Joint International Tropical Medicine Meeting

JITMM 2023

“Achieving the SDGs: Human and AI-driven Solutions for Tropical Medicine in a Changing World”

13-15 December 2023

Eastin Grand Hotel Phayathai, Bangkok, Thailand

Abstracts Book

Hosted by

Mahidol University
Faculty of Tropical Medicine

Co-Organizers:

Mahidol University

Mahidol University
Faculty of Medicine Siriraj Hospital

กรมควบคุมโรค
Department of Disease Control

Chula
Chulalongkorn University

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- Faculty of Tropical Medicine, Mahidol University
- Mahidol University
- Faculty of Medicine Siriraj Hospital, Mahidol University
- Department of Disease Control, Ministry of Public Health (MOPH)
- Faculty of Medicine, Chulalongkorn University
- Mahidol-Oxford Tropical Medicine Research Unit (MORU)
- Southeast Asian Ministers of Education Organization (SEAMEO) TROPMED Network

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Wednesday 13 December 2023

S01: Opening Ceremony

8.30-10.00hr

Report
Weerapong Phumratanaprapin
Chair, JITMM 2023 Organizing Committee
Dean, Faculty of Tropical Medicine, Mahidol University

Welcome Address
Wanna Hanshaoworakul
Medical Physician, Advisor Level,
Department of Disease Control, Thailand Ministry of Public Health

Apichat Asavamongkolkul
Dean, Faculty of Medicine Siriraj Hospital, Mahidol University

Chanchai Sittipunt
Dean, Faculty of Medicine, Chulalongkorn University

Nicholas Day
Director, Mahidol Oxford Tropical Medicine Research Unit

Pratap Singhasivanon
Secretary General/Coordinator, SEAMEO TropMed Network

Welcome Remarks
Banchong Mahaisavariya
President, Mahidol University

8.30-10.00hr

Opening Ceremony

Chairperson: -

Invited speaker:

1. mRNA vaccines: Pandemic Preparedness and Beyond

Kiat Ruxrungtham

Other (Chula Vaccine Research Center (Chula VRC), Chulalongkorn University)

Abstract No.: ABS0002304

mRNA vaccines: Pandemic Preparedness and Beyond

Kiat Ruxrungtham

Authors: Kiat Ruxrungtham

Affiliation: Faculty of Medicine, Chulalongkorn University

No abstract available

Keyword: No abstract available

Wednesday 13 December 2023

S02: Reaching out across continents: Public Health support between Asia and Africa

10.30-12.00hr

Room A

Wednesday 13 December 2023

S02: Reaching out across continents: Public Health support between Asia and Africa

10.30-12.00hr

Room A

Chairperson:
1. Leo Braack

Invited speaker:

1. REACHING OUT ACROSS CONTINENTS: PUBLIC HEALTH SUPPORT BETWEEN ASIA AND AFRICA
Poe Poe Aung
Other (Maastricht University, Netherlands)

2. SUPPORT FOR CONTROL OF INVASIVE *Anopheles stephensi*
Susanta Kumar Ghosh
Other (ICMR-National Institute of Malaria Research, Bangalore, India)

Abstract No.: ABS0002138

REACHING OUT ACROSS CONTINENTS: PUBLIC HEALTH SUPPORT BETWEEN ASIA AND AFRICA

Poe Poe Aung

Authors: Poe Poe Aung[1], Wulan Aldillah Wulandhari[1], Kallista Chan[2], Leo Braack[1]

Affiliation: [1]Malaria Consortium Asia, Bangkok, Thailand; [2]London School of Hygiene and Tropical Medicine, London, UK

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 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 will be conducted in November 2023 in Cameroon, collaborating with Cameroon's national epidemiological surveillance unit, Ministry of Public Health Cameroon and academic institutions. We will bring key representatives from three African countries, Thailand and Mexico to Cameroon, for risk assessment and mitigation of arbovirus disease transmission and preparedness of outbreak response for arbovirus diseases. Lessons learnt highlighted the need for effective planning and coordination, ensuring correct timing commitment from partner institutions, 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.

Keywords: Arboviruses, South-South Exchange Visits, Africa, Asia

Abstract No.: ABS0002141

SUPPORT FOR CONTROL OF INVASIVE Anopheles stephensi

Susanta Kumar Ghosh

Authors: Susanta Kumar Ghosh[1]* Chaitali Ghosh[2]**

Affiliation: 1. ICMR-National Institute of Malaria Research, Bangalore, India.
2. Tata Institute for Genetics and Society, Bangalore, India.

* Expert Member, RBM Vector Control Working Group (VCWG) Task Team on Anopheles stephensi in Africa
** Member, RBM Vector Control Working Group

Anopheles stephensi commonly known as Asian Malaria Mosquito is an invasive malaria vector. To date, besides Sri Lanka (2017) and Yemen (2021), this species has been detected in African countries of Djibouti (2012), Ethiopia (2016), Sudan (2016), Somalia (2019), Nigeria (2020), Ghana (2022) and Kenya (2022) and Eritrea (2022). Glen Liston in 1901 first described An. stephensi from the village Ellichpur (now Achalpur), Amravati district, Maharashtra, India. South Asia and the Arabian Peninsula is the home of this malaria vector. There are three biological forms known as type, intermediate, and mysorensis. In urban settings, type form tends to be anthropophilic (prefer human blood), endophagic (prefer to feed indoors), endophilic (prefer to inhabit/rest indoors), and their larval stages can be found in artificial containers (e.g., water barrels, wells, fountains, cisterns, overhead tanks). In contrast, in rural settings, the mysorensis form is considered to be zoophilic (prefer animal blood), exophilic (prefer to inhabit/rest outdoors), and their larval stages are found in irrigation canals, ponds, stream pools, and stream margins. There is a necessity on what vector strategies would be most appropriate to halt the march of An. stephensi. Since 2019 World Health Organization (WHO) to ASTMH 71st Annual Meeting at Seattle in 2022, and recently RBM-Vector Control Working Group (VCWG) in Accra, Ghana (6 to 8 February 2023), WHO Regional Response meeting in Addis Ababa, Ethiopia (8 to 10 March 2023) and a convene meeting on `Improving Larval Source Management in Africa' in Addis Ababa, Ethiopia (15 and 16 September 2023)

Keywords: Anopheles stephensi, Variants, Malaria, Invasion, India, Africa

Wednesday 13 December 2023

S03: Improving Biopreparedness

10.30-12.00hr

Room B

Wednesday 13 December 2023

S03: Improving Biopreparedness

10.30-12.00hr

Room B

Chairperson:
1. CAPT Andrew Letizia
2. LCDR Nathaniel Christy

Invited speaker:

1. SARS-CoV-2, Influenza, and Dengue virus circulation dynamics in Kelantan and Klang Valley regions of Western Malaysia
Kim-Kee Tan
Other (Universiti Malaya)

2. Trends in respiratory virus infections in relation to the COVID-19 pandemic in Lao P.D.R: a hospital-based surveillance study
Koukeo Phommasone
Other (Lao-Oxford-Mahosot Hospital-Wellcome Trust research Unit)

3. SEROSURVEILLANCE FOR TROPICAL INFECTIOUS DISEASES: BOLSTERING LAB CAPACITY THROUGH MULTIPLEXING TECHNOLOGIES
Keersten Ricks
Other (USAMRIID)

4. SARS-CoV-2 Risk Factors and sero-prevalence in minimally vaccinated individuals in Papaua New Guinea
FRANCIS LELNGEI
Other (CENTRAL PUBLIC HEALTH LABORATORY, NATIONAL DEPARTMENT OF HEALTH, PAPUA NEW GUINEA)

Abstract No.: ABS0002306

SARS-CoV-2, Influenza, and Dengue virus circulation dynamics in Kelantan and Klang Valley regions of Western Malaysia

Kim-Kee Tan

Authors: Kim-Kee Tan

Affiliation: University of Malaya Tropical Infectious Diseases Research & Education Centre

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002182

Trends in respiratory virus infections in relation to the COVID-19 pandemic in Lao P.D.R: a hospital-based surveillance study

Koukeo Phommasone

Authors: Koukeo Phommasone[1], Danoy Chommanam[1], Nathaniel C Christy[2], Touxiong Yiaye[1], Soulichanya Phoutthavong[1], Patsalin Keomoukda[1], Sompong Thammavong[1], Thipsavanh Bounphiengsy[1], Thongsavanh Lathsachack[1], Latsaniphone Boutthasavong[1], Bountoy Sibounheuang[1], Ooyanong Phonemixay[1], Siribun Panapruksachat[1], Viladeth Praphasiri[3], Sommay Keomany[4], Bounthavy Chaleunphon[5], Phouvieng Douangdala[6], Matthew T Robinson[1], Elizabeth Batty[7], Manivanh Vongsouvath[1], Andrew G Letizia[2], Mayfong Mayxay[1,8],Audrey Dubot-Pérès[1,10], Elizabeth A Ashley[1,9]

Affiliation:[1]Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit, Microbiology Laboratory, Mahosot Hospital, Vientiane, Lao PDR; [2]U.S. Naval Medical Research Unit TWO (NAMRU-2), Singapore and Phnom Penh, Cambodia; [3]Xiengkhuang Provincial Hospital, Phonsavan District, Xiengkhuang Province, Lao PDR; [4] Salavan Provincial Hospital, Salavan Province, Lao PDR; [5]Attapu Provincial Hospital, Attapu Procince, Lao PDR; [6] Luangnamtha Provincial Hospital, Luangnamtha Province, Lao PDR; [7]Mahidol Oxford Tropical Medicine Research Unit; [8]University of Health Sciences, Ministry of Health, Vientiane, Lao PDR; [9] Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, UK; [10] Unité des Virus Émergents (UVE: Aix-Marseille Univ-IRD 190-Inserm 1207), Marseille, France.

Background: Circulation of influenza and other seasonal respiratory viruses changed dramatically during the COVID-19 pandemic, thought due to control measures put in place to reduce transmission of SARS-CoV-2. This study aimed to determine the trends of SARS-CoV-2, influenza A, influenza B and respiratory syncytial viruses (RSV) in patients presenting with acute respiratory infections (ARI).

Methods: This prospective study was conducted in four provincial hospitals across Lao PDR. Participants of all ages who met our case definition for an ARI (axillary temperature ≥ 37.5°C or history of fever, AND cough or other respiratory symptoms/signs OR loss of smell and/or taste) presenting to the hospital less than 10 days after symptom onset were eligible to be enrolled. Nasopharyngeal (NP) and throat swabs were taken for SARS-CoV-2 E-gene, influenza A, influenza B and human respiratory syncytial virus probe based real-time RT PCR assay.

Findings: A total of 4,334 patients were recruited between March 2021 and July 2023, of whom 928 (22%) were children less than 5 years old. Seven percent of patients (302) had a qSOFA score □2. SARS-CoV 2 was detected in 19.2% patients, followed by influenza A, influenza B and RSV (9.2%, 7.7% and 5.4%, respectively). There were 167 patients with at least two viruses detected. Influenza viruses and RSV were not detected while COVID-19 control measures were implemented.

