Differences were identified in the relative abundance of 97 miRNAs in EVs compared to that of adult whole worms. Among the major miRNAs of EVs, there were both highly conserved molecules and those specific to parasitic worms. It can be assumed that *O. felineus* microRNAs can modulate the same target genes as their human homologues. Among the predicted target genes in the human genome, enrichment was observed in the epithelial-mesenchymal transition pathway, protein secretion, PI3K-Akt signaling pathway and others. Analysis of transcriptomes of human H69 cholangiocytes revealed 773 differentially expressed genes after the treatment with EVs. The Fisher test showed the enrichment of DEGs with predicted target genes for parasitic microRNAs. Thus, we have demonstrated the data indicating the regulatory role of parasitic microRNAs in the regulation of human cholangiocyte gene expression. The study of parasitic secretory microRNAs provides the opportunity to identify new mitogenic biologicals created during co-evolution of the parasite and the host. The study is supported by the Russian Science Foundation (№24-44-00048).

Abstract Reference: 20596
Mode of Presentation: Poster Presentation
Topic: Session 3 - One Health

Coverage, adequacy, and utilization of Long-Lasting Insecticidal Nets (LLINs) among Forcibly Displaced Myanmar Nationals (FDMNs) in Bangladesh

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Abstract Content

Malaria elimination efforts in Bangladesh face numerous challenges including the presence of Forcibly Displaced Myanmar Nationals (FDMNs), also known as Rohingya. This study aimed to assess LLIN coverage, adequacy, and utilization among the FDMN population. A cross-sectional study was conducted between July and October 2023 to evaluate LLIN coverage, adequacy and utilization in FDMN settlements. The study focused on how FDMNs in malaria-endemic areas accept, utilize and maintain LLINs in their daily lives particularly for pregnant women and children under five. A total of 600 individuals participated in the survey. The majority respondents (66.5%) were females, with ages ranging from 26 to 42 years. Education levels were low, with nearly 70% having no formal education. While 98.2% of respondents reported owning LLINs, 44.3% of households lacked sufficient nets. Over half of respondents reported that none of their household members slept under LLINs, primarily due to insufficient quantities (86.7%) or damaged nets (10.4%). The survey revealed that 65.7% individuals on the interview night slept under LLINs. However, utilization rates were 77.4% among pregnant women and \78.3% children under five. Only half of the respondents reported hanging LLINs correctly in the evenings. Washing practices varied, with 60.4% washing LLINs more than four times in the last three months. Despite high LLIN ownership among FDMNs, challenges regarding adequacy, access, and utilization remain. Suboptimal utilization rates among vulnerable groups like pregnant women and young children necessitate targeted interventions.

Abstract Reference: 20597
Mode of Presentation: Poster Presentation
Topic: Session 2 - Bacteriology

Development and initial evaluation of DNA aptamers for the early detection of leptospirosis

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Abstract Content

Leptospirosis, caused by the pathogenic *Leptospira*, remains a public health concern in the Philippines with an increasing prevalence in major urban areas due to flooding caused by climate change. Current methods of detection including culture, microscopy, and serological assays are laborious and take time to yield results. Given the potential fatality of leptospirosis, early-stage detection is critical for effective medical intervention. Aptamers, an emerging diagnostic tool, are single-stranded oligonucleotides currently being explored as an antibody alternative. This technology could enhance point-of-care diagnostics, potentially addressing the gap in disease diagnosis. Aptamers were selected against *Leptospira* species in commercial vaccines through the Systematic Evolution of Ligands by Exponential Enrichment (SELEX). This procedure involved repeated exposure and screening of single-stranded DNA to the antigen followed by PCR amplification and oligo capture. Fourteen rounds of selection were performed resulting in enriched oligo pools. Next-generation sequencing (NGS) was done on Rounds 8, and 10 to 14. Fifteen representative seed sequences from the overrepresented clusters were analyzed through surface plasmon resonance (SPR) and significant signal was detected in four candidate aptamers. Sixteen aptamer pair combinations were screened through the enzyme-linked aptamer sandwich assay (ELAA) to determine the best performing pair. Results indicate that the AP1-AP5 aptamer combination had the highest affinity to the *Leptospira* antigen. Aptamers were successfully developed and evaluated to detect the pathogen *Leptospira* through cell-SELEX, SPR, and ELAA. Further evaluation of these aptamers should be conducted to determine their potential as a new diagnostic tool for the early detection of leptospirosis.

Abstract Reference: 20598
Mode of Presentation: Poster Presentation
Topic: Session 3 - One Health

Association between climate variability and malaria in a high-risk area of Kenya

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Abstract Content

Climate is an important factor that affects mosquito-borne disease transmission as the vectors are sensitive to climate variations. A mosquito-borne disease model based on climate data is often robust at predicting disease outcomes. The major objective of the present study is to develop a district level malaria prediction model. This presentation reports the important climate variables that are associated with malaria cases in Mbita District, Homabay County, in western Kenya. This district is one of the most prone areas to malaria transmission in Kenya. Using distributed lag nonlinear models, the monthly malaria cases from 2016 to 2023 were regressed on Indian Ocean Dipole Index (DMI), Nino3.4 Index, maximum temperature, minimum temperature, rainfall and lake water level. As the area borders Lake Victoria, the water level was also considered. The relative risk (RR) with 0-month lag increased as the DMI, Nino3.4 Index, rainfall and lake water level increased. The RR with 2-month lag increased as the maximum temperature increased, but the magnitude of risk decreased above 26℃. The minimum temperature was also associated with higher RR at a 2-month lag. The results suggest that these variables are potential predictors for forecasting malaria transmission in Mbita District.

Abstract Reference: 20601
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Assessing LAMP technology for malaria parasites' DNA detection in Thai clinical settings

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Abstract Content

Eiken Chemical Co., Ltd (EIKEN) has developed three LAMP kits for detecting malaria parasites' DNA: *Plasmodium* spp. (Pan)-LAMP, *P. falciparum* (Pf)-LAMP, and *P. vivax* (Pv)-LAMP. These kits were evaluated for their efficacy in clinical settings in Thailand. A total of 349 patients suspected of malaria were tested in collaboration with the Hospital for Tropical Medicine at Mahidol University from November 2019 to June 2022. DNA was extracted from dried blood samples on filter papers using EIKEN's PURE method. Tests were conducted using Pan-LAMP, Pf-LAMP, and Pv-LAMP kits and results were compared with conventional methods such as microscopy and PCR. Microscopy identified 125 malaria cases with positive parasitemia including 17 Pf, 103 Pv, 3 *P. knowlesi* (Pk), 1 *P. malariae* (Pm), and 1 *P. ovale* (Po). Pf-LAMP tests showed positive for all the 17 Pf cases, and Pv-LAMP tests showed positive for all the 103 Pv cases. Additionally, Pan-LAMP tests demonstrated positive for the 3 Pk, 1 Pm, and 1 Po identified microscopically. There were also 14 LAMP-positive cases with negative microscopy, among which PCR confirmed 1 Pf and 1 Pk. Furthermore, Pv-LAMP detected a mixed infection of Pv with Pf in one case which was initially determined by both microscopy and Pf-LAMP; this was confirmed by PCR. The LAMP kits demonstrated potential for effective malaria diagnosis in areas with dominantly prevalent Pv and the presence of Pk, offering a valuable tool for field diagnosis.

Keywords: LAMP kits, Malaria diagnosis, *Plasmodium* species, DNA detection

Abstract Reference: 20610
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

Two decades of Japanese encephalitis vectors surveillance in Indonesia: A mini-review

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Abstract Content

Japanese encephalitis is a complicated health issue in Southeast Asian countries, especially Indonesia. This disease spreads through the bite of Culex mosquitoes and causes brain inflammation, neurological complications, and even death, particularly in children and the elderly. The spread of the Japanese encephalitis virus (JEV) can be prevented through the crucial role of vector surveillance, which allows for the collection of epidemiological data, identification, monitoring of vector populations, and the subsequent direction of public health policies. To investigate the vector surveillance implemented in Indonesia over the previous 20 years on the JE vector, as well as potential future issues, we searched for articles published between January 2004 and May 2024. We analyzed the number of papers that met our inclusion criteria based on country, sample type, and year of collection. Of the 79 papers identified from PubMed, ScienceDirect, Google Scholar, and Medline indexes, 13 papers met the inclusion criteria. Based on these papers, there has been extensive surveillance of the Japanese encephalitis vector in Indonesia, especially in Bali and West Kalimantan, because these two provinces are endemic areas for JEV. Only two publications carried out genotyping on JEV-positive samples, and the genotypes found were genotypes I and IV. Surveillance research on Japanese encephalitis vectors in Indonesia has been widely conducted. However, the detection and genotyping of JEV originating from vectors are still rarely performed. It is necessary to conduct further surveillance in other provinces using more specific methods to determine the spread of the JEV genotype in Indonesia.

Abstract Reference: 20627
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

Effectiveness test from the combination of *Annona muricata* leaf extract and *Citrus sinensis* rind extract on in vitro *Pediculus humanus capitis* mortality

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Abstract Content

The transmission of *Pediculus humanus capitis* is easy and fast, and the side effects are very dangerous for children. Because of this, natural remedies are needed to prevent this condition from spreading. One of the most effective natural ingredients for treating this disease is *Annona muricata* leaves. These leaves contain various secondary metabolites, such as acetogenin and *Citrus sinensis* rind. This determines the effectiveness of combining the extract of *Annona muricata* leaf and *Citrus sinensis* rind on the mortality rate of patients with this condition. This study used a true experimental design with a posttest-only control group design for *Pediculus humanus capitis*. This study consisted of positive control group using 1% permethrin (K+), negative control group using aquadest (K-) and 5 treatment groups using a combination of *Annona muricata* leaf extract and *Citrus sinensis* rind extract in a ratio of 30:70 (P1), 40:60 (P2), 50:50 (P3), 60:40 (P4), 70:30 (P5). This study was carried out 3 times replication the observation of mortality *Pediculus humanus capitis*. The treatment group had a mortality percentage from the highest to the lowest at 120 minutes, P3 (60%), P1 (53.33%), P5 (46.67%), as well as P2 and P4 (40%). The results of the one-way ANOVA test showed that $p< 0.05$. The combination of *Annona muricata* leaf extract and *Citrus sinensis* rind extract is effective in causing mortality in *Pediculus humanus capitis*.

Keywords: *Annona muricata* leaf, *Citrus sinensis* rind, Mortality, Pediculoside, *Pediculus humanus capitis*.

Abstract Reference: 20629
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Genome-wide survey of malaria-associated loci in the Negrito groups of Malaysia

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Abstract Content

The Negrito populations of Southeast Asia have been regarded as the earliest settlers of the region. Their historical association with regions of high malaria endemicity makes them unique subjects for studying genetic adaptations to malaria. Genome-wide association studies (GWAS) involving malaria have mainly focused on African populations, whereas indigenous groups from malaria-endemic regions of Southeast Asia have been largely neglected. This study aims to investigate the presence and frequency of malaria-related SNPs among Malaysian Negritos. Single Nucleotide Polymorphisms (SNP) data from three Malaysian Negrito groups: Jehai, Kintaq, and Batek, were reanalyzed for this study. The data was generated using Illumina Omni 2.5 array in a previous study. Malaria-related SNPs were obtained from the GWAS catalog (https://www.ebi.ac.uk/gwas/) using the trait label "malaria". Of the 158 malaria-related SNP loci identified from the GWAS catalog, only 9 were present in the Negrito SNP array data. Preliminary results revealed that the risk allele frequencies for rs12590640 and rs12788102 were greater than 70% among all three Negrito groups. These findings indicate that while there is some overlap between malaria-associated SNPs in African and SEA populations, significant differences that warrant further investigation may exist. Future research will focus on testing for natural selection on malaria-related genes in Negritos to understand the evolutionary pressures and potential adaptations to malaria in these indigenous populations.

Abstract Reference: 20631
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Identification of a novel *P. falciparum* protein regulating gametocyte microtubule density and shape

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Abstract Content

The *Plasmodium falciparum* gametocyte is responsible for transmission from humans to mosquitoes. As gametocytes mature in the bone marrow (Stage I-IV), they develop a subpellicular microtubule structure, which is disassembled (Stage V) resulting in the characteristic falciform shape and extravasation from the bone marrow. We have identified a putative microtubule organizing center (MTOC)-localized protein and investigated its role in regulating gametocyte microtubule density and shape. We established knockout (KO) and smFPV5-tagged (WT) parasite lines and performed asexual and gametocyte growth assays. Immunofluorescence confocal microscopy was used to determine localization and microtubule structure and density. We examined Giemsa-stained slides of KO and WT parasites using image analysis (Fiji) to measure and quantify gametocyte shape (curvilinearity). Asexual growth rate and gametocyte maturation were not significantly different between WT and KO parasites. However, KO gametocytes displayed significantly increased tubulin and more dispersed DAPI signal as compared to the WT across Stages II, III, IV, and V ($p < 0.05$). Furthermore, KO Stage V gametocytes displayed significantly straighter morphology as compared to the characteristic sickle shape seen in WT Stage V gametocytes ($p < 0.0001$). These data further characterize the gametocyte MTOC and highlight the role of global microtubule organization during *P. falciparum* gametocyte development. Perturbing the fine microtubule equilibrium responsible for the shape and deformability of mature gametocytes may increase splenic clearance and impact transmission. Displaying no significant homology to host proteins, this protein is a potential target for transmission-blocking interventions.

Abstract Reference: 20638
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

Sub-therapeutic plasma lumefantrine concentrations in the Papua New Guinea Defence Force personnel, a concern for inducing lumefantrine resistance in *Plasmodium falciparum* malaria

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Abstract Content

The Australian Defence Force Malaria and Infectious Disease Institute (ADFMIDI) together with the Papua New Guinea Defence Force (PNGDF) have recently been conducting cross-sectional vector borne disease epidemiological surveys across PNGDF military bases. In PNG, first-line treatment of uncomplicated *Plasmodium falciparum* is the artemisinin based combination therapy of artemether-lumefantrine. During a 2023 survey of PNGDF members in Lae, Morobe Province, participants were asked whether they had taken any antimalarial drugs in the previous four weeks. Twenty of 186 (11 %) answered “Yes”. Since lumefantrine (LF) has a relatively long plasma elimination half-life ($T_{1/2}$ 3 to 6 days), and because of the potential for emerging resistance to LF in PNG, we measured LF and its primary metabolite, desbutyl-lumefantrine (LFm) concentrations in plasma samples collected from survey participants using a validated liquid chromatography mass spectrometry (LC-MS/MS) assay. LF was measured in all 20 plasma samples from those who answered “Yes” to having taken antimalarials (mean of 465 ng/mL, range 19.1 to 1,940 ng/mL). Surprisingly, of the other participants (n=166) who answered “No” to taking antimalarials in the past four weeks, we randomly screened 35 plasma samples and of these 23 (66%) had a mean LF concentration of 32.2 ng/mL (range less than low limit of quantitation of 1 ng/mL to 113.6 ng/mL) by LC-MS/MS. Given that a day 7 treatment threshold LF concentration is considered to be at least 175 ng/mL, many PNGDF members had sub-therapeutic plasma LF concentrations that may drive *P. falciparum* LF resistance in Morobe Province, PNG.

Abstract Reference: 20642
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

Mosquito larvae distribution and habitat abundance in relation to malaria prevalence in Shagari, Yola South Local Government Area, Adamawa State, Nigeria

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Abstract Content

Mosquitoes are widely distributed throughout the world and breed in different water bodies, with species preferring specific water qualities and habitats. The study aims to survey mosquito breeding habitats and malaria prevalence in Shagari, Yola South Local Government Area, Nigeria. Samples were randomly collected from seven (7) households in seven (7) communities. A reconnaissance visit was made to communities and GPS coordinate recorded. Consent was sought for blood samples collection for malaria parasitological investigation using the methods described by Cheesbrough. Data were analyzed using Epidata, Statistical Package for the Social Science (SPSS), MS Excel, and Chi-square. Malaria prevalence was 74.6% with 51.9% males and 48.1% females. Highest and lowest malaria prevalence was recorded in Unguwan-b 19.4% and Wuro-modibbo 5.7% respectively. Age group 5-10 years had highest prevalence 35.5% and age group 21-30 years had least prevalence 14.3%. Participants with primary education level had the highest prevalence 37.9% and pre-primary with the lowest at 5.1%. Students had highest prevalence by occupation with 58.8%, followed by no occupation 15.5%. Lelewalji and Shagari phase I community had more larval habitats. The study identified 2,696 mosquito larvae including *Culex* 71.0%, *Anopheles* 28.9% and *Aedes* 0.1%. The larval habitats identified in the study area showed that mosquito larvae were abundance in streams 25.7%, with domestic containers being the least 2.3%. The study identified *Culex* mosquitoes as the predominant malaria parasite. The presence of *Aedes*, *Culex* and *Anopheles* could contribute to the high malaria prevalence in the study area.

Abstract Reference: 20643
Mode of Presentation: Poster Presentation
Topic: Session 2 - Vector-Borne Diseases

Prevalence of theileria, borrelia, anaplasma in ticks (Acari: Ixodidae) in Korea

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Abstract Content

Ticks transmit several zoonotic pathogens including Anaplasma, Borrelia, Babesia. The Borrelia is causative agent of Lyme disease, and the sporozoan parasites Anaplasma and Babesia / Theileria lead to anaplasmosis and babesiosis, respectively. In order to investigate the prevalence of these tick-borne pathogens, ticks were collected in Gangwon province in 2022 and 2023 in Republic of Korea. A total of 32,452 ticks were collected at four regions, the dominant tick was *H. longicornis*, followed by *H. flava* and *Ixodes niponensis*. The nymphs appeared from April and peaked in June, and number of the collected adults peaked in June and then steadily decreased. On the other hands, the collected number of larva was increased from June, and peaked in September. The tick-borne pathogens were detected using PCR and the infective rates of Anaplasma, Borellia, and Theileria were 3.52%, 3.72%, and 15.2%, respectively. The infection rates appeared from April and peaked in June or July in adults and nymph ticks, whereas the infection rates increased form August and peaked on September in larvae. These suggest that there might be a close relationship between the pathogens in ticks and the outbreaks of infection in humans and animals.

Abstract Reference: 20652
Mode of Presentation: Poster Presentation
Topic: Session 2 - Entomology

Nation-wide surveillance of tick (Acari: Ixodidae) infestations of humans in Singapore

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Abstract Content

Singapore is a tropical island-nation densely populated sometimes described as a ‘Garden City’ due to its abundant greenspaces and rich wildlife. However, this combination of factors also creates a favourable nexus for the spillover of ticks (and their associated pathogens) from wildlife to humans. Despite the rich diversity of local ticks and their public-health importance, the epidemiology of tick-infestations in Singapore has received little attention. Analysing data from the national tick surveillance program, cases submitted to the National Public Health Laboratory, and literature records, this study presents 51 cases of human tick-infestation in Singapore, involving 128 specimens from 11 species. Most of these infestations were locally acquired (88%), the remaining were acquired overseas involving either non-established (8%) or locally present (4%) tick species. Only *Dermacentor*, *Haemaphysalis*, *Ixodes*, and *Amblyomma* genera were found to bite humans locally. *Dermacentor auratus* was responsible for most of the infestations (58%), with its immature life-stages (larvae and nymphs) causing the majority of the infestations (93%). Most infestations occurred on the head (63%) including: otoacariasis (32%), periorbital-infestation (21%) and scalp-infestation (10%). A detailed re-examination of local *Haemaphysalis nadchatrami* specimens lead to their reassignment as *Haemaphysalis papuana*, a closely related species and responsible for 3 local cases of human-infestation. Identifying human-biting ticks in Singapore helps: to gain realistic insights into tick-borne pathogens risk considering their confirmed and/or potential vectorial capabilities; to adjust public-health monitoring and response; to develop and implement adapted landscape management and control measures; and to enhance public education to minimize the tick-bite risk.

Abstract Reference: 20656
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

A pilot study using LAMP in a field setting by ADF for Malaria surveillance with PNGDF

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Abstract Content

In May 2023 the Australian Defence Force Malaria and Infectious Disease Institute (ADFMIDI) collaborated with the Papua New Guinea Defence Force (PNGDF) to conduct a health survey of PNGDF members and their families living on Igam Barracks in Lae, PNG. A pilot study involving Loop Mediated Isothermal Amplification (LAMP) (Meridian Bioscience - Alethia) testing was run concurrently with Malaria Ag *P.f*/Pan RDTs (Bioline) and WHO accredited level 1 and 2 microscopy performed on the PNGDF member samples (n=185). Malaria detection and speciation PCR was conducted on return to Australia. The pilot study was used to implement and validate the use of LAMP in a field setting to examine such factors as sensitivity, specificity, financial cost, personnel and labour cost, throughput, and ease of use. LAMP was shown to be an effective tool for malaria detection in a survey setting.

Abstract Reference: 20657
Mode of Presentation: Poster Presentation
Topic: Session 2 - Vector-Borne Diseases

The *Culex tritaeniorhynchus* as the potential vector for bovine ephemeral fever virus transmission

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Abstract Content

A recent study in Taiwan has revealed new insights into bovine ephemeral fever (BEF), a viral disease causing significant economic losses in cattle farming. Traditionally attributed to *Culicoides*, this research presents the first experimental evidence of BEFV transmission by *Culex tritaeniorhynchus*. The study assessed the vector competence of five mosquito species in transmitting BEFV using RT-PCR. Between 2017 and 2018, 4,435 mosquitoes were collected from five cattle farms in Taiwan. The dominant species was *Cx. tritaeniorhynchus* (93.89%), followed by *Anopheles sinensis* (3.31%), *Culex quinquefasciatus* (1.56%), *Culex pipiens molestus* (0.79%), and *Armigeres subalbatus* (0.45%). BEFV infection was primarily found in *Cx. tritaeniorhynchus*. Experiments showed that *Cx. tritaeniorhynchus* were highly susceptible to BEFV, with a 100% susceptibility rate via intrathoracic injection and then a 60% oral transmission rate of BEFV via the saliva of *Cx. tritaeniorhynchus*. At 28°C, 20% of these mosquitoes became infected after oral ingestion, with higher temperatures increasing susceptibility. At 32°C, 10 days after oral infection, susceptibility reached 36.67 ± 5.78%. These findings suggest that *Cx. tritaeniorhynchus* as the potential vector in the BEFV transmission cycle in Taiwanese cattle farms.

Abstract Reference: 20658
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

Iris setosa Pall. ex Link extract induces apoptosis-like programmed cell death in *Acanthamoeba castellanii* and *Acanthamoeba polyphaga* trophozoites

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Abstract Content

Acanthamoeba keratitis (AK) is a sight-threatening and difficult-to-treat ocular infectious infection. The nonnegligible side effects of current AK therapeutics emphasize the urgent necessity to develop a safe and effective therapeutic drug for AK. In this study, we analyzed the amoebicidal activity of *Iris setosa* Pall. ex Link extract (ISE) on *Acanthamoeba* and its underlying amoebicidal mechanism was investigated. Whole body of *I. setosa* Pall. ex Link was collected and extracted. ISE was further fractioned into five subfractions by sequential extraction with *n*-hexane, chloroform, ethyl acetate, *n*-butanol, and water. The amoebicidal activity of extracts against *Acanthamoeba castellanii* and *Acanthamoeba polyphaga* and the cytotoxicity against human corneal epithelial cells (HCE-2) were analyzed by cell viability assay. The underlying amoebicidal mechanism of the *n*-butanol subfraction of ISE (ISE-BuOH) was investigated in *A. castellanii* and *A. polyphaga* via apoptosis-related assays, mitochondrial membrane potential (MMP) change, and ATP assays. ISE induced significant morphological changes in *Acanthamoeba* trophozoites and showed amoebicidal activity against *A. castellanii* and *A. polyphaga*. ISE-BuOH revealed a selective amoebicidal activity against the *Acanthamoeba* species with no significant cytotoxicity in HCE-2 cells. ISE-BuOH induced apoptosis-like programmed cell death (PCD) in amoebae characterized by DNA fragmentation, increased ROS production, mitochondrial dysfunction via loss of MMP and ATP level, and increased caspase-3 activity. Partial cysticidal activity of ISE-BuOH was also detected. ISE-BuOH revealed a promising amoebicidal activity to *Acanthamoeba* trophozoites by inducing a PCD event and showed partial cysticidal activity. ISE-BuOH could be a potential source in developing a therapeutic drug for AK.

Abstract Reference: 20659
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

A gene drive that reduces Plasmodium fertility and could end malaria

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Abstract Content

Gene drives have the power to eradicate pests or pathogens. CRISPR/Cas technology has made gene drives precise and simple to make. Gene drives to control mosquitoes that spread malaria are being deployed, but the malaria pathogen itself has not yet been targeted. We aimed to build and test a gene drive in rodent *Plasmodium berghei*. We built a homing, sex biasing gene drive designed to convert all parasites to females, which would thus collapse the population because it would be unable to have sex to infect mosquitoes. Our gene drive disrupts a gene essential for male development in malaria parasites. We fed our gene drive parasites plus target parasites to mosquitoes to enable them to mate. Our gene drive line mated with the target line. All the progeny produced by this mating lacked the male development gene, which had been replaced by the gene drive cassette. The progeny were infectious and successfully infected naïve mice, which became symptomatic. However, these mice were not infectious to new mosquitoes because they made no male gametes, so transmission was stopped. Our modelling of a *P. falciparum* gene drive indicates that fewer then 0.1% of a population needs to be inoculated for the gene drive to achieve population collapse of the parasite in ~5 years. Deployment of a gene drive pathogen has massive safety, ethical, moral, social, and regulatory challenges. Nevertheless, malaria defies efforts at global eradication, and a gene drive strategy could be a decisive new tool to end malaria.

Abstract Reference: 20666
Mode of Presentation: Poster Presentation
Topic: Session 3 - One Health

Inappropriate antibiotic prescribing in febrile children under five years old in West Africa

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Abstract Content

Antimicrobial resistance is a global health concern, particularly in sub-Saharan Africa. With the decrease in malaria incidence, the proportion of non-malarial febrile illnesses is rising in hospital diagnosis. Diagnosis of febrile children without specific symptoms is often challenging, which may lead to indiscriminate antibiotic prescribing. The aim of the present study was to reveal the level of inappropriate antibiotic prescriptions in febrile children under 5 years old in The Gambia, West Africa. The study also identified contributing factors to inappropriate prescriptions. The dataset included 1028 febrile children reported at Fajara site in Medical Research Council Unit the Gambia between July 2017 and August 2018. Although antibiotic treatment was unnecessary for 439 children, 233 (53%) of them were inappropriately prescribed antibiotics. Log-binomial multiple regression analysis identified two interaction terms which contributed to inappropriate antibiotic prescriptions. Hospitalized children with dual diagnoses were twice more likely to have inappropriate antibiotic prescriptions compared to outpatients with single diagnosis (adjusted RR = 2.08; 95% CI: 1.10 -3.95). Hospitalized children with an underlying heart condition were also twice more likely to receive inappropriate antibiotic prescription than outpatients without the condition (adjusted RR = 2.30; 95% CI: 1.01 -5.28). The risk of inappropriate antibiotic prescriptions increased by 20% in the 3-4 year old age group compared to 0-2 year old group (adjusted RR = 1.20; 95% CI: 1.02 -1.42). The present study confirmed that inappropriate antibiotic prescribing is common in the studied clinic. Caution is warranted when considering antibiotics for febrile children with these contributing factors.

Abstract Reference: 20670
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

Efficacy of ivermectin identified by high-throughput screening against *Clonorchis sinensis* larvae

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Abstract Content

Food-borne flukes are a new public health issue and praziquantel (PZQ) remains the only treatment option. Unfortunately, PZQ efficacy is staged and exhibits a tremor effect only in adults without affecting young and nonaging larvae. Given the empty drug pipelines and the lack of alternative treatment options, developing new drugs has become paramount. Insect repellent activity against C.sinensis larvae was evaluated by applying HTS to a compound library consisting of a total of 308 FDA-approved drugs. Among the selected drugs, ivermectin showed a deep inhibitory effect against contorchiasis larvae. Therefore, in this study, the larval efficacy of ivermectin against C.sinensis was evaluated. Cystic larvae of C.sinensis were 12.5, 25, 50, and 100 μM ivermectin, which were not affected by 24-hour exposure. However, the larval efficacy for the concentrations tested after 48 hours of drug exposure was 0, 36.9, 38.2, and 38%, respectively. An additional increase in larval efficacy was observed after 72 hours, reaching 53.4, 58.6, 74.7, and 70.1% for the four mentioned aform concentrations, respectively. In conclusion, ivermectin found with HTS showed inhibitory activity against C.sinensis larvae in vitro. Further studies investigating the insect repellent effect of ivermectin on adult and juvenile C.sinensis using animal models will need to be conducted.