Conclusion: COVID-19 control measures had an added benefit to prevent other respiratory virus infections in Laos. Lifting the restrictions led to a resurgence of influenza A, influenza B and RSV.

Keywords: COVID-19, Respiratory virus infection, acute respiratory infection, Lao PDR

Abstract No.: ABS0002222

SEROSURVEILLANCE FOR TROPICAL INFECTIOUS DISEASES: BOLSTERING LAB CAPACITY THROUGH MULTIPLEXING TECHNOLOGIES

Keersten Ricks

Authors: Ricks, Keersten

Affiliation: Diagnostic Systems Division, United States Army Medical Research Institute of Infectious Diseases

Introduction: The spread of infectious disease continues to present a challenge for global force health protection and public health initiatives, as was evidenced by the Ebola outbreak in West Africa, the SARS-CoV-2 pandemic, and the recent mpox outbreak. Access to sustainable tools for pathogen detection and surveillance is critical to stay ahead of potential outbreaks in non-human and human populations. Methods: An integrated, customizable diagnostic system that uses molecular assays in combination with immunodiagnostic methods provides the highest confidence in a diagnostic result. As an example, we present serosurveillance results from a recent observational study screening Malaysian Armed Forces pre and post 90-day deployments to Sabah, Malaysia, where there is high risk of exposure to pathogens causing tropical fevers. Results: Serum samples were screened for seroconversion to Plasmodium spp, arboviruses, and henipaviruses using multiplexed serologic panels from Walter and Eliza Hall Institute (WEHI), USAMRIID, and Uniformed Services University, respectively. The USAMRIID panel screened for exposure to hantaviruses, Crimean-Congo Hemorrhagic Fever virus (CCHFV), tick borne encephalitis virus (TBEV), alphavirus spp., and flavivirus spp. Three samples seroconverted seroconversion for panflavivirus, one borderline seroconverted for HTNV, and one borderline seroconverted for TBEV. We plan to send a flavivirus specific serology panel to further tease out specific IgG responses in the deployed MAF battalions. Conclusion: By developing a sustainable diagnostic program and transitioning these capabilities to our in-country collaborators, we have the best chance rapidly responding to endemic, emerging, and re-emerging tropical infectious diseases.

Keywords: serology, multiplex, capacity building, diagnostic toolbox, biosurveillance

Abstract No.: ABS0002227

SARS-CoV-2 Risk Factors and sero-prevalence in minimally vaccinated individuals in Papaua New Guinea

FRANCIS LELNGEI

Authors: Francis Lelngei

Affiliation: Central Public Health Laboratory, PNG

No abstract

Keyword: No abstract

Wednesday 13 December 2023

S04: Climate Change Impacts on Human Health (SEAMEO TROPMED Network)

10.30-12.00hr

Room C

Wednesday 13 December 2023

S04: Climate Change Impacts on Human Health (SEAMEO TROPMED Network)

10.30-12.00hr

Room C

Chairperson:
1. Pratap Singhasivanon

Invited speaker:

1. VULNERABILITY OF HEALTHCARE FACILITY TO INUNDATION AND SEA LEVEL RISE: A CLIMATE CHANGE SCENARIO IN MALAYSIA
Noraishah Mohammad Sham
Other (Institute for Medical Research (IMR) Malaysia)

2. Heat Strain Score Index Among Hospital Healthcare Workers in Batangas, Philippines and its Association with Level of Cognitive Function
Crystal Amiel Estrada
Other (University of the Philippines Manila College of Public Health)

3. Climate Change and Health Impacts: Thailand Perspectives
Kraichat Tantrakarnapa
Faculty of Tropical Medicine, Mahidol University (Social and Environmental Medicine)

4. Association of ambient temperature with daily non-accidental and cause-specific mortality in a northern state of Malaysia
Rohaida Ismail
Other (Institute for Medical Research, Ministry of Health Malaysia)

5. Addressing Antimicrobial Resistance through the One Health Approach in a Changing Climate
Maria Margarita Lota
Other (Faculty, Department of Medical Microbiology, College of Public Health, University of the Philippines Manila)

Abstract No.: ABS0002174

VULNERABILITY OF HEALTHCARE FACILITY TO INUNDATION AND SEA LEVEL RISE: A CLIMATE CHANGE SCENARIO IN MALAYSIA

Noraishah Mohammad Sham

Authors: Noraishah MS[1], Wan Nurul Farah WA[1], Yannie AB[2] and Rohaida I[1]

Affiliation:[1]Environmental Health Research Centre. Institute for Medical Research, National Institutes of Health, Ministry of Health Malaysia. 40170 Shah Alam, Selangor, Malaysia

[2]Coastal Management and Oceanography Research Centre. National Water Research Institute of Malaysia (NAHRIM). Ministry of Natural Resources, Environment and Climate Change (NRECC). 43300 Seri Kembangan, Selangor, Malaysia

According to National Oceanic and Atmospheric Administration, United States Agency, global mean sea level is projected to increase by at least one foot above 2000 levels by the end of the century although greenhouse gas emissions remain relatively low in the following decades. This study aims to assist healthcare facilities managers by establishing a baseline for climate change resilience in healthcare facilities by prioritizing adaptation methods and reducing the health effects of climate change. The spatial variation of the sea level change is estimated by assimilating the global mean sea level projections from the Atmosphere–Ocean coupled Global Climate Model/General Circulation Model simulations to the satellite altimeter observations along the subject coastlines. Sea level rise projections for the years 2050 and 2100 were produced based on the statistical analysis of the tide gauge data obtained and satellite altimeter data observed along the Malaysian coast. Impact of sea level rise on the healthcare facilities was assessed at 147 hospitals and 1,143 health clinics in Malaysia. The assimilated projections showed that the sea level around the Peninsular Malaysia coastline is projected to rise with a mean in the range of 0.253 m to 0.517 m in 2100. The assessment showed that four hospitals and twenty-nine health clinics were currently prone to SLR and increments of another four and thirty-seven affected hospitals and health clinics by year 2100. As a result, this study might serve as a roadmap for developing strategies to boost stimulatory effects and carry out vulnerability assessments in healthcare facilities.

Keywords: sea level rise; Malaysia; climate projection; healthcare facilities

Abstract No.: ABS0002187

Heat Strain Score Index Among Hospital Healthcare Workers in Batangas, Philippines and its Association with Level of Cognitive Function

Crystal Amiel Estrada

Authors: Alcantara-dela Luna, Jelyne A.[1], Lomboy, Marian Fe Theresa C.[2], Mira, Rachel Nona C.[3], **Estrada, Crystal Amiel M.**[2], Fadrilan-Camacho, Vivien Fe F.[2], Quizon, Romeo R.[2]

Affiliation: [1]College of Public Health, University of the Philippines Manila; [2]Department of Environmental and Occupational Health, College of Public Health, University of the Philippines Manila; [3]College of Nursing, University of the East Ramon Magsaysay Memorial Medical Center

Background: The increasing temperature being recorded globally raises concerns for the health and safety of workers. The Philippines lacks information on the impact of heat strain on cognition, especially among hospital healthcare workers (HCWs). Hence, this study aims to determine the association between heat strain score index and level of cognitive function among HCWs.

Method: A total of 449 HCWs participated in a cross-sectional study and answered a self-administered online questionnaire. To evaluate the level of heat strain experienced by the participants, the Heat Strain Score Index was utilized while PROMIS Cognitive Function Measure version 2.0 (Adult Short Form 8A) was used to measure the level of cognitive functioning of HCWs. Multiple logistic regression was employed to measure the relationship between the heat strain score index and the level of cognitive function.

Results: The findings revealed that only 11.6% of HCWs were categorized under the alarm and danger levels (2.7%) of the heat strain score index. However, the majority (57.9%) of HCWs were found to have worse cognitive function than the average of the reference population. Lastly, after holding other variables constant, the likelihood of having worse cognitive function increased by 3.6 times when the heat strain of HCWs was at unsafe level.

Conclusion: This study highlights the importance of considering heat strain as a potential contributor to the cognitive function impairment experienced by HCWs suggesting that hospital administrators should review their programs related to occupational health with focus on environmental heat.

Keywords: heat strain, cognitive function, healthcare workers, Philippines

Abstract No.: ABS0002208

Climate Change and Health Impacts: Thailand Perspectives

Kraichat Tantrakarnapa

Authors: Kraichat Tantrakarnapa

Affiliation: Department of Social and Environmental Medicine, Faculty of Tropical Medicine, Mahidol University

Introduction: Climate Change was raised as global issue together with other aspects, influences human health impacts. The risk depends on many factors such as age, health status, socio-economic including topography and location. In Thailand, there are many mentioned impacts from climate change include the physical, biological factors, ecology and human health system.

Method: We downscale the Global Climate Model (GCM) for Thailand for different IPCC scenarios every 10 years period until year 2100. The analysis of extreme event of high temperature and health related disease were analyzed. A two-stage time-series approach was applied to assess the association between non-optimum temperatures and the hospital admission.

Results: Trend of temperature from the current situation period (2021-2030) to 2100 are significantly increased. We observed a J-shaped relationship with the risk of hospital admissions increasing for both cold and hot temperatures. Hot temperatures were responsible for most of the Afs (Attributable Fraction) of hospital admissions, with 6.71% (95% CI: 5.80%, 7.41%) for outpatient visits and 4.50% (95% CI: 3.62%, 5.19%) for inpatient visits.

Conclusion: This study reveals that low and high temperature has a high significant impact on hospital admissions. The current findings could provide evidence for policymakers to development national adaptation measures or strategies and mitigation measures the effects of climate change on health, especially temperature exposure.

Keywords: Climate Change, Health Impacts, Thailand, Global Climate Model

Abstract No.: ABS0002181

Association of ambient temperature with daily non-accidental and cause-specific mortality in a northern state of Malaysia

Rohaida Ismail

Authors: Rohaida Ismail[1], Hadita Sapari[2], Wan Rozita Wan Mahiyuddin[1], Mohamad Rodi Isa[2], Mohamad Ikhsan Selamat[2]

Affiliation: [1]Environmental Health Research Centre, Institute for Medical Research, National Institutes of Health, Ministry of Health Malaysia, Selangor, Malaysia; [2]Department of Public Health Medicine, Faculty of Medicine, Universiti Teknologi MARA, Selangor, Malaysia

Introduction: Many epidemiological studies have provided evidence on the relationship between extreme temperatures with natural cause mortality in temperate-climate countries. However, heat mortality is becoming a global public health concern that particularly relevant for warm climate regions. Thus, this study aimed to examine the association between ambient temperature and non-accidental mortality including cardiovascular and respiratory mortality in a tropical area of Malaysia. Methods: Daily data on meteorology, air pollutants, non-accidental and cause specific mortality during 2011-2020 were obtained for in a northern state of Malaysia. A quasi-Poisson generalized linear regression with a distributed lag non-linear model (DLNM) were applied to estimate the temperature and mortality association. Results: A non-linear U-shaped relationship was found between temperature and mortality with a minimum mortality temperature (MMT) of 28.4°C. High temperature exposure was associated with immediate effect of non-accidental mortality; this had persisted until lag 3 days. Effect estimates are interpreted as the relative risk of mortality when the temperature exposure differs were found to be higher for non-accidental and cause-specific respiratory mortality. For age specific, extreme temperatures exposure increased the risk of mortality among elderly (age more than 65 years old) during hot and cold temperature. Conclusion: These findings indicated that the daily fluctuation of non-accidental and cause-specific respiratory mortality was associated with ambient temperature, and in specific age group. Understanding the relationship would be helpful for stakeholders to efficiently formulate the health management including public health promotion and warning systems for communities.

Keywords: temperature; non-accidental mortality; cardiorespiratory mortality; Malaysia

Abstract No.: ABS0002234

Addressing Antimicrobial Resistance through the One Health Approach in a Changing Climate

Maria Margarita Lota

Authors: Maria Margarita M. Lota

Affiliation: College of Public Health, University of the Philippines Manila (TROPMED Philippines)

No abstract available

Keyword: No abstract available

Wednesday 13 December 2023

S05: Unveiling Host-Parasite Interactions through Mosquito Microbiome

10.30-12.00hr

Room D

Wednesday 13 December 2023

S05: Unveiling Host-Parasite Interactions through Mosquito Microbiome

10.30-12.00hr

Room D

Chairperson:
1. Sirasate Bantuchai
2. Wang Nguitragool

Invited speaker:

1. Understanding and exploiting the microbiome for mosquito control
Grant Hughes
Other (Liverpool School of Tropical Medicine)

2. Curbing malaria: the implication of mosquito microbiota in blocking the Plasmodium parasites
Yuemei Dong
Other (W. Harry Feinstone Department of Molecular Microbiology and Immunology, Bloomberg School of Public Health, Johns Hopkins University)

3. Unraveling the impact of mosquito symbionts on vector-borne disease transmission in a changing world
Panpim Thongsripong
Other (Florida Medical Entomology Laboratory, University of Florida)

Abstract No.: ABS0002235

Understanding and exploiting the microbiome for mosquito control

Grant Hughes

Authors: Grant Hughes

Affiliation: Centre for Neglected Tropical Disease, Liverpool School of Tropical Medicine

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002236

Curbing malaria: the implication of mosquito microbiota in blocking the Plasmodium parasites

Yuemei Dong

Authors: Yuemei Dong

Affiliation: W. Harry Feinstone Department of Molecular Microbiology and Immunology, Bloomberg School of Public Health, Johns Hopkins University

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002145

Unraveling the impact of mosquito symbionts on vector-borne disease transmission in a changing world

Panpim Thongsripong

Authors: Panpim Thongsripong

Affiliation: Florida Medical Entomology Laboratory, University of Florida

The natural distribution and diversity of eukaryotic, microbial, and viral symbionts in mosquitoes, along with their interactions with human activities, remain areas of limited understanding. It is crucial to understand how the mosquito microbiome and virome respond to a changing world, as these microbes, both collectively and individually, have the potential to significantly influence the transmission of vector-borne diseases (VBD) and public health. In this presentation, we exemplify how mosquito symbionts can impact VBD transmission by describing an experiment that investigated the influence of Ascogregarina culicis, a common mosquito-specific Apicomplexan parasite, on Aedes aegypti's fitness and susceptibility to dengue virus infection. Our findings underscore the intricate, yet widespread, relationship between vectors, their symbionts, and pathogens, emphasizing the need for a deeper, comprehensive understanding of how habitats influence mosquito symbionts. Particularly, we question whether human-driven landscape changes can alter the composition of the vector microbiome and virome. Leveraging Next Generation Sequencing and bioinformatic tools, we observed a decrease in diversity within the vector-associated microbiome along a gradient of increasing habitat modification. Conversely, host species emerged as a pivotal factor in shaping the vector's virome. Consequently, anthropogenic habitat changes are likely to exert the greatest influence on the distribution of vector-associated viruses, facilitating the spread of invasive vector species. Collectively, our studies advance the current understanding of the socio-ecological drivers behind disease emergence, with the potential to contribute to a predictive model of infectious disease emergence influenced by human activities and urbanization.

Keywords: symbionts, VBD transmission, Ascogregarina culicis, Aedes aegypti

Wednesday 13 December 2023

S06: Innovative Approaches to Disease Prevention and Control (Thai Language)

10.30-12.00hr

Room E

Wednesday 13 December 2023

S06: Innovative Approaches to Disease Prevention and Control (Thai Language)

10.30-12.00hr

Room E

Chairperson:
1. Benjamaporn Pinyopornpanich
2. Darinda Rosa

Invited speaker:

1. Practical use of Urine RDT for opisthorchiasis screening in upper northestern Thailand
Sasithorn Tangsawad
Other (Office of Disease Prevention and Control 8 Udonthani Department of Disease Control, MOPH)

2. Royal Biosafety Mobile Unit vehicle from COVID-19 to screening and diagnosing Liver cancer and Cholangiocarcinoma with Ultrasound For the quality of life for Thai people
Jutikarn Phukowluan
Other (Division of Communicable Diseases, Department of disease control)

3. IRIS Recognition
Suthat Chottanapund
Other (Institute for Urban Disease Control and Prevention, Department of Disease Control)

4. The Implementation Mechanism to Reduce HIV-Related Stigma and Discrimination in Thailand (Crisis Response System: CRS)
Niwat Suwanphatthana
Other (Stigma and Discrimination Coordinator, UNAIDS Thailand)

5. Development of CRS in Thailand
Siriporn Monyarit
Other (Office of Disease Prevention and Control Region 6 Chonburi, Department of Disease Control, Ministry of Public Health, Thailand)

6. Justice system to Protect Rights Violation and Discriminations
Chantima Thanasawangkul
Other (Senior Public Prosecutor Executive Director’s office of Legal Development Office of Attorney General)

7. A successful establishment of Paralegals as Human Rights Defenders in Thailand
Journee Siriphan
Other (Director of Foundation for AIDS Rights)

Abstract No.: ABS0002312

Practical use of Urine RDT for opisthorchiasis screening in upper northestern Thailand

Sasithorn Tangsawad

Authors: Sasithorn Tangsawad

Affiliation: Office of Disease Prevention and Control 8 Udonthani Department of Disease Control, MOPH

No abstract available

Keywords: No abstract available

Abstract No.: ABS0002247

Royal Biosafety Mobile Unit vehicle from COVID-19 to screening and diagnosing Liver cancer and Cholangiocarcinoma with Ultrasound For the quality of life for Thai people

Jutikarn Phukowluan

Authors: Jutikarn Phukowluan

Affiliation: Division of Communicable Diseases, Department of disease control tigma and Discrimination Coordinator, UNAIDS Thailand

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002244

IRIS Recognition

Suthat Chottanapund

Authors: Suthat Chottanapund

Affiliation: Institute for Urban Disease Control and Prevention, Department of Disease Control

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002313

The Implementation Mechanism to Reduce HIV-Related Stigma and Discrimination in Thailand (Crisis Response System: CRS)

Niwat Suwanphatthana

Authors: Niwat Suwanphatthana

Affiliation: Stigma and Discrimination Coordinator, UNAIDS Thailand

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002238

Development of CRS in Thailand

Siriporn Monyarit

Authors: Siriporn Monyarit

Affiliation: Office of Disease Prevention and Control Region 6 Chonburi, Department of Disease Control, Ministry of Public Health, Thailand

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002241

Justice system to Protect Rights Violation and Discriminations

Chantima Thanasawangkul

Authors: Chantima Thanasawangkul

Affiliation: Senior Public Prosecutor Executive Director’s Office of Legal Development Office of Attorney General

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002242

A successful establishment of Paralegals as Human Rights Defenders in Thailand

Jarunee Siriphan

Authors: Jarunee Siriphan

Affiliation: Director of Foundation for AIDS Rights

No abstract available

Keyword: No abstract available

Wednesday 13 December 2023

Vector-borne diseases identification and quantification vectored by mosquitoes using the QIAcuity DigitalPCR System and qPCR by QIAGEN and Biodesign

12.00-13.00hr

Room E

Wednesday 13 December 2023

Vector-borne diseases identification and quantification vectored by mosquitoes using the QIAcuity DigitalPCR System and qPCR by QIAGEN and Biodesign

12.00-13.00hr

Room E

Chairperson: -

Invited speaker:

-

Wednesday 13 December 2023

S07: Road to Zero Death in Dengue: A Call for Action

13.45-15.15hr

Room A

Wednesday 13 December 2023

S07: Road to Zero Death in Dengue: A Call for Action

13.45-15.15hr

Room A

Chairperson:
1. Nattachai Srisawat
2. Usa Thisyakorn

Invited speaker:

1. RECENT ADVANCES IN DENGUE MANAGEMENT: A FOCUS ON FLUID MANAGEMENT
NGUYEN TRONG PHU TRAN
Other (Tropical Medicine Cluster - Chulalongkorn University)

2. Novel biomarkers to predict severe dengue.
Umaporn Limothai
Other (chulalongkorn university)

3. Dengue vaccine: an update
Pope Kosalaraksa
Other (Department of Pediatrics, Faculty of Medicine, Khon Kaen University)

Abstract No.: ABS0002131

RECENT ADVANCES IN DENGUE MANAGEMENT: A FOCUS ON FLUID MANAGEMENT

NGUYEN TRONG PHU TRAN

Authors: PHU NGUYEN TRONG TRAN[12], NATTACHAI SRISAWAT[1-6]

Affiliation: [1]Tropical Medicine Cluster, Chulalongkorn University, Bangkok, Thailand; [2]Faculty of Medicine, Chulalongkorn University; [3]Excellence Center for Critical Care Nephrology, King Chulalongkorn Memorial Hospital, Bangkok, Thailand; [4]Critical Care Nephrology Research Unit, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand; [5]Center for Critical Care Nephrology, The CRISMA Center, Department of Critical Care Medicine, University of Pittsburgh, School of Medicine, Pittsburgh, PA, USA; [6]Academy of Science, Royal Society of Thailand, Bangkok, Thailand.

Introduction: While most cases of dengue are self-limiting or present with mild symptoms, the concern over severe dengue persists. Supportive care plays a pivotal role in managing severe dengue, with a primary focus on fluid management.

Methods: This narrative review explores the current literature concerning recent advancements in fluid management for dengue infection.