Abstract Reference: 20681
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

Unraveling the immunomodulatory role of macrophages in giardiasis: A transcriptome-based study

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Abstract Content

Giardiasis, a gastrointestinal disease caused by *Giardia intestinalis*, leads to childhood morbidity and mortality in developing countries. This disease mainly affects school children, particularly those living in the rural parts of Malaysia. The latest report in 2019 has shown that the overall mean rate of giardiasis in Malaysia is 13.7%. *G. intestinalis* developed sophisticated, yet not completely disclosed mechanisms to escape the host immune system and growth in the intestine. The underlying cellular and molecular mechanisms of giardiasis, including the role of lamina propria immune cells, such as macrophages that contribute to parasite control are poorly understood. To characterize the role of macrophages and how these antigen-presenting cells subsequently modulate host immune response, the main objective of this study is to characterize the immunomodulatory roles of THP-1-derived human macrophages in response to *G. intestinalis* infection using a transcriptome-based approach. THP-1-derived human macrophages will be co-cultured with *G. intestinalis* trophozoites at various time points, followed by the assessment of nitric oxide, cytokines, and chemokines production. Additionally, the release of macrophage extracellular traps following stimulation will be examined. Differential expression of immune-related genes will be identified using RNA sequencing, and the transcriptomics data will be validated with real-time PCR. The findings of this study will serve as a platform to unravel novel gene networks and signaling pathways involved in the pathogenesis of human giardiasis. Findings from this project will facilitate the future application of macrophage-based approach for the design and development of immunotherapeutic in giardiasis.

Abstract Reference: 20683
Mode of Presentation: Poster Presentation
Topic: Session 2 - Vector-Borne Diseases

Concurrent infection of dengue and malaria: An unusual case report

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Abstract Content

Dengue fever and Malaria are endemic diseases often occur in Southeast Asia, including Indonesia.[1] Malaria and dengue have similar clinical features. Concurrent malaria and dengue infection is a serious disease that rarely documented. We report the case of a 33 years old male patient with fever since 4 days before admission. Patients also complain of pain, joint and muscle pain and nausea. The patient is a soldier who has a history of service in Papua and has experienced similar complaints. He was diagnosed with malaria in 2022 and received 1x4 tablet DHP treatment for 3 days. On physical examination, the abdomen found enlarge of spleen. Laboratory examination results thrombocytopenia. In the peripheral blood smear, *Plasmodium vivax* was found with 2,746 parasites/μL of blood support of Vivax Malaria. The patient was diagnosed with Dengue Fever and Malaria Vivax which given DHP 1x4 tablets for 3 days, primaquine 1x1 tablet for 14 days. Concurrent infections of malaria and dengue virus can be severe symptoms, including fever, headache, myalgia, nausea, and stomach discomfort.[3] Dengue is diagnosed on the presence of IgM or low platelets. Malaria diagnosed through a blood smear, which P. vivax hypnozoites are frequently reactivated from latent stage, resulting in clinical relapses.[4] DHP and primaquine antimalarial medications enabled the patient to recover quickly. The patient's clinical status improved after beginning the anti-malarial regimen, highlighting the need of evaluating multiple diseases in places where dengue fever and malaria are prevalent.

Abstract Reference: 20685
Mode of Presentation: Poster Presentation
Topic: Session 2 - Bacteriology

Targeting ESKAPE pathogens: Isolation and characterization of bacteriophages from environmental samples

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Abstract Content

The indiscriminate use of antibiotics causes the appearance of multidrug-resistant bacteria (MDR), which has been classified by WHO as a serious global health concern, affecting healthcare and the economy. ESKAPE (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species) pathogens are the most common MDR bacteria that causes nosocomial infection which leads to the increased morbidity and mortality of patients. To fight against MDR bacteria, new antibiotics and alternative therapies are urgently needed. Bacteriophage therapy has been gaining interest as an alternative treatment against MDR bacteria. However, to date, only a small portion of bacteriophages and their target hosts have been thoroughly studied and identified. Therefore, it is of utmost importance to continue our efforts in discovering and characterizing novel bacteriophages capable of effectively targeting these MDR bacteria. This proposed study focuses on the isolation and characterization of bacteriophages obtained from sewage and soil samples. A total of four lytic bacteriophages were isolated against *Klebsiella pneumoniae*, five against *Pseudomonas aeruginosa*, and one against *Acinetobacter baumannii*. These isolated bacteriophages were then further purified and amplified. Purified bacteriophages will then be characterized by examining their stabilities under different pH and temperatures. Host range analysis against the clinical strains of MDR bacteria will be performed using the double agar overlay method. The findings of this study will serve as a platform for discovering novel bacteriophages with promising antimicrobial properties to control nosocomial infections associated with ESKAPE pathogens.

Abstract Reference: 20697
Mode of Presentation: Poster Presentation
Topic: Session 2 - Vector-Borne Diseases

Japanese encephalitis in an immunocompromised host – A case of diagnostic challenge

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Abstract Content

Japanese encephalitis (JE) is a vector-borne disease with significant public health and clinical concern due to its high case-fatality rate of 30% and long-term neurological sequelae of 30-50% in survivors. We reported a case of JE encephalitis, highlighting the diagnostic challenges. 27-year-old gentleman who underwent stem cell transplant 2 years ago for relapsed acute leukemia, presented with fever for 3 days. His Glasgow coma scale (GCS) was 13 with no neurological deficit or meningism. Dengue point-of-care(POC) test showed positive IgM with negative NS1 Ag and IgG. Cerebrospinal fluid (CSF) was acellular with normal protein and glucose. Magnetic resonance imaging demonstrated bilateral high frontal white matter and corpus callosum lesions with abnormal signal in left medial temporal lobe. There were no features to suggest dengue infection. He was commenced on intravenous (IV) ceftriaxone and acyclovir and when his GCS dropped to 9, IV methylprednisolone 1000mg OD was given for 5 days. His CSF bacteria and viral panels were negative. He started to improve 3 days later and recovered with no neurological sequelae. His autoimmune screen and CSF dengue PCR (acute and convalescent samples) were negative. CSF JE IgM on both occasions were positive with increasing optical density. His convalescent serum JE IgM was positive and Dengue POC test showed negative NS1 with positive IgM and IgG. Diagnosis of JE encephalitis remained a challenge to clinicians in Sarawak. Cross-reactivity between JE with dengue is common as both belong to the Flavivirus family.

Abstract Reference: 20702
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Exploring the antimalarial potential of a novel synthetic immunomodulatory heterocycle in a murine model

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Abstract Content

Malaria remains a major global health threat emphasizing the need for an effective and safe antimalarial agent. In our efforts towards the development of new immunochemotherapeutic approaches to tackle malaria, different classes of new heterocyclic compounds having immunomodulatory potential are synthesized and evaluated through *in-vitro* antimalarial screening. Further *in vivo* assessment of the lead compound was then done against *P. berghei* ANKA infection in a mouse model. The *in-vitro* cytotoxicity and hemolytic assays were performed and antimalarial activity was assessed using the schizont maturation inhibition assay. The *in vivo* antimalarial efficacy was assessed using suppressive test and a combination of Artemether + Lumefantrine was used as a positive control. Other parameters such as parasitaemia levels, host survival rates, lymphocyte subsets, cytokine profiles, liver and kidney function tests and quantification of reactive oxygen species (ROS) and nitric oxide (NO) levels were also studied to check the efficacy and safety of treatment. The findings revealed a significant reduction in parasitaemia and prolonged host survival after treatment with the lead compound. The newly identified molecule balanced cytokine levels and improved lymphocyte subset responses, enhancing antimalarial activity while minimizing inflammation and tissue damage. Increased ROS and NO levels suggested that the compound regulates oxidative stress and immune pathways. This study emphasizes the importance of versatile immunomodulatory heterocyclic small molecules in antimalarial drug development. The research findings highlighted that the identified lead can suppress parasitic growth and has strong immunomodulatory effects, providing promising evidence for further investigation.

Abstract Reference: 20705
Mode of Presentation: Poster Presentation
Topic: Session 2 - Bacteriology

Identification and immunogenicity of outer membrane peptides for shigella vaccine development

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Abstract Content

Shigella, a Gram-negative bacterium, causes shigellosis and presents challenges in treatment due to antibiotic resistance. Developing vaccines against prevalent *Shigella* serotypes could significantly reduce shigellosis incidence. This study aimed to identify the HLA class II bound peptides and assess their immunogenicity as potential candidates for *Shigella* vaccine development. THP-1 human macrophage cell lines were infected with clinical strains of *Shigella flexneri* 2a. The bacterial peptides bound to HLA class II molecules of infected THP-1 cells were analyzed and identified using an immunopeptidomics approach. Fourteen peptides were predicted by PSORTb, CELLO, and Gneg-mPLoc as *Shigella* outer membrane proteins. Among these, twelve proteins were conserved across *Shigella* species and showed no significant similarity to human proteomes. Outer membrane receptor FepA and TonB-dependent receptor were predicted to possess numerous antigenic B- and T-cell epitopes. Recombinant truncated proteins were constructed for immunogenicity assays. *Shigella*-infected rat serum was obtained by immunizing rats with outer membrane proteins (OMPs) and surface associated proteins (SAPs) of *S. flexneri* 2a. Immunogenicity was assessed by quantifying IgG response from immunized rat serum using the recombinant truncated proteins in immunoblot and ELISA assays. Recombinant truncated FepA and TonB showed strong reactivity with OMPs- and SAPs-immunized rat serum. In conclusion, recombinant truncated FepA and TonB are promising candidates for the development of epitope-based universal *Shigella* vaccine, with efficacy to be further evaluated in animal immunization studies.

Abstract Reference: 20707
Mode of Presentation: Poster Presentation
Topic: Session 3 - Vector-Borne Diseases

Rapid and precise identification of *Bartonella henselae* using quantitative PCR assay on clinical samples

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Abstract Content

Bartonellosis may cause variety of emerging infectious diseases in humans that can be difficult to diagnose. Cat scratch disease (CSD) is a worldwide preventable zoonotic disease caused by a Gram-negative bacterium, *Bartonella henselae (B. henselae*). We have validated two rapid, highly sensitive and specific, duplex, real-time polymerase chain reaction (PCR) assays on TaqMan probes to simultaneously detect and differentiate *B. henselae* and *B. quintana.* The TaqMan probe–based assays have high specificity and sensitivity, and good reproducibility for simultaneous detection of *B. henselae* and *B. quintana*. Between 1st September 2023 – 30th April 2024, 79 clinical samples from patients were tested for Bartonella PCR at Rickettsial Laboratory of Institute for Medical Research, Setia Alam, 33% (26/79) samples were tested positive for *B. henselae* and none detected for *B. quintana.* Out of 26 samples, 5 were lymph nodes and 21 samples were blood. 19% (5 / 26) of the positive samples were Opthamology cases and 81% (11/26) were Medical cases. 4/5 lymph nodes detected for *B.henselae* were cases of necrotising granulomatous lymphadenitis. 11.5% (3/26) of positive samples were from confirmed to be from immunocompromised patients while the rest were either immunocompetent or unknown status. The conventional diagnosis of *Bartonella* spp. infections is hampered by the slow, fastidious growth characteristics of *Bartonella* spp. PCR assay for *B.henselae* detection is a cost-effective, sensitive and reliable methods; and are thus suitable for clinical diagnosis, epidemiological surveys, and surveillance of Cat Scratch Disease.

Abstract Reference: 20710
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Exploring the therapeutic efficacy of ethanolic flower extract of *Calotropis procera* in combination with *Artemether lumefantrine* in *Plasmodium berghei* infected mice

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Abstract Content

Antimalarial drug resistance poses a significant challenge towards global efforts to combat malaria. Plant-derived antimalarials are indispensable for malaria treatment and serve as a foundation for the development of new drugs. In the present study, an ethanolic flower extract of *Calotropis procera* (EFECP) was used for treatment along with the standard antimalarial drugs Artemether and Lumefantrine (AL) to improve its therapeutic activity. The suppressive efficacy of EFECP in combination with AL was assessed in *P. berghei* infected mice (ANKA strain) using Knight and Peters (1980) method. Assessment of parasitaemia and Mean survival time was studied along with immunological and biochemical parameters which included analysis of cell surface expression, nitric oxide levels, Reactive Oxygen Species and Cytokine analyses etc. The results demonstrated enhanced suppressive efficacy of the EFECP, accompanied by 100% mean survival time when given along with AL. Further, the combination treatment exhibited improved immunological responses. Biochemical analysis also highlighted the safety of combination treatment. Combination therapy is fast replacing monotherapy in the treatment of infectious diseases and *Plasmodium* resistance to artemisinin–based combination therapies (ACTs) is an emerging challenge. Our findings affirm the immense potential of EFECP + AL combination in rapid suppression of the parasite with safety to visceral organs of the host.

Abstract Reference: 20719
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

Biogeography of freshwater snails (Mollusca: Gastropoda) in various agro-ecological zones across six provinces of South Africa

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Abstract Content

Freshwater gastropods are recognised for the role they play as intermediate hosts of trematodes of veterinary and public health importance. Their population dynamics and biodiversity are affected by human and animal activities. Climatic and environmental factors, exacerbated by introduction of invasive snails may lead to displacement or decline in the biodiversity of autochthonous snail populations. However, these changes often go unnoticed due to poor monitoring and surveillance. This study assessed the geographic distribution and diversity of freshwater snails in six provinces of South Africa. Localities with different agro-ecological conditions were selected for the survey and 3360 snails were collected from 26 randomly selected habitats were animal and/or human activities occurred. Snail were identified based on the COI and 16S genes. Spatial distribution maps showing the distribution and abundance of snails across the different sites were generated using Arc-GIS. Thirteen freshwater snail species were identified from five families; Lymnaeidae, Planorbidae, Thiaridae, Physidae and Gastrodontidae. The highest snail density and species diversity was recorded in the hot semi-arid steppe region of Limpopo province, Tzaneen. *Bulinus truncatus* was the only species collected in the cold semi-arid steppe. *Physa acuta*, *Pseudosuccinea columella* and *Terabia granifera* were the most distributed, and utilised variety of habitats. *Physa acuta* was the most abundant species, but *P. columella*was found in most agro-ecological zones. This was not surprising as these species are invasive in South Africa.

Abstract Reference: 20725
Mode of Presentation: Poster Presentation
Topic: Session 3 - One Health

Nanopore sequencing for the comprehensive and accurate elucidation of the "nemabiome" in dogs, humans and other animals.

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Abstract Content

Gastrointestinal nematodes (GINs) severely affect animals, including humans, by causing serious morbidity whilst also exacerbating cycles of poverty. Commonly used diagnostics for GIN detection are often insensitive, e.g. microscopy, whilst more sensitive molecular techniques, e.g. quantitative PCR (qPCR), may only target a few species. More recently, attempts to characterise all GIN species simultaneously, i.e. the "nemabiome" have been developed using next-generation sequencing (NGS). To date, these methods have relied on short-read NGS platforms that can only detect limited genera and for some taxa they are unable classify to a species level. Improving upon this, we demonstrate how a nanopore sequencing approach can accurately characterise the complete nemabiome from animals and humans. Through targeting of both internal transcribed spacer regions of the clade V nematodes and 18S ribosomal RNA gene of other key taxa in clades I, II and IV we have shown our assay can provide a comprehensive characterisation of GIN diversity. Moreover, the performance of our assay was found to be equivalent to highly sensitive and specific qPCRs for key GIN species. Overall, long-read nanopore sequencing offers unparalleled accuracy in species classification and enables a more comprehensive characterization of GIN communities, surpassing the identification capabilities of previously available technologies.

Abstract Reference: 20727
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Anemia among children in malaria endemic areas

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Abstract Content

Studies on malaria and/or Soil Transmitted Helminths (STHs) in malaria-endemic areas are important because these parasitic diseases put children at higher risk for anemia. Malaria causes red blood cells (RBCs) destruction, while STH, specifically, hookworms attach to host’s intestinal walls and destroy RBCs, both resulting in low hemoglobin levels known as anemia. Therefore, a cross-sectional study (n=381) was conducted to determine the anemia status among children 1 to 18 years old in four highly malaria-endemic municipalities of Palawan, the Philippines. Stool was used to determine STH prevalence using Kato-katz technique, blood was collected for malaria and anemia detection, while serum sample was utilized to measure serum ferritin and transferrin for Iron Deficiency Anemia (IDA) detection, respectively. A total of 402 children were enrolled in the study and were interviewed for demographic profile. All had their blood taken, however, only 167 submitted stool samples. The overall prevalence of malaria was found to be 2.7% (n=11), while STH prevalence was 37.7% (n=63). Out of the 11 malaria positive patients, 27% (n=3) have anemia. On the other hand, 46.4% of STH positive children have anemia. Furthermore, only 1 participant was diagnosed with IDA. Our study suggests that the adjusted association between malaria and anemia is not statistically significant (p=0.375). Meanwhile, STH was significantly associated (p=0.006) with anemia (AOR = 2.94, 95% CI = 1.37, 6.32).

Abstract Reference: 20730
Mode of Presentation: Poster Presentation
Topic: Session 3 - Vector-Borne Diseases

Scrub typhus seropositivity in Malaysia between 2016-2021: A six-year trend

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Abstract Content

Scrub typhus is a vector-borne zoonotic disease caused by the obligate intracellular Gram-negative bacterium *Orientia tsutsugamushi*. The pathogen is transmitted by the bite of larval stage trombiculid mites (chiggers) residing in small mammals. The diagnosis of the disease is challenging due to its similarity to other febrile illnesses. This study aimed to analyse the trend of scrub typhus seropositivity in Malaysia over a six-year period. Serological assay using the indirect immunoperoxidase procedure was conducted on patient samples collected from major hospitals across the five regions in Malaysia from 2016 to 2021. The serological data includes antibody titres against *O. tsutsugamushi*. Descriptive statistics were employed to characterize the patterns of scrub typhus seropositivity over the six-year period. Scrub typhus seropositivity showed a fluctuating trend between 2016-2021. In 2016, it was 22.4%, declining to 15.0% and 21.8% in 2017 and 2018 respectively. Seropositivity peaked in 2019 at 28.4% before decreasing to about 15% in 2020 and 2021. Sarawak in the East Malaysia region had the highest scrub typhus seropositivity rate at 40.7% whereas the Southern region was lowest at 4.0% cumulatively. Both males and females had similar seropositivity rates, with the highest occurrence in the 41-65 years age group in 3 out of the 6 studied years. In conclusion, the study on scrub typhus seropositivity in Malaysia over six years highlighted fluctuating rates across regions and age groups. The programmes of enhancing the surveillance, public awareness, vector control, healthcare training, and further research should be applied to address this epidemiological trend effectively.

Abstract Reference: 20731
Mode of Presentation: Poster Presentation
Topic: Session 2 - Bacteriology

Genome sequencing of A methicillin-resistant *Staphylococcus warneri* clinical isolate from Terengganu, Malaysia

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Abstract Content

Bacteraemia due to *Staphylococcus warneri*, a coagulase-negative staphylococci, is rare and occasionally infections are associated with medical indwelling devices. This opportunistic pathogen is generally resistant to β-lactams. Here, the draft genome of a methicillin-resistant *S. warneri* strain MR-SwaC109 which was isolated from the blood of an 84-year-old male patient in Hospital Besut, Terengganu in 2022 was presented. Phenotypic antimicrobial resistance was determined by disk diffusion using a panel of 30 antibiotics from 20 antimicrobial classes. Whole genome sequencing was performed using the Illumina iSeq 100, sequences assembled using UniCycler and analysed using standard bioinformatics tools. *S. warneri* MR-SwaC109 was resistant to four tested antibiotics: penicillin, oxacillin, cefoxitin and teicoplanin. The assembled genome comprised of a circular chromosome of 2,591,075 bp over 29 contigs. PlasmidFinder revealed two plasmid replicons, i.e., Inc18/*rep16*, designated pSwaC109-1 (14,843 bp) and Rep3/*rep5d* designated pSwaC109-2 (5,494 bp). pSwaC109-1 harboured the *blaZ* β-lactamase gene while the chromosome of SwaC109 contained the *mecA* methicillin-resistance gene (found in an SCC*mec* type IV (2B) element). Besides, a number of virulence genes responsible for cellular adherence (*atl*, *ebp*, and *sdrE*), lytic enzymes (*sspB*, *sspC*, *hysA*, *geh*, *lip*, *sspA*, and *nuc*), immune evasion (capsule) and secretion system (*esaG*) were also found in the genome. To our knowledge, this is the first genome description of a *S. warneri* clinical isolate from Malaysia. Our study provides a valuable genomic context of the genes contributing to antibiotic resistance and virulence of *S. warneri*.

Abstract Reference: 20734
Mode of Presentation: Poster Presentation
Topic: Session 2 - Vector-Borne Diseases

Scabies infection induces the non-histaminergic itch pathway

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Abstract Content

Scabies is one of the most common skin diseases worldwide and is caused by the parasitic mite *Sarcoptes scabiei*. Unbearable itch is the cardinal symptom of scabies. Scratching in response to itching facilities the entrance of pathogenic bacteria into the skin and can lead to life-threatening sequelae. The mechanisms underlying the scabies itch are poorly understood, hence scabies itch targeted therapies are missing. Due to the non-responsiveness to anti-histamines, a histamine-independent pathway is proposed for scabies itch. We aimed to investigate the expression of non-histaminergic itch markers (MRGPRX2, tryptase, periostin, NK1R, epidermal nerve fiber density (ENFD) and substance P) *ex-vivo* over a course of scabies infection in a scabies pig model. Skin biopsies from three scabies infected pigs were collected pre-infection and 2, 4, 8, 12 and 20 weeks post-infection. Primary antibodies for above listed markers and cy-3 labelled secondary antibodies were used immunohistologically. Aperio FL slide scanner and QuPath software were used to image and quantify itch markers. We observed significant increase in typtase$^+$ mast cells, MRGPRX2 positive cells, periostin, and NK1R expression, and reduced ENFD at 2 Weeks post-infection, coinciding with clinical onset of the scabies-associated itch in this model. We propose that scabies infection induces the non-histaminergic pathway.

Abstract Reference: 20740
Mode of Presentation: Poster Presentation
Topic: Malaria

Improving surveillance of *Plasmodium knowlesi* infections using serological exposure markers

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Abstract Content

Plasmodium knowlesi is increasingly becoming a leading cause of malaria in Southeast Asia. It is a zoonotic parasite that is transmitted from macaques (natural hosts) to humans through the bite of an infected Anopheles mosquito. Surveillance and diagnosis of *P. knowlesi* infection is confounded by lack of specific targets in rapid diagnostic tests and morphological similarities to other *Plasmodium* spp (such as *P. falciparum and P. malariae)* when using a blood smear. Addressing these concerns, the Mueller laboratory is developing and validating the detection of *P. knowlesi* specific antibodies in human sera samples to be used as serological exposure markers (SEMs) that can identify individuals with recent exposure to *P. knowlesi* infection. A multiplexed Luminex bead assay was utilised to detect *P. knowlesi* antibodies against key blood-stage parasite proteins. Magnetic beads coupled to *P. knowlesi* antigens were incubated with plasma samples from individuals from longitudinal cohort studies with known *P. knowlesi* infection status. At ICTMM, we aim to present how effectively the SEMs can classify individuals as having a past exposure to *P. knowlesi* using a machine learning algorithm. Knowledge of the past exposure complimented with molecular approaches (such as qPCR) will aid in understanding the transmission dynamics of *P. knowlesi* which can guide control measures that are urgently needed to reach malaria elimination in the Southeast Asian region as set by the Asian Pacific Malaria Elimination Network.

Abstract Reference: 20742
Mode of Presentation: Poster Presentation
Topic: Session 2 - Malaria

Intermittent preventive treatment for forest goers by forest malaria workers: An observational study on a key intervention for malaria elimination in Cambodia

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Abstract Content

Cambodia targets *P. falciparum* malaria elimination by 2023, aligning with WHO's Mekong Malaria Elimination program. The Intermittent Preventive Treatment for Forest Goers (IPTf) project aimed at forest-specific malaria elimination. The study aims to pinpoint the main factors driving malaria transmission in Cambodian forests and evaluate the initial implementation and effectiveness of IPTf in accelerating the elimination of malaria. From March 11, 2019, to January 30, 2021, an intervention program took place in isolated forests in Northeast Cambodia. The first phase focused on observing forest goers (FGs), documenting their malaria risk. In the second phase, a monthly artesunate-mefloquine IPTf was implemented by forest malaria workers conducting interviews, blood collection, and IPTf administration. Throughout the study period, 2198 FGs were involved in 3579 interviews. Following IPTf implementation, PCR-confirmed malaria prevalence significantly decreased from 2.9% to 0.5% for *P. falciparum* and from 21.0% to 4.7% for *P. viva*x. The intervention phase demonstrated a rapid decline in *P. falciparum* prevalence among mobile and previously inaccessible populations, while also revealing a higher *P. falciparum* infection risk associated with activities inaccurately labelled as farming, underscoring the need for customized interventions. The successful implementation of IPTf in Cambodia's remote forests has markedly decreased malaria prevalence among high-risk groups. Cambodia's National Malaria Program has acknowledged this strategy as essential for malaria elimination intervention, endorsing forest-specific approaches to meet the 2025 goal of eradicating all human malaria species in Cambodia.

Abstract Reference: 20744
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

Spatial distribution of *Plasmodium falciparum* infections in a high-risk area bordering Lake Victoria

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Abstract Content

A geographical distribution pattern of *Plasmodium falciparum* infections is often highly heterogeneous. It is important to identify factors shaping the spatial pattern for planning an effective intervention. The objective of the present study was to recognize the spatial pattern of *P. falciparum* infections in a high-risk area bordering Lake Victoria in Kenya and to identify the factors shaping the pattern. RDT (rapid diagnostic test) based *P. falciparum* infection data were obtained from a cohort study that followed over 400 residents in Suba South District, Homabay County in western Kenya. We analyzed the dataset considering the spatial autocorrelation, age, gender, bednet use and timing of survey using the Bayesian statistical method. The spatial analysis recognized at least two hot spot areas. The analysis also found that bednet use reduced the risk of infection by 12%, but the effect was not statistically significant (PR: 0.88, 95% CI: 0.72 - 1.03). Although males tended to have a higher risk, the effect of gender was not statistically significant either (PR: 1.18, 95%CI: 0.94-1.43). On the other hand, timing of survey was statistically significant (the statistics is not shown here because of its complexity). Since age was highly correlated with netuse, it was excluded from the optimal model. The results suggest high spatial and temporal heterogeneities of infections in the area. Currently we are conducing further analyses to identify key spatial factors such as elevation and distance from water sources.

Abstract Reference: 20745
Mode of Presentation: Poster Presentation
Topic: Session 2 - Bacteriology

Multidrug-resistant organisms in healthcare-associated infections: A growing concerns of antimicrobial sensitivity in low- and middle-income settings

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Abstract Content

Healthcare-associated infections (HAIs) represent a significant cause of mortality and morbidity among inpatients. HAIs are often caused by multidrug-resistant organisms, limiting effective antimicrobial options, especially in low- and middle-income (LMIC) settings. This review aims to evaluate the most common causes of HAIs and to determine the sensitivities of antimicrobials in treating these infections. A total of 109 isolates were studied, consisting of 49 isolates from healthcare-associated bloodstream infections and 60 isolates from ventilator-associated pneumonia collected from February 2023 to May 2024 from Universitas Sumatera Utara Hospital. Microorganism identification and antibiotic resistance were determined using the VITEK 2 Compact system according to the Clinical and Laboratory Standards Institute (CLSI) guidelines. *Staphylococcus aureus* (22.4%), coagulase-negative staphylococci (16.3%), *Klebsiella pneumoniae* (12.4%), and *Escherichia coli* (12.4%). For VAP, the main pathogens were *Acinetobacter baumannii* (21.6%), Candida spp. (18%) and *Pseudomonas aeruginosa* (15%). Results also showed that 53% of BSI and 52% of VAP cases were multidrug-resistant organisms (MDRO). None of the Enterobacteriaceae isolates from BSI and VAP samples were sensitive to ampicillin, ampicillin-sulbactam, or ceftriaxone. MSSA isolates showed moderate sensitivity to most antibiotic classes except to vancomycin and tigecycline. *Acinetobacter baumannii* showed highest sensitivity to tigecycline (69%) and amikacin (46%), but low sensitivity to ceftriaxone (8%) and meropenem (38%) in treating VAP. The results highlight the diminishing effectiveness of first-line and even reserved antimicrobials in treating HAIs. There is a critical need to raise awareness about antibiotic use.