Results: While the 2009 WHO guideline has gained widespread acceptance as standard practice, its fluid management protocol lacks robust supporting evidence. Little new evidence has emerged to inform the development of an updated guideline. Several controversies surrounding fluid resuscitation in severe cases, including the optimal choice of crystalloid fluids, the role of colloids in preventing and resuscitating shock, and the use of fluid boluses, among other questions, require attention. Novel insights into fluid management for dengue may arise from the study of critically ill patients, especially those with sepsis. The results of the FEAST trial have led to a revised WHO recommendation, advocating for the use of smaller volumes of fluid administered over longer periods for resuscitating children. Buffered solutions had been endorsed over normal saline in recent Sepsis guidelines, yet recent important evidence (PLUS, BaSICs and an updated meta-analysis of randomized trials) found insignificant difference in mortality and other secondary outcomes. The role of colloid fluids, particularly albumin, has been found to be not superior to crystalloids (CRISTAL, CHEST, CRYSTMAS, 6S-trial, and ALBIOS), yet they might have a reparative effect on the glycocalyx layer. However, generalizing these findings to severe dengue management should be done cautiously, considering the

Keywords: dengue, fluid management

Abstract No.: ABS0002142

Novel biomarkers to predict severe dengue.

Umaporn Limothai

Authors: Umaporn Limothai[1-3], Nattachai Srisawat[1-3]

Affiliation:[1]Tropical Medicine Cluster, Chulalongkorn University, Bangkok, Thailand.; [2]Excellence Center for Critical Care Nephrology, King Chulalongkorn Memorial Hospital, Bangkok, Thailand.; [3]Center of Excellence in Critical Care Nephrology, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand.

Introduction: Early predictive biomarkers of severe complications may improve case management, reduce unnecessary hospital admissions, and lower dengue-related mortality. This study aimed to identify novel early predictors associated with progression to severe dengue.

Methods: Narrative review of current literature.

Results: Various host and viral factors have been studied to identify biomarkers of severe dengue disease. Recent breakthroughs in omics approaches and machine learning algorithms enabling the discovery of novel clinically usable biomarkers such as a combination of gene expression markers and microRNAs. However, its performance in a large and diverse prospective cohort remains unknown.

Conclusion: Many novel promising biomarkers for predicting severe dengue were identified. It is crucial to test the feasibility, utility, performance, and validity of these biomarkers before implementing them in routine clinical care.

Keywords: severe dengue, predictive biomarker, omics approaches

Abstract No.: ABS0002248

Dengue vaccine: an update

Pope Kosalaraksa

Authors: Pope Kosalaraksa

Affiliation: Department of Pediatrics, Faculty of Medicine, Khon Kaen University

No abstract available

Keyword: No abstract available

Wednesday 13 December 2023

S08: Free Paper I: Malaria

13.45-15.15hr

Room B

Wednesday 13 December 2023

S08: Free Paper I: Malaria

13.45-15.15hr

Room B

Chairperson:
1. Nicholas Day
2. Pyae Linn Aung

Invited speaker:

1. ASSESSING RECEPTIVITY TO MALARIA USING CASE SURVEILLANCE AND FOREST DATA IN A NEAR-ELIMINATION SETTING IN NORTHEAST THAILAND
Rebecca Walshe
Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

2. INTERACTIVE GENETIC EPIDEMIOLOGY TOOLS FOR SURVEILLANCE OF DRUG-RESISTANT MALARIA PARASITE STRAINS
Ethan Booth
Other (Mahidol Oxford Research Unit)

3. COMPARATIVE ANALYSIS OF MACHINE LEARNING AND TIME SERIES MODELS IN FORECASTING MONTHLY MALARIA INCIDENCE IN GOA, INDIA
Syed Shah Areeb Hussain
Other (ICMR - National Institute of Malaria Research)

4. MALARIA VECTOR IDENTIFICATION USING CONVOLUTIONAL NEURAL NETWORKS MODEL
Peeyush Mittal
Other (Indian Council of Medical Research- National Institute of Malaria Research, India)

5. THE AGREE TRIAL TO REDUCE PRETERM BIRTH IN KENYAN WOMEN AT RISK OF MALARIA IN PREGNANCY
Kevin Kain
Other (University of Toronto, UHN-Toronto General Hospital)

6. Population genomics and transcriptomics of Plasmodium falciparum in Cambodia and Vietnam uncover key components of the artemisinin resistance genetic background
Zbynek Bozdech
Other ()

Abstract No.: ABS0002086

ASSESSING RECEPTIVITY TO MALARIA USING CASE SURVEILLANCE AND FOREST DATA IN A NEAR-ELIMINATION SETTING IN NORTHEAST THAILAND

Rebecca Walshe

Authors: Walshe R[1], Pongsoipetch K[2], Mukem S[2], Sudathip P[3], Kitchakarn S[3], Maude RR[1], Maude **RJ**[2,4]

Affiliation:[1]Faculty of Medicine, Ramathibodi Hospital, Mahidol University, Bangkok, Thailand; [2]Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [3]Division of Vector Borne Diseases, Department of Disease Control, Tiwanond Road, Nonthaburi 11000 Thailand; [4]Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, UK

Introduction: Thailand aims to eliminate malaria by 2024. Understanding the receptivity of local areas to malaria allows the appropriate targeting of interventions. Forest coverage is known to be associated with malaria risk, as an environment conducive to both vector breeding and high-risk human behaviours.

Methods: Geolocated, anonymized, individual-level surveillance data from 2011- 2021 from the Thai DVBD was used to calculate incidence and estimated Rc at village level. Forest cover was calculated using raster maps of tree crown cover density and year of forest loss from the publicly available Hansen dataset. Incidence and forest cover were compared graphically and using spearman's rho. The current foci classification system was applied to the last 5 years (2017-2021) and forest cover compared between the classifications. A simple risk score was developed to identify villages with high receptivity.

Results: Indigenous Annual Parasite Index (API) and approximated Rc were higher in villages in highly forested subdistricts, and with higher forest cover within 5km. Forest cover was also higher in malaria foci which consistently reported malaria cases each year than those which did not.

Conclusion: There was a positive association between forest coverage around a village and indigenous malaria cases. Most local transmission was seen in the heavily forested subdistricts on the international borders with Laos and Cambodia, which are where the most receptive villages are located. These areas are at greater risk of importation of malaria due to population mobility and forest-going activities. Combining forest cover and recent case surveillance data with measures of vulnerability may

Keywords: Receptivity, Malaria, Transmission, Indigenous, Surveillance, Forest

Abstract No.: ABS0002040

INTERACTIVE GENETIC EPIDEMIOLOGY TOOLS FOR SURVEILLANCE OF DRUG-RESISTANT MALARIA PARASITE STRAINS

Ethan Booth

Authors: Ethan Booth[1], Varanya Wasakul[1], Tess Verschuuren[1], Olivo Miotto[1,2]

Affiliation: [1]Mahidol-Oxford Tropical Medicine Research Unit, Mahidol University, Bangkok, Thailand; [2]Nuffield Department of Medicine, University of Oxford, Oxford, UK.

Introduction: The rapid emergence and spread of drug-resistant malaria threaten elimination efforts in the Greater Mekong Subregion (GMS). The GenRe-Mekong project, in collaboration with National Malaria Control Programs (NMCPs), conducts genetic surveillance of Plasmodium falciparum to monitor drug resistance in the GMS. Translating the generated genetic data into graphic outputs easily interpreted by NMCPs requires extensive analyses, posing a major challenge that demands powerful and intuitive tools.

Methods: We developed the grcMalaria package for genetic analyses and drug resistance mapping using the R language. The package processes standardized genetic surveillance data, as defined by the SpotMalaria Data Dictionary, using public-domain libraries and data sources. Its companion Web-based interface is based on the R Shiny platform, allowing interactive usage of the R package without requiring programming knowledge.

Results: The grcMalaria package turns genotyping data into intuitive geographical maps of drug resistance, allele prevalence, diversity, and relatedness with minimal coding. It also provides clustering analyses that identifies and maps genetically similar strains. Furthermore, the grcMalaria Web application provides easy-to-use access to key features of grcMalaria, bypassing the need for R installation and scripting.

Conclusion: The grcMalaria R package and web application offer easy access to crucial information on the spread of drug-resistant parasite strains, and help predict changes in drug efficacy at regional, national, provincial and district levels. These tools render genetic epidemiological analysis accessible and allow NMCPs to integrate and contextualize their findings within broader regional analyses, strengthening future elimination strategies.

Keywords: Plasmodium falciparum, Antimalarial Resistance, Genetic data, Data visualization, R language, Shiny

Abstract No.: ABS0002078

COMPARATIVE ANALYSIS OF MACHINE LEARNING AND TIME SERIES MODELS IN FORECASTING MONTHLY MALARIA INCIDENCE IN GOA, INDIA

Syed Shah Areeb Hussain

Authors: Hussain SSA

Affiliation:
1. ICMR - National Institute of Malaria Research;
2. Academy of Scientific and Innovative Research;
3. Indian Institute of Technology, Delhi;
4. ICMR - National Institute of Cancer Prevention and Research;
5. International Centre for Genetic Engineering and Biotechnology

Introduction: As we move towards malaria elimination in India, forecasting malaria incidence has compelling public health significance for effective resource allocation. Therefore, in this study the comparative performance of several machine learning and time-series models was assessed, for forecasting case incidence under the changing scenario of malaria in Goa, India.

Methods: Monthly maximum, minimum and average of five meteorological variables -temperature, rainfall, relative humidity, pressure, and wind speed, were used to forecast malaria in Goa. SHAP analysis was conducted to identify the most relevant predictors. Three machine learning models (Support vector machines, Random Forest and XGBoost) and four types of time series models (exponential smoothening, ARIMA, SARIMA and SARIMAX) were trained using data from 2010-2020. Forecasts were made for the year 2021, and validated against the actual case incidence. An additional machine learning model was also trained which incorporated time-series variables from ARIMA models.

Results: The three machine learning models produced more precise results with low confidence intervals but lacked accuracy (RMSE=24.28-80.79) as they were not able to account for the decreasing trend in malaria incidence. In contrast, the time series models (in particular the ARIMA models) produced significantly more accurate results (RMSE=1-6.06), but with low precision i.e. high confidence intervals. Adding time series variables as additional predictors in machine learning models significantly improved their accuracy (RMSE=1.6-8.4) while preserving the high precision of these models.

Conclusion: Combining time-series terms within machine learning models can incorporate the best of both worlds and significantly improve forecasting accuracy and precision.

Keywords: Malaria, Machine Learning, Time-Series Modelling, Forecasting, India

Abstract No.: ABS0002081

MALARIA VECTOR IDENTIFICATION USING CONVOLUTIONAL NEURAL NETWORKS MODEL

Peeyush Mittal

Authors: Peeyush[1,2] , Hussain SSA[1,2] Suchi Tyagi[1,2], Himmat Singh[1,2]

Affiliation:[1]ICMR-National Institute of Malaria Research; [2]Academy of Scientific and Innovative Research

Introduction: Recent advances in AI/ML, show great potential in forecasting diseases, Species and non-invasive diagnostics in Vector Borne Diseases. In India, thousands of mosquitoes are collected for entomological studies. However, morphological identification of these vectors is tedious, time consuming and error prone. In this study Convolutional neural network (CNN) was used to build a compact on-site tool for easy, fast and accurate species identification.

Methods: Model was trained using, high quality images of mosquitoes captured using Digital and Mobile cameras (total 296) attached to dissection microscope. Captured images of Indian malaria and dengue vectors were fed to CNN models. Model was trained for binary identification of An. Stephensi against other mosquito species in python. Images were resized to 256x256 and 16 2D CNN layers with 20 epochs were used to train model on the dataset.

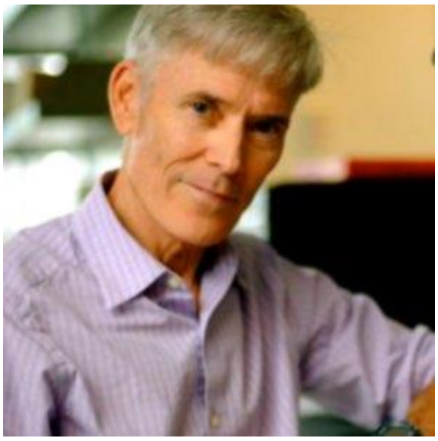
Resuls: Precision, recall and accuracy of trained CNN model was 1 indicating model was trained perfectly. Model performance was tested using 5 images withheld from the training dataset and 5 images obtained from online datasets. The trained model identified An. stephensi 6 times with an overall accuracy of 60%. The model showed 80% accuracy for withheld dataset which consisted of higher resolution images and similar background/lighting features. in contrast accuracy of identification in online dataset which had more diverse features was only 40%.

Conclusion: The CNN model performs well for datasets with similar features, but needs to be trained with more diverse datasets for improving accuracy for images captured in the field, with more diverse features.

Keywords: Malaria, Anopheles, Artificial Intelligence, Mosquito Identification.

Abstract No.: ABS0002185

THE AGREE TRIAL TO REDUCE PRETERM BIRTH IN KENYAN WOMEN AT RISK OF MALARIA IN PREGNANCY



Kevin Kain

Authors: Kevin Kain[1,2], Julie Wright[1,2], Hellen Barsosio[3], Feiko ter Kuile[3,4]

Affiliation: [1]Sandra A. Rotman Laboratories, Sandra Rotman Centre for Global Health, UHN-Toronto General Hospital, Toronto, ON, Canada; [2]Tropical Disease Unit, Division of Infectious Diseases, Department of Medicine, University of Toronto, Toronto, Ontario, Canada; [3]KEMRI Centre for Global Health Research (CGHR), Kisumu, Kenya; [4]Liverpool School of Tropical Medicine, UK

Introduction: Preterm birth (PTB) is the leading cause of death in children under-five globally. 14.9 million babies are born preterm each year, with one million dying in their 1st month of life. PTB is also a leading cause of long-term physical, neurodevelopmental, and socioeconomic impact in survivors. 80% of PTB cases occur in Asia and sub-Saharan Africa. Infections during pregnancy are risk factors. The mechanisms underlying PTB are unclear and there has been no decrease in PTB in the last decade. SDGs cannot be achieved without addressing PTB.

Methods: We hypothesized that common infections lead to sequential disruptions of inflammatory and angiogenic pathways that result in placental vascular insufficiency and PTB. Moreover, that low L-arginine-nitric oxide bioavailability increases this risk. We conducted analyses of inflammatory, angiogenic, and markers of L-arginine-NO bio-availability across pregnancy in multiple studies of women in sub-Saharan Africa.

Results: Women with inflammatory markers (e.g., sTNFR2) in the highest quartile before 24 weeks and women with anti-angiogenic factors (e.g., sEndoglin) in the highest quartile at 28–33 weeks had an increased relative risk of PTB. Low levels of bioavailable L-arginine were associated with altered inflammatory and angiogenic pathways.

Conclusion: Our studies support the hypothesis that dietary L-arginine or L-citrulline (which converts into L-arginine in vivo) may reduce PTB. This sets the stage for the AGREE trial now starting in Kenya: RDBPC trial of L-citrulline vs placebo in 2960 pregnant women. Primary endpoint: reduce adverse birth outcomes by 25% RRR; Secondary endpoints: reduce neonatal sepsis, pre-eclampsia; and neurocognitive deficits.

Keywords: Malaria, Malaria in pregnancy, SDGs, preterm birth, adverse birth outcomes

Abstract No.: ABS0002203

Population genomics and transcriptomics of Plasmodium falciparum in Cambodia and Vietnam uncover key components of the artemisinin resistance genetic background

Zbynek Bozdech

Authors: Zbynek Bozdech

Affiliation: Nanyang Technological University, Singapore

The emergence and spread of Plasmodium falciparum lineages resistant to artemisinins is threatening the efficacy of Artemisinin Combination Therapies (ACTs), the global first-line treatment for falciparum malaria. Artemisinin resistance is a complex genetic trait in which nonsynonymous SNPs in PfK13 cooperate with other, currently unknown, genetic variations to mediate the resistance phenotype. To identify these new molecular factors, we carried out population genomic/transcriptomic analyses of P. falciparum collected from patients with uncomplicated malaria in Cambodia and Vietnam between 2018 and 2020. GWAS confirmed the strong association of mutations in PfK13, in particular C580Y, with artemisinin resistance, but also uncovered significant associations with several additional polymorphisms, including PfRad5 in which two nonsynonymous mutations (N1131I and N821K) were independently associated with artemisinin resistance since its emergence. In addition, an intronic SNP in the gene encoding a WD40 repeat-containing protein on chromosome 11 (PfWD11) was associated. Population transcriptome analyses revealed a defined set of genes whose steady-state levels of mRNA and/or alternatively spliced or antisense transcripts correlated with artemisinin resistance. Using transcriptomics of sequential parasite samples after the start of ACT treatment, we also characterized in vivo transcriptional responses to artemisinins and demonstrated the capacity of the resistant parasites to decelerate their intraerythrocytic developmental cycle, which can contribute to the resistant phenotype. During this process, both PfRAD5 and PfWD11 appear to upregulate an alternatively spliced isoform suggesting a contribution to the protective response to artemisinins. Comparison with historical samples indicated that PfRad5 and PfWD11 have been under selective pressure since the emergence of artemisinin resistance in the Greater Mekong Subregion as covariates of PfK13. Hence both genes now represent new high-confidence markers presumably as the key elements of the artemisinin resistance genetic background.

Keywords: Plasmodium falciparum, Cambodia and Vietnam, artemisinin resistance

Wednesday 13 December 2023

S09: Evolution, Transmission, and Vaccination of Hand, Foot, and Mouth Disease

13.45-15.15hr

Room C

Wednesday 13 December 2023

S09: Evolution, Transmission, and Vaccination of Hand, Foot, and Mouth Disease

13.45-15.15hr

Room C

Chairperson:
1. Weerawan Hattasingh
2. Supawat Chatchen

Invited speaker:

1. Evolution of Enterovirus Variants Associated with Hand, Foot, and Mouth Disease Outbreaks in Thailand
Yong Poovorawan
Other (Faculty of Medicine, Chulalongkorn University)

2. Tracking Transmission of Enterovirus Causing Hand, foot, and mouth disease (HFMD) in a Kindergarten-Based Setting in Bangkok
Supawat Chatchen
Faculty of Tropical Medicine, Mahidol University (Tropical Pediatrics)

3. Efficacy and safety of Enterovirus 71 vaccine in young children
Tawee Chotpitayasunondh
Other (President, Pediatric Infectious Disease Society of Thailand)

Abstract No.: ABS0002192

Evolution of Enterovirus Variants Associated with Hand, Foot, and Mouth Disease Outbreaks in Thailand

Yong Poovorawan

Authors: Yong Poovorawan, Jiratchaya Puenpa

Affiliation: Center of Excellence in Clinical Virology, Faculty of Medicine Chulalongkorn University

Infection associated with human enterovirus (EV) can be asymptomatic or result in a wide range of symptoms from mild to severe. EV infection disproportionately affects children

Keywords: Enterovirus, Hand, Foot, and Mouth Disease, Thailand

Abstract No.: ABS0002134

Tracking Transmission of Enterovirus Causing Hand, foot, and mouth disease (HFMD) in a Kindergarten-Based Setting in Bangkok

Supapawat Chatchen

Authors: Chatchen S[1], Sittikul P[1], Yodsawat P[1,2], Nuanpirom J[1,2], Kosoltanapiwat N[1], Batty EM[1,3], Sangket U[2], and Thaipadungpanit J[1,3]

Affiliation: [1]Mahidol University; [2]Prince of Songkla University; [3]University of Oxford

Introduction: Hand, foot, and mouth disease (HFMD) is caused by single positive-stranded RNA viruses in the Enteroviruses genus. It is highly transmissible among children less than five years old. Enterovirus A71 (EV-A71) and coxsackievirus are significant causes of epidemic HFMD worldwide, especially in children aged from birth to five years old. The outbreaks are seasonally reported in kindergartens worldwide, including in Thailand. We conducted a prospective cohort study of children attending five kindergartens during 2019 and 2020. We used molecular genetic techniques to investigate the characteristics of the spreading patterns of HFMD in a school-based setting in Bangkok, Thailand.

Methods: Enterovirus clusters were identified by partial 5' UTR sequencing analysis as a low-resolution preliminary grouping tool. The Sequence-Independent, Single-Primer Amplification (SISPA) was performed. The portable Oxford Nanopore Sequencing Technology was used. We used the ligation, PCR-free, multiplexing native barcode kit and MinION in WGS. Finally, WGS data were analyzed using long-read bioinformatics tools.

Results and Conclusion: We identified 22 index cases of HFMD (symptomatic infections) and 25 cases of enterovirus-positive asymptomatic contacts. EV-A71 was the most common enterovirus detected, and most of the infected persons (8/12) developed symptoms. Other enteroviruses included coxsackieviruses (CVs) A4, CV-A6, CV-A9, and CV-A10 as well as echovirus. Two occurrences of a single clone causing an infection cluster were identified (EV-A71 C1-like subgenotype and coxsackievirus A6). Random amplification-based sequencing using MinION (Oxford Nanopore Technology) helped identify viral transmission between two closely related clones. Surveillance of highly contagious enterovirus in communities is essential for disease notifications and Controls.