Abstract Reference: 20746
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

Assessment of the application value of the FA280—a fully automated fecal analyzer for diagnosing clonorchiasis: A mixed-method study

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Abstract Content

The traditional fecal examinations like Kato-Katz (KK) method are labor-intensive, time-consuming, and poorly accepted. The FA280, an innovative automatic fecal analyzer, reduces the labor intensity and increases efficiency. Evaluating its application in clonorchiasis diagnosis is essential to advance disease detection. A mixed-method design was employed. The quantitative study for performance assessment involved a diagnosis test conducted in Xinhui District, Guangdong, China, comparing the detection rate and agreement between the FA280 and the KK method. The qualitative study applied the semi-structured individual interviews with medical staff and institution managers to respectively explore the applicability and promotion potential of the FA280. The data was analyzed through thematic analysis. The quantitative study involved 1000 participants. The FA280 and the KK method each detected clonorchiasis at a 10.0% positive rate, with a 96.8% overall agreement rate. No significant difference was found in the agreement between two methods ($P > 0.99$). The kappa value was 0.82 (95% *CI*: 0.76–0.88), showing almost perfect agreement. The qualitative study, with three medical staff and two managers, founded the FA280 was superior in learning, detection and results, and has high acceptance. The benefits, challenges and suggestions of FA280 promotion were also mentioned. The high consistency between FA280 and KK method results suggested a good performance for the FA280. Insights gathered from interviews indicated its potential as a primary diagnostic method for clonorchiasis. Our study assessed the performance, applicability, and scalability of the FA280 in clonorchiasis diagnosis, thereby contributing to the control of the disease.

Abstract Reference: 20763
Mode of Presentation: Poster Presentation
Topic: Session 3 - Entomology

Establishment allele-specific PCR targeting locus 1016 in voltage-gated sodium channel gene in *Aedes aegypti* laboratory strain

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Abstract Content

The efficacy of control measures against *Aedes aegypti* mosquitoes, the primary vector of the dengue virus, is jeopardized by the emergence of insecticide resistance. Molecular detection of knockdown resistance (*kdr*) in the voltage-gated sodium channel provides pivotal information associated with pyrethroid resistance. This study expedited the identification of the *kdr* gene targeting position 1016 in domain II, segment 6 of voltage-gated sodium channel via allele-specific PCR (AS-PCR). Laboratory strains of F1106 *Ae. aegypti* reared in the Insectarium of the Medical Entomology Unit, Institute of Medical Research, were utilized. The establishment of robust AS-PCR protocol, achieved through PCR optimization, is crucial for enhanced specificity in discriminating substitutions of valine to glycine at position 1016 in *Ae. aegypti* laboratory strain, which then served as the standard amplification reference. DNA was extracted and subjected to AS-PCR using specific primers. The establishment of a gradient PCR protocol, with temperatures ranging from 50 to 60°C, was executed to determine the optimal annealing temperature for the primers. The findings indicated that the optimal annealing temperature was 58°C. The electrophoresis gel of targeted sequences revealed distinct bands at molecular weight of 592bp and 348 bp. As the test sample is the susceptible strain, single nucleotide analysis demonstrated the absence of mutations at position 1016 in the VGSC gene. In conclusion, AS-PCR can serve as a reference for the rapid detection of V1016G mutations in wild-caught *Ae. aegypti*, providing a valuable diagnostic tool and allowing for the distinction between heterogeneous and homogeneous resistance populations through gel electrophoresis analysis.

Abstract Reference: 20764
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

Detection and quantification of viable helminth eggs in Brazilian sewage sludge as an epidemiological tool

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Abstract Content

Soil-transmitted helminths (STH) infections, neglected diseases with significant underreporting, pose a challenge to epidemiological monitoring, impacting billions of people worldwide, especially those in socioeconomic vulnerability. In this scenario, sewage monitoring appears to be an alternative to assist in epidemiological surveillance, allowing for the detection and quantification of viable helminth eggs on a large scale. This study aimed to analyze the presence of STH eggs in sewage sludge collected over the last triennium (2021-2023) from eight wastewater treatment plants located in socioeconomically distinct areas in Brazil’s Central-West Region. The method employed centrifugation and flotation using a zinc sulfate solution (d = 1.30 g/mL) for the recovery of helminth eggs from the sewage sludge samples, followed by microscopic analysis using a Sedwick-Rafter chamber. The area with the lowest monthly income presented an average of four times more helminth ova (16.61 eggs/g DM; $p < 0.05$) than the most economically favored region analyzed (3.56 eggs/g DM). Eggs from 12 distinct genera were observed, with *Hymenolepis* spp. (44.28%), *Ascaris* spp. (19.27%), *Trichuris* spp. (7.87%) and *Toxocara* spp. (7.25%) being the most identified. Our results emphasize the socioeconomic factor of STH infections and indicate regions with a higher incidence of STH eggs. This information offers valuable insights for the epidemiological surveillance of these frequently underreported infections that affect the poorest and most deprived communities. Identifying the areas and populations at higher risk of helminth infection, especially those in socioeconomic vulnerability, is crucial to understand and mitigate the impact of these infectious diseases on public health.

Abstract Reference: 20767
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

P230 as a *Plasmodium vivax* gametocyte biomarker in Southwestern India: Implications for transmission dynamics

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Abstract Content

Plasmodium vivax, the most prevalent malaria infection in South Asia, complicates elimination efforts due to its early gametocyte appearance, which enables mosquito infectiousness before diagnosis. Elimination strategies of identifying and targeting highly expressed gametocyte genes in regional isolates can impact transmission intensity overcoming seasonal variations. Human blood samples infected with *Pv* were collected from the southwestern coastal region of India. Total RNA was extracted using TRIzol method and RT-qPCR was performed to quantify and compare the expression of gametocyte-specific genes *P25*, *P230*, *P48/45*, and *HAP2*, with *seryl-tRNA synthetase* as the endogenous control. RT-qPCR analysis revealed that among the examined gametocyte-specific genes, *P230* exhibited the highest expression levels, followed by *P25* and *HAP2*, with *P48/45* showing the lowest expression. Additionally, these genes' expression levels and trends remained consistent throughout the malaria transmission seasons. The distinct expression pattern of gametocyte-specific genes in *Pv*, with *P230* being the most highly expressed, suggests that *P230* could serve as a more effective biomarker than *P25*, traditionally used for *P. falciparum*. The consistent expression levels of these genes across malaria transmission seasons indicate that seasonal variations do not significantly affect gametocyte gene expression in *Pv* isolates. Our study highlights the need for region-specific studies and tailored malaria elimination strategies, emphasizing *P230* as a key target for interventions in *Pv* endemic areas. The stable expression of gametocyte genes across seasons supports the robustness of these biomarkers for year-round monitoring and control efforts.

Abstract Reference: 20769
Mode of Presentation: Poster Presentation
Topic: Session 3 - Entomology

Forcipomyia (Lasiohelea) biting midges as a new vector candidate for leishmaniasis transmission in Thailand

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Abstract Content

The identification of vectors for leishmaniasis transmission in Thailand remains uncertain, despite sandflies being conventionally recognized as the primary vectors. Experimental evidence reviled that biting midges are more likely the natural vectors of *Leishmania* (*Mundinia*) species. While *Culicoides* has received substantial attention, *Forcipomyia* has been relatively overlooked due to the limitation of morphological and molecular data. To date, 33 subgenera have been described but only species of subgenus *Lasiohelea* feed on vertebrate hosts. Accordingly, we speculate that *Forcipomyia* (*Lasiohelea*) spp. might serve as vectors of *Mundinia* leishmaniasis in the country. This study aims to investigate the potential role of *Forcipomyia* biting midges as leishmaniasis vectors in Thailand, using integrated morphological and molecular approaches. **S**weep nets were used to collect the *Forcipomyia* midges around the patient's house in Nakhon Si Thamarat, Southern Thailand. Primary morphological screening of *Lasiohelea* was based on the presence of well-developed cibarium armature, 2Rs cell extending beyond middle of anterior margin, one spermatheca without neck, and wings with dense microtrichia. Phylogenetic analysis of *COI* gene was conducted to establish phylogenetic consistency within *Forcipomyia* subgenera clades. *Leishmania* 18s qPCR was also employed for parasite detection. Morphological and molecular data support the identification of *Forcipomyia* (*Lasiohelea*) specimens. Notably, 18s qPCR results indicate the presence of *Leishmania* in such specimens. Essentially, our findings represent the first evidence of natural *Leishmania* infection within *Forcipomyia* (*Lasiohelea*) midges. This discovery implicates *Forcipomyia* (*Lasiohelea*) in the epidemiology of the disease.

Keywords: *Forcipomyia* biting midges, leishmaniasis vector, phylogenetic analysis, Thailand.

Abstract Reference: 20770
Mode of Presentation: Poster Presentation
Topic: Session 2 - Vector-Borne Diseases

Dengue and the bonded heart: Case series of dengue myocarditis

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Abstract Content

Dengue infection is arthropod borne flaviviridae infection that is endemic in tropical countries. Dengue infection causes asymptomatic infection to severe dengue shock syndrome with multi organs involvement. We reported a case series of dengue myocarditis that occurred in a pair of spouse. Case 1-The Wife 59 years old lady, underlying hypertension, dyslipidaemia was presented with fever for 5 days, associated with cough, loose stools and myalgia and reduced effort tolerance.On examination, she was tachycardiac and had crepitation over her right lung field. Dengue NS1 and IgG was positive. Electrocardiogram showed T inversion over inferior leads, creatinine kinase (CK) was 1065U/L (normal range: <200U/L), Troponin I was 90ng/L (normal range: <15.6ng/L). Chest X ray showed right sided pleural effusion. She was diagnosed as severe dengue in critical phase in compensated shock complicated with myocarditis and leaking. ECHO showed no abnormality. Case 2-The Husband 59 years old gentleman,underlying dyslipidemia was presented with fever for 5 days, associated with cough, nausea, myalgia and loose stool. Dengue NS1 and IGG were positive. Electrocardiogram showed T inversion over V3-V6 with raised cardiac biomarkers-creatinine kinase was 494 U/L and increased to 685 U/L, Troponin I was 56.9 Diagnosis of dengue fever in critical phase complicated with myocarditis was made. Dengue myocarditis is an uncommon and likely under-diagnosed complication. Diagnosis of dengue myocarditis remains challenging due to heterogenous manifestation from asymptomatic to severe cardiogenic shock.

Abstract Reference: 20783
Mode of Presentation: Poster Presentation
Topic: Session 2 - Bacteriology

Tuberculosis-destructed lung and a devastating déjà vu of tuberculosis mortalities: A case report of an 11-year-old girl - the last surviving daughter

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Abstract Content

Tuberculosis-destroyed lung poses a significant public health challenge, especially in developing countries. We report a case of an 11-year-old girl with Rifampicin-Resistant Tuberculosis (RR-TB) complicated by a destroyed right lung and Major Depressive Disorder, following the loss of all six elder sisters to similar disease. An 11-year-old girl presented with a 6-month history of chronic cough and constitutional symptoms. Imaging revealed a complex right pleural effusion, and RR-TB was diagnosed on tuberculosis workups. Her family history included six sisters who died from RR-TB complications. Social factors included false beliefs, non-compliance, and inadequate TB treatment and surveillance. Her 10-month hospitalization was complicated with TB-immune reconstitution syndrome (TB-IRIS), major depressive disorder, refusal of treatment, and complex social issues. Management comprised of respiratory support, intensive second-line anti-TB regimen, an 8-week steroid course, and psychological care. Immunological workups were unremarkable. A two-year treatment plan and a multidisciplinary, multilevel compliance-enforcing measures were implemented and were successful so far. Throughout follow-ups, she remained stable with Long Term Oxygen Therapy (LTOT) and reduced effort tolerance (NYHA Class III). Meanwhile, stringent surveillance identified her father and elder brother as RR-TB cases, both of whom were treated with the appropriate regimen. Tuberculosis with post-tubercular lung destruction and complex compliance issue are manageable with vigilant, comprehensive, and highly-attentive multidisciplinary care from primary to tertiary level. Managing tuberculosis-destroyed lung with complex social issues is a significant challenge. Collaborative, multidisciplinary care can make a difference, and together, we can drive meaningful change

Abstract Reference: 20786
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

Proteasome mutation promotes resistance to artemisinin in *Plasmodium falciparum*

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Abstract Content

Malaria parasites increasingly develop resistance to all drugs available in the market, hampering the goal of reducing malaria burden. Therefore, understanding the resistance mechanisms is crucial for developing treatments with improved and sustainable efficacy in the future. Clinical artemisinin resistance has been associated with mutations in the *k13* gene, nevertheless, mutations in different parts of the ubiquitin-proteasome system (UPS) modulate artemisinin susceptibility in malaria parasites. The UPS is crucial throughout the parasite's life cycle and involves a protein posttranslational modification, named ubiquitination that is recognized by the 26S proteasome. The type of ubiquitination defines if proteins are recycled or degraded by the proteasome. The initial step of substrate processing by the proteasome is recognizing a ubiquitylated substrate, mediated by the ubiquitin receptors within the base subcomplex of the 19S RP, including the rpn2. One mutation, rpn2^{E738K}, was found in *P. chabaudi* artemisinin-resistant parasite line. Using a *P. falciparum* strain, we investigated this mutation and found it gives dihydroartemisinin resistance to the parasites, with the proteasome playing a key role in this resistance due to the reduction of polyubiquitinated proteins. Additionally, we introduced this mutation to the K13^{C580Y} mutant parasites, and preliminary studies revealed that the proteasome mutation was masked by the K13 mutation. Thus, by conducting additional research, we can be able to clarify the K13 mutation mechanism that confers parasite resistance and highlight the critical function of the UPS in the dihydroartemisinin mode of action.

Abstract Reference: 20787
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

Molecular mechanisms for artemisinin-piperaquine resistance in *Plasmodium falciparum*

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Abstract Content

Malaria causes half a million deaths annually. Despite efforts to eradicate it, *Plasmodium's* resistance to available antimalarial drugs has been a challenge in disease control. Artemisinin-based combination therapies (ACTs) are the most widely used treatment, however, resistance has also emerged. One of these combinations is the dihydroartemisinin-piperaquine. Its resistance has been linked to the $K13^{C580Y}$ mutation, *pfcrt* SNPs, and variations in plasmepsin2/3 (pm2 and pm3, respectively) and *pfmdr1*. We generated *P. falciparum* Dd2 parasite lines with copy number variations in *pm2* or a *pm3-1* hybrid gene on a southeast-Asian genetic background. A decrease in mdr1 copy number was observed, leading to higher susceptibility to mefloquine, mirroring findings in Southeast Asia. This suggests that mdr1 reduction is an adaptation to plasmepsin amplification, rather than a direct process of selection for piperaquine resistance. We also observed higher resistance to dihydroartemisinin with plasmepsin 2 amplification, similar to the *pfk13* mutant. Using verapamil (CRT inhibitor) and elacridar (MDR1 inhibitor) we observed that pm2 and pm3-1 amplifications increased piperaquine resistance, similar to what is reported in Cambodian *P. falciparum*. Studies associate *crt* mutations with piperaquine resistance in the context of amplified plasmepsin genes. Our findings suggest that *plasmepsin* and *mdr1* variants create a genetic background that favors *crt* mutations. Our results demonstrate a complementary mechanism involving *plasmepsins, mdr1*, and *crt* in piperaquine resistance. To further study underlying mechanisms, we generated new transgenic lines with the $K13^{C580Y}$ mutation and *pm2 and pm3-1* variations to unveil DHA-PPQ resistance mechanisms.

Abstract Reference: 20818
Mode of Presentation: Poster Presentation
Topic: Session 2 - Bacteriology

Streptococcus pyogenes infections in the tropics

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Abstract Content

Streptococcus pyogenes (group A or GAS) infections are a significant public health problem causing Scarlet Fever, skin and soft tissue infections (impetigo, cellulitis and abscesses) and life-threatening puerperal sepsis, Toxic Shock Syndrome (TSS) and necrotising fasciitis (NF) & tropical ulcer (NTU). Risk factors include poor sanitation, malnutrition, weakened immunity and over-crowding of homes allowing spread between occupants. NF of limbs was first managed effectively in the 1920s by Meleney in Beijing with deep incisional drainage of the fascial layers. The necrotising infection needs early recognition as associated septicaemia and TSS cause a rejection psychosis. Diagnosis includes differentiation from gas gangrene (myonecrosis), which is not associated with GAS as it does not penetrate the fascial layer; hence amputation is not needed. GAS causes rapidly advancing necrotic thrombosis of subcutaneous vessels, up to 2 cms daily (mark with pen), limiting antibiotic penetration. Treatment needs fasciotomy, high dose intravenous (IV) penicillin, careful anticoagulation and management of the TSS. NTU occurs in epidemics during water-logged conditions associated with poor sanitation. It also occurs individually. Treatment requires debridement and systemic penicillin with eradication of GAS carriage. Prevention and control include provision of clean water, sanitation and hygiene to reduce GAS colonisation of skin and mucosal surfaces and transmission within the population, aided by public health education. Antibiotic use is not required. Vaccination will be of immense benefit when available.

Abstract Reference: 20819
Mode of Presentation: Poster Presentation
Topic: Session 2 - Bacteriology

Wound healing with sugar paste without antibiotic use

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Abstract Content

Ancient Egyptians used sugar mixed with lard for wound healing while others used honey. Sugar debrides the wound and inhibits bacterial growth. It also has an osmotic effect enhancing serum exudation and development of granulation tissue. A modern sugar paste was produced at Northwick Park Hospital (NPH) pharmacy incorporating granulated sugar, polyethylene glycol (PEG) and hydrogen peroxide (H_2O_2) as thick and thin preparations. The paste could not be sterilised but both PEG and H_2O_2 are bactericidal rendering the paste safe. Experiments were conducted in deep subcutaneous wounds made on a pig, which has similar skin and subcutaneous tissue to humans. Comparison was made between cling film, sugar paste, chlorhexidine and chlorite solution (EUSOL). Photography and histological sections were performed weekly. Wounds healed within one week with plain film or sugar paste, were delayed by 2 weeks with chlorhexidine and 6 weeks with EUSOL. In hospital, wounds healed in 19 / 20 patients given NPH sugar paste. Deep cavities in the neck, liver and buttock healed within 3 weeks and large bed sores within 6 weeks. For cavities, the thin paste was instilled through a catheter once daily. Wounds and bed sores were packed with thick paste held in place with bandages changed twice daily. At final healing, wounds bled due to well-vascularised granulation tissue when the paste was stopped. Sugar is a good alternative for managing wounds infected with antibiotic-resistant bacteria. It also removes odour. Avoiding unnecessary use of antibiotics is desirable and now achievable.

Abstract Reference: 20825
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

AIDS with cerebral toxoplasmosis in beta thalassemia major: An unusual case report

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Abstract Content

Thalasemia major patients have a high incidence of transfusion-transmitted infections, primarily as a viral infections acquired via blood transfusion, such as HIV.[1] Toxoplasmosis is a major cause of central nervous system infection in HIV/AIDS patients don't receive proper prophylaxis.[1] We report the case of a 25 y.o female patient with complaints of decreased consciousness accompanied by fever, severe headache and vomiting. The patient has thalasemia since birth with 2-3 bags of transfusion every month and iron chelating. On physical examination, there was temporalis muscle atrophy, oral thrush, stiff neck. Laboratory showed HIV Elisa and Anti Toxo IgG positive. Head MSCT showed multiple supra-infratentorial lesions with irregular borders with cystic components suspicious for SOP Infectious Process, Hydrocephalus non communincans. MRI Brain shows multiple brain abscesses accompanied by meningoencephalitis and ventriculitis which causes non-communicating hydrocephalus. The patient was given Cotrimoxazole therapy 3x960 mg, Pyrimethamine loading 200 mg followed by 1x75 mg, Clindamycin 3x600 mg, Nystatin drop 3x4 cc, Deferipron 3x1000 mg and other symptomatic therapy. Transfusion Transmitted Infections primarily affect people who require blood transfusions, such as thalassemia major and been linked to worse survival rate.[3] Dysfunction of erythroid differentiation to bone marrow microenvironment damage and stromal cell impairment by HIV.[4] Even after anti-toxoplasma medication, the mortality of HIV-associated TE during hospitalization remains high.[5] Major patients with multitransfused β-thalassemia are constantly at high risk of getting transfusion-transmitted infections with poor prognosis of Toxoplasmosis leads to death or disability in HIV

Keyword**:** *AIDS, Thalasemia, Transfusion-Transmitted Infections*

Abstract Reference: 20831
Mode of Presentation: Poster Presentation
Topic: Session 2 - Bacteriology

A case of ceftazidime-intermediate meliodosis - A worrying phenomenon

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Abstract Content

Malaysia is endemic for melioidosis. It is a serious infectious disease caused by *Burkholderia pseudomalle*i (*Bp*). Melioidosis can affect both humans and animals, with a wide range of symptoms that can vary from localised skin infection to severe septicaemia. [1] Ceftazidime is a the treatment of choice for intensive phase due to its effectiveness in *Bp*. In general, most of the bacteria strain in Malaysia are sensitive strain. [2,3] However, the emergence of multidrug-resistant strains risk treatment failure and reliance on carbapenems [4]. We report a case of ceftazidime-intermediate Bp in an immunocompromised host. A previously healthy 40-year-old woman presented with nephrotic syndrome. She was diagnosed with systemic lupus erythematosus (SLE) and received intravenous (IV) hydrocortisone 100mg TDS for 37 days and IV methylprednisolone 500mg OD for 2 days. She developed septic shock with pneumonia requiring mechanical ventilation support. She had cavitating pneumonia of lungs and splenic abscess. Her initial blood culture yield ceftazidime-susceptible *Bp*. After 19 days of IV ceftazidime, she was persistently bacteremic and her blood culture yield ceftazidime-intermediate *Bp*. She was commenced on 21 days of IV meropenem. During hospitalisation, she suffered from catheter-related bloodstream infection and ventilator-associated pneumonia. She was also colonized with carbapenem-resistant *Enterobacterales* (CRE). She was discharged well from this infection after 101 days. Ceftazidime-intermediate in *Bp* is potentially inducible or mixed strains infection could occur. If unaware might lead to treatment failure and life-threatening events. Prolonged use of broad-spectrum antimicrobials, such as carbapenem increased risk of CRE.

Abstract Reference: 20835
Mode of Presentation: Poster Presentation
Topic: Session 1 - Virology

Prevalence of coxsackievirus A6 among suspected enteroviruses cases in 2023: Insights from Malaysia

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Abstract Content

Coxsackievirus A6 (CVA6) is an important enteroviruses (EVs) serotype linked to hand, foot, and mouth disease (HFMD) worldwide. This study determined the prevalence, demographic distribution, and clinical presentation of CVA6 cases in Malaysia. Clinical samples, including throat/rectal swabs, stools, CSF, and vesicular lesions, were subjected to in-house enterovirus RT-qPCR assays targeting pan-enteroviruses (Pan-EV), enterovirus A71 (EV-A71), coxsackievirus A16 (CVA16), CVA6 and enterovirus D68 (EV-D68). Laboratory and clinical data were analyzed retrospectively. Of 850 samples, 13.00% (111/850) tested positive for enteroviruses. CVA6 was the most prevalent serotype, accounting for 25.89% (29/111), followed by CVA16 at 16.07% (18/111). EV-A71 and EV-D86 were detected at a rate of 0.89% (1/111). The remaining enterovirus cases were not otherwise subtype specified. CVA6 cases peaked from June to August 2023, with an average detection rate of 34.00%. The majority of CVA6 infections were reported among children 1–5 years old (55.17%), followed by infants (37.93%), and markedly reduced in older children aged 6-12 years old (6.90%). Rashes over extremities were reported in all CVA6 cases, while fever and oral lesions were observed in 89.66% and 58.62% of cases, respectively. Meningoencephalitis complications were seen in 17.24% of the patients. CVA6 detection in rectal swab specimens exhibited a lower CT value (mean 24.61, SD 2.99) compared to throat swabs (mean 27.57, SD 4.70). CVA6 is the most prevalent enterovirus serotype in Malaysia, especially in cases with extremities blisters, oral lesions, and fever. Additionally, we highlighted the potential of rectal swabs as the optimal specimen for CVA6 detection.

Abstract Reference: 20839
Mode of Presentation: Poster Presentation
Topic: Session 1 - Virology

A retrospective study on Tuberculosis Preventive Therapy (TPT) commenced among people living with HIV (PLHIV) in a single centre in Malaysia.

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Abstract Content

TB caused 7.5 million infections and caused 1.3 million deaths. TB manifests as active TB (aTB) soon after infection or later which is latent TB infection (LTBI). 5-10% of LTBI cases develop into aTB. TPT is effective in preventing aTB from LTBI. PLHIV have 18.0 times higher risk to acquire TB. Guidelines suggest TPT for PLHIV. This study aimed to examine the TB infection rate among PLHIV in relation to TPT commencement. Retrospective analysis of HIV new cases aged 18-year-old and above, in Miri Hospital from 2010-2022. Data was routinely collected administrative data. TPT used was isoniazid for 6-9 months. 342 new cases were included. 86.3% were male with a median age of 31-year-old (IQR of 13). Mode of transmission included homosexual activities (51.5%), heterosexual activities (35.7%), and bisexual activities (11.4%). Median CD4 at presentation was 240 (IQR 282). 86.3% survived for a median of 56 months (IQR of 46). 18.4% had TB and 71.4% were diagnosed within 30 days of HIV diagnosis. Higher proportion of PLHIV who succumbed to HIV had TB, 56.2%, as compared to those who survived, 15.6% ($p<0.005$). 17.3% commenced on TPT. Among these, 2 of those who received TPT (3.4%) developed TB, as compared to 21.2% among those who did not receive TPT ($p<0.005$). TPT is effective in preventing TB among PLHIV. However, initiation of TPT should not be a blanket rule to prevent TPT-related complications which delayed the ART initiation which is the key for immune reconstitution.

Abstract Reference: 20845
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

Development of a spirulina feed effective only for the two larval stages of *Schistosoma mansoni*, not the intermediate host snail.

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Abstract Content

Current control of schistosomiasis relies mainly on mass drug administration of praziquantel. However, persistent reinfection and high costs require targeting the larvae as the source of infection and molluscs as intermediate hosts. The use of the molluscicide niclosamide is less common due to its high environmental toxicity and high cost. Serendipitously, we discovered that a feed derived from the cyanobacterium Arthrospira (Spirulina) platensis significantly reduces the release of infected larvae in snails. Snails fed with spirulina exhibited up to an 88% reduction in the release of cercariae, with the effect being concentration-dependent, particularly early in the infection period. Spirulina was also found to be non-toxic and extremely safe for both snails and Japanese medaka. In addition, its direct effect on cercariae was studied and it induced larval mortality. In particular, linoleic acid, one of the components of spirulina, was found to be responsible for this effect. These results suggest that spirulina may be a new feed concept that has a direct effect on schistosome larvae within infected snails and on larvae released from snails, without exhibiting environmental toxicity.

Abstract Reference: 20849
Mode of Presentation: Poster Presentation
Topic: Session 3 - Vector-Borne Diseases

The neglected tropical disease: Scrub typhus

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Abstract Content

Scrub typhus is a zoonotic vector borne rickettsial infection that is endemic in rural areas of Southeast Asia including India, Thailand, Korea, Australia, Russia, The Pacific Islands, and Japan. It is a neglected tropical disease with high mortality if untreated. We report a case of scrub typhus with classical presentation of fever and eschar in our centre located in Johor (North Malaysia). A 80 year old lady with underlying hypertension and dyslipidaemia with no history of hospitalisation, presented left leg wound for 1 week associated with fever, she could not recall preceded sting or bite.She visited primary health clinic and was given a course of oral cloxacillin, however she did not feel better and noticed rash on her trunk. On examination, she was haeomodynamically stable and an eschar noted on her anterior left ankle. She has maculopapular rash on her trunk. Her bloods tests show haemoglobin 10.9g/dl, white blood cell 4.56 x 10^9/L, platelet 186 x 10^9/L, urea 3.6 mmol/l, sodium 124mmol/L, potassium 3.3mmol/L, creatinine 95 umol/L, aspartate transaminase 81mmol/l, alanine transaminninase 66mmol/l, C-reactive protein 59,8 mmol/l. A provisional diagnosis of rickettsial infection was made. She was given oral doxycycline. Both her eschar and blood rickettsial polymerase chain reaction tests showed *Orientia Tsutsugamushi* DNA detected. Scrub typhus is an endemic disease in Malaysia. Clinicians should include it as one of the differentials in approach to manage patients presented with febrile illness.

Abstract Reference: 20852
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

Cerebral toxoplasmosis in HIV patients with opportunistic infections and severe bacterial pneumonia: A case report

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Abstract Content

Cerebral toxoplasmosis and severe bacterial pneumonia, particularly from MRSA, are significant concerns in HIV patients with weakened immune systems. Delays in diagnosis and management heighten mortality risk. Therefore, understanding comorbid diseases in HIV patients is crucial for improving clinical outcomes. A 27-year-old male presented with decreased consciousness, seizures, and cerebral toxoplasmosis in stage IV HIV with wasting syndrome and MRSA. The patient was unaware of his HIV status, which had progressed to stage IV without ARV treatment. Laboratory tests confirmed HIV, and severe bacterial pneumonia from MRSA was diagnosed. MRI showed multiple brain masses consistent with toxoplasmosis. CSF examination indicated positive Pandy and Nonne tests and increased total protein. The patient received anti-toxoplasma and ARV therapy as per guidelines, alongside anti-TB therapy and corticosteroids to manage clinical manifestations. Prognosis depends on the response to anti-TB therapy and CD4 count improvement. Cerebral toxoplasmosis in HIV patients with severe bacterial pneumonia is challenging to manage. Early diagnosis and treatment are critical to reducing fatal complications. Enhanced education on ARV adherence and opportunistic infection prevention is essential to lower mortality rates in HIV patients. This case underscores the importance of holistic management for HIV patients with opportunistic infections and severe bacterial pneumonia. Early diagnosis and intervention are key to improving patient prognosis. Patient education on adherence to ARV usage and the prevention of opportunistic infections will help reduce mortality rates in such cases.