Keywords: Enterovirus, whole genome sequencing, Oxford Nanopore Technology, MinION, SISPA

Abstract No.: ABS0002249

Efficacy and safety of Enterovirus 71 vaccine in young children

Tawee Chotpitayasunondh

Authors: Tawee Chotpitayasunondh

Affiliation: Queen Sirikit National Institute of Child Health

No abstract available

Keyword: No abstract available

Wednesday 13 December 2023

S10: Updates on P. knowlesi Research

13.45-15.15hr

Room D

Wednesday 13 December 2023

S10: Updates on P. knowlesi Research

13.45-15.15hr

Room D

Chairperson:
1. Wang Nguitragool

Invited speaker:

1. Prevalence of simian malaria in long-tailed macaques of Peninsular Malaysia
Yee Ling Lau
Other (Universiti Malaya)

2. UNVEILING THE ANTHROPOZOONOTIC POTENTIAL: HUMAN-TO-ANOPHELES DIRUS MOSQUITO TRANSMISSION OF PLASMODIUM KNOWLESI MALARIA THROUGH MEMBRANE FEEDING ASSAY
Sirasate Bantuchai
Faculty of Tropical Medicine, Mahidol University (Mahidol Vivax Research Unit (MVRU))

3. ADAPTATION of PLASMODIUM KNOWLESI TO INVADE DUFFY-NEGATIVE ERYTHROCYTES
Wang Nguitragool
Faculty of Tropical Medicine, Mahidol University (Molecular Tropical Medicine and Genetics)

4. Reassessing merozoite invasion processes using Plasmodium knowlesi
Robert Moon
Other (London School of Hygiene & Tropical Medicine)

Abstract No.: ABS0002195

Prevalence of simian malaria in long-tailed macaques of Peninsular Malaysia

Yee Ling Lau

Authors: Amirah Amir[1]*, Shahhaziq Shahari[1], Mohd Lutfi Abdullah[2], Jeffrine J. Rovie-Ryan[2], Georges Snounou[3], **Yee-Ling Lau**[1]

Affiliation: [1]Department of Parasitology, Faculty of Medicine, University Malaya, 50603 Kuala Lumpur, Malaysia; [2]National Wildlife Forensic Laboratory, Ex-situ Conservation Division, Department of Wildlife and National Parks Peninsular Malaysia, 56100 Kuala Lumpur, Malaysia; [3]CEA-Université Paris Sud 11-INSERM U1184, Immunology of Viral Infections and Autoimmune Diseases (IMVA) IDMIT Department IBFJ DRF, Fontenay-aux-Roses, France

Malaria is one of the deadliest human parasitic diseases causing an estimated 409000 deaths in 2019 (WHO, 2020). There has been recent interest in zoonotic malaria as an emerging disease as we observe a rise in the number of knowlesi malaria cases together with the recent discovery of cynomolgi and inui malaria in humans in southeast asia. However, very little is known about the epidemiology of simian malaria amongst its natural host, the macaques. In this study, we determined the prevalence of simian malaria infection in wild long tailed macaques from Peninsular Malaysia. Blood samples from wild macaques were collected by the Department of Wildlife and National Parks Peninsular Malaysia. The samples were subjected to nested PCR (targeting the Plasmodium small subunit ribosomal RNA (18S rRNA) gene). A total of 410 macaques from 12 states were sampled. More than half (49.8%) of the sampled macaques tested positive for malaria. Majority (93.9%) of the infected macaques were infected with more than one Plasmodium species. Wild macaques in Pahang had the highest prevalence of malaria (100%), followed by Johor (54.4%), Terengganu (52.5%), Selangor (49.2%), Kelantan (48.4%), Perak (25.7%), Perlis (16.7%), Negeri Sembilan (5.3%). Wild macaques from Melaka, Kedah, Putrajaya and Wilayah Persekutuan were negative for malaria. Overall, Plasmodium inui was the most prevalent species infecting the macaques followed by P. fieldi, P. cynomolgi, P. coatneyi, and P. knowlesi. Studies to ascertain the vectors for simian malaria and their bionomics should also be done in these areas to evaluate the risk of zoonotic

Keyword: transmission to humans. This would be useful for the planning of simian malaria control strategies in the future.

Keywords: simian malaria, macaque, zoonosis, Plasmodium)

Abstract No.: ABS0002173

UNVEILING THE ANTHROPOZOONOTIC POTENTIAL: HUMAN-TO-ANOPHELES DIRUS MOSQUITO TRANSMISSION OF PLASMODIUM KNOWLESI MALARIA THROUGH MEMBRANE FEEDING ASSAY

Sirasate Bantuchai

Authors:

Affiliation: [1]Mahidol Vivax Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand; [2]Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand; [3]Department of Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand.

Malaria remains to be a significant disease and the goal of eradication faces new challenges. In Thailand there has been a surge in zoonotic Plasmodium knowlesi malaria, and incidents have been reported in individuals who have not had prior exposure to the forest in endemic regions. This suggests that there may have been a shift from animal-to-human as in anthropozoonotic change in the transmission of knowlesi malaria in Thailand. To investigate this possibility, we explored the transmission dynamics by using a direct membrane feeding assay to infect Anopheles dirus colony with P. knowlesi infected blood. Nested-PCR assay was employed for species identification. Two oocysts were detected from two mosquitoes including the detection of sporozoites in the salivary glands. These findings warrant additional investigation such as controlled human malaria infection studies to better understand the transmission dynamics of P. knowlesi in Thailand

Keywords: Plasmodium knowlesi, mosquito infection, membrane feeding assay, anthropozoonotic, anopheles dirus

Abstract No.: ABS0002226

ADAPTATION of PLASMODIUM KNOWLESI TO INVADE DUFFY-NEGATIVE ERYTHROCYTES

Wang Nguitragool

Authors: Zinga M[1,2], Mohring F[3], Chainarin S[4], Ibrahim A[3], Ngernna S[1] Turkiewicz A[3], Campino S[3], Clark TG[3,5], Miao J[6], Cui L[6], Roobsoong W[4], Sattabongkot J[4], Moon R[3*], and Nguitragool W[1,4*]

Affiliation: [1]Department of Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol University, Thailand; [2]Department of Medical Parasitology, Catholic University of Health and Allied Sciences, Tanzania; [3]Department of Infection Biology, Faculty of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, UK; [4]Mahidol Vivax Research Unit, Faculty of Tropical Medicine, Mahidol University, Thailand; [5]Department of Infectious Disease Epidemiology, Faculty of Epidemiology and Population Health, London School of Hygiene and Tropical Medicine, UK; [6]Department of Internal Medicine, Morsani College of Medicine, University of South Florida, USA

Plasmodium knowlesi, a zoonotic malaria species, has become a significant public health concern in Southeast Asia. Despite progress in eliminating other human malaria parasites in Malaysia and southern Thailand, *P. knowlesi* cases have surged. Like *Plasmodium vivax*, *P. knowlesi* relies on Duffy-Antigen Receptor for Chemokine (DARC) in invading human erythrocytes and is thought to affect only Duffy-positive individuals. However, our current research demonstrates *P. knowlesi*\'s surprising invasion adaptability. We found that this parasite can overcome its dependence on DARC, adapting in lab conditions to invade and replicate within Duffy-negative (Fy-) erythrocytes. This adaptation, unrelated to DARC binding, remains stable and unaffected by α-DARC antibodies. Genomic analysis revealed a recombination between the parasite\'s similar genes, dbpα and dbpγ, creating a new chimeric gene. Through targeted genetic reversal, we confirmed its necessity for invading Duffy-negative erythrocytes. This discovery sheds light on *P. knowlesi*\'s invasion plasticity, vital for understanding its potential transmission beyond Southeast Asia and the intricate host cell tropism of *P. vivax*. This insight into atypical invasion pathways holds significance for malaria research and potential future interventions.

Keywords: Duffy, *Plasmodium knowlesi*, *Plasmodium vivax*, invasion, malaria

Abstract No.: ABS0002177

Reassessing merozoite invasion processes using *Plasmodium knowlesi*

Robert Moon

Authors: Melissa N Hart [1, 2], Franziska Mohring[1], Sophia M DonVito[1], James A Thomas[1], Nicole Muller-Sienerth[3], Gavin J Wright[3, 4], Ellen Knuepfer[2, 5], Osamu Kaneko[6], Helen R Saibil[7], Moritz Treeck[5], Kazuhide Yahata [6, 8], Robert W Moon[1]

Affiliation: [1]London School of Hygiene & Tropical Medicine; [2]Royal Veterinary College; [3]Wellcome Trust Sanger Institute; [4]University of York; [5]The Francis Crick Institute; [6]Nagasaki University; [7]Birkbeck; [8]Ehime University

The adaptation of P. knowlesi (Pk) to culture in human erythrocytes presents exciting opportunities to study erythrocyte invasion biology. Two major protein families have been studied extensively in P. falciparum (Pf): the erythrocyte binding-like proteins (EBPs/EBAs) and the reticulocyte binding-like proteins (RBLs/RHs). These proteins are hypothesized to have overlapping but critical roles during the invasion process. In Pk, the protein repertoire is smaller, comprising one EBL (DBPa) and one RBL (NBPXa),) that are both essential for invasion of human erythrocytes. We leverage the unique biological features of Pk, where merozoites are twice the size of Pf and have an elongated polarized shape. Using live microscopic analysis, our aim is to gain a deeper understanding of the distinct invasion stages and the roles of the PkEBP/RBL families in this process.

Employing a conditional DiCre approach, we\'ve demonstrated distinct roles for the two families at different invasion stages, including a specific role for RBL proteins in the initial identification and deformation of target host erythrocytes. Furthermore, we\'ve unearthed new features that prompt a significant reassessment of invasion. Notably, we\'ve discovered that Pk merozoites can engage in productive gliding motility prior to invasion, and we\'ve corrected a longstanding assumption in merozoite topology – the merozoite apex is actually located in the wider end of the cell, contrary to prior beliefs. These findings unveil new aspects of this complex process and introduce fresh tools and techniques to deepen our understanding of invasion across all malaria parasite species.

Keywords: P. knowlesi, erythrocyte, invasion, genome-editing, motility

Wednesday 13 December 2023

S11: Applications of AI-based Mathematical Modeling in Health Science Research

13.45-15.15hr

Room E

Wednesday 13 December 2023

S11: Applications of AI-based Mathematical Modeling in Health Science Research

13.45-15.15hr

Room E

Chairperson:
1. Wirichada Pan-ngum
2. Sompob Saralamba

Invited speaker:

1. EARLY WARNING SYSTEMS FOR MALARIA OUTBREAKS IN THAILAND: AN ANOMALY DETECTION APPROACH
Oraya Srimokla
Other (University of Oxford)

2. Studying a Mathematical Model for the 5th Wave of Covid-19 Outbreak in Thailand.
PANNATHON KREABKHONTHO
Other (Faculty of Science, Mahasarakham University)

3. ASSESSING THE IMPACTS OF HOUSEHOLD CONTACTS IN COVID-19 TRANSMISSION DYNAMIC MODELING THROUGH SMALL-WORLD NETWORK
Thanagun Dheravijaranaynkul
Other (Chulalongkorn University)

4. PANDEMIC PARAMETERS OPTIMIZATION FROM MODIFIED SEIQR MODEL ON COVID-19 USING DIFFERENTIAL EQUATIONS, NEURAL NETWORKS AND BAYESIAN INFERENCE: THAILAND DATA
Jayakrit Hirisajja
Other (Faculty of Science, Chiang Mai University)

Abstract No.: ABS0002100

EARLY WARNING SYSTEMS FOR MALARIA OUTBREAKS IN THAILAND: AN ANOMALY DETECTION APPROACH

Oraya Srimokla

Authors: Srimokla O[1] , Pan-Ngum W[2,3], Choosri N[4], Saralamba S[2]

Affiliation:[1]University of Oxford; [2]Mahidol-Oxford Tropical Medicine Research Unit; [3]Mahidol University; [4]Chiang Mai University

Background: As malaria remains a persistent health threat, rapid identification of malaria infections and active surveillance tools are essential to achieve malaria elimination in Thailand. Through this study, an anomaly detection system is built as an early warning method for malaria outbreaks in Thailand.

Methods: To capture unusual malaria activity in Thailand, statistical, machine learning, and threshold-based anomaly detection algorithms are developed and compared. A user interface is designed for anomaly detection, allowing the Thai malaria surveillance team to apply anomaly detection algorithms and visualise areas with unusual malaria activity.

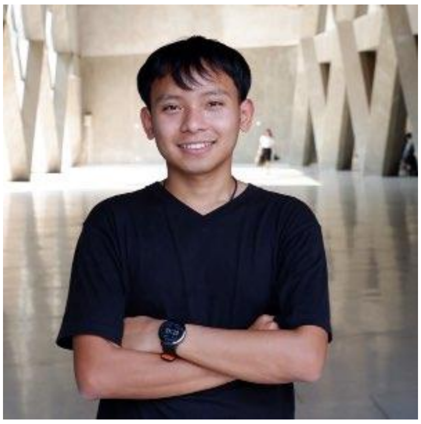
Results: 9 anomaly detection algorithms were developed and their ability to detect verified outbreaks was evaluated using Thai malaria data from 2012 to 2022. The historical average threshold-based method triggered three times fewer alerts, while correctly identifying the same number of verified outbreaks. A limitation present is the small number of verified outbreaks; further consultation with the Division of Vector Borne Disease could help identify more verified outbreaks. The dashboard (https://moru.shinyapps.io/MalariaAnomalyDetectionApp/) allows disease surveillance professionals to easily identify and visualise unusual malaria activity at a provincial level across Thailand.

Conclusion: An improved early warning system is proposed to support malaria elimination in Thailand. Anomaly detection algorithms are developed, compared, and functionalised to easily integrate into the existing malaria surveillance system. An anomaly detection dashboard for Thailand is built and supports early detection of abnormal malaria activity. Overall, the proposed early warning system improves identification of provinces with impending outbreaks and can be easily integrated with Thailand's malaria surveillance system.

Keywords: Anomaly, Malaria, Outbreak, Warning

Abstract No.: ABS0002053

Studying a Mathematical Model for the 5th Wave of Covid-19 Outbreak in Thailand.



PANNATHON KREABKHONTHO

Authors: Pannathon Kreabkhontho[1] and Thitiya Theparod[1*]

Affiliation: Mahasarakham University

COVID-19 is a disease that spreads from person to person. In Thailand, there has been an outbreak of the COVID-19 Omicron variant in the fifth wave, with a high number of infected individuals. This has prompted researchers to be interested and create a mathematical model. The model consists of various population groups, including the group of individuals at risk of infection, the group of individuals at risk who have been vaccinated, the group of infected individuals, the group receiving treatment in hospitals, the group in ICU care, the group recovering from ICU treatment in hospitals, the group of individuals who have recovered from infection, and the group of individuals who have succumbed to the infection. In our investigation of COVID-19 spread and the effectiveness of vaccination, we determined crucial epidemiological factors, including the endemic equilibrium and the basic reproduction number. We then conduct mathematical and numerical analysis of the model. Our findings indicate that the endemic equilibrium is stable whenever R0>1 and unstable when R0

Keywords: COVID-19, Basic reproduction number, Equilibrium point, Mathematical model

Abstract No.: ABS0002143

ASSESSING THE IMPACTS OF HOUSEHOLD CONTACTS IN COVID-19 TRANSMISSION DYNAMIC MODELING THROUGH SMALL-WORLD NETWORK

Thanagun Dheravijaranaynkul

Authors: Thanagun Dheravijaranayankul

Affiliation: [1]Chulalongkorn University

This study explores the pivotal role of household contacts in COVID-19 transmission dynamics by employing a novel approach that integrates two-layer contact networks and agent-based modeling (ABM). The investigation investigate into the nuances of contact patterns, distinguishing interactions occurring within households (within-household layer) from those taking place between households (across-household layer). Six distinct scenarios are simulated to assess the efficacy of diverse non-pharmaceutical interventions (NPIs).

In the baseline scenario with no interventions, the disease follows expected patterns. In Scenario 1, reducing interactions with individuals outside the household yields a marked reduction in disease transmission. Scenario 2, which focuses on minimizing interactions among household members, also demonstrates effectiveness in reducing disease transmission. Scenarios 3 and 4, similar to Scenarios 1 and 2, respectively, yet involving targeted interventions based on visible symptoms, demonstrate that applying interventions at a later stage results in only modest adjustments in peak infection rates and total fatalities. Scenario 5, characterized by a significant reduction in all interactions, effectively mitigates disease spread.

These findings underscore the paramount significance of early interventions, particularly during the asymptomatic phase of infection, for effectively managing outbreaks. The timely implementation of non-pharmaceutical interventions, especially those geared towards reducing interactions with individuals outside one\'s household, remains a critical strategy in disease control.

Keywords: mathematical modeling, transmission dynamics, COVID-19, small-world network, household contact

Abstract No.: ABS0002079

PANDEMIC PARAMETERS OPTIMIZATION FROM MODIFIED SEIQR MODEL ON COVID-19 USING DIFFERENTIAL EQUATIONS, NEURAL NETWORKS AND BAYESIAN INFERENCE: THAILAND DATA

Jayakrit Hirisajja

Authors: Hirisajja J[1], Chaijaruwanich J[2], Laosiritaworn Y[3], Pan-ngum (Pongtavornpinyo) W[4]

Affiliation: [1]Ph.D\'s'Degree Program in Computer Science, Department of Computer Science, Faculty of Science, Chiang Mai University; [2]Department of Computer Science, Faculty of Science, Chiang Mai University; [3]Department of Physics, Faculty of Science, Chiang Mai University; [4]Department of Tropical Hygiene and Mahidol-Oxford Tropical Medicine Research Unit (MORU), Faculty of Tropical Medicine Mahidol Universityahidol-Oxford Tropical Medicine Research Unit (MORU), Faculty of Tropical Medicine, Mahidol University

Since the COVID-19 pandemic emerged, the epidemiological model for infectious diseases of Susceptible, Infected, and Recovered (SIR) type has been used to understand and forecast the transmission and assess the impacts of various interventions in the pandemic. While the virus is spreading, various strategies were used, including Non-Pharmacuitical Interventions (NPIs) and vaccination. In simple models, transmission parameters would be assumed to be fixed even though it is dynamically determined by circulating variants and on-going interventions. We propose using the Neural Network approach to solve or approximate the solution in the transmission dynamic model represented by a set of differential equations describing the disease progression. By integrating the Neural Network, recognized as a universal approximator, with SEIQR(Suspect-Expsed-Infected-Quarantine-Recovery) differential equation and utilizing government public data, the Neural Networks can effectively track variations of SEIQR parameters in pandemic data. This optimized Neural Network yields a temporal function detailing the transition rates across compartments, providing insights into the epidemic characteristics and dynamics. Employing the Julia programming language with the SciML and Turing package, we developed Neural Networks capable of capturing step-changed transition rates among E, I, Q, and R compartments based on simulated data. To align with stochastic data of Thailand\'s'COVID-19 epidemic, Bayesian inference was incorporated into the Neural Network model, producing output as a posterior distribution parameter that can successfully encapsulate the evolving transition values of Thailand\'s'COVID-19 data. Amidst the virus\'s'shifting dynamics, the results suggest underscoring our approach\'s'efficacy in providing insight information for dealing with public health crises.

Keywords: COVID-19, SIR Epidemic model, SEIQR, Differential Equations, Neural Network, Bayesian Inference

Wednesday 13 December 2023

S12: Biology and Drug Discovery of Pathogenic Free-living Amoeba

15.45-17.15hr

Room A

Wednesday 13 December 2023

S12: Biology and Drug Discovery of Pathogenic Free-living Amoeba

15.45-17.15hr

Room A

Chairperson:
1. Pichet Ruenchit
2. Kasem Kulkeaw

Invited speaker:

1. UPDATE ON DIAGNOSIS AND TREATMENT OF FREE-LIVING AMOEBA: LEARNING FROM UNSUCCESSFUL AND SUCCESSFUL TREATMENTS
Patsharaporn Techasintana Sarasombath
Other (Department of Parasitology, Faculty of Medicine Siriraj Hospital, Mahidol University)

2. DRUG DISCOVERY FOR PATHOGENIC FREE-LIVING AMOEBAE
Christopher Rice
Other (Purdue University)

3. BIOLOGY AND ADVANCED TECHNOLOGY FOR THE STUDY OF FREE-LIVING AMOEBA
Kasem Kulkeaw
Other (Faculty of Medicine Siriraj Hospital Mahidol University)

Abstract No.: ABS0002140

UPDATE ON DIAGNOSIS AND TREATMENT OF FREE-LIVING AMOEBA: LEARNING FROM UNSUCCESSFUL AND SUCCESSFUL TREATMENTS

Patsharaporn Techasintana Sarasombath

Authors: Kedsara Panyasu, **Patsharaporn T. Sarasombath**

Affiliation: Siriraj Integrative Center for Neglected Tropical Parasitic Diseases, Department of Parasitology, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, Thailand

Introduction: Free-living amoebae are typically found in various environments such as soil, dust, and freshwater. Among these, four genera of amoebae, Naegleria, Balamuthia, Acanthamoeba, and Sappinia, can cause diseases in both humans and animals. Naegleria fowleri leads to acute fulminant brain damage called primary amebic meningoencephalitis (PAM), while Acanthamoeba spp. and Balamuthia mandrillaris cause granulomatous amebic meningoencephalitis (GAE), both with mortality rates exceeding 95%. Effective treatments for PAM and GAE are currently lacking.

Objective: To determine factors affecting treatment outcomes in patients with N. fowleri and B. mandrillaris brain infections, and assess the effectiveness of available treatment regimens and procedures.

Methods: We systematically searched Ovid MEDLINE, Scopus, PubMed, Google Scholar, and additional sources for studies providing original data on diagnosed free-living amoeba brain infections, symptom onset, treatment regimens, time to initial treatment and outcomes.

Conclusion: Recommended PAM treatments often involve a combination of amphotericin B, azithromycin, fluconazole, rifampin, miltefosine, and dexamethasone, due to their success in PAM survivors. Therapeutic hypothermia has shown some effectiveness in a few PAM survivors, while hypertonic saline treatment has limited data on efficacy. For GAE from B. mandrillaris, a regimen comprises flucytosine, pentamidine, fluconazole, sulfadiazine, and azithromycin or clarithromycin, but effectiveness remains low. Nitroxoline is a promising option for GAE, used successfully in one case. Further research and treatment options are crucial for enhancing clinical outcomes.

Keywords: free-living amoeba, Naegleria fowleri, Balamuthia mandrillaris, Sappinia, treatment, primary amebic meningoencephalitis, brain infection, amoebae

Abstract No.: ABS0002214

DRUG DISCOVERY FOR PATHOGENIC FREE-LIVING AMOEBAE

Christopher Rice

Authors: Christopher A. Rice[1,2], Chenyang Lu[1] and Dennis E. Kyle[2].