Keywords: Cerebral Toxoplasmosis, HIV, Opportunistic Infection, Bacterial Pneumonia

Abstract Reference: 20854
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

Merozoite Surface Protein-1 (PkMSP1) domain analysis: In search for a genetic marker for *Plasmodium knowlesi*

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Abstract Content

MSP-1 protein is known for its crucial role as a vaccine target, epidemiological study, and cross-species. This study aims to determine the target polymorphic domain that can be further utilized as a genetic marker for developing a genotyping procedure for epidemiology surveillance during a malaria outbreak. PkMSP1 consists of nine domains; four of which were variable domains. Seventy (70) clinical samples confirmed positive for *P. knowlesi* by Nested-PCR were subjected to this study. Sets of primer represent variable domains (Domain II-PKD2; Domain IV- PKD4; Domain VI- PKD6 and Domain VIII- PKD8) and one conserved domain (Domain III- PKD3) was generated, underwent a nested PCR and capillary electrophoresis. Using Size polymorphism analysis, 9 samples (12.85%) showed a product size determined at least in only one domain, whereas 61 samples (87.15%) showed a product size at multiple domains. PKD6 appeared most frequently across the domain. Out of 70 samples PKD6 was detected in 65 samples (92%) followed by PKD8 (48 samples: 68.6%), PKD2 (33 samples: 47%), PKD4 (29 samples: 41.4%) and PKD3 (13 samples: 18.6%). These findings suggested that PKD6's might represent the predominant strain indicating that these strains either are more prevalent or have a higher transmission rate among the studied population. However, a limitation we encountered was that the samples may not be representative of the broader parasite population. Therefore, more samples from different localities or geographical differences need to be incorporated in the future study to reflect the true diversity of the domain accurately.

Abstract Reference: 20859
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

Assessing artemisinin resistance: Molecular and structural validation study

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Abstract Content

The development of artemisinin resistance is attributed to genetic modifications within the *Plasmodium falciparum* kelch 13 (Pfk13) propeller gene. This study aimed to validate selected Kelch 13 mutations identified in Malaysian isolates by generating transgenic Kelch 13 mutant *Plasmodium falciparum* strains using CRISPR-Cas9 technology. Validation involved in-vitro Ring Stage Survival Assay, computational-aided approaches, and the generation of recombinant proteins for binding interaction studies between PfK13 and artemisinin. Four distinct mutant parasite lines and protein variants (V494I, L598G, S600C, and N537I) were created and assessed. Transgenic parasites carrying PfK13S600C, PfK13V494I, and PfK13N537I mutations exhibited significantly higher survival rates in RSA_{0-3} assays, whereas PfK13L598G demonstrated sensitivity to artemisinin treatment. Additionally, a model structure for PfK13 was established, evaluating binding energy during PfK13-artemisinin engagement through computational-aided methods. Results indicated less stable complexes formed by all four mutant proteins, suggesting increased artemisinin resistance due to higher binding energies than the wild-type K13 protein. However, in the recombinant protein analysis, only two mutations, V494I and N537I, were successfully expressed out of the four. Compared to the wild-type PfK13-WT, transgenic parasite lines carrying mutants PfK13-V494I and PfK13-N537I exhibited altered binding interactions with artemisinin, potentially diminishing the drug's effectiveness and contributing to resistance. While various factors contribute to artemisinin-based combination therapy (ACT) treatment failures, this study may support the hypothesis that mutations alter the binding site within the β-propeller region, potentially impacting artemisinin efficacy against the parasite.

Abstract Reference: 20860
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

Emergence of *P. cynomolgi* and potential issues in management of zoonotic malaria in Malaysia

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Abstract Content

The first case of naturally acquired human infection with *Plasmodium cynomolgi* in Malaysia was reported in 2014. Since then, there had been no misdiagnoses of *P. vivax* as *P. cynomolgi* until April 2023, when a 33-year-old male working in the Malaysian Forestry Department was initially diagnosed with *P. knowlesi* malaria through microscopy. EDTA-preserved blood sample was sent to the National Public Health Laboratory in Kota Bharu, to undergo PCR confirmation of species. Despite re-examination and a PCR assay using the abTES™ Malaria 5 qPCR II Kit (AITbiotech, Singapore), the sample was identified as *P. vivax*. However, further DNA sequencing revealed sequences resembling *P. cynomolgi*, rather than *P. vivax*. The same sample was then sent to IMR for further analysis. In IMR, the microscopic examination showed features characteristics of *P. vivax*. Nested PCR and qPCR assays for both human and simian malaria indicated a mixed infection of *P. vivax* and *P. cynomolgi* , which was then confirmed through sequencing and corroborated by MAPELAB Spain. This discovery raises several important issues: 1) existence and distribution of cynomolgi malaria in 1Malaysia, 2) possible misdiagnosis of *P. cynomolgi* that may morphologically resemble *P. vivax*, 3) nature of transmission of zoonotic malaria among humans, 4) has the sylvatic cycle of animal malaria been broken?; and lastly, 5) what will be the impact of additional simian malaria infection on the national malaria control programs in relation to vector control, cost of potential outbreak and public health care and burden of diagnosis to the hospitals and laboratories

Abstract Reference: 20870
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

In silico prediction of G-quadruplex forming sequences in protozoan genomes, spotlight on Leishmania

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Abstract Content

Parasitic protozoans including *Plasmodium*, *Leishmania* and *Trypanosoma* are pathogens causing infectious diseases like malaria, leishmaniasis and chagas diseases, respectively. These protozoans have genomes with varing GC content, which may lead to different frequencies of Guanine quadruplex (G-quadruplex) formation. G-quadruplexes are atypical nucleic acid structures known to regulate gene expression in mammalian cells. Their role in protozoans is a growing area of interest in parasitology. To investigate G-quadruplex in these pathogenic protozoans, we predicted the potential G4 forming sequences (PQS) in the genome of several protozoa using a qualified tool called pqsfinder and obtained the loci of these PQSs at first. Our results showed that *Leishmania spp.* had the highest PQS amount and density compared to *Plasmodium* and *Trypanosoma*. Notably, PQSs in *Leishmania* were found right upstream of gene coding regions, suggesting the role of G-quadruplex on regulating gene expression. We also observed repetitive patterns of PQS distribution in certain genomic regions of *Leishmania*. To detect these singular potential G4 forming regions (SPQRs), we developed an algorithm origin from Hankel Matrix and identified several SPQRs in *Leishmania* genome. Interestingly, these SPQRs occurred in the region of genes coding important proteins in *Leishmania* transformation, such as heat shock proteins and amastin. It implies that G-quadruplex may be involved in the unique poly-cistronic post-transcriptional regulation of transformation-associated genes in *Leishmania*. In the future, we will experimentally elucidate G-quadruplex formation and further study the mechanism of G-quadruplex-mediated post-transcriptional regulation of gene expression.

Abstract Reference: 20871
Mode of Presentation: Poster Presentation
Topic: Session 3 - Entomology

First molecular evidence of Herpetomonas-like species in mosquitoes collected from southern Thailand

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Abstract Content

Mosquitoes are known to transmit a wide range of human pathogens, including viruses, protozoa, and filarial worms. To date, only avian trypanosomes are known to be transmitted by mosquitoes. However, information on their potential as vectors of medically important trypanosomatids, a large group of unicellular parasites such as *Trypanosoma* and *Leishmania*, remains largely unknown. In this study, a total of 90 mosquitoes were collected from the household of a patient with a history of visceral leishmaniasis in Songkhla province, southern Thailand. The mosquito collection was identified as *Armigeres* spp. (92.2%), *Aedes* spp. (4.5%) and *Culex* spp. (3.3%). To detect trypanosomatids in mosquitoes, small subunit ribosomal RNA-specific PCR (*SSU rRNA*-PCR) was performed on extracted genomic DNA from each mosquito. Both male and female mosquitoes were tested for the presence of trypanosomatids. Out of 90 samples, 48 samples, including all mosquito genera and sexes, were positive for *SSU rRNA*-PCR. Based on Sanger plasmid sequencing and BLASTn analysis, the parasite detected was genetically similar to *Herpetomonas nabiculae*, a monoxenous trypanosomatid that primarily infects insects, with 91% identity. Although no human-infecting trypanosomatid was detected in the mosquito samples collected in this study, our data provide the first molecular evidence of *Herpetomonas* infection in mosquitoes in the southern part of Thailand, thus filling the knowledge gap on trypanosomatid biology in Thai mosquitoes.

Abstract Reference: 20872
Mode of Presentation: Poster Presentation
Topic: Session 3 - Entomology

Seasonal occurrence of hard ticks (Acari: Ixodidae) on vegetation in Nagasaki City, Japan

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Abstract Content

In Japan, the number of cases of tick-borne diseases, such as severe fever with thrombocytopenia syndrome, has continued to increase over the past decade. The majority of cases have been reported from western prefectures, including Nagasaki. Despite the emphasis on disease prevention, few studies have explored the tick ecology in Nagasaki. Hence, we conducted monthly collections of hard ticks for 24 consecutive months (from March 2022 to February 2024) on a mountain trail near Nagasaki City to reveal the temporal variation in hard tick species. Ticks were sampled by dragging a sheet of white flannel fabric on vegetation for one hour in each collection, involving two investigators. Tick species at each stage were identified morphologically using identification keys. A total of 6,112 ticks (61 adults, 1,595 nymphs, and 4,456 larvae) belonging to 3 genera and 9 species were collected. The collected species included *Amblyomma testudinarium*, *Haemaphysalis flava*, *H. formosensis*, *H. hystricis*, *H. longicornis*, *H. megaspinosa*, *Ixodes nipponensis*, *I. ovatus*, and *I. turdus*. The most abundant species were *H. formosensis*, followed by *H. flava*, and *H. hystricis*. Phenological patterns of each species were determined. *H. formosensis* and *H. flava* showed a similar seasonal trend, with their nymph stage peaking in winter. In contrast, *H. hystricis* exhibited a different seasonal trend, with adult and nymph stages peaking in warmer seasons. The study's findings offer insights into tick dynamics and species composition in Nagasaki, guiding future research on tick ecology and disease transmission, and aiding targeted control strategies for tick populations.

Abstract Reference: 20885
Mode of Presentation: Poster Presentation
Topic: Session 2 - Bacteriology

Case report: *Streptococcus suis* infection in human

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Abstract Content

Streptococcus suis (S. suis) is a gram-positive bacteria that is one of the leading infections in swine industry worldwide. However, it is also an emerging zoonotic pathogen that causes severe human infections such as meningitis, septicemia, and arthritis- commonly acquired through exposure to contaminated pigs or pig meat. We report a case of a 60 years old lady with no prior medical illness, who presented to us with fever and altered behaviour for 3 days. A lumbar puncture was performed as she came in with symptoms suggestive of menigitis. Opening pressure during LP was high at 43mm/Hg. The gram stain came back to be Gram positive cocci in chain, hence she was given IV dexamethasone and IV C-penicillin. Subsequent CSF and blood culture both turned out to be Streptococcus suis. After a further history taking, we found out that she lives in a viilage in Long Anab Baram, whereby there was a sudden death of pigs about a year ago. We are however not sure about how they disposed of the corpse. She achieved complete recovery after completion of IV C-Penicillin. She did not develop any carditis or arthritis. To minimize the infections by S. suis, we should improve public awareness by education and popularization. With this, more clinicians will be able to pick up S. suis cases with clinical symptoms and predisposing risk factors, hence receive adequate care while waiting for laboratory confirmation.

Abstract Reference: 20886
Mode of Presentation: Poster Presentation
Topic: Session 3 - One Health

Factors related to knowledge and motivation in preventive education of *Opisthorchis viverrini* among students of teacher training institutions in Laos

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Abstract Content

Opisthorchis viverrine (OV) is a foodborne trematode that is caused by eating raw fish, and OV is endemic in Laos. To promote OV preventive education in the school, it is necessary to provide students in the teacher training institutions (TTI) with correct knowledge and motivation for preventive education. However, the status of students' knowledge and motivation for OV preventive education has not been clarified. This study aimed at clarifying factors influencing students' knowledge and motivation for preventive education of OV infection. Data were collected from 268 students in the faculty of education at the National University of Laos in 2023 using a self-administered questionnaire. The questionnaire consisted of knowledge and consciousness about OV infections, preventive behaviors, information sources on OV infection, learning experience and motivation on preventive education, etc. Factors related to knowledge and motivation for teaching OV preventive education were evaluated by logistic regression analysis. The average of students' age was 20.6±2.6 years. The percentage of the students who knew the lifecycle of OV was 59.2%, and that of risk of animal free-ranging was 16.7%. 29.3% of the students responded that squeezing lemon could sterilize raw fish. The results of logistic regression analysis showed that knowledge level has a significant influence on "OV infection is preventable", "Opportunity of OV infection", and "Multiple sources for OV infection". In addition, teaching motivation has a significant influence on the "Importance of providing OV preventive education to school children", "Experience of learning about health education on parasitic diseases", and "OV infection is preventable.

Abstract Reference: 20900
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

Protection induced by heterologous vaccination targeting *Toxoplasma gondii* CST1 or MIC8 antigens

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Abstract Content

Homologous immunization of virus-like particles (VLPs) expressing the *Toxoplasma gondii* microneme protein 8 (MIC8) or cyst wall protein (CST1) was proven to be highly efficacious experimental toxoplasmosis vaccines in mice. Yet, the efficacy of heterologous immunization using recombinant baculovirus (rBV) and VLP platforms under distinct intensity of infections remains unreported. In this study, rBVs and VLPs expressing either MIC8 or CST1 were heterologously administered in mice and the resulting protection was evaluated after challenge with heavy (900 cysts) or light (45 cysts) *T. gondii* ME49 infectious doses. Heterologous immunization elicited antigen-specific IgG antibody responses in sera. CST1-induced markedly higher fecal IgA, brain IgG responses, and germinal center B (GC B) cell responses than those elicited by MIC8 upon light infection conditions. While pro-inflammatory cytokine productions and the overall cyst counts were similar for the two vaccine groups, IFN-γ induction and cyst burden were significantly lower in the lightly-infected CST1 than in the MIC8 group. These findings highlight the differential potential of MIC8 and CST1 as promising candidates for heterologous vaccine design against toxoplasmosis considering the variance in infection intensity.

Abstract Reference: 20902
Mode of Presentation: Poster Presentation
Topic: Session 3 - Vector-Borne Diseases

Trends in leishmaniasis: A 30-year review in an endemic area in the south of Madrid Community

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Abstract Content

In Spain, autochthonous leishmaniasis is caused by *Leishmania infantum*, and transmitted by *Phlebotomus* sandflies. The global incidence is 0.73 cases/100.000 inhabitants, and visceral leishmaniasis (VL) and cutaneous leishmaniasis (CL) are the main forms of clinical manifestations. Years ago, in Fuenlabrada, south of the Madrid Community, the biggest leishmaniasis outbreak in Europe was reported. In this study, the aim was to analyse trends in the diagnosis, management, epidemiology, and clinical presentation of leishmaniasis cases which diagnosed at the Severo Ochoa University Hospital (SOUH), a secondary hospital in south of Madrid. A retrospective review of clinical histories and databases was carried out. Statistical analysis was performed using Epidat and geographic distribution by Google Maps. This study was approved by the Clinical Research Ethics Committee of SOUH. Between 1992 and 2022, 145 of leishmaniasis cases were diagnosed, 127 (87.6%) out of them presented VL and 18 (12.4%) CL. Simultaneous CL and VL was recorded in one case, and 12 VL patients showed infrequent histologic locations of *Leishmania* parasites. Considering before, during and after Fuenlabrada´s outbreak, the incidence of VL fluctuated between 5.2, 8.3 and 0.5 VL cases/100 000 inhabitants, respectively. VL-HIV coinfection was more frequent before outbreak. In contrast, during and after outbreak, the VL was mainly detected in adults >60 years-old and non-HIV immunosuppressed individuals. Over the years, the pentavalent antimonial was replaced by amphotericin B, and molecular diagnosis was introduced in last years. The early diagnosis, prompt treatment and measures of public health changed the leishmaniasis epidemiology allowing its control.

Abstract Reference: 20905
Mode of Presentation: Poster Presentation
Topic: Session 3 - Vector-Borne Diseases

Surveillance of chagas disease in Spain

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Abstract Content

Chagas Disease (CD) is a silent parasitic infection caused by the protozoan *Trypanosoma cruzi*. In Spain, where the vector transmission does not exist, the parasite has been transmitted through blood transfusion, organ transplants, laboratory accidents, and mainly from mother to child (congenital CD). The aim of this study was to evaluate the microbiological diagnosis as an indicator of CD surveillance in areas where CD is not endemic. Retrospective and prospective review of databases of Reference and Research Laboratory for Parasitology of National Centre for Microbiology of Instituto de Salud Carlos III was carried out. The first acute CD case was diagnosed in 1982, a laboratory accident case. Between 1997 and 2023, 32 000 and 18 600 serum and blood samples were tested by serological and molecular tools. The first congenital CD case occurred in 2001, 51 cases more was confirmed up to 2018, after that no more cases was diagnosed. Two cases by organ transplant and five by blood transfusion were confirmed. The number of chronic CD cases was >10 000. The cases distribution increased up to 2010, after that decreased because of screening and diagnosis are performed at hospitals and after 2020 for pandemic Covid-19. Given the CD is detected in chronic phase, CD is not notifiable, for that reason microbiological data could give a good information about epidemiological situation of CD, both where CD is endemic and not. In order to complete the information a network of CD laboratories has been promoted.

Abstract Reference: 20909
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

The exstence of *Plasmodium* sp parasites in Nagur Village, Tanjung Beringin District, Serdang Bedagai Regency, North Sumatra Province Indonesia

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Abstract Content

Plasmodium sp. is a parasite that causes malaria, one of the world's deadliest infectious diseases. Nagur Village, Tanjung Beringin District, Serdang Bedagai Regency, North Sumatra Province is an endemic area for malaria. A total of 43 cases were discovered in 2023. The research conducted in May 2024 aimed to determine the presence of the *Plasmodium sp* parasite, assess the history and identify the risk factors for malaria. The method used was to visit the houses with malaria cases and the surrounding areas to conduct peripheral blood smear examinations. The researchers requested the respondents to provide their malaria history, symptoms, and risk factors through a questionnaire. Among the 38 respondents (50.7%) who had contracted malaria within the past 1 week to 2 years, 75 respondents participated. The results of peripheral blood examination revealed that 6 respondents (8%) were infected with malaria; 5 of them (6.7%) were infected with *P. vivax*, and 1 respondent (1.33%) was infected with *P. falciparum.* Interestingly, all respondents infected with malaria did not exhibit any symptoms at the time their blood was drawn for examination. The most common risk factor for contracting malaria was sitting outside the house at night, reported by as many as 58 respondents (77.3%). This was attributed to the research area's location on the coast with hot weather. In conclusion, the study found the presence of *Plasmodium vivax* and *Plasmodium falciparum* parasites in the area.

Abstract Reference: 20911
Mode of Presentation: Poster Presentation
Topic: Session 3 - Vector-Borne Diseases

Detection of *Trypanosoma evansi* and *Theileria/Babesia* sp. in the tabanids (Diptera: Tabanidae) of Nueva Ecija, Philippines

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Abstract Content

Hematophagous flies from the family Tabanidae (Arthropoda: Diptera) are important nuisance pests and disease vectors in animals. Recently, protozoan infections initially restricted to animals, such as babesiosis (*Babesia* sp.), theileriosis (*Theileria* sp.), and surra (*Trypanosoma evansi*) have been reported in humans. In this study, the potential exposure of humans to the protozoans *Babesia* sp., *Theileria* sp., and *Tr. evansi* were determined through molecular approaches. Nzi traps were installed near backyard farms in Brgy. Catalanacan, Science City of Muñoz, Nueva Ecija, Philippines for the collection of tabanids. The species, relative abundance and density of the collected tabanids were recorded. The occurrence of *Trypanosoma evansi* (n = 383) and *Theileria/Babesia* sp. (n = 382) in the proboscis of tabanids were determined using conventional PCR. The presence of human blood among the samples positive for the target protozoans was also used as an indicator of potential human blood feeding by the tabanids. A total of 4,317 tabanids were collected belonging to *Tabanus partitus* (99.95%) and *Ta. reducens* (0.05%). The recorded occurrences for *Tr. evansi* and *Theileria/Babesia* sp. were 47.26% (181/383) and 31.15% (119/382), respectively. The co-occurrence of the parasites was detected in 6.01% (23/383) of the proboscis tested. Twelve samples found positive for *Theileria/Babesia* sp. were sequenced and found to be from the genus *Theileria*. While 18.41% (51/277) of the samples positive for either protozoan have detectable human DNA. The results indicate potential human exposure to *Tr. evansi*, *Babesia* sp., and *Theileria* sp. through tabanid bites.

Abstract Reference: 20912
Mode of Presentation: Poster Presentation
Topic: Session 1 - Virology

Study protocol of immune responses to SARS-COV-2 vaccination and infection in a longitudinal sampling amidst the COVID-19 pandemic in Malaysia

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Abstract Content

This study protocol aims to evaluate the durability and functionality of SARS-CoV-2 Ancestral strain (Wuhan-Hu-1)-specific immune responses induced by COVID-19 vaccination and natural infection over a 12-month period. Between March 2021 and May 2022, 400 participants were enrolled concluding in May 2023. Two main groups of participants: (1) serologically SARS-CoV-2-naïve individuals receiving the BNT162b2 primary series vaccination and (2) those who recently recovered from COVID-19 infection within 30 days, regardless of vaccination history were included in the study. Additionally, a subset of 45 participants with selected COVID-19 exposure histories provided peripheral blood mononuclear cells (PBMCs) for cross-sectional analysis six months after enrolment. This study assesses the host-pathogen interactions central to the development of COVID-19 immunity. With enrolment spanning two years of the pandemic, most participants exhibited mixed SARS-CoV-2 exposures—via vaccination and infection—resulting in diverse subgroups of interest. Analyses include serology kinetics, memory cells ELISpots, B cells repertoire analysis, cytokine/chemokine profiling, and proteomic pathway will comprehensively examine the immune response against the SARS-CoV-2, thus informing and potentially predicting dynamic longitudinal responses against new more transmissible, immune-evasive SARS-CoV-2 variants.

Abstract Reference: 20927
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

Characteristics of imported malaria cases in China from 2012 to 2021

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Abstract Content

To analyze the characteristics of imported malaria cases in China from 2012 to 2021, aiming to gain insights into the imported malaria epidemic and formulate effective prevention and control measures accordingly. Data on imported malaria cases in China over the past 10 years were collected from the relevant literature from 2012 to 2021. The number of cases, species composition, geographical distribution, and fatal cases were analyzed. The chi-square (χ^2) test was used to compare case-fatality rates among regions. Results From 2012 to 2021, imported cases dominated in China, with Africa being the primary source of importation, followed by Asia. A total of 26,287 imported malaria cases (98.71% of all cases) were reported nationwide, among which falciparum malaria accounted for 64.02%, vivax malaria for 23.20%, ovale malaria for 8.96%, *malariae* malaria for 2.28%, and mixed infections for 1.55%. Affected by the COVID-19 pandemic, the number of imported malaria cases from 2017 to 2021 decreased by 37.37% compared to 2012-2016, with Africa (8,731 cases, 86.57%) and Asia (1,255 cases, 12.44%) remaining the primary sources of importation. The imported malaria epidemic remains prominent, necessitating strengthened surveillance and management, improved diagnosis and treatment of imported malaria cases, and reduced occurrence of fatal cases.

Abstract Reference: 20928
Mode of Presentation: Poster Presentation
Topic: Session 3 - Vector-Borne Diseases

In vitro validation of antileishmanial property of Nimbolide on miltefosine resistant *L. donovani* parasite

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Abstract Content

Visceral leishmaniasis (VL) is a vector-borne disease caused by *Leishmania donovani*, a protozoan parasite. VL is a severe form of leishmaniasis and is fatal if left untreated. Leishmania has developed resistance to most of the drugs used for its treatment, including Miltefosine (MIL). So, it is important to find new antileishmanial molecules to stop the spread of *L. donovani* parasites that MIL does not kill. Neem (Azadirachta indica) leaf extracts have shown potent antileishmanial properties (in vitro and in vivo). Among them, Nimbolide (NB), has been reported to have anti-bacterial and anti-cancer activities. In the present study, we investigate the antileishmanial properties of Nimbolide against MIL-resistant and MIL-sensitive *L. donovani.* MTT assay and growth curve analysis revealed that NB inhibits promastigote dose-dependently. SEM analysis revealed that NB treatment clearly impacted promastigote size and morphology. Flow cytometry analysis shows that NB treatment altered mitochondrial superoxide production, mitochondrial membrane potential, cell cycle, and cell proliferation. NB treatment reduced the intracellular amastigote infectivity and this was further confirmed by reduced IL-10 cytokine expression in *L. donovani* infected human macrophages (THP-1 cell line) Thus, Nimbolide could be a promising drug candidate to treat Leishmaniasis as well as control the emergence of MIL resistant parasites.

Abstract Reference: 20934
Mode of Presentation: Poster Presentation
Topic: Session 3 - Vector-Borne Diseases

Eliminating Lymphatic Filariasis (LF) in endemic areas through online/off-line mass drug administration (MDA) data collection using geospatial smart survey and dashboard (MyGeoLFEP)

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Abstract Content

Lymphatic Filariasis Elimination Program (LFEP) in Malaysia was launched in 2002 under the global initiative of the World Health Organization (WHO) to reduce the prevalence of lymphatic filariasis (LF) to a level where it is no longer a public health concern. Conventional MDA faces challenges due to time-consuming manual surveys and extensive workforce requirements, especially in remote areas. To address this, the MyGeoLFEP project was introduced to enhance MDA efficiency. This digital solution streamlines data entry, enables real-time reporting, and monitors MDA progress. MyGeoLFEP features geolocation integration for efficient follow-ups and dashboard integration for enhanced visibility. The project has significantly reduced time spent on data management, accurately determined population coverage, and enabled efficient follow-ups with dropout cases. A notable feature of MyGeoLFEP is its offline data capability, which allows for data collection even in the absence of internet network, with automatic transmission once the network resumes. In terms of data security MyGeoLFEP uses the ArcGIS Enterprise platform located in the Malaysian Health Data Warehouse (MyHDW) data center. This project has successfully reduced the required workforce and man-days for MDA, resulting in over 50% reduction in operating costs. This innovation marks a substantial step toward eliminating LF as a public health concern in Malaysia by increasing MDA efficiency and achieving significant cost reduction in operations.

Abstract Reference: 20936
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

G6PD deficiency and other red blood cell disorders in malaria endemic regions in Indonesia

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Abstract Content

Malaria parasite has been infecting humans for millions of years in which both the parasite and the host co-evolved with each giving selection pressure to each other. Humans will try to evade the infection by modifying the immune system or the red blood cells. Thus, in regions where malaria is still endemic, high prevalence of red blood cells disorders are found. This pilot study aims to map prevalence of G6PD deficiency, Southeast Asian Ovalocytosis (SAO) and Hemoglobin E (HbE) in Kalimantan, the Indonesian part of Borneo Island. Preliminary result using PCR/RFLP and sequencing showed that in regions where malaria rate is high, as in central Kalimantan (n is 283), G6PD deficiency, SAO and HbE prevalences are 25.8%, 4.6% and 9.9% respectively, compared to north Kalimantan (n is 293) where malaria rate is very low, G6PD deficiency, SAO and HbE prevalences are only 0.6%, 1,1% and 1,7% respectively. These red cell disorders give some degree of protection to malaria infection when inherited in heterozygous condition as in the case of SAO. G6PD deficiency are marked with acute hemolytic anemia upon exposure to oxidative agents. HbE on the other hand, can cause red cell instability when exposed to oxidants as well. G6PD deficiency presents certain degree of hemolytic severity when exposed to both malaria infection and oxidative drugs such as primaquine which may be exacerbated when inherited with SAO and/or HbE.

Abstract Reference: 20938
Mode of Presentation: Poster Presentation
Topic: Session 3 - One Health

Prospective real-world study comparing the safety and effectiveness of Nimesulide with available anti-pyretic and analgesics for treatment of fever or fever with pain

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Abstract Content

Pyrexia is a condition where body temperature exceeds the normal range due to elevation in the core temperature. Pain is a complex experience, influenced by biological, psychological, and social factors. Nimesulide, a relatively selective COX-2 inhibitor NSAID, known for its potent analgesic, antipyretic, and anti-inflammatory effects. Primary objective was to assess and compare the efficacy of Nimesulide, Ibuprofen+Paracetamol and Paracetamol in subjects with fever or fever with pain. Secondary objective was to assess and compare its safety. 303 subjects were statistically analyzed which included 101 subjects in Group 1 (Nimesulide 100mg), 101 subjects in Group 2 (Ibugesic 400mg + Paracetamol 325mg) and 101 subjects in Group 3 (Paracetamol 650mg). In fever, after 15 minutes, temperature decreases were statistically significant ($p<0.001$). At 1 & 2 hours, Group 1 showed a significantly greater reduction compared to Groups 2 and 3 ($p<0.05$). Group 1 exhibiting the largest reductions at 4, 6, 24, 48, and 72 hours, maintaining it through Day 8. In fever with pain, Group 1 consistently demonstrating greater reductions than Group 2 ($p<0.05$). By Day 1, reductions in VAS scores remained significant across all groups, with notable differences between Group 1 & Group 2 ($p<0.0001$). Days 2 and 3 showed significant VAS score reductions, with Group 1 differing significantly from Group 2. Day 4 to Day 8, significant reductions were maintained in all groups, particularly on Day 6 ($p<0.05$). To conclude that Nimesulide demonstrates superior efficacy compared to both Ibuprofen+Paracetamol and Paracetamol in managing fever & pain over 10 days

Abstract Reference: 20940
Mode of Presentation: Poster Presentation
Topic: Session 3 - Bacteriology

TB-LyoAmp: An alternative tool to WHO-endorsed PCR methods for rapid detection of *Mycobacterium tuberculosis* in low-resource settings

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Abstract Content

Although there are many rapid test kits for Mycobacterium tuberculosis (MtB) based on combinations of loop-mediated isothermal amplification (LAMP) and lateral flow assays (LFAs), most of them are in a wet format which requires cold chain logistics and storage that lowers their suitability for tropical low-resource settings. To this end, we have designed a lyophilized LAMP-LFA test kit housed in dry cassettes named “TB-LyoAmp”. This kit possesses high specificity for TB detection, with the sensitivity approaching a single cell of MtB. As of July, 2024 we have established that it has a minimum shelf-life of 5 months at room temperature, equivalent to nearly 2 years and 9 years at 4 °C and -20 °C, respectively, per the Q10-Accelerated Ageing Technique. With a short turnaround time (75 min); high portability and ease of use; and likely low production and utilization costs, TB-LyoAmp has potential to bridge the gap in TB detection by either replacing or used alongside current WHO-endorsed methods i.e., real-time PCR and cell culture, in rural resource-limited settings.

Abstract Reference: 20946
Mode of Presentation: Poster Presentation
Topic: Session 3 - Bacteriology

Neglected yet critical: A case series on lepromatous leprosy with Lucio phenomenon, experience from Central Pahang Lead Hospital, Malaysia

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Abstract Content

Hansen's disease, caused by *Mycobacterium leprae*, remains a significant global health issue, with around 200,000 new cases reported annually. Lepromatous leprosy, a severe form, can be complicated by Lucio phenomenon (LP), characterized by necrotising skin lesions. Delayed diagnosis can lead to significant morbidity and mortality. This retrospective review analysed three cases of lepromatous leprosy with LP at Hospital Sultan Haji Ahmad Shah, from January 2023 to June 2024. Data on demographics, clinical presentations, diagnostics, treatments, and outcomes were collected, with photographic documentation obtained with patient consent. A 71-year-old woman presented with intermittent fever, weight loss, and chronic ulcerations. Diagnosed with multibacillary leprosy with LP, she was treated with MDT, resulting in healing of skin ulcers and residual hypopigmentation. A 78-year-old man presented with pneumonia, necrotic skin lesions and LP. He succumbed from secondary infections despite MDT treatment. A 66-year-old indigenous man presented with extensive ulcerations and LP in septic shock, with skin biopsy confirming lepromatous leprosy. He however suffered cardiac arrest prior to commencement of MDT. Lucio phenomenon, marked by severe immune-mediated vasculitis, is a rare but life-threatening complication of lepromatous leprosy. It is often misdiagnosed due to its rarity and similarity to other conditions. Accurate diagnosis requires a high index of suspicion and laboratory confirmatory testing. Accurate diagnosis with appropriate treatment is crucial in preventing severe outcomes in leprosy. There is a need for increased awareness and training among healthcare providers to recognise and manage Lucio phenomenon effectively.

Abstract Reference: 20947
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

A pilot trial to establish an induced blood stage malaria infection model in healthy Tanzanian adults with varying prior exposure to *P. falciparum*.

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Abstract Content

Controlled human malaria infection (CHMI) studies are crucial in assessing potential malaria interventions and understanding immune protection to inform malaria vaccine development. Induced blood stage malaria infection (IBSM) offers a more precise means for proof-of-concept testing of blood-stage interventions through bypassing the pre-erythrocytic stages of malaria infection. For the first time, we establish an IBSM model in an endemic region in a trial involving twelve healthy adult participants residing in Bagamoyo, Tanzania. Participants were enrolled into "low"(n=6) and "high"(n=6) prior malaria exposure groups as defined by baseline anti-schizont IgG levels below the 25th and above the 75th percentiles of a previously established local population scale, respectively. Participants were inoculated with approximately 1000 chloroquine-sensitive *P. falciparum* 3D7 clone-infected erythrocytes and monitored for 28 days at the Ifakara health Institute clinical trial facility in Bagamoyo. Blood samples were collected for safety and immunology assessments. Parasite quantification by *P. falciparum* qPCR was done at least once daily throughout the 28 days of in-house observation. Participants were administered rescue treatment at 500 parasites/µl or at 200 parasites/µl if accompanied by malaria signs or symptoms and empirically at the end of the 28 days observation period. We have demonstrated that IBSM is safe and well tolerated in Tanzanian adults, with frequencies and severity of adverse events in keeping with those of previous CHMI studies in Africa.9 of 12 participants developed qPCR detectable parasitemia. Some participants reached significantly higher parasite loads compared to naïve UK adults in IBSM studies, with significantly fewer adverse events.

Abstract Reference: 20948
Mode of Presentation: Poster Presentation
Topic: Session 3 - Vector-Borne Diseases

Clinical cure of severe diffuse cutaneous leishmaniasis cases due to *Leishmania amazonensis* in Bolivia using a combination of pentavalent antimonials and miltefosine

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Abstract Content

Bolivia is endemic for cutaneous leishmaniasis (CL) with sporadic cases of visceral leishmaniasis (VL). Diffuse cutaneous leishmaniasis (DCL) is the most infrequent clinical presentation, with *Leishmania amazonensis*, *Leishmania mexicana* and *Leishmania waltoni* as agents in the New World. DCL is characterized by multiple diffuse nodular non-ulcerative skin lesions with great abundance of parasites, negative reaction to Montenegro skin test (Leishmanin), and resistance to treatment. The first description of DCL was published in 1948 by Prado Barrientos in Bolivia, and only three other cases were identified in this country by our team. The last two cases were registered in the Amazonian departments of Pando and Beni, respectively, in the northern region near the border with Brazil. Both cases had a long history of slowly progressive disease with multiple diffuse nodular skin lesions with abundant amastigotes, molecularly confirmed as *L. amazonensis*, and resistance to multiple treatments with pentavalent antimonials and amphotericin B, including liposomal presentation. Both cases showed clinical cure after treatment with a combined course of pentavalent antimonials and miltefosine for 28 days at conventional doses, without relapse at 6-8 months. The cases are being followed clinically and future parasitological and molecular studies are pending to evaluate the presence of parasites using multiple tools. This presentation is accompanied by an interesting iconography that shows the pre- and post-treatment clinical characteristics and the results of the parasitological studies. Apparently, this combination of drugs is an effective alternative and a hope for treating DCL (included in the most neglected human diseases).

Abstract Reference: 20949
Mode of Presentation: Poster Presentation
Topic: Session 3 - Bacteriology

Molecular serotyping of invasive pneumococcal clinical isolates from a tertiary medical centre in Malaysia

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Abstract Content

Pneumococcal disease can result in significant morbidity or mortality. In developing nations, it affects the extremes of age and the World Health Organization (WHO) estimates that 1 million children die of pneumococcal infections annually. We aim to investigate the prevalence of *Streptococcus pneumoniae* serotypes from sterile samples. Ninety-seven stocked isolates from sterile sites (blood, bronchoalveolar lavage (BAL), pleural fluid and cerebrospinal fluid (CSF)) from 2016 until 2021 at the Diagnostic Microbiology Laboratory in Universiti Malaya Medical Centre, were revived and reconfirmed to be *Streptococcus pneumoniae* via PCR targeting the capsular polysaccharide biosynthesis (cpsA) gene. These isolates were subjected to multiplex serotyping through conventional PCR for 44 primer pairs. Capsular serotyping was done in 9 multiplex reactions. The most common invasive specimen was from blood (n=79), followed by BAL (n=14), CSF (n=2) and pleural fluid (n=2). Out of the 44 serotypes tested, only 17 serotypes were present. The most common serotype was 6A/6B/6C/6D (n=28), followed by 19F (n=12) and 19A (n=8). With the introduction of the pneumococcal vaccine into the National Immunization Programme, it is anticipated that the serotypes not covered by the vaccine will be more prevalent. Our study highlights the common serotypes prevailing in sterile specimens from our centre. More surveillance will be needed in the post-vaccination era. Ethical approval has been sought (MECID no. 2020224-8308). This study was funded by Pfizer Global Medical Grants (Grant #75500549, IF019-2023).

Abstract Reference: 20953
Mode of Presentation: Poster Presentation
Topic: Session 3 - Entomology

The relationships between microbiome diversity and epidemiology in domestic species of malaria-mediated mosquitoes of Korea

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Abstract Content

Microbiota in the mosquito plays an important role in their behavior and vector competence. The composition of their microbiome is strongly influenced by the environment, especially their habitat. The microbiome profiles of adult female *Anopheles sinensis* mosquitoes from malaria hyperendemic and hypoendemic areas in Republic of Korea were compared using 16S rRNA Illumina sequencing. In different epidemiology groups, the alpha and beta diversity analyses were significant. The major bacterial phylum was Proteobacteria. The most abundant species in the microbiome of hyperendemic mosquitoes were the genera *Staphylococcus*, *Erwinia*, *Serratia*, and *Pantoea*. Notably, a distinct microbiome profile characterized by the dominance of *Pseudomonas synxantha* was identified in the hypoendemic area, suggesting a potential correlation between the microbiome profiles and the incidence of malaria cases.

Abstract Reference: 20954
Mode of Presentation: Poster Presentation
Topic: Session 3 - Entomology

An AI-IoT integrated system for real-time monitoring of vector mosquito populations

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Abstract Content

The risk of mosquito-borne diseases such as malaria, dengue, and chikungunya is escalating due to climate change and increased international transportation. Rapid detection of vector mosquito species from the Aedes, Anopheles, and Culex genera is essential for effective vector control. Currently, mosquito population monitoring depends on manual efforts by experts, which limits efficiency. To address this issue, we propose an integrated AI-IoT system designed for real-time mosquito detection in natural environments. Our system includes an imaging trap device functioning as an edge device for automatic collection of mosquito and environmental data. Deep learning models are employed to ensure accurate mosquito identification, and an integrated management pipeline coordinates multiple trap devices across various locations. Data is analyzed on a centralized server, which manages these edge devices, while environmental factors such as temperature, humidity, and gas concentrations are also monitored. The system utilizes the Faster-RCNN detector with a ResNet50 backbone, trained on 3,000 images collected from the wild, particularly in livestock facilities. Each image includes an average of 5.1 mosquito instances. The system achieves up to 86.8% mean Average Precision for detecting Aedes albopictus, Aedes vexans, Anopheles spp., and Culex pipiens, with an Intersection over Union threshold of 0.50. Future research will extend the system to include additional flying insects associated with livestock diseases, adapt it for broader applications, and refine ecosystem models to enhance proactive vector control measures.

Abstract Reference: 20955
Mode of Presentation: Poster Presentation
Topic: Session 3 - Entomology

Chromosome-level genome assembly of *Anopheles sinensis*

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Abstract Content

Malaria, declared eradicated in South Korea in 1979, began re-emerging in 1993, with approximately 500 cases annually, predominantly near the border. Understanding the genome of local Anopheles mosquitoes is crucial for investigating this pattern, but their genomes have been poorly characterized until now. We present a novel chromosome-level genome assembly of Anopheles sinensis, a principal malaria vector in Korea. This new assembly represents a significant improvement over the previously available scaffold-level genome, achieved through a hybrid assembly approach utilizing Oxford Nanopore Technologies (ONT) data. The assembly consists of 3 chromosomes and 34 unplaced sequences, encompassing a total length of 229 Mbp. It exhibits exceptional contiguity with an N50 of 91 Mbp and an L50 of 2. BUSCO analysis indicates a high degree of completeness, with a score of 97.6%, underscoring the assembly's robustness and fidelity. Furthermore, we have annotated 13,491 genes and 17,214 proteins, thereby providing an extensive genomic resource. This advanced assembly facilitates numerous research opportunities in the biology and ecology of Anopheles sinensis. It enables investigations into the genetic mechanisms underlying insecticide resistance, the identification of potential molecular targets for innovative malaria control strategies, and the examination of evolutionary adaptations that enhance the vectorial capacity of Anopheles sinensis. Additionally, the high-quality chromosome-level assembly supports comparative genomics studies with other Anopheles species, contributing to a deeper understanding of malaria transmission dynamics. Taken together, this novel assembly constitutes a critical resource for advancing malaria research and developing effective vector control measures, thereby making a substantial contribution to global health.

Abstract Reference: 20956
Mode of Presentation: Poster Presentation
Topic: Session 3 - Entomology

Ultrasound induces changes in host-seeking behavior and modulates sensory gene expression in *Aedes aegypti*

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Abstract Content

The spread of mosquito-borne infectious diseases contributes significantly to global mortality and disease burden. Various electronic mosquito repellents (EMRs) using sound have been developed and commercialized as preventive measures. However, the effectiveness of these EMRs on mosquitoes remains unclear. This study presents experimental evidence demonstrating that ultrasound of different frequencies and sound pressures differentially affects the host-seeking behavior of Aedes aegypti females. Non-blood-fed, inseminated female *Ae. aegypti* mosquitoes, aged 5–7 days, were used for all experiments. Ultrasound was generated using a waveform generator (33500B Series, Agilent Technologies, Santa Clara, CA, USA). Behavioral tests (survival test, wind tunnel test, two-part chamber assay, arm-in-cage test) were conducted alongside molecular experiments to determine the mosquitoes' response to ultrasound and any changes in specific mRNA expression. Bioassay experiments revealed that ultrasound at frequencies of 30-100 kHz and pressures of 90-110 dB significantly disrupted CO_2-oriented behavior and indoor invasion. Additionally, prolonged exposure (>24h) to high-pressure ultrasound reduced attraction to human arms. At the molecular level, there was no change in the expression of the odorant receptor co-receptor gene (AaOrco) in ultrasound-treated mosquitoes. However, the CO_2 receptor gene (AaGr3) was downregulated, and the putative hearing-related gene (AAEL009258) was upregulated. This study demonstrates that high-pressure ultrasound disrupts host-seeking behavior and alters the expression of host-seeking related genes in *Ae. aegypti*. A better understanding of the molecular and neural mechanisms underlying the effect of ultrasound on mosquito behavior is crucial for addressing the current issues related to EMR efficacy.

Abstract Reference: 20957
Mode of Presentation: Poster Presentation
Topic: Session 3 - Bacteriology

Geospatial analysis of serology titres of *Burkholderia pseudomallei* in Central Pahang: A year-long study of melioidosis endemicity

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Abstract Content

Melioidosis, caused by Burkholderia pseudomallei (*BP)*, presents a significant public health challenge in Pahang State, Malaysia. It mimics other febrile tropical illnesses, often leading to empirical treatment based on clinical suspicion. This underscores the need for alternative diagnostic tools especially when cultures yield negative results. The value of serological tests in guiding the diagnosis of melioidosis remains uncertain, especially in endemic regions like Central Pahang. This study evaluated serology samples for *BP* sent from 4 central Pahang hospitals from January 1st to December 31st, 2023. Serology samples were matched with the geographical addresses of the respective patients. Addresses were geocoded into GPS coordinates and analysed using QGIS to map and assess the spatial distribution of serology titres and sample quantity across Central Pahang. Samples with non-traceable addresses were excluded. A total of 828 serology samples were collected, with 37 duplicates and 15 with incomplete data, leaving 776 samples for analysis. Of these, 69 samples were from outside Central Pahang. Among the 707 relevant samples, 45% were serology positive and 55% serology negative. This study showed that some areas in Central Pahang demonstrate elevated serology titres, suggesting a predisposition to exposure rather than active infection. Further study is needed to determine baseline serology levels for these localities, which could help establish a diagnostic baseline in the future. This study highlighted clusters with elevated serology titres. These findings may suggest for targeted public health interventions and policy adjustments in diagnostic and management strategies in high-risk areas.

Abstract Reference: 20959
Mode of Presentation: Poster Presentation
Topic: Session 3 - Entomology

Susceptibility status of *Culex quinquefasciatus*, *Culex gelidus* and *Culex tritaeniorhynchus* larvae against temephos, cypermethrin and lambdacyhalothrin from East Dagon Township, Yangon, Myanmar

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Abstract Content

Insecticide resistance has caused a negative impact on the efficacy of insecticide-base approaches in Integrated Vector Management (IVM) Programme and become a great issue globally. Study on insecticide resistance was scared or null in Myanmar. This study aims to investigate the larval susceptibility status of three species *Culex* larvae namely, *Culex quinquefasciatus*, *Culex gelidus* and *Culex tritaeniorhynchus* collected from cattle farm in East Dagon Township located in Yangon, Myanmar. The larval bioassay was performed according to WHO standard protocol. The diagnostic (0.012 mg/L) and operational (1.0 mg/L) dosage of temephos were used for bioassay. For comparison purpose, similar dosages of cypermethrin and lambdacyhalothrin were used. The 24 hours post treatment mortality was used as indicator to determine the susceptibility status of the *Culex* larvae. Our study revealed that *Cx. quinquefasciatus* and *Cx. tritaeniorhynchus* larvae were resistant against diagnostic dosage of all tested larvicides. While *Cx. gelidus* was resistant against 0.012 mg/L of cypermethrin and lambdacyhalothrin, but susceptible against of temephos. On the other hand, all *Culex* species tested against operational dosage of larvicides were highly susceptible to lambdacyhalothrin, followed by temephos and cypermethrin. By conducting resistance study on *Culex* mosquitoes in Myanmar, the Ministry of Health and local authority can develop targeted and sustainable strategies to manage mosquito populations and reduce the burden of vector-borne diseases.

Abstract Reference: 20960
Mode of Presentation: Poster Presentation
Topic: Session 3 - Entomology

Adulticide susceptibility status of black flies, *Simulium duolongum* and *Simulium jeffreyi* from Malaysia

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Abstract Content

Black fly is incriminated as vector for human onchocerciasis. In Malaysia, research on black fly were mainly focused on the morphology, vector distribution, living patterns and DNA barcoding. However, there is no study reported on the susceptibility status of black fly. Thus, this study aims to investigate the susceptibility status of *Simulium duolongom* and *Simulium jeffreyi* against DDT, dieldrin, propoxur, malathion and permethrin which collected from Janda Baik, Selangor. Adult bioassay was performed according to the WHO Standard Protocol. Both *S. duolongum* and *S. jeffreyi* were completely susceptible to DDT, propoxur, malathion and permethrin with 100% mortality but exhibited resistance to dieldrin with 81.82% and 27.09% mortality, respectively. These findings established a baseline data on insecticide resistance of black flies in Malaysia.

Abstract Reference: 20963
Mode of Presentation: Poster Presentation
Topic: Session 3 - Vector-Borne Diseases

Prevalence and factors associated with *Trypanosoma cruzi* (Chagas, 1909) infection in dogs from the Brazilian semi-arid region

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Abstract Content

Trypanosoma cruzi is the etiological agent of Chagas disease and the vectors are triatomine insects. According to the World Health Organization (WHO), it is one of the most important infections related to poverty and precarious living conditions in Latin America. Dogs and cats can become infected, but its importance in the transmission cycle differs between regions. The objective of this study was to determine the prevalence and factors associated with chagasic infection in dogs in the municipality of Mãe d'Água, a region with a hot and dry semi-arid climate, average annual precipitation of 800 mm, average annual temperature of 25°C and affected by prolonged droughts. Samples were collected from dogs from rural and urban areas, males and females over six months of age. Diagnosis of infection was performed by Nested PCR of 145 blood samples, using the primers TCZ1 (5′-CGAGCTCTTGCCCACACGGGTGCT-3′) and TCZ2 (5′CCTCCAAGCAGCGGATAGTTCAGG-3′). The prevalence of infection was 44.8% (47.1% in urban areas and 42.6% in rural areas). Factors associated with infection were proximity to natural ecotopes such as flagstones, stones and other rock formations (OR = 2.21; 95% CI) and contact with cats (OR = 2.09; 95% CI). The infected dogs lived on the outskirts of the municipality close to rocky outcrops, transitional forests and stony soil. The high prevalence of natural infection is a warning sign for planning more effective control measures and actions to promote human and animal health.

Abstract Reference: 20965
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

Plasmodium vivax malaria: Case report

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Abstract Content

Malaria is the infection caused by inoculation with the mostly obligate intraerythrocytic protozoa of the genus Plasmodium. Kalimantan have low and stable transmission of Plasmodium falciparum and Plasmodium vivax, there are relatively high case numbers in the province of East Kalimantan. This case report will discuss a case of relapse vivax malaria with thrombocytopenia. We present a rare case in a 31-year-old male who came to the hospital with fever since 19 days. Patients also complain of headache, fatigue, abdominal pain, and nausea. The patient is civil engineering. The patient works in the forests of East Kalimantan. The patien had history of malaria one year ago. On physical examination, the abdomen found enlarge of spleen and liver. Laboratory examination results thrombocytopenia. In the peripheral blood smear, *Plasmodium vivax* was found with 1,746 parasites/µL of blood support of Vivax Malaria. The Malaria Vivax which given DHP 1x4 tablets after 3 days, primaquine 1x1 tablet after 14 days. Malaria diagnosed through a blood smear, which P. vivax hypnozoites are frequently reactivated from latent stage, resulting in clinical relapses. DHP and primaquine antimalarial medications enabled the patient to recover quickly. Monitoring therapy was done on the eighth day, with microscopic examination, and the result was negative malaria plasmodium. Malaria is the infection caused by inoculation with the mostly obligate intraerythrocytic protozoa of the genus Plasmodium. Malaria can be prevented by avoiding mosquito bites and by taking medicines

Keyword: *Malaria Vivax, Plasmodium, Fever, Relaps*

Abstract Reference: 20969
Mode of Presentation: Poster Presentation
Topic: Session 1 - Parasitology

Prevalence of *Eimeria* spp. in buffalo calves of Mumbai region and its Theraputic management

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Abstract Content

This study aimed to investigate the prevalence and control of gastrointestinal parasites, with a focus on *Eimeria* spp. infections in buffalo calves in the Mumbai region at organized farms over a period from April 2023 to January 2024. A total of 254 faecal samples were collected and analyzed using both conventional and Polymerase Chain Reaction (PCR) for a comprehensive assessment. The results revealed an overall 48.81 percent prevalence of gastrointestinal parasitic infections, with *Eimeria* spp. being the most predominant at 27.95 percent with mixed helminth infections. Seasonal analysis indicated the highest prevalence during the rainy season (33.33%), with lowest in the summer (19.04%). Treatment was evaluated. Amprolium showed a reduction in oocyst counts by an average of 96.46%, whereas Toltrazuril resulted in a slightly higher average reduction of 97.34 percentage. Which showed Toltrazuril was deemed more efficious over Amprolium. The study underscores the significance of regular monitoring and tailored interventions in managing parasitic infections in buffalo calves.

Keywords- GI parasites, *Eimeria* species, anticoccidials

Abstract Reference: 20970
Mode of Presentation: Poster Presentation
Topic: Session 3 - Parasitology

Detection of benzimidazole resistance in *Haemonchus contortus* population using allele-specific PCR in Maharashtra state of India

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Abstract Content

In the present study, an allele specific PCR (AS-PCR) was employed to detect genotypic and allelic frequencies of *Haemonchus contortus* populations collected from abattoirs located at 4 different regions of Maharashtra. The frequency of resistant genes was found twice compared to susceptible genes. The heterozygous samples were combined with resistant samples because the presence of heterozygous population indicates its predisposition to transform in to the resistance alleles. The observed anthelmintic resistance percentage were 80.00%, 73.33%, 73.33% and 60.00% in sheep, while 80.00%, 80.00%, 60.00% and 73.33% were observed in goats of Western Maharashtra, Marathwada, Vidarbha and Konkan regions, respectively. In all the regions, the observed resistant percent was more than 50 percent indicating the development of high level of benzimidazole resistance in both hosts i.e., sheep and goat. Genotype and allele frequencies **-** maximum resistance against benzimidazole was observed in Marathwada region with the genotype frequency of 0.6 and the frequency of resistant allele of 0.765 from both sheep and goats. In Western Maharashtra, the genotype frequency and frequency of resistant allele was 0.56 and 0.675 respectively.

Abstract Reference: 20977
Mode of Presentation: Poster Presentation
Topic: Session 3 - Vector-Borne Diseases

Seroprevalence of *Trypanosoma evansi* in cattle in Northern and Northeastern Thailand using an in vitro cultivated crude antigen in an iELISA

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Abstract Content

Antibody detection using indirect ELISA with crude antigens of *T. evansi* is a powerful tool recommended by the OIE for detecting the carrier status of *T. evansi*. However, crude antigens were often produced using experimental animals, which raised ethical concerns. To reduce the use of experimental animals, in vitro cultivation of *T. evansi* has been developed. This study aims to use an in vitro produced *T. evansi* crude antigen in the iELISA to measure the seroprevalence of *T. evansi* infection in cattle. Briefly, serum samples were collected from 410 dairy and beef cattle in Northern and Northeastern Thailand between June and December 2023. An iELISA using in vitro cultivated *T. evansi* Thai strain crude antigens were developed. The result showed that the overall seroprevalence of *T. evansi* infection in cattle was 18.29% (75/410) (95% CI: 14.55%-22.03%). There were *T. evansi* seropositives in dairy and beef cattle by 19.03% (95% CI: 13.91%-24.14%), and 17.39% (95% CI: 11.91%-22.87%), respectively. Out of 61 farms, 34 farms (55.74% (95% CI: 43.27%-68.20%)) were seropositive for *T. evansi*. *T. evansi* seroprevalence was higher in the Northern region (24.73%, 95% CI: 18.46%-30.99%) compared to the North Eastern region (13.16%, 95% CI: 8.77%-17.55%). The highest seroprevalence was observed in Phrae at 32.18% (28/87). In conclusion, we successfully developed an iELISA using in vitro cultivated *T. evansi* Thai strain as crude antigen and employed for diagnosing *T. evansi* in cattle.

Keywords: indirect ELISA, in vitro produced crude antigen, *Trypanosoma evansi*, Thai strain

Abstract Reference: 20980
Mode of Presentation: Poster Presentation
Topic: Session 3 - Malaria

Insecticide-treated ceiling nets to combat partial artemisinin resistant malaria in tropical Africa

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Abstract Content

Artemisinin resistance has now emerged in eastern Africa and urgent action is needed (Dhorda M, Kaneko A, et al. Science 2024). As part of a multipronged approach, we evaluated novel vector control tools, such as Olyset®Plus ceiling net (2% permethrin+1% piperonyl butoxide). We conducted a two-arm cluster randomized controlled trial with 10 clusters per arm during 2021–2023 on Mfangano Island in western Kenya. Olyset®Plus ceiling nets were installed in the intervention arm. Malaria prevalence in children at 12 months post-intervention was measured during cross-sectional school surveys. Cumulative malaria incidence in all age groups during a 12-month follow-up post-intervention was tracked monthly in a community cohort. Malaria infection was determined using malaria rapid diagnostic test. Olyset®Plus ceiling nets were installed in 1006 houses (mean coverage: 93.4%). Eight hundred six eligible children were recruited in the control- and 831 in the intervention- arms to determine malaria prevalence. At 12 months post-intervention, malaria prevalence was 30.1% (95%CI: 27.1–33.3) in the control- and 16.4% (14.0–19.2) in the intervention- arms (prevalence ratio 0.55; 95% CI: 0.33–0.91, p=0.056). Two hundred six eligible persons were recruited in the control- and 266 in the intervention- arms to determine malaria incidence. During the 12-month follow-up, malaria incidence was 0.11 per person-year (ppy) (0.07–0.15) in the control- and 0.05 (0.02–0.09) ppy (1.21–1.65) in the intervention- arms (incidence rate ratio 0.47; 95% CI: 0.24–0.95, p=0.030). Olyset®Plus ceiling nets protect against malaria in addition to the effects of existing control interventions.

Abstract Reference: 20981
Mode of Presentation: Poster Presentation
Topic: Session 3 - One Health

Targeted health education module among school children for control of soil-transmitted helminth infections: A systematic review and meta-analysis

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Abstract Content

Soil-transmitted Helminth (STH) infections may contribute to morbidity, including malnutrition, decreased growth and development, anaemia, and reduced cognitive function which influence afflicted children’s educational attainment and quality of life. Focused health education interventions can greatly enhance understanding, beliefs, and behaviours related to cleanliness, which are crucial for effectively preventing and managing STH infections. The main objective of this review is to evaluate the effectiveness of health education interventions in reducing the prevalence and intensity of STH infections among school children. The review used the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) criteria. A total of 1,606 Studies were initially gathered through a primary literature search. After eliminating duplicates, 762 studies were screened for their title. 42 studies were shortlisted for full-text assessment based on their abstracts. Following a thorough review of the full texts, six (6) studies were ultimately selected for this review. The findings of this systematic review and meta-analysis highlight the significant impact of targeted health education modules on reducing the prevalence and intensity of soil-transmitted helminth (STH) infections among school children. The pooled data from six studies involving 7,789 participants demonstrated reduced STH infection rates and improved knowledge, attitudes, and practices (KAP) related to hygiene and infection prevention. This review underscores the importance of targeted health education in the fight against STH infections. By improving hygiene practices and raising awareness about transmission and prevention, health education can play a crucial role in reducing the burden of STH infections among school-aged children.

Abstract Reference: 20983
Mode of Presentation: Poster Presentation
Topic: Session 3 - Bacteriology

Genetic polymorphisms among the pulmonary tuberculosis caused by Malaysia-Specific *Mycobacterium tuberculosis* strain: Sit745/Eai1-Mys

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Abstract Content

Key factors influencing tuberculosis development include host genetics, the genetic diversity of Mycobacterium tuberculosis, and environmental conditions. The East-African-Indian (EAI) lineage is the predominant lineage in Southeast Asia, India, and East Africa. A recent finding has identified SIT745/EAI1-MYS, a sub-lineage of EAI, as the geographically specific M. tuberculosis strain in Malaysia. This study aimed to investigate the role of IFN-γ-(+874)-A/T and IL10-(-1082)-A/G SNPs with TB disease susceptibility among patients infected with M. tuberculosis SIT745/EAI1-MYS strain. A cross-sectional study was conducted between three groups of subjects consisted of TB patients infected with M. tuberculosis SIT745/EAI1-MYS strain (n=9), TB patients of non-M. tuberculosis SIT745/EAI1-MYS strains (n=9), and healthy controls (n=9). The genetic variation in IFN-γ-(+874)-A/T and IL10-(-1082)-A/G A/G SNPs were detected using allele-specific PCR and analyzed for their association with TB risk and severity. The results indicated a higher frequency of the IFN-γ-(+874)-TT and IL-10-(-1082)-AG genotypes among TB patients compared to healthy controls. The IFN-γ (+874)-AA and IL-10-(-1082)-AG genotypes were more prevalent among TB patients infected with the SIT745/EAI1-MYS M. tuberculosis strains compared to non-SIT745/EAI1-MYS, indicating a possible link between these genotypes and more severe TB symptoms. Although there is no significant correlation between the IFN-γ-(+874)-A/T and IL10-(-1082)-A/G polymorphisms with the susceptibility or severity of TB due to the small sample size, this initial strain-specific association could suggest that genetic factors may interact with particular M. tuberculosis strains to influence disease severity.

Abstract Reference: 20984
Mode of Presentation: Poster Presentation
Topic: Session 3 - Virology

Use of rabies immunoglobulin in cattle exposed to rabies virus with dog bite site above the neck region in Maharashtra

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Abstract Content

A total of 132 cases in cattle and buffaloes with dog bite site above the neck region were studied for the time of onset of symptoms of rabies and distance from the brain. Reported 100 percent fatality, even after post exposure vaccination alone, were confirmed using direct fluorescent test and RT-PCR using N gene amplification. The prediction of onset of time of symptom stands to be very accurate in cattle and buffaloes, in cases under study. The prediction of incubation varied in calf, heifers ranges from 15 days to 20 days in dog bite site above the neck region. Intervention with local instillation of diluted rabies immunoglobulin @100 IU, at each site of bite within seven days after the dog bite, prevented the death of 100 percent in treatment group. The study concluded the need for use of rabies immunoglobulin (RIG) as local instillation and the dog bite wound above the neck region should be considered as Category III and should be treated with vaccine and RIG as a post exposure regime.

Abstract Reference: 20992
Mode of Presentation: Poster Presentation
Topic: Session 1 - One Health

Development of an anticancer agent based on cell therapy using Toxoplasma GRA16

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Abstract Content

Anticancer effect focused on the mechanisms induced by parasites is a new approach to enhancing therapeutic effects for cancer drug development. It is known that Toxoplasma gondii (T. gondii) is one of the anticancer parasites and has been shown to inhibit cancer growth. Our previous study elucidated that T. gondii dense granule protein 16 (GRA16) binds to Herpesvirus Associated Ubiquitin Specific Protease (HAUSP) and Protein Phosphatase 2A-regulatory subunit B55 (PP2A-B55) in cancer cells. We tried to elucidate that GRA16 as a crucial protein for studies evaluating the anticancer effect and analyzed the signaling mechanisms that could inhibit cancer growth when GRA16 was expressed in various cancer cells. Our results show that GRA16 in cancer cells could induce cell-cycle arrest and apoptosis via the HAUSP/PTEN/AKT/P53 and PP2A-B55/AKT/NF-kB pathways, thereby increasing the sensitivity of anticancer drugs. Moreover, we confirmed how GRA16 can regulate the expression and activity of hTERT and how it affects telomere shortening before apoptosis. In colorectal carcinoma cells (HCT116), GRA16 inhibited hTERT expression and phosphorylation, inhibited telomerase activity, and induced telomere shortening. We revealed that the central mechanism regulating hTERT expression and activity of GRA16 is HAUSP/PTEN/AKT/STAT3/E2F1/c-Myc pathway. Through the above results, we demonstrated that T. gondii-derived GRA16, which binds to HAUSP and PP2A-B55, regulates PTEN, NF-kB, AKT, and hTERT in cancer cells and induces cell-cycle arrest, telomere shortening, and apoptosis. We suggest that GRA16 can be applied for the novel anticancer agents.

MSPTM STUDENT COMPETITION – RAPID ORAL PRESENTATION

MSPTM STUDENT COMPETITION – RAPID ORAL PRESENTATION

Abstract Reference: 20047
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Epidemiology

Determining Acute Undifferentiated Febrile Illness (AUFI) cases among outpatients in different localities of Malaysia

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Abstract Content

Acute Undifferentiated Febrile Illness (AUFI) may occur throughout the year and some especially in rainy and post-rainy season. Acute undifferentiated febrile illness (AUFI) connotes fever of <14 days duration without specific aetiology. This case is emerging globally with various types of respiratory pathogens reported influenza virus, some coronaviruses, respiratory syncytial virus, *Klebsiella pneumoniae* and so forth. In Malaysia, AUFI cases were understudied, which are demanding to perform a health surveillance of AUFI with clinical symptoms that mimicking among the etiologies. An observational cross-sectional surveillance study was conducted from February until June 2023 focusing on respiratory infections that have pandemic potential in three localities in Peninsular of Malaysia. A total of 409 patients participated in the study and were interviewed for demographic backgrounds, and review of symptoms followed by oral swab (VTM) sample collection. All samples were subjected to the commercially available Fast Track Diagnostic (FTD®) Respiratory Pathogens 33 multiplex test. There were 27.9% (n=114/409) patients with positive cases of respiratory pathogens. The most predominant pathogen in this study was human rhinovirus with 6.4% (n=26), followed by influenza A (n=20; 4.9%), enterovirus (n=13; 3.2%), coronavirus-NL63 (n=12; 2.9%) and adenovirus (n=10; 2.4%). All risk factors were analysed by log-linear modelling. Age group of less than 20 years was the significant risk factors for Influenza A (p=0.027; x2=10.969), while according to sex, female was the significant factors for coronavirus NL-63 infection (p=0.033; x2=4.521). The present study highlights the importance of AUFI surveillance in differentiating the various etiologies for respiratory infections.

Abstract Reference: 20056
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Malaria

Biodiversity and distribution of *Anopheles stephensi* bioforms: Implications for malaria vector control in Rajasthan, India

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Abstract Content

Anopheles stephensi, a primary malaria vector in Rajasthan, India, poses a persistent threat with year-round malaria transmission. The species exhibits three distinct bioforms—type, mysorensis, and intermediate distinguished by egg ridge counts. This study focuses on unraveling the spatial distribution of these bioforms in both rural and urban landscapes, considering their diverse capacities for malaria transmission. Systematic collection of gravid mosquitoes and larvae occurred across various habitats in Rajasthan. Gravid females underwent egg laying, followed by meticulous morphometric analysis to quantify egg ridges. Simultaneously, an in-depth examination of larval habitats aimed to identify bioform-specific preferences. The comprehensive collection yielded approximately 15,000 ± 200 *Anopheles stephensi* eggs from 45 localities (11 Urban & 34 Rural) across 8 Rajasthan districts. Morphometric analysis of 3,569 eggs highlighted the prevailing dominance of mysorensis over intermediate and type. Notably, mysorensis and intermediate bioforms were more prevalent in rural areas, while the type bioform predominated in urban settings. Mysorensis-bioform consistently dominated rural locales across seasons, while the type bioform exhibited a preference for indoor breeding in structures like underground and cement tanks, contrasting with other bioforms favoring outdoor breeding sites. The observed direct proportionality (r=0.55) between egg size and ridge count underscores a nuanced aspect of their biology. Importantly, no reproductive isolation was noted among these bioforms. Mysorensis-bioform emerges as a prominent entity, guiding targeted control strategies. Understanding at the subspecies level, especially considering the type bioform's vector efficacy, informs effective control-measures based on its distinctive breeding site selection in this region.

Abstract Reference: 20162
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Emerging Infectious Diseases

Morphology and phylogenetic analysis of Angiostrongylus malaysiensis

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Abstract Content

Angiostrongylus cantonensis and *A. malaysiensis* are cryptic species with similar morphological, life cycle and genetic characteristics, making their distinction challenging. Accurate identification of these *Angiostrongylus* species is crucial for diagnosing and managing their zoonotic diseases. Thus, this study aimed to update the morphological identity of *A. malaysiensis* through scanning electron microscopic data and to molecularly characterize its phylogenetic relationships across different countries. In this study, adult worms were initially identified based on morphological characteristics and further confirmed as *A. malaysiensis* using ITS2 sequences, validated through NCBI blast results. Scanning electron microscope photography revealed that the morphology of *A. malaysiensis* has similar ultrastructure characteristic with *A. cantonensis* including the number and arrangement of sensory papillae at anterior extremity and presence of papilliform structure at the terminal end rays adult male. Phylogenetic analysis was conducted using the existing ITS2 sequences and three newly designed genetic markers: NAD1, NAD4, and 12S genes. The findings indicated a close relationship between the *A. malaysiensis* from this study and those from Phatthalung, Thailand, and Laos. All markers proved effective in differentiating closely related *Angiostrongylus* species. Furthermore, the study revealed that while the ITS2 gene remains conserved, the NAD1, NAD4, and 12S genes exhibit variability, suggesting their suitability for discriminating intraspecies variations and for population genetic studies.

Abstract Reference: 20164
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Malaria

Rosetting of *Plasmodium knowlesi*-infected red blood cells

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Abstract Content

Malaria continues to be the most lethal parasitic disease, responsible for over 608,000 deaths in 2022. The rise of zoonotic forms of malaria, particularly *Plasmodium knowlesi*, presents a significant challenge to the elimination efforts in Asia. A critical feature of primate malaria, including *knowlesi* malaria, is the capacity for rosetting. This process, where infected Red Blood Cells (iRBCs) adhere to uninfected RBCs (uRBCs), leads to the blockage of microvasculature in vital organs and hampers the clearance of the parasite, which can result in severe malaria cases. While extensively studied in *P. falciparum*, our understanding of rosetting in other types of malaria, specifically those not caused by the *Laverania* subgenus, is still limited. In this study, we reveal that *P. knowlesi* is capable of forming stable rosettes with *Macaca mulatta* RBCs in a laboratory setting, without the need for antibodies or serum factors. Using a cloned line of *P. knowlesi*, we observed that the ability to form rosettes can be sustained through a process of enrichment, but interestingly, this trait reverses approximately 53 days after enrichment. This suggests a mechanism of epigenetic regulation similar to that seen in *P. falciparum*. Additionally, we've developed a new imaging flow cytometric technique to measure rosette formation quantitatively and efficiently. These discoveries enhance our comprehension of the pathogenesis of severe *knowlesi* malaria and establish a foundation for future *in vivo* studies on rosetting, a critical step in developing new chemotherapeutic treatments.

Abstract Reference: 20190
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Dengue

The dengue disquisition: A low-cost public housing conundrum in Klang Valley, Malaysia

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Abstract Content

Dengue remains the most rapidly advancing vector-borne disease in the world, and while the disease burden is predominantly in low-to-middle-income countries, the association with poverty remains in question. Consequently, a study was undertaken to evaluate the prevalence of anti-dengue antibodies among individuals residing in the People's Housing Program (*Projek Perumahan Rakyat – PPR*), a government-sponsored low-cost housing initiative targeting low-income earners, commonly referred to as the bottom 40 (B40). These types of public housing often face challenges such as substandard housing facilities thus this study investigates several social determinants of health, including the economic, environmental, and social conditions that shape the health of individuals. The research was conducted over a period of 18 months across 14 PPRs in the Klang Valley, Malaysia. The seroprevalence of DENV infections analysed against intrinsic and extrinsic factors revealed a high seroprevalence of anti-dengue immunoglobulin G (IgG) at 78.2% (CI: 74.0 – 82.0) among the 436 residents while seroprevalence of anti-dengue IgM was at 0.9% (CI: 0.25 – 2.3) and was significantly associated with age, income, location, waste bin conditions as well as, presence of stagnant water bodies around the compound. Findings from this study highlight an acute need for improvements in the environmental and societal health of those residing in PPRs, apart from continuous community empowerment to ensure preventive measures taken to eradicate dengue are sustainable.

Abstract Reference: 20211
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Malaria

Emerging trends of low-density zoonotic malaria, *Plasmodium cynomolgi*, in Peninsular Malaysia

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Abstract Content

Plasmodium cynomolgi, a simian malaria parasite, has been reported to cause naturally acquired human infection and poses a threat to malaria elimination in Malaysia. Recently, nine cases of *P. cynomolgi* naturally acquired human infections have been reported in Peninsular Malaysia in four states, namely Perak, Negeri Sembilan, Melaka, and Kelantan. This study aims to determine the occurrence of *P. cynomolgi* in other parts of Peninsular Malaysia. Blood samples were obtained from 635 indigenous community samples from Kedah, Selangor, Pahang, Melaka, and Negeri Sembilan. Malaria was screened by microscopy and species-specific nested polymerase chain reaction (PCR) using extracted DNA from blood samples to detect the presence of *Plasmodium* species. No malaria parasites were detected under the microscope, but PCR analysis confirmed the presence of malaria. Overall, there were 40 cases of *P. vivax*, 24 cases of *P. cynomolgi*, 22 cases of *P. knowlesi*, 8 cases of *P. falciparum*, 3 cases of *P. inui*, and 1 case of *P. malariae*. *P. cynomolgi* was identified in 6 single-species infections and 18 mixed-species infections. It was found in every state where samples were collected. This raises concerns about *P. cynomolgi* potentially becoming a public health issue, similar to *P. knowlesi*. If this happens, accurately estimating *P. cynomolgi* prevalence would be challenging due to morphological similarities with *P. vivax*, along with mild or asymptomatic cases. Thus, the National Malaria Elimination Strategic Plan should target low-density and/or asymptomatic human and zoonotic malaria parasite carriers using highly sensitive molecular diagnostic tools in high-risk areas during surveillance studies.

Abstract Reference: 20223
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Parasitology

Molecular identification of human hookworm infections among refugee communities in Malaysia

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Abstract Content

Hookworm infection remains a significant public health challenge worldwide, particularly among marginalized and displaced populations such as refugees. In Malaysia, where a substantial number of refugees seek shelter, the prevalence of hookworm infections among these communities is of particular concern. Accurate species identification is essential for effective treatment and control strategies. However, there is a lack of recent data on the species composition of hookworm infections among refugee communities in Malaysia. This study aimed to identify the prevalence and species identity of hookworm infections among refugee communities in Malaysia. A total of 418 fecal samples were collected from refugees and examined using microscopy. Of these, 20 samples (4.8%) tested positive for hookworm infections. A two-step PCR-based method targeting the 28S rRNA-ITS2 region was used to identify infections by *Necator americanus* and *Ancylostoma* spp. PCR products positive were sequenced bidirectionally, and sequences were analyzed through BLAST and phylogenetic analysis. Sequencing of PCR products confirmed that 17 (85%) of 20 samples were identified as *Necator americanus*, with no detection of *Ancylostoma* spp. infections in this study. This study highlights the prevalence of hookworm infection among refugee communities in Malaysia and provides insights into the distribution of hookworm species. Understanding the species composition is essential for intervention strategies and implementing targeted control measures to mitigate the burden of hookworm infection in vulnerable populations.

Abstract Reference: 20227
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Protozoa Diseases

Molecular diversity and epidemiology of canine haemoparasites in Tamil Nadu, India

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Abstract Content

Vector-borne diseases pose a significant threat to dogs in India, with their distribution influenced by a combination of environmental and social factors. In recent years, an increase in disease transmission has been reported due to factors such as globalization, unplanned urbanization, and climatic changes. Currently, vector-borne diseases such as babesiosis, ehrlichiosis, trypanosomosis, hepatozoonosis, and anaplasmosis are mainly affecting canines in India. In the present study, the dogs were presented to Madras Veterinary College Teaching Hospital with wide range of clinical signs i.e., fever, vomiting, diarrhoea, epistaxis, haematuria, hematochezia, ecchymosis on the body surface, icteric mucous membranes, enlarged lymph nodes, and limb oedema. Upon PCR screening of 200 blood samples collected from suspected dogs, babesiosis was found to be the most prevalent protozoan disease (39/200, 19.5 %). Following babesiosis, the order of prevalence was anaplasmosis (18/200, 9 %), ehrlichiosis (16/200, 8 %), hepatozoonosis (15/200, 7.5 %) and trypanosomosis (3/200, 1.5 %). Among babesiosis, *Babesia vogeli* (23/39) was found to be more prevalent than *Babesia gibsoni* (16/39). Many cases were identified as co-infections, contributing to secondary complications such as immune-mediated hemolytic anemia (IMHA) or immune-mediated thrombocytopenia (IMTH) in dogs. Despite receiving blood transfusions, the survival prospects of the dogs were declining due to their compromised immune system. This epidemiological study could aid in enhancing our understanding of the transmission dynamics of the parasites and in developing mitigation strategies.

Abstract Reference: 20230
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Parasitology

Epidemiology of soil-transmitted helminth (STH) infections among the Negritos in Malaysia: Highlighting the associated-risks of moderate to severe infections

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Abstract Content

Soil-transmitted helminth (STH) infections remain a significant challenge within the Orang Asli communities, despite public health efforts. To investigate the present epidemiological landscape of STH infections and the associated risks of moderate to severe STH infections, we recruited 259 participants from the Negrito tribe, encompassing individuals from Bateq, Jahai, Kintaq, and Kensiu subtribes across four states in Peninsular Malaysia. The fecal samples underwent parasitological examinations, including direct fecal smear, formol-ether concentration, and Kato-Katz techniques. Additionally, we collected sociodemographic, behavioural, and environmental data using pretested questionnaires to identify associated risk factors. The overall prevalence of STH infection was 63.30% (n=164), where the participants were infected with at least one type of STH species. The most dominant STH species was *Trichuris trichiura (*57.92%), followed by *Ascaris lumbricoides* (35.52%), and hookworm (8.88%). Double infections were the most prevalent (50.60%, n=83), followed by single infections (27.80%, n=72) and triple or more infections (9%, n=5.50). Additionally, we found that those with close contact with soil had 1.94 times greater risks (95% CI: 1.2, 3.3; P=0.012) of STH infection than those without. Males had 1.98 times greater STH infection risk (95% CI: 1.0, 3.9; P=0.047) than females. They also faced 2.22 times greater risk (95% CI: 1.2, 4.1; P=0.012) of moderate to heavy *T. trichiura* infection, while children under 12 years old had 2.47 times greater risk (95% CI: 1.1, 5.4; P=0.024) of moderate to heavy *A. lumbricoides* infection. These findings highlighted the ongoing challenge of STH infections in Orang Asli communities, urging targeted interventions.

Abstract Reference: 20236
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Parasitology

Molecular detection of *Microsporidia* spp. among Rohingya school children in Selangor

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Abstract Content

Microsporidia are obligate intracellular spore-forming protozoan parasites, which over 17 species have been discovered to infect humans. Two species that are commonly reported as the etiological agents in humans are Enterocytozoon bieneusi (*E. bieneusi)* and Encephalitozoon intestinalis *(E.intestinalis)*. In Malaysia, there is recent concern among the Rohingya community to contract any emerging diseases including this parasitic infection which requires rapid diagnosis of the parasites for detection of microsporidiosis. Hence, in this study, multiplex Polymerase Chain Reaction (PCR) techniques will be performed to detect *E. bieneusi* and *E.intestinalis* in human stool samples. A total of 91 stool samples have been collected from Rohingya school children in Selangor and will undergo DNA extraction followed by optimization of the PCR amplification. The amplified DNA will be visualised onto gel electrophoresis for detection of *E. bieneusi* and *E.intestinalis*. In this study, it is expected to have the presence of *E. bieneusi* and *E.intestinalis* among the samples with the presence of mixed infection by both species in a single sample. The presence of *E. bieneusi* and *E.intestinalis* in this target population may related to their hygienic lifestyles and exposure to their environment but since microsporidiosis exhibit it clinical manifestation within immunocompromised population more severely compared to immunocompetent individuals, it may be challenging for diagnosis of microsporidiosis among asymptomatic population such as children. Therefore, in order to achieve comprehensive understanding in detection of microsporidiosis, a thorough molecular studies of microsporidia species is required for rapid and accurate diagnosis of this disease.

Abstract Reference: 20238
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Parasitology

Prevalence of *Blastocystis hominis* infection, risk factors and its association with nutritional status among orang Asli Negrito in peninsular Malaysia

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Abstract Content

Blastocystis hominis is a common protozoan parasite found in the human gastrointestinal tract, with varying prevalence rates worldwide. However, epidemiological findings and its potential impact on nutritional status among the Orang Asli (OA) Negrito population in Peninsular Malaysia remain understudied. In this study, 259 participants from the Negrito OA tribe, (subtribe Kintak, Bateq, Jahai, Kensiu and Mendriq) underwent stool examination for intestinal protozoa. Both parasitological (direct fecal smear and trichrome staining method) and molecular identification (PCR) were performed. Of the 259 samples, 40 samples (15.4%) were found positive with *Blastocystis hominis* with majority (65.0%) of the infected participants was from Bateq subtribe in Pahang. Significant associations were observed between *Blastocystis* infection and individuals who always neglect to wash their hands after using toilet (p=0.001) and those who always walk or run barefoot (p=0.001). Additionally, a significant association was detected between *Blastocystis* infection and soil-transmitted helminth (STH) infections (p=0.04) as well as underweight children under 10 years old (p=0.04). However, no significant association was found between *Blastocystis* infection and anemic individuals (p=0.17). This study sheds light on the prevalence and risk factors of Blastocystis hominis infection among the Orang Asli Negrito population in Peninsular Malaysia. The observed associations with nutritional status suggest a potential synergistic effect, emphasizing the necessity for continued and focused research to enhance health outcomes within this community.

Abstract Reference: 20246
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: One Health

Serological diagnosis of congenital toxoplasmosis

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Abstract Content

The diagnosis of congenital toxoplasmosis is challenging due to the diverse range of clinical symptoms it shows, and the limitations of available diagnostic methods. This study aims to describe the serodiagnosis and clinical manifestations of congenital toxoplasmosis. A total of 50 neonates with suspected congenital toxoplasmosis were included in this study. The first samples for IgM and IgG antibodies were screened by ECLIA. For positive results of congenital toxoplasmosis, second serum samples were requested within 2-4 weeks. Out of the 50 first serum samples, the seroprevalence of congenital toxoplasmosis IgG antibodies was 58%. No IgM antibody was detected. The analysis of the paired serum samples was performed only in 12 patients and showed that 24% may have acquired passive immunity from the mother. According to gender, the female had a higher seroprevalence [17 (68.0%)] than the male [12 (48.0%)]. In terms of the age group, the highest seroprevalence was 56.5% (n=26) in the age group (0 -10) days. Furthermore, the majority of cases were asymptomatic (72%), and a few neonates presented symptoms including prematurity (8%) followed by SGA (6%). There is no association between the clinical presentation and the congenital toxoplasmosis. A high seroprevalence of congenital toxoplasmosis was found in this study. The use of paired samples can facilitate the categorization of cases into acute and possible passive immunity from mothers, as well as enhance the precision of diagnosis, particularly in nations that have restrictions on molecular testing.

Abstract Reference: 20290
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Microbiology

Impact of scabies and urbanization on skin microbiome dynamics in Peninsular Malaysian Orang Asli Communities

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Abstract Content

Scabies pose significant public health challenges globally, especially in Malaysia, disproportionately affecting underserved Orang Asli communities. To address these issues, we investigated scabies among Orang Asli communities in Peninsular Malaysia and its association with the skin microbiome. We conducted a burrow-ink test to detect scabies and used validated questionnaires to gather anthropometric, demographic, and socioeconomic data. From 117 participants , we collected 351 skin swab samples from the forehead, volar forearm, and toeweb, from which DNA was extracted. Shotgun sequencing characterized the skin microbiome composition, and we constructed a Metagenomic Assembled Genomes (MAGs) database from the samples. We recovered 848 prokaryotes, 29 eukaryotes, with over 50% potentially novel MAGs, highlighting the richness of the Orang Asli skin microbiome. Our results revealed a distinct Orang Asli microbiome compared to urban populations, with a higher abundance of Proteobacteria, twice the alpha-diversity ($p=6.00 \text{ x } 10^{-6}$), and a unique profile based on Bray-Curtis dissimilarity analysis ($p=0.001$, $R^2=0.103$). In a comparative study between Orang Asli with scabies and healthy Orang Asli, the samples with scabies displayed distinct beta-diversity ($p=0.001$, $R^2=0.021$), and multiple microbiome species were differentially abundant compared to healthy controls. Orang Asli with scabies exhibited significantly higher abundance of multiple Proteobacteria species, including *Acinetobacter* and *Aeromonas*, compared to healthy controls. These findings underscore the unique skin microbiome profile of Orang Asli communities compared with the general populations and the scabies-associated skin microbiome. Further investigation into the complex interplay between urbanization, skin infections, skin microbiome, and holistic skin health in Orang Asli communities is warranted.

Abstract Reference: 20300
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Parasitology

Genomic analysis of sag surface antigen loci in *Eimeria tenella*

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Abstract Content

Poultry coccidiosis is an intestinal disease caused by obligate intracellular parasites of the genus *Eimeria*. The principal surface antigen gene family in *Eimeria tenella* (EtSAG) has been categorized into three sub-families (SAGa, SAGb and SAGc), each suggested to be involved in host attachment and invasion, presenting promising targets for coccidiosis control. Here, full-length genomic sequences of EtSAG loci from isolates representing diverse continents including North America (United States), Asia (Malaysia and Japan) and Africa (Nigeria) were investigated. Alignment with the reference *E. tenella* Houghton strain revealed 50 out of 87 EtSAGs displaying variations in the exons and/or introns, with 28 (46.7%), 21 (80.7%) and one (100%) EtSAGs from SAGa, SAGb and SAGc sub-families, respectively. Mutations in the SAGa members (n=19, 67.9%) were mainly detected in the exon sequences, while mutations in SAGb members (n=10, 47.6%) were predominantly in both exon and intron sequences. Among these sub-families, SAGc was the most polymorphic (averaging one variant per 271 bp), followed by SAGb (one variant per 448 bp) and SAGa (one variant per 584 bp). Notably, mutations detected in the exons were primarily non-synonymous (n=46, 66.0%), resulting in amino acid changes. Comparison between isolates revealed the exon mutations were of low frequency and sparsely distributed, with about half of the mutations exclusively detected in the isolates from North America and Africa. This comprehensive genomic analysis sheds light on the genetic diversity of EtSAGs, laying the foundation for the development of targeted control strategies for coccidiosis.

Abstract Reference: 20312
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Malaria

Sustainability of a malaria programme in a decentralized health system: A case study of stakeholders in Kanchanaburi province, Thailand

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Abstract Content

Community health workers (CHWs) are a key component of national malaria elimination strategies in the Greater Mekong Subregion. Their various roles include testing for malaria which has contributed to early detection among at-risk populations in border communities. To maintain uptake and provision of their services, it has been proposed to expand their roles beyond malaria. How this is best implemented depends on local context and health priorities. The current decentralization of the health system in Thailand provides the opportunity for the optimal model to be decided at provincial level. This study uses qualitative interviews to explore perceptions of stakeholders concerning the sustainability of community-based malaria services in endemic communities in Kanchanaburi province in western Thailand. The study is extended from a multi-country project (2021-2023) investigating the prospect for role expansion of CHWs in near elimination setting in Southeast Asia. Here we highlight preliminary results from key informant interviews with malaria programme implementers. Results suggest that there is a large prospect for role expansion in highly endemic communities. Several factors include: (1) malaria post workers in some communities were found to be officially integrated as primary care unit staff; (2 primary care centers were newly established to enhance CHWs' capacity to provide essential medicines, including antimalarials; and (3) increasing demand for migrant health services, particularly for pregnancy care and tuberculosis, were reported among populations seeking shelter. Findings suggest the role expansion is possible within the context of decentralized system and has strong potential for ensuring the sustainability of community-based malaria care.

Abstract Reference: 20324
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Entomology

The discovery of novel point specific mutations, P1585R and F1695L in northern peninsular Malaysia populations of *Aedes albopictus* (Skuse)(Diptera: Culicidae)

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Abstract Content

Controlling *Aedes* is mainly by the means of synthetic insecticides application, ensuing insecticide resistance. Monitoring susceptibility profiles of *Aedes* vectors and the mechanisms involved is crucial in devising efficient vector control strategies. In this study, we assessed larval and adult susceptibility status to several insecticides in five populations of *Ae. albopictus* from Northern Peninsular Malaysia (Penang and Perlis) and examined the association between pyrethroid resistance and *kdr*-mutations. *Ae. albopictus* larvae were subjected to temephos larvicides, showing very low mortality across all field strains. Adult females were tested against several insecticides, with varying degrees of resistance observed. All strains resistant to 0.1% propoxur and 0.25% primiphos methyl. The Perlis populations are profoundly resistant towards 0.25% permethrin (mortality; KB: 34% and KTT: 49%) and 0.03% deltamethrin (mortality; KB: 4% and KTT: 11%) as compared to the Penang populations. The synergist assay of Perlis strains showed minimal restoration of susceptibility post-exposure to deltamethrin, ruling out the primary role of metabolic mechanism causing resistance. Moreover, the detection of the F1534L mutation in pyrethroid-resistant *Ae. albopictus*, initially detected in Shah Alam, along with newly discovered non-synonymous mutations like P1585R and F1695L at regions DIII and DIV, implies that the spread of resistance genes might be underway in other strains too. The resistance of *Aedes* mosquitoes to insecticides in Northern Malaysia is caused by heavy insecticide use in agriculture and vector control, along with possible introduction of resistance genes from nearby countries.This scenario could greatly impact Malaysia's vector control efforts, urging the search for alternative solutions.

Abstract Reference: 20333
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Parasitology

How good is molecular techniques as opposed to microscopic-based techniques for soil-transmitted helminth diagnosis? A systematic review and meta-analysis

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Abstract Content

The advancement of molecular diagnostics, such as polymerase-chain reaction (PCR), presents an invaluable modality in fighting against soil-transmitted helminth (STH) infection, thus aligns with the WHO 2021-2030 roadmap. Although microscopic-based techniques are usually adequate, they lack sensitivity to diagnose low-intensity infection, and often, a combination of different techniques is needed to diagnose each STH species accurately. Besides, PCR enables the simultaneous detection of multiple species, making it beneficial for diagnosing various STH infections. This study evaluates the diagnostic accuracy of PCR compared to microscopic-based techniques in diagnosing four common STH infections. A literature search was done in PubMed, ProQuest, Ovid, EBSCO, WorldCat, medRxiv, and bioRxiv-a total of 36 eligible studies screened from 4.297 studies were included in the analysis. QUADAS-2 showed a low risk of bias, while funnel plots, Egger's regression, and Begg's correlation tests indicated some publication bias for selected studies in our analysis. PCR demonstrated sensitivity and specificity ranging from 69.3-89.7% and 82.3-96.3%, respectively, while positive and negative predictive values ranged from 33.9-67.9% and 97.1-97.7%, respectively. Diagnostic odds ratios of PCR were also assessed, with a result ranging from 17.1-77.9. The next step to be considered is systematically evaluating PCR performance, standardizing, and harmonizing the PCR protocol, thus ensuring constant results across the laboratories. Altogether, our findings proved the high diagnostic accuracy of PCR compared to microscopic-based techniques, implicating its use for diagnosing STH infections along with its ability to detect low-intensity infections, therefore targeting STH elimination in 2030 is achievable.

Abstract Reference: 20341
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Emerging Infectious Diseases

Predictors of mortality in leptospirosis cases, Indonesia

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Abstract Content

Leptospirosis is a priority zoonotic in Indonesia. The mortality rate of leptospirosis cases ranges from 5-20%. Predictors of leptospirosis mortality include older age, oliguria, shortness of breath, icteric, decreased platelets, and increased potassium; creatinine; Bilirubin; ureum. Analyze the relationship of mortality predictor factors with mortality of leptospirosis patients in Demak Regency, Indonesia. Demographic data, clinical symptoms, and laboratory results were obtained from hospital medical record data in Demak Regency for 2018-2023. The study design used was a retrospective cohort. Mortality predictors were analyzed with Cox regression. The study found that leptospirosis patients were more male (58.9%) with mean age±SD = 47.96±15.753. As many as 30.1% of patients died out of a total of 73 patients hospitalized. Causes of death included: platelet levels of <100,000 cells/mm (47.5%); creatinine levels > 3 mg/dL (50.0%); urea levels >90 mg/dL (51.35%); icteric (64.2%); oliguria (31.25%); dyspnea (58.82%); myalgia (29.69%), and comorbidities (34.62%). Five independent risk factors associated with mortality have been identified, including platelet levels of <100,000 cells/mm (HR: 5.30; CI 95%: 1.56-17.96; *p-value*: 0.0014); creatinine levels >3 mg/dL (HR: 4.04; CI 95%: 1.48-10.9; *p-value*: 0.0026); urea levels >90 mg/dL (HR: 6.12; 95% CI: 1.80-20.73; *p-value*: 0.0004); icteric (HR: 3.36; CI 95%: 1.54-8.50; *p-value*: 0.0055); and dyspnea (HR: 13.62; CI 95%: 3.18-58.35; *p-value*: 0.001). Platelets, creatinine, ureum, icteric, and dyspnea are predictors of leptospirosis mortality.

Abstract Reference: 20363
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Malaria

Epidemiological risk factors associated with *Plasmodium cynomolgi* infection among *Macaca fascicularis* in Peninsular Malaysia

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Abstract Content

Malaria caused by *Plasmodium* remains one of the most important infectious diseases worldwide despite continuous efforts to control the infection especialy in developing countries. In Malaysia, primate malaria is naturally found in long-tailed macaques (*Macaca fascicularis*). These primates may harbours a number of malaria parasites that are zoonotic (*P. knowlesi*, *P. cynomolgi* and *P. inui*). Recent cases of human malaria involving *P. cynomolgi* infection in Peninsular Malaysia and in other Southeast Asian countries has heightened the need to study the ecology and transmission patterns of this parasite. The present study aims to determine the molecular prevalence and epidemiological risk factors associated with *P. cynomolgi* infection among *M. fascicularis* in Peninsular Malaysia. Blood samples were collected from 1587 free-ranging macaques from 122 locations in Peninsular Malaysia, and subjected to *P. cynomolgi* detection by nested PCR amplification. In total 48.4% of the macaques were infected with *Plasmodium* with the highest infection rates attributed to *P. cynomolgi* (28.9%). Significantly higher ($p<0.05$) prevalence of infection was observed in the juvenile female macaques (37.1%), those inhabiting forested areas (33.4%), habitats at elevations between 60 to <80m above sea level (53.1%), and >60km away from the coast (62.3%). Hotspots of infection were detected in a number of locations with the Mid-eastern region of the country having the highest infection rates (43.7%). Multivariate logistic regression revealed that the age of the macaques, spatial zones, and habitat elevation were significant risk factors for *P. cynomolgi* infection. This study constitutes the first attempt in Southeast Asia to screen a large number of macaques to determine the epidemiological risk factors of *P. cynomolgi* infection. This emerging zoonosis is of serious concern for public health, and the epidemiological data obtained in this study may be used for planning and implementing effective control measures for *P. cynomolgi* infection in the country.

Abstract Reference: 20376
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Parasitology

Development and survivability of strongyle free-living stage larvae in different environments and soil-type conditions

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Abstract Content

Strongyle is a harmful parasite in horses, and its infestation poses a threat to the host's health. In managing an impactful parasite control program, understanding the environmental conduciveness of the shed parasite’s egg survives the full life cycle is crucial in a tropical ambience. Studies that describe these tendencies are limited to temperate countries' environments. Fresh faeces droppings collected from horses were cultured in the laboratory using pasture on four types of common soils in Malaysia. The soil types are sphagnum, omnibus, saprolitic, and antisols placed in rectangular wood panels kept at different temperatures at 21±1°C, 26±1°C, 29±1°C, and 32±1°C for 30 days. The Baermann technique was used to extract larvae from faecal samples. Larvae development and survivability were viewed under a microscope (x10). In conclusion, it showed that the development of strongyle larvae does influenced by temperature which is 21 ± 1 °C where the larvae developed longer compared to 32 ± 1 °C where the larvae developed faster. Meanwhile the survival rate or larvae influenced by different type of soils which sphagnum soil has higher survival rate (30.71%) compared to omnibus soil (16.50%).

Abstract Reference: 20383
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Entomology

Employing environmental DNA analysis to detect *Aedes aegypti* larvae DNA in water samples: Next generation technique for dengue vector surveillance

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Abstract Content

Aedes aegypti surveillance methods in Indonesia are performed by collecting larvae in artificial water containers in households. However, this practical use of conventional surveillance approaches is limited by the dependence on manual processes and taxonomic expertise. Also, this technique has the disadvantage of relying on in situ identification of larvae which has the opportunity for misidentification in differentiating *Ae. aegypti* or other species of mosquitoes. Surveillance strategies that yield reliable data are required for a better comprehension of mosquito diversity and abundance, thereby enhanced vector control program. The environmental DNA (eDNA) analysis is a promising and reliable technique to detect *Ae. aegypti* in artificial water containers. This study aimed to apply eDNA metabarcoding approach for the detection of *Ae. aegypti* larvae DNA. This study assessed water samples associated *Ae. aegypti* DNA detection by sampling 100 sites in North Jakarta in the rainy season (January-February 2023) and dry season (May-June 2023). DNA sequencing data were analyzed in mBRAVE yielded four genera and species identified. Our results showed *Ae. aegypti* and *Culex nigripalpus* DNA detected in dry season and *Ae. aegypti*, *Megaselia scalaris*, *Chironomus striatipennis* were detected in the rainy season, indicating the presence of *Ae. aegypti* in the area and the risk of Dengue transmission mostly in the rainy season. Whereas *Ae. aegypti* larvae are more common during the rainy season than during the dry season, *Ae. aegypti* larvae DNA is present in two seasons. It indicates that the eDNA method is a reliable technique and completes conventional surveillance.

Abstract Reference: 20387
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: One Health

Point of care diagnostics approach in understanding fungal diversity applications in selected shrimp aquaculture ponds

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Abstract Content

Safeguarding food safety and public health in today's food industry necessitates an integrated One Health approach that recognises the intricate connection between environmental, animal, and human health factors, particularly in the management of fungal infections within shrimp aquaculture. In this study, the fungal diversity in shrimp aquaculture has been explored by establishing propagation method of fungal species from shrimp, sediment, and water samples collected from shrimp aquaculture farms in Selangor, Malaysia. Fungi were propagated on Sabouraud Dextrose Agar (SDA), then subcultured for pure cultures. Macroscopic and microscopic analyses were then employed to observe fungal morphology for identification. Vitek® MS (MALDI-TOF MS) was utilized for identification of fungal isolates present in human specimens exclusively, out of the all the fungal isolates obtained. As the result of fungal propagation, a total of 31 fungal isolates were isolated. The three most significant genera were *Aspergillus* sp., *Penicillium* sp., and *Fusarium* sp., being the dominating species. About 5 fungal isolates were identified using Vitek® MS (MALDI-TOF MS) indicating that they may also become pathogenic to human upon consumption. Subsequently, all the fungal isolates were sent for sequencing after PCR. The sequences were then analysed for further studies such phylogenetic analysis. Overall, this study advances our understanding of fungal diversity in shrimp aquaculture, perhaps leading to more sustainable management practices. The ultimate goal would be establishing ONE health system that prioritises safety throughout the entire food supply chain, emphasizing the implementation of good management practices.

Abstract Reference: 20535
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: New Technologies in Tropical Disease Studies

Development of transdermal nanofiber patch with diclofenac relief myofascial pain

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Abstract Content

Diclofenac sodium (DS), a nonsteroidal anti-inflammatory drug, is commonly prescribed for moderate pain. However, oral administration of DS often causes gastrointestinal irritation. Transdermal drug delivery systems (TDDSs) offer a non-invasive alternative, delivering the medication directly through the skin and avoiding irritation. Polyvinyl alcohol (PVA) emerged as a system for drug delivery applications due to its biocompatibility and large loading capacity. Thus, the aim of this study was to develop a polyvinyl alcohol (PVA) transdermal patch containing DS using the electrospinning method. Experimentation explored two PVA concentrations (10% w/v and 20% w/v) and flow rates (6 mm/h and 3 mm/h) to identify the optimal parameters for patch production. After experimenting, a 20% w/v and a 6 mm/h flow rate were identified as optimal. To assess their stability, additional patches were produced using the same parameters. Fourier Transform Infrared (FTIR) spectroscopy was used to analyze the chemical composition of the patches and confirm the presence and distribution of DS within the PVA matrix. The FTIR spectra of both initial and repeated patches showed characteristic peaks of DS, indicating its stable encapsulation within the PVA matrix. Notably, a distinct peak at around 3328 cm', and additional peaks at 1725 cm' and 1572 cm' confirmed that DS was amorphously distributed within the PVA matrix. Overall, the innovative Diclofenac Sodium (DS)-loaded nanofibers have the potential to serve as effective biomaterial patches for transdermal administration, enhancing carrier retention and facilitating controlled drug release.

Abstract Reference: 20553
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Malaria

In silico modelling of triple artemisinin-based combination therapies to inform dosing in areas with emerging antimalarial drug resistance

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Abstract Content

Declining antimalarial drug efficacy poses a significant threat to malaria control worldwide. The firstline treatment for *P. falciparum* malaria combines artemisinin derivatives with a long-acting partner drug. These artemisinin-based combination therapies (ACT) have proven very successful in maintaining high cure-rates. However, recent decreases in ACT efficacy have led to the necessary development and testing of new drugs and therapies, such as triple ACTs (TACT), where the ACT is administered alongside a third antimalarial drug. Some promising candidate TACTs are currently in clinical trials; and whilst essential, clinical trials are an extremely time and resource intensive way to learn more about candidate regimens. Mathematical modelling of the underlying drug-parasite dynamics can be a cost-effective and ethical way to simulate efficacy of novel regimens, informing effects in varied scenarios. We have developed an in silico pharmacokinetic-pharmacodynamic model that incorporates parent-metabolite profiles, drug-drug interactions, parasite life-cycle and age-specific killing effects. It was previously applied to dihydroartemisinin-piperaquine-mefloquine and was able to accurately estimate efficacy in the populations where clinical trials were conducted. We have performed a simulation study of the TACT artemether-lumefantrine-amodiaquine, using published pharmacokinetic and pharmacodynamic parameters to explore treatment outcomes in a variety of settings. This flexible model allows for evaluation of potential cure rates at different levels of resistance to each of the three antimalarials, and for a variety of possible interaction scenarios. This model framework can be used to explore likely efficacy in different populations and inform TACT dosing schedules and local treatment policy.

Abstract Reference: 20554
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Malaria

Association of novel IgG3 allele with malaria in children from Sepik region of Papua New Guinea

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Abstract Content

Malaria causes death and severe illness in children under five years of age. Recent work has established the importance of malaria-specific IgG3 in malaria immunity. Antibody allotypes due to single nucleotide polymorphisms (SNPs) in IgG3-Fc regions can modulate IgG3 Fc-mediated functions. A novel IgG3 allele, G3m29, was recently reported in pregnant women from Sepik, Papua New Guinea (PNG), and was shown to have enhanced affinity to FcγRIIa. We hypothesized that the prevalence of G3m29 in this population was associated with protection from *Plasmodium* species infections in children. In a longitudinal study cohort of children aged 1-3 years (N=203), with multiple *Plasmodium* species infections from the Sepik region in PNG, we amplified the Fc region of IgG3 by polymerase chain reaction using $\mathrm{C_H}2$ and $\mathrm{C_H}3$ specific primers. We then used Sanger sequencing to identify SNPs and compared to the reference alleles of immunogenetics (IMGT) database. We identified that 78% of the cohort were either heterozygous (n=82, 40%) or homozygous (n=77, 38%) for G3m29. We found a decrease in total number of *Plasmodium* infections in children with potential G3m29 allele compared to non-G3m29 allele carriers (β= -1.736, 95% CI [-3.39,-0.079], p <0.05). This effect was most pronounced for *P. vivax* asymptomatic infections (β=-1.06, 95% CI [-2.01,-0.12], p <0.05). G3m29 carriers had significantly lower levels of total IgG and IgG1 to *P. vivax* vaccine candidate proteins than non-G3m29 carriers. In conclusion, the G3m29 allele is highly prevalent in the Sepik region of PNG and might be involved in protection against *Plasmodium vivax* infections.

Abstract Reference: 20678
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Microbiology

Draft genome of a multidrug- and methicillin-resistant *Staphylococcus capitis* blood isolate from Terengganu, Malaysia

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Abstract Content

Staphylococcus capitis is associated with nosocomial bloodstream infections. Here, we present the draft genome of *S. capitis* strain ScaC49, obtained from blood culture of a 57-year-old female patient admitted to Hospital Sultanah Nur Zahirah, Terengganu, Malaysia in 2022. Phenotypic antimicrobial resistance (AMR) was determined by disk diffusion. Whole genome sequencing was performed on the short-read DNBSEQ-BGISEQ-500 platform and sequences were assembled using Unicycler. The draft genome sequence is 2,599,777 bp assembled into 29 contigs with three putative plasmids, designated pScaC49-1 (RepA_N/*rep39*, 30,352 bp), pScaC49-2 (Rep3/*rep5c*, 5,948 bp), and pScaC49-3 (RepL/*rep10*, 2,465 bp). ScaC49 is a multidrug- and methicillin-resistant strain phenotypically resistant to nine antimicrobial classes. The phenotypic AMR profile was in concordance with the predicted AMR gene(s), i.e., β-lactams (*mecA* in SCC*mec* type IV(2B) element and *blaZ*), fusidic acid (*fusB*), phosphonic acid (*fosBx1*), trimethoprim (*dfrC*), aminoglycosides (*aph(2’’)-aac(6’)*), teicoplanin (*vraS* and *walK*) and constitutive macrolide-lincosamide-streptogramin B (cMLSB) phenotype (*ermC*). In addition, mutation in *gyrB* that confers fluoroquinolone resistance, and genes encoding multidrug efflux pumps, i.e., *mdeA*, *sdrM*, *sepA*, and *qacB* could mediate resistance to aminoglycosides, penam/β-lactams, tetracyclines along with disinfectants and antiseptics were presented in ScaC49. Virulence genes that enabled cell adherence (*atl*, *ebh*, *ebp*, *icaA*, *icaB*, *icaC*, and *icaR*), immune evasion (*adsA*, *capB*, *capC*, and *manA*), and encode hydrolytic enzymes (*geh*, *lip*, and *nuc*), and toxin (*hlb*-β hemolysin) were also identified. The discovery of multidrug- and methicillin-resistant *S. capitis* that possessed numerous virulence factors in Terengganu warrants continuous vigilance.

Abstract Reference: 20728
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Covid

Immunogenic responses of T-cells and memory B-cells towards the spike-protein of SARS-CoV-2 among individuals who have received three doses of the COVID-19 vaccine

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Abstract Content

With most of the world’s population already vaccinated against COVID-19, the generation of durable immune responses by the COVID-19 vaccines were unclear, particularly in a 3-dose vaccination regimen. The immune response that evaluates the durability of immune protection is known as the adaptive immune response, where T-cells and memory B-cells play important roles towards the effectiveness of a vaccines durability. In this study, we investigated the activation of T-cells and intracellular cytokines production by T-cells, as well as the generation of IgG^+ memory B-cells targeting the SARS-CoV-2’s spike-protein among COVID-19 vaccinated individuals at two-weeks (T1), six-to-eight months (T2), and 12-months (T3) after receiving a booster vaccination dose of the BNT162b2-Pfizer/BioNTech. The individuals had been primarily vaccinated with either the BNT162b2 vaccine (categorized as PPP) or the CoronaVac-Sinovac (categorized as the SSP group) before receiving the booster vaccination dose. Our study exhibits that activation of CD4+ T-cells (CD25+/CD69+ and CD134+/CD137+) and CD8+ T-cells (CD25+/CD69+ and CD69+/CD137+), as well as Th1 (IL-2) and Th2 (IL-4) intracellular cytokines production by T-cells increased at T2 for both vaccination groups, and IgG^+ memory B-cells were detectable (50-100%) up to the T3 timepoint. These results suggest that the T-cells can be activated during an exposure or infection towards COVID-19 and undergo SARS-CoV-2 infected cells removal, and the memory B-cells may reproduce plasma cells and specific-antibodies towards SARS-CoV-2, essentially producing immune protection up to 12-months after the booster vaccination.

Abstract Reference: 20761
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Microbiology

Antimicrobial resistance profiling of clinical methicilin-resistant *Staphylococcus aureus* (MRSA) from Terengganu, Malaysia

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Abstract Content

Methicillin-resistant *Staphylococcus aureus* (MRSA) has becoming increasingly prevalent worldwide, as it continues to evolve and develop resistance to multiple antibiotics. The emergence of inducible macrolide-lincosamide-streptogramin B (iMLSB) phenotype may lead to clinical failures in clindamycin treatment. This study aims to determine the antimicrobial resistance profile of 44 MRSA isolates, i.e., 27 hospital-associated (HA) isolates, eight community-associated (CA) isolates and nine isolates of unknown origin (from other hospitals), collected from Hospital Sultanah Nur Zahirah, Terengganu, Malaysia from 2022 to 2023. The antimicrobial resistance profiles against 26 antibiotics from 18 antimicrobial classes were determined using the Kirby-Bauer disk diffusion method, while MLSB resistance phenotypes were detected using the D-test. The MRSA isolates showed full resistance towards penicillin and cefoxitin, while resistance to ciprofloxacin, moxifloxacin, oxacillin, and cefoperazone were detected in >50% of isolates. Rifampin, novobiocin, teicoplanin, fosfomycin, and ceftaroline were fully active with 100% susceptibility rate. iMLSB phenotype was the most common MLSB resistance phenotype (27.3%, *n*=12), followed by macrolide-streptogramin (MS) (13.6%, *n*=6), constitutive resistance (cMLSB) (6.8%, *n*=3) and lincosamide (L) (2.3%. *n*=1). Additionally, 54.7% (*n*=22) isolates were susceptible to the MLSB antibiotics. There was a high prevalence of MDR among the HSNZ MRSA isolates, with all isolates being MDR. The highest level of resistance was against nine antimicrobial classes (4.5%, *n*=2) while resistance to four and five classes were the most common (22.7%, *n*=10), followed by three (9.1%, *n*=4) and six classes (18.2%, *n*=8). The high prevalence of MDR and inducible clindamycin resistance among the HSNZ MRSA isolates warrants further vigilance.

Abstract Reference: 20798
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Virology

Potent chikungunya virus inhibition and potential therapeutic targets of *Streptomyces* sp. KSF103 ethyl acetate extract

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Abstract Content

Chikungunya fever, a global viral disease lacking effective vaccines or drugs, necessitates insecticide use to control *Aedes* mosquito transmission. This study investigated the ethyl acetate (EA) extract of *Streptomyces* sp. KSF103 on CHIKV replication via *in vitro* assay in C6/36 mosquito cell lines. A viral yield reduction assay was performed to determine the effect on CHIKV replication during *in vitro* by quantifying the reduction in CHIKV infectious plaques and the quantity of CHIKV progeny's RNA. The C6/36 cell lines were exposed to lower than the maximum non-toxic dose (MNTD) of EA extract in pre- and post-treatments. The post-treatment was the most effective approach for the extract to restrict the CHIKV replication by 95.2% at 7 µg/mL, with an EC_{50} of 0.217 ± 0.102 µg/mL. The EA extract suppressed CHIKV replication in a dose-dependent manner in a plaque assay. Significant interactions between dodemorph and selagine with CHIKV nsP3 in molecular docking studies suggest that nsP3 could be the target for the EA extract against CHIKV. This study suggests that the EA extract is a potential anti-CHIKV agent. Additional studies on anti-entry and time of-addition assay will gain a better understanding of the inhibition properties of EA extract against CHIKV.

Abstract Reference: 20817
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Diagnostic Technology

In silico design of DNA-Aptamers targeting HPV 16 E6/E7 oncoproteins: Pioneering low-cost, protein-based diagnostics for holistic cervical cancer detection

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Abstract Content

Human papillomavirus (HPV) 16 is a leading cause of cervical cancer, driven by the E6 and E7 oncoproteins that disrupt tumor suppressor proteins. Early detection of these oncoproteins is crucial, highlighting the need for a cost-effective diagnostic technique to improve early diagnosis and treatment. This study aims to develop in silico-based DNA Aptamers targeting HPV16 E6 and E7 oncoproteins and evaluate its potential as a novel diagnostic tool for holistic cervical cancer detection. Quantitative analysis using Autodock Vina, PLIP, and GROMACS showed that DNA-Aptamers bound specifically with high stability and high affinity towards E6 and E7 oncoproteins, -18.9 and -16.0 kcal/mol, respectively. Validation of the generated DNA-Aptamers specificity and sensitivity binding against these HPV oncoproteins were evaluated using aptahistochemical staining on 30 cervical cancer tissue samples, ranging from precursor lesions to invasive cancers. Results indicated that the DNA-Aptamers bound specifically against E6 and E7 oncoproteins in the nuclear of abnormal squamous intraepithelial lesion, which coincided with the in-silico analyses. The DNA-Aptamers able to sensitively detect these oncoproteins at the early precursor cervical lesions, although the cells morphology was not transforming into cancerous yet. These HPV16 E6 and E7 DNA-Aptamers hold promising potential as innovative bioreceptors, paving the way for cost-effective, protein-based diagnostic tools like biosensors and aptahistochemical assays, which could revolutionize early cervical cancer detection.

Abstract Reference: 20847
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Emerging Infectious Diseases

Genetic profiling of microsporidium spp. in fecal samples: A molecular approach

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Abstract Content

Microsporidium is an intestinal protozoan parasite that causes disease in most animal groups and has recently been identified as a significant cause of infection in immunocompromised patients. *Enteropcytozoan bieneusi* (EB), *Encephalitozoaon intestinalis* (EI), *Encephalitozoaon cuniculi* (EC), and *Encephalitozoaon hellem* (EH) are the most common microsporidia parasites to infect human. Although microsporidium microscopic inspection is rapid and accurate, it is limited to genus-level identification. Consequently, the goal of the current study is to enhance and apply a molecular approach to verify microscopy results. A common genus and EB, EI, EC, and EH were assessed in 41 archived stool samples utilizing specific PCR based on the SSU rRNA gene and sequencing. Gram-chromotrope (GC) was used to stain the samples for microscopy examination. Microscopically, 33 samples (80.5%) were positive for *Microsporidium spp.*, whereas only 3 (7.3%) samples were positive for EB by PCR when tested for all samples. Using Maximum-Likelihood, Bayesian, and Maximum parsimony Method phylogenetic analysis, it was discovered that all three of the samples are related to other immunocompromised human patients from Malaysia and Chinese patients with diarrhoea. To determine if molecular analysis can fully replace the microscopic diagnosis, additional samples and evidence are required to evaluate the detection and identification of *Microsporidium spp*. using molecular methods

Keywords: Microsporidium, Fecal samples, SSUrRNA, Immunocompromised, PCR

Abstract Reference: 20856
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Drugs and Drug Resistance

Genomic insights into multidrug-resistant Salmonella strains in Taiwan: Mechanisms of resistance and epidemiological implications

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Abstract Content

The rise of multidrug-resistant (MDR) *Salmonella* strains, including *Salmonella* Agona and *Salmonella* Goldcoast, poses serious public health challenges in Taiwan. *S*. Goldcoast, first identified in 2014, has seen increased MDR infections since 2018. *Salmonella* Anatum (group E) and *Salmonella* Typhimurium (group B) also exhibit notable MDR profiles, complicating treatment. This study investigates the genomic characteristics and antibiotic resistance mechanisms of *S*. Agona and *S*. Goldcoast strains in Taiwan, focusing on resistance genes and phylogenetic relationships. Stool samples from a patient in northern Taiwan yielded two Salmonella strains. Whole-genome sequencing (WGS) provided genomic sequences. Serotyping confirmed *S*. Agona and *S*. Goldcoast. Antibiotic resistance profiles and comparative analysis of *S*. Agona strains assessed MDR prevalence and genetic clustering. WGS identified resistance genes on a 278 kb plasmid. About 50% of *S*. Agona strains exhibited MDR, while the majority were susceptible. *S*. Agona strains belonged to a limited genetic cluster, suggesting recent acquisition of resistance genes. *S*. Goldcoast showed consistent resistance genes across strains, indicating a shared evolutionary history. Similarity in resistance genes or plasmids between strains suggested possible intra-patient gene transfer. Azithromycin resistance was traced to known genes. This study highlights the urgent emergence of MDR *Salmonella* strains in Taiwan, particularly *S*. Goldcoast. Genomic surveillance is essential to monitor and control antibiotic resistance. Understanding resistance mechanisms is crucial for effective treatment strategies.

Abstract Reference: 20883
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Tropical Medicine

CpG-adjuvanted virus-like particle vaccine induces protective immunity against *Leishmania donovani* infection

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Abstract Content

Visceral leishmaniasis (VL) poses a significant public health challenge due to the lack of an approved human vaccine. This study aimed to enhance the efficacy of a virus-like particle (VLP) vaccine expressing the *Leishmania donovani* promastigote surface antigen (PSA) adjuvanted with CpG oligodeoxynucleotide (CpG-ODN). We examined the immune responses elicited in mice following subcutaneous immunization with PSA-VLPs co-formulated with CpG-ODN, and assessed its efficacy upon challenge infection with mCherry (mCh)-expressing *L. donovani* promastigotes. Our findings revealed that PSA-VLP vaccination with CpG-ODN significantly elevated the levels of parasite-specific IgG, IgG1, IgG2a, and IgG2b antibodies in the serum. Additionally, vaccinated mice exhibited enhanced germinal center B cells, as well as splenic $CD4^+$ and $CD8^+$ T cell activities, compared to unimmunized mice. Importantly, PSA-VLPs and CpG-ODN vaccination reduced the levels of inflammatory cytokines IFN-γ and IL-6 in visceral organs, leading to decreased total parasite burden and providing effective protection against *L. donovani* challenge. These findings indicate that CpG-ODN markedly boosts the protective immunity conferred by PSA-VLPs vaccination against *L. donovani*, offering a promising step towards the development of an effective VL vaccine.

Abstract Reference: 20888
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Emerging Infectious Diseases

Within-household transmission of chikungunya virus during an outbreak in Cambodia

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Abstract Content

Chikungunya virus (CHIKV) is a major public health concern in Cambodia, with evidence suggesting an increased risk of household transmission during outbreaks. This study investigated the rate of secondary household transmission of CHIKV and identified potential risk factors. A prospective, multicenter surveillance study was conducted during CHIKV outbreaks in 2021/2022 in four Cambodian provinces. Index cases were identified at referral hospitals and diagnosed with acute CHIKV infection within 48 hours of symptom onset. Household members with negative IgM and IgG antibodies at baseline were included in symptom surveillance and followed up with serology at 6 weeks. Symptomatic participants were tested for new CHIKV infections using molecular assays. Among 150 household members from 46 index cases, 75 were seronegative for CHIKV at baseline. Of these, 55 completed follow-up, and 21 (38%) developed CHIKV infections, 10 (18%) symptomatic and 11 (20%) asymptomatic. Most symptomatic infections occurred within a few days of the index case's diagnosis. Frequent symptoms included fever, joint pain, headache, rash, and fatigue. Higher infection rates were associated with a larger household size, close family relationship to the index case, and not using mosquito coils. No significant demographic factors were associated with infection risk. The high rate of secondary household CHIKV transmission underlines the need for targeted in-home prevention, including vector control. Further research on dominant mosquito vectors and indoor/outdoor exposure is needed to confirm these findings in different settings and refine intervention strategies to better protect vulnerable populations and manage CHIKV outbreaks effectively.

Abstract Reference: 20904
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Neglected Tropical Diseases

The tale of two queens: Spatio temporal analysis of geo-helminths in Sabah

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Abstract Content

Soil-transmitted helminth (STH) infections are a major public health concern, especially affecting school-aged children in tropical regions. This study developed, implemented, and evaluated a health education module aimed at controlling STH infections among pre-school children in Kota Belud, Sabah. Using the Fuzzy Delphi Method (FDM), experts designed the module, which included comic books, drawings, and health talks to teach key preventive measures like handwashing, soap use, deworming, wearing shoes, and safe drinking water. The research was conducted in three phases: development of the health education module, a parasitological survey, and a cluster-randomized controlled trial (cRCT). The parasitological survey involved stool sample examinations using the Kato-Katz technique to determine STH infection prevalence. The cRCT compared an intervention group (receiving the health education module and deworming) with a control group (receiving only deworming). Geographic Information System (GIS) technology was used for spatiotemporal analysis of STH infection distribution and its correlation with environmental factors such as rainfall, temperature, and soil type. This study advances the understanding of STH epidemiology and illustrates the practical application of health education in disease prevention. By using interactive and culturally appropriate materials, the study effectively promoted better hygiene practices and awareness. Future research should examine the long-term effects of such educational interventions and their potential for broader application.

Abstract Reference: 20942
Mode of Presentation: MSPTM Student Competition – Rapid Oral Presentation
Topic: Entomology

Resistance profiling of *Aedes aegypti* from a Dengue hotspot: Assessing resistance levels at intensity concentrations

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Abstract Content

Dengue is the fastest spreading vector-borne viral disease, endemic in over 100 countries. In Malaysia, dengue cases surged by 86.3% in 2023, reaching 123,133 cases with 100 deaths compared to 2022. With no specific antiviral treatments and the limited availability of a safe tetravalent dengue vaccine, insecticides remain the primary intervention for controlling dengue vectors. This study examined the resistance of *Aedes aegypti* from a hotspot locality in Klang Valley to pyrethroids and organophosphates via WHO adult bioassay. Resistance was evaluated by increasing the insecticide concentration to 5x and 10x from the initial discriminating concentration. Findings indicated an absence of adult mosquito mortality among tested insecticides at discriminating concentrations. However, mortality increased in response to exposure at intensity concentrations, showing a trend of rising mortality as concentrations escalated from 5x to 10x. Despite this increase, mortality did not reach susceptibility levels, with most recorded mortalities being less than 98%, except for one insecticide from the organophosphate group, pirimiphos-methyl. This study underscores the importance of assessing resistance intensity to quantify the resilience of *Aedes aegypti* to insecticides, providing crucial insights into their survival rates at both discriminating and elevated concentrations. Understanding the degree of resistance helps in formulating effective vector control strategies. The findings highlight the necessity for continuous monitoring and adaptive management of insecticide use to combat the rising threat of insecticide resistance in dengue vectors, ensuring the efficacy of control measures and protecting public health.

MSPTM STUDENT COMPETITION - POSTER PRESENTATION

MSPTM STUDENT COMPETITION – POSTER PRESENTATION

Abstract Reference: 20178
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Malaria

Essential role of pleckstrin homology domain-containing protein 1 (PH1) in AMA1 secretion during erythrocyte invasion by *Plasmodium yoelii*

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Abstract Content

Malaria, caused by *Plasmodium* parasites, is a significant public health concern. In the mammalian host, parasites must multiply within erythrocytes; thus, the invasion into erythrocytes is a critical step. The proteins secreted from the micronemes play essential roles in orchestrating this intricate process; therefore, unraveling the molecular mechanism underlying such secretion holds the promise of elucidating novel targets for drug intervention. Our previous investigations in *Plasmodium yoelii* demonstrated that deleting APH, one of the Pleckstrin Homology (PH) domain-containing proteins, impaired asexual growth and erythrocyte invasion. These phenotypes were likely linked to impaired secretion of MTRAP and AMA1. Based on the hypothesis that other PH domain-containing proteins are also involved in microneme secretion, we generated a transgenic *P. yoelii* 17XL line wherein the PH1 gene locus can be inducibly excised. Moreover, PH1 deletion impaired the translocation of AMA1 to the merozoite surface but did not affect that of MTRAP. Indirect fluorescence assay revealed Myc-tagged APH colocalized with MTRAP, while Myc-tagged PH1 did not colocalize with AMA1 and MTRAP. Our observation for PH1 is consistent with *P. falciparum* PH2, which was required for the secretion of EBL, another microneme protein, but did not colocalize with EBL (Ebrahimzadeh et al. 2019).

Abstract Reference: 20330
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Parasitology

Study on intestinal parasitic infections and gut microbiota in cancer patients at a tertiary teaching hospital in Malaysia

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Abstract Content

Intestinal parasitic infections (IPIs) can pose significant risks to cancer patients due to heightened susceptibility to opportunistic infections, which lead to severe morbidity and mortality. Recent studies indicate that intestinal parasites may disrupt the gut microbiota's balance as they share the same niche. However, there is limited understanding of these interactions in Malaysia. To assess the connection between intestinal parasites and gut microbiota composition in cancer patients, a study was conducted. Stool samples from 134 cancer patients undergoing active treatment or newly diagnosed were collected and examined for the presence of intestinal parasites. The study compared 33 microscopically positive stool samples and 20 negative samples against 17 healthy controls using 16S RNA sequencing of the V3-V4 region to evaluate gut microbial composition. This study observed significant differences in microbiota diversity and composition between cancer patients and healthy controls ($p < 0.001$). Notably, parasite-infected patients show a distinct bacterial composition compared to non-infected based on Bray-Curtis ($p=0.041$) and Jaccard ($p=0.021$) measurement. Parasite-infected patients showed an enrichment of *Enterococcus* and a reduction of *Faecalibacterium prausnitzii* compared to non-infected and control groups. Further analysis identified specific variations among different parasitic infections. Patients with *Entamoeba* and *Cryptosporidium* infections exhibited increases in obligate anaerobic bacteria. Those infected with microsporidia showed significant alterations in *Enterococcus* levels, while bacteria from the *Clostridiales* order, *Faecalibacterium*, *Parabacteroides*, *Collinsella*, *Ruminococcus*, and *Sporosarcina* decreased compared to the non-infected. These findings underscore the importance of understanding and managing the interactions between intestinal parasites and gut microbiota to improve cancer patient's outcome.

Abstract Reference: 20380
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Helminths Biology and Control

Taurine alleviates liver fibrosis induced by *Clonorchis sinensis* via acting on hepatic stellate cells

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Abstract Content

Clonorchis sinensis is a zoonotic trematode that parasitizes in the bile duct and gall bladder of animals and humans, which can cause liver fibrosis and even cholangiocarcinoma. Taurine can protect the liver from damage by benefiting liver cells’ repairing and regenerating. This study aimed to investigate the effect of taurine on liver fibrosis caused by *C. sinensis* via acting on hepatic stellate cell (HSC). The mice infected with *C. sinensis* were treated with taurine with the healthy mice as the control. The livers were extracted for hematoxylin-eosin (HE) and Masson staining. The primary HSC of mice were extracted for qRT-PCR and Western Blot (WB). In vitro experiments, HSC-T6 stimulated by *C. sinensis* excretory-secretory products (CsESPs) was treated with taurine. Both primary HSC and HSC-T6 were used to extract total RNA and protein, then qRT-PCR and WB were conducted to identify the expression of α-smooth muscle actin (α-SMA), Collagen I (Col1A1), Collagen III (Col3A1). Results of HE and Masson staining showed that mice livers treated with taurine were not serious compared with those of the infected group. Both WB and qRT-PCR showed that α-SMA, Col1A1 and Col3A1 in the primary HSC in taurine treated group decreased significantly ($P<0.01$) compared with those in *C. sinensis* infected group. The vitro experiments had the same trend, but the Col3A1 showed less significance ($P<0.05$) by WB. Our results clarify that taurine can alleviate liver fibrosis caused by *C. sinensis* by acting on HSC, which provides new idea and potential therapeutic target for the treatment.

Abstract Reference: 20400
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Dengue

Insecticide resistance profile and mechanisms of insecticide resistance in field *Aedes albopictus* in Northern Taiwan

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Abstract Content

Aedes albopictus serves as a significant vector for arboviruses. It can transmit a range of arboviruses such as yellow fever, dengue, and Zika. Previous findings indicated that insecticide resistance was absent in *A. albopictus* populations from Taiwan. However, due to increased imported dengue cases in northern Taiwan in recent years, the massive application of pyrethroid-based insecticides is now underway. In the present study, we assessed the insecticide resistance status of 9 field populations of *A. albopictus* to deltamethrin (0.03% diagnostic dose (DD)), lambda-cyhalothrin (0.08% DD), permethrin (0.4% DD), bendiocarb (0.2% DD) and pirimiphos-methyl (60 mg/m² DD). Furthermore, we conducted synergism tests by using piperonyl butoxide (PBO) to determine whether cyctochrome P450 monooxygenases are involved. Subsequently, we conducted kdr mutation screening (I1532, F1534) for all the populations to determine the presence of any genetic mutations underlying the reduced insecticide susceptibility. Deltamethrin, lambda-cyhalothrin, permethrin, bendiocarb and pirimiphos-methyl caused 32-78%, 44-88%, 27-77%, 69-100%, 92-100% mortality, respectively. Nevertheless, the mortality of 9 field populations increased up to 99% upon pre-exposed to PBO synergist. Among the field populations, only 11.8% individuals (I1532V) from 5 population were observed. Of these individuals, 85% showed heterozygous mutations, and the other 15% showed homozygous mutations in I1532V. The result indicates that metabolic resistance involving cyctochrome P450 monooxygenases is the major factor resulting in reduced susceptibility of field populations to test insecticides. Though the frequency of kdr mutation is low, long term insecticide susceptibility monitoring programs on the target population is required to ensure effective control.

Abstract Reference: 20412
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Malaria

Investigating the Plasmodium transmission blocking activity of platelet factor peptides

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Abstract Content

There is a recognised need to develop new therapies against *P. falciparum*, both to safeguard against emerging resistance and to eliminate the transmission capable lifecycle forms called gametocytes. Our research group, with collaborators, has used a molecular and chemical biology approach to develop novel antimalarials with a unique mechanism of action against blood stage Plasmodium. Based on the structure of the human protein PF4, a novel engineered peptide termed PDIP, has potent activity. PDIP selectively enters parasitised erythrocytes and causes death by lysis of the parasite's digestive vacuole. With known biological similarities between the blood stage and gametocytes we sought to determine whether PDIP was similarly active against gametocytes and other transmission stages. We found no direct gametocytocidal effects of PDIP, however PDIP-fluorochrome conjugates rapidly enter gametocyte infected erythrocytes, localise within the cytosol, and persist within the cell for several days, highlighting their specificity. Novel peptide drug conjugates (PDCs) of PDIP covalently linked to known antimalarial compounds, which use the PDIP scaffold to selectively deliver the compound to the parasite, have direct killing and inhibit further activation during gametogenesis. We are working with collaborators to determine the effects of PDIP in the full mosquito transmission infection model, and against sporozoite viability, which are ongoing. This project reinforces the selectivity of membrane active proteins against their target pathogens, and supports PDIP as a novel compound to target Plasmodium. We also validate the PDC approach as a strategy for selective delivery of potent antimalarial compounds to the gametocyte.

Abstract Reference: 20450
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Malaria

The intrinsically disordered region of *Plasmodium berghei* ookinete membrane protein OSCP is involved in adhesion to the mosquito midgut

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Abstract Content

When ingested by *Anopheles* mosquitoes, *Plasmodium* protozoa transform into motile ookinetes, which attach to and penetrate the midgut cells, eventually maturing into oocysts on the basal side. Previously, we identified a membrane protein, Ookinete Surface and Oocyst Capsule Protein (OSCP), which affects ookinete motility and oocyst wall formation (Nakayama et al. 2021) . We observed that the antibody against amino acids (aa) 926–939 of OSCP inhibit ookinete motility, suggesting they are involved in parasite adhesion. We focused on the region around aa 926–939 using an *in silico* approach. The flanking regions, predicted by PlasmoDB and PONDR to contain intrinsically disordered regions (IDRs), were identified as Front IDR (aa 860–925) and Rear IDR (aa 939–1068). These regions were expressed and purified as GST fusion recombinant proteins in *Escherichia coli*. Subsequently, ELISA, immunostaining, and pull-down assays were assess their interactions with the mosquito midgut. The Front IDR recombinant protein adhered to mosquito midgut proteins in the cell membrane fraction, as revealed by ELISA. Immunostaining revealed adherence to the luminal side of the midgut cells. The binding strength increased with decreasing salt concentration, and suggested the involvement of electrostatic interactions. The pull-down assay detected multiple proteins binding to the Front IDR recombinant protein, which are currently being identified. Our study suggests that the Front IDR at aa 860–925 in the OSCP is associated with ookinete attachment to the mosquito midgut via electrostatic interactions. This insight provides a new perspective on how ookinetes recognize the mosquito midgut.

Abstract Reference: 20454
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Dengue

The effect of artificial light at night on *Aedes aegypti* larvae and its carry-over effect on adult traits

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Abstract Content

Aedes aegypti is anthropophilic and the primary vector of dengue virus in urban areas. The physiological state and behavior of mosquitoes may be influenced by increased artificial light at night (ALAN). Previous researches focused on the direct effect of ALAN on adult mosquito, but the effect of ALAN on larvae were largely ignored. The present study examined the effect of ALAN on larval development, and its carry-over effect on adult mosquitoes, including flight activity, blood feeding, and fecundity of *Aedes aegypti*. The ALAN-exposed larvae were kept under 13.5:10.5 h (L:D) photoperiod with light intensity of 1000 lux and 200 lux; for the control, no ALAN exposure in the dark period. The mosquito was exposed to 12:12 h (L:D) during the adult stage. The result showed that no significant difference was found between the ALAN-exposed group and the control in the larvae development traits. In contrast, the carry-over effect of ALAN was significant. ALAN-exposed female mosquitoes showed significantly higher percentage of blood-feeding (70.4% and 66.4% on 28-day and 35-day ages, respectively) and fecundity (58 and 46 eggs per female on 28-day and 35-day ages, respectively), compared to control group (blood-feeding: 29.5% and 26.8%; fecundity: 26, 22 eggs per female) but no significant difference was observed in adult flight activity. The result suggest that ALAN may have increased the larval nutrient consumption, resulting in larger adult body size. The change in adult body size may thus explain their increased percentage of blood-feeding, and fecundity. The phenomenal potentially increase the adult vectorial capacity.

Abstract Reference: 20456
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Dengue

Insecticide resistance in *Aedes aegypti* from Southern Taiwan

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Abstract Content

Aedes aegypti is the primary vector for vector-borne diseases including dengue fever. In 2023, a total of 24,727 dengue cases was reported in Kaohsiung and Tainan, Southern Taiwan, accounting for 92.6% of the total dengue case reported in Taiwan. Pyrethroid fogging is commonly used mosquito control in southern Taiwan. However, intensive use of insecticides leads to development of insecticide resistance in *Aedes* mosquito. In the present study, *Aedes aegypti* were collected from six districts in Tainan city and Kaohsiung city, Taiwan. The field populations were tested using Standard WHO bioassay with diagnostic doses of five insecticides, namely 0.03% deltamethrin, 0.05% lambda-cythalothrin, 0.4% permethrin, 0.2% bendiocarb, 60 mg/m^2 pirimiphos-methyl to determine their resistance levels by comparing with laboratory susceptible strain (Bora-Bora strain). Subsequently, synergistic test using piperonyl butoxide (PBO) was employed to examine the possibility of cytochrome P450 monooxygenases. The field populations were also screened to detect the presence of *kdr* mutations (i.e., V1016G, S989P and F1534C). The laboratory strain had mortality over 98% in all of the insecticides. All field populations exposed to those aforementioned insecticides produced averaged mortalities in the range of range 1.1-44.1%, 4.4-61%, 4.4-7.2%, 89.9-98.3%, and 0-54.4%, respectively. The mortalities below 98% indicate resistance. Knockdown resistance (*kdr*), mutation in VGSC and enhanced cyctochrome P450 are the major mechanisms underlying the reduced efficiency of pyrethroid insecticides. This study demonstrates pyrethroid resistance and its underlying mechanisms in six field populations in southern Taiwan. This information provides the authorities crucial information to facilitate future vector control program.

Abstract Reference: 20484
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Tick-borne Diseases

Peptidomic analysis of canine hepatozoonosis; A preliminary study

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Abstract Content

Canine Hepatozoonosis is one of the most important canine vector borne diseases (CVBD). *Hepatozoon canis* develops a complicated life cycle and manifests a wide range of symptoms from asymptomatic to life-threatening stage. Several techniques can be used to diagnose *Hepatozoon canis* infection. This study aimed to explore the utility of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) in distinguishing peptide barcodes in serum samples from healthy control dogs and *H. canis* infected dogs. Serum samples were collected from two healthy control dogs ($n = 2$) and five *H. canis* infected dogs ($n = 5$). All spectra derived from MALDI-TOF MS were analyzed using Metaboanalyst 6.0. In the mass range of 1,000–6,000 Da, 1792 peptides were detected. Both serum peptide barcodes were clearly classified into two clusters, as presented by orthogonal partial least squares discriminant analysis model (orthogonal PLS-DA), indicating differences in peptide expression. The volcano plot displayed 78 up-regulated peptides and 35 down-regulated peptides. Furthermore, the peptides at m/z 2883.40, 2892.06, 3040.26, 3086.19, and 3212.07 significantly differed between the investigated groups. Peptide barcode generated by MALDI-TOF MS could serve as a diagnostic tool for screening Canine Hepatozoonosis; however, verification through a larger sample size and association with clinical data are required.

Abstract Reference: 20512
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Vector Control

The role of cuticular hydrocarbon and synergist on escaping response of Aedes mosquito from deltamethrin-treated surface

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Abstract Content

Insecticide residual spraying, exploiting the resting behavior of female mosquito after a blood meal, is gaining popularity to control *Aedes aegypti*. However, mosquitoes tend to avoid or prematurely escape the treated area before receiving lethal dose. The behavioral response of field resistant mosquito (LY, high resistant; QZ, low resistant) and laboratory susceptible strain (Bora-bora) to deltamethrin treated surface was examined. We examined the role of cuticular hydrocarbon and piperonyl butoxide (PBO) synergist on escaping response of susceptible Bora-bora *Aedes* mosquito exposing to deltamethrin-treated surface. To this end, the test mosquitos were treated hexane on appendages and PBO 1hrs before the behavioral assay. The result shows the escape response of LY (17.9%±5.4%) are lower than QZ (60.0%±4.9%) and Bora-Bora (44.6%±11.4%). In addition, approximately 25% individuals from LY spent 50 min to escape the treated area; while QZ spent 3 min to escape the treated area. The % escaping of Bora-bora strain recorded 32.2%± 10.9% and 48.3%±4.3% under pretreatment of Hexane and PBO both show no significant difference with non-exposed individuals (44.6%±11.4%). The pre-treatments of hexane (90.6%±1.6%) and PBO (67.6%±6.4%) significantly increased the % knockdown compared to non-exposed (hexane: 14.4%±5.9%; PBO: 0%±0%). Additionally, significant higher mortality was observed under hexane (88.3%±7.1%) and PBO pre-treatment (75.9%±4.2%) compared to non-exposed (hexane: 32.8%±14.3%; PBO: 0%±0%). The result indicated the variability of behavioral response is related to physiological resistance of mosquito. Cuticular hydrocarbon and synergist affect escaping response of *Aedes* mosquito from deltamethrin-treated surface and resulting in substantial knockdown and mortality in mosquito.

Abstract Reference: 20700
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Rabies

Knowledge, attitudes and practices towards rabies among healthcare workers in Cambodia – A national survey

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Abstract Content

Combined efforts on dog vaccination, timely post-exposure prophylaxis (PEP) and raised awareness are needed to reach the objective of zero human deaths due to dog-mediated rabies by 2030 launched by the quadripartite. In Cambodia, awareness of healthcare workers towards rabies has never been assessed. A large online national survey was launched among a random sample of public and private health facilities between 09/2023 and 05/2024 to assess the knowledge, attitude and practices (KAP) towards rabies of healthcare workers. A total of 1,227 facilities ranging from small private cabinets to national hospitals completed the survey. Respondents were mainly doctors (40.0%) and nurses (30.8%) with a strong male bias (72.5%). Although main species, symptoms and transmission modes were well known, five main knowledge gaps were identified: (i) PEP is necessary even for minor wounds, (ii) one can be exposed when slaughtering rabid animals but not when touching rabid people or animals (iii) timely and complete PEP is extremely efficient, (iv) after symptom onset, rabies is 100% lethal (v) dogs can transmit the virus before exhibiting clinical signs. Incorrect opinions on the major role of non-owned stray dogs should also be addressed. Concerning practices, 86.8% (79.7-91.7) of the 59.7% (54.7-64.6) of respondents who had experienced a bite within their household had sought PEP. Multivariable logistic regression highlighted main variables linked to good KAP. By identifying key knowledge gaps and profiles and facilities with the weakest KAP, this study will help better target effective rabies training programs for healthcare workers.

Abstract Reference: 20897
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Microbiology

Studying host preference and its contribution to the co-occurrence of entomopathogenic nematodes mentors

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Abstract Content

Biodiversity plays a critical role in maintaining ecosystems by providing sustainable food chains and supporting the general wellness of organisms. Biodiversity is enhanced when species can coexist stably, which can be promoted by niche partitioning. Entomopathogenic Nematodes (EPNs) are an interesting group of organisms because multiple species can co-occur in the same ecosystem while using the same resources. EPNs are obligate parasitic nematodes that kill their insect hosts, which are crucial for their reproduction. They are globally used for agricultural purposes as environmentally friendly insecticides. EPNs are successful biological insecticides, providing an alternative to chemical insecticides, and they contribute significantly to biological control. EPNs might use niche partitioning to decrease competition and increase their survival rates. Understanding their behavior is vital for addressing gaps in existing research on biodiversity, host preference, and environmental factors. We hypothesize that EPNs co-occur due to their preference for infecting different host species, which mitigates competition. This research involves an in-depth analysis of nematode abundance in different sections of chemotaxis assays. We examined three EPNs: Steinernema affine, S. costaricense, and S. krausse. They were exposed to four different host species: Acheta domestica, Galleria mellonella, Manduca sexta, and Tenebrio molitor. Over 24 hours, we observed their host preferences. Our chemotaxis assays showed that different EPN species have distinct host preferences, potentially allowing for resource partitioning in their natural habitats and avoiding competition. Understanding these dynamics is essential for enhancing biodiversity and promoting sustainable ecosystems.

Abstract Reference: 20945
Mode of Presentation: MSPTM Student Competition – Poster Presentation
Topic: Parasitology

Diagnostic capabilities of rSjTPx-1 for detecting schistosome infection in pigs

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Abstract Content

Zoonotic schistosomiasis, caused by *Schistosoma japonicum*, remains a public health issue in endemic regions like the Philippines. The presence of animal reservoir hosts, including water buffaloes, dogs, and pigs, complicates control efforts. Pigs, in particular, lack standard sensitive and specific diagnostic tools for schistosome infection. This study assessed the diagnostic performance of recombinant *S. japonicum* thioredoxin peroxidase 1 (rSjTPx-1), a sensitive and specific biomarker, using enzyme-linked immunosorbent assay (ELISA) to detect seropositive results in humans and water buffaloes. Archived pig sera (n=70) from a schistosomiasis-endemic area in Jaro, Leyte, Philippines, were tested for *S. japonicum* infection using both soluble egg antigen (SEA) ELISA and rSjTPx-1 ELISA, with negative controls (n=8) from a non-endemic area. Receiver operating characteristic curve analysis determined the cut-off value for rSjTPx-1 seropositivity, while a t-test identified significant differences between samples with high and low optical density (OD) values from rSjTPx-1 enzyme-linked immunosorbent assay. The cut-off for rSjTPx-1 was set at 0.2850, with an area under the curve (AUC) of 0.7875, while soluble egg antigen had a cut-off of 0.1971 and an AUC of 0.5286. The results indicated a 25.71% seropositivity for rSjTPx-1 and 58.75% for SEA. There was a significant difference between high and low OD values (p-value: 0.0007). This study confirms the potential of rSjTPx-1 enzyme-linked immunosorbent assay for detecting schistosome infection in pigs, demonstrating good sensitivity and specificity compared to SEA-ELISA. Field testing in pigs should be done to compare the recombinant antigen ELISA with stool microscopy.