Affiliation: [1]Department of Comparative Pathobiology, Purdue University, West Lafayette, IN, USA.
[2]Center for Tropical and Emerging Global Diseases, University of Georgia, Athens, GA, USA.

Pathogenic free-living amoebae (Balamuthia mandrillaris, Acanthamoeba castellanii and Naegleria fowleri) cause several neglected human diseases. To raise awareness, B. mandrillaris and A. castellanii have both been described to cause cutaneous infections as well as diseases of the brain known as Granulomatous Amoebic Encephalitis (GAE). Acanthamoeba can also cause ocular keratitis. N. fowleri exclusively causes a brain disease known as Primary Amoebic Meningoencephalitis (PAM). Due to the known difficulties in treating these diseases, the unmet clinical need is for highly potent and quickly acting therapeutics and rapid diagnostics. An additional need is for potent cysticidal action for diseases caused by Acanthamoeba and Balamuthia. Herein, we report our efforts for screening the world's largest known number of drugs to identify potentially new anti-amoebic therapeutics. We used CellTiter-Glo 2.0 high-throughput screening methods to screen various drug libraries in search for new active chemical scaffolds against pathogenic FLA. From our initial screen of ~13,500 compounds against logarithmic trophozoites we validated 63 hits against B. mandrillaris, 32 against A. castellanii, and 53 against N. fowleri via dose response assessment. Lastly, we will provide an update on new highly sensitive and specific diagnostic tools developed for Balamuthia mandrillaris. This is by far the largest screen of drugs for these neglected amoebae and these data identify new repurposing drug candidates for the treatment of amoebic diseases and by developing rapid diagnostics hand -in-hand we hope this will eventually help bring down the mortality of patients from amoebic diseases.

Keywords: free-living amoeba, Balamuthia mandrillaris, Acanthamoeba castellanii, Naegleria fowleri, CNS disease, eye disease.

Abstract No.: ABS0002136

BIOLOGY AND ADVANCED TECHNOLOGY FOR THE STUDY OF FREE-LIVING AMOEBA

Kasem Kulkeaw

Authors: Kulkeaw K[1], Tongkrajang N[1], Kobpornchai P[1,2], Whangviboonkij N[1], Panadsako N[3], Pengsart W[4], Chaisri U[5]

Affiliation: [1]Siriraj Integrative Center for Neglected Parasitic Diseases, Department of Parasitology, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, 10700, Thailand; [2]Siriraj-Long Read Lab, Faculty of Medicine Siriraj Hospital, Mahidol University; [3]Graduate Study School, Faculty of Medicine Siriraj Hospital, Mahidol University, Nakhon Pathom 73170, Thailand; [4]Hollywood International Ltd., Thailand; [5]Department of Pathology, Faculty of Tropical Medicine, Mahidol University

Introduction: Free-living amoeba are capable of adapting to survive in different microenvironments. Balamuthia mandrillaris is a rare pathogenic, free-living amoeba causing fatal brain damage. The mechanism underlying cell damage remains limited. This presentation aims to update the biology of B. mandrillaris and provide advanced tools for the study of amoeba biology.

Methods: A clinical isolate of B. mandrillaris trophozoites was examined using a coculture with human neural cells in a 2D and 3D culture, including spheroid and organoid. Host-parasite interactions were observed using confocal and holotomographic microscopes.

Results: B. mandrillaris trophozoites protrude invadopodia-like structure into human neural cells. Endocytosis of human protein and lipid was in various forms, including membrane-bound granules, nonmembranous granules, and cytoplasmic dispersion. Inhibition of trogocytosis could not stop this process. The use of 3D cell culture allows observation of human neuron cell damage and identification of brain trauma biomarkers.

Conclusion: B. mandrillaris trophozoites ingest human cell components independent of phagocytosis and trogocytosis. The 2D and 3D coculture of the trophozoites yielded different behaviors. Interpretation of the data obtained from the different culture platforms should be considered before generalizing the information into a human context.

Keywords: Free-living amoeba; Balamuthia mandrillaris; spheroid; cerebral organoid; host-parasite interaction; neglected parasitic disease

Wednesday 13 December 2023

S13: Advancing Knowledge of Cryptic Intraerythrocytic Infections in Plasmodium vivax Malaria

15.45-17.15hr

Room C

Thursday 13 December 2023

S 13: Advancing Knowledge of Cryptic Intraerythrocytic Infections in Plasmodium vivax Malaria

15.45-17.15hr

Room C

Chairperson:
1. Wanlapa Roobsoong

Invited speaker:

1. PLASMODIUM VIVAX CRYPTIC ERYTHROCYTIC INFECTIONS
Hernando del Portillo
Other (Institute for Global Health (ISGlobal), Hospital Clínic - Universitat de Barcelona, Barcelona, Spain)

2. MECHANISTIC INSIGHTS AND FUNCTIONAL STUDIES OF PLASMODIUM VIVAX INTRASPLENIC INFECTIONS
Carmen Fernández
Other (Institute for Global Health (ISGlobal), Hospital Clínic - Universitat de Barcelona, Barcelona, Spain)

3. 3D PRINTED BONE-MARROW-ON-A-CHIP AND BLOOD RHEOLOGY CHALLENGES
Aurora Hernandez-Machado
Other (Institute of Nanoscience and Nanotechnology (IN2UB), University of Barcelona)

4. TOWARDS AN ENGINEERED VASCULARIZED BONE-MARROW-ON-CHIP TO UNDERSTAND PLASMODIUM VIVAX CRYPTIC NICHES: PRELIMINARY RESULTS ON DEVICE ASSEMBLY
Cristina C. Barrias
Other (i3S - Instituto de Investigação e Inovação em Saúde, Universidade do Porto)

Abstract No.: ABS0002266

PLASMODIUM VIVAX CRYPTIC ERYTHROCYTIC INFECTIONS

Hernando del Portillo

Authors: Hernando del Portillo

Affiliation: Institute for Global Health (ISGlobal), Hospital Clínic - Universitat de Barcelona, Barcelona, Spain

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002267

MECHANISTIC INSIGHTS AND FUNCTIONAL STUDIES OF PLASMODIUM VIVAX INTRASPLENIC INFECTIONS

Carmen Fernández

Authors: Carmen Fernández

Affiliation: Institute for Global Health (ISGlobal), Hospital Clínic - Universitat de Barcelona, Barcelona, Spain

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002269

3D PRINTED BONE-MARROW-ON-A-CHIP AND BLOOD RHEOLOGY CHALLENGES

Aurora Hernandez-Machado

Authors: Aurora Hernandez-Machado

Affiliation: Institute of Nanoscience and Nanotechnology (IN2UB), University of Barcelona

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002270

TOWARDS AN ENGINEERED VASCULARIZED BONE-MARROW-ON-CHIP TO UNDERSTAND PLASMODIUM VIVAX CRYPTIC NICHES: PRELIMINARY RESULTS ON DEVICE ASSEMBLY

Cristina C. Barrias

Authors: Cristina C. Barrias

Affiliation: i3S - Instituto de Investigação e Inovação em Saúde, Universidade do Porto

No abstract available

Keyword: No abstract available

Wednesday 13 December 2023

S14: Japanese Virology Focusing on Emerging Viruses

15.45-17.15hr

Room C

Wednesday 13 December 2023

S14: Japanese Virology Focusing on Emerging Viruses

15.45-17.15hr

Room C

Chairperson:
1. Kei Sato
2. Keita Matsuno

Invited speaker:

1. Evolution of SARS-CoV-2 and beyond
Kei Sato
Other (The Institute of Medical Science, The University of Tokyo)

2. EMERGING TICK-BORNE BUNYAVIRUS INFECTIONS
Keita Matsuno
Other (International Institute for Zoonosis Control, Hokkaido University)

3. AN EXPERIMENTAL PLATFORM FOR DENGUE RESEARCH
Tomokazu Tamura
Other (Hokkaido University)

Abstract No.: ABS0002105

Evolution of SARS-CoV-2 and beyond

Kei Sato

Authors: Kei Sato[1,2]

Affiliation:
[1]The Institute of Medical Science, The University of Tokyo, Japan
[2]The Genotype to Phenotype Japan (G2P-Japan) Consortium

SARS-CoV-2, the causative agent of COVID-19, emerged at the end of 2019. During its global spread over the past 3 years, SARS-CoV-2 has been highly diversified, and these SARS-CoV-2 variants have been considered to be the potential threats to the human society. In order to elucidate the virological characteristics of newly emerging SARS-CoV-2 variants in real-time, I launched a consortium called “The Genotype to Phenotype Japan (G2P-Japan)” in January 2021. With the colleagues who joined the G2P-Japan consortium, we have revealed the virological characteristics of SARS-CoV-2 variants. In May 2023, WHO declared the end of the Public Health Emergency of International Concern (PHEIC) for COVID-19. However, “the next pandemic” will come in the future, and we need to gather our wisdom learned from the COVID-19 pandemic for the preparedness of future pandemic. Here, I will talk about our findings on SARS-CoV-2 variants and future perspectives to combat the outbreaks and pandemic that will happen in the future.

Keywords: SARS-CoV-2; Pandemic; Outbreak; One health

Abstract No.: ABS0002199

EMERGING TICK-BORNE BUNYAVIRUS INFECTIONS

Keita Matsuno

Authors: Matsuno K[1,2,3,4]

Affiliation:
[1]International Institute for Zoonosis Control, Hokkaido University
[2]Institute for Vaccine Research and Development, Hokkaido University
[3]One Health Research Center, Hokkaido University

The order Bunyavirales is composed of a wide variety The order Bunyavirales is composed of a wide variety of tri-segmented negative-strand RNA viruses with over 400 species. Recent emergences of a series of tick-borne bunyavirus diseases raise attention to divergent bunyaviruses maintained in ticks. Severe fever with thrombocytopenia syndrome (SFTS) caused by SFTS virus (SFTSV) grouped into the genus Bandavirus, family Phenuiviridae, is one of the emerging tick-borne bunyavirus diseases in Asian countries, firstly identified in China. SFTSV and tick-borne phenuiviruses have been found in a number of countries. In our study, novel phenuiviruses in ticks collected in Japan and Zambia and also non-human lethal cases of SFTSV infection in captive cheetahs in a zoo in Japan were found. In 2019, we discovered a novel bunyavirus genetically classified into the genus Orthonairovirus, family Nairoviridae, designated as Yezo virus (YEZV) from a patient showing a febrile illness after a tick bite in Hokkaido, Japan. YEZV infection has been retrospectively confirmed in seven cases showing an acute febrile illness with leukocytopenia and thrombocytopenia after tick bite. YEZV is genetically closely related to orthonairoviruses causing human febrile illness in China. YEZV infection was also identified in ticks and wild animals in Hokkaido, suggesting endemic circulation. Our studies on emerging bunyavirus diseases will broaden the landscape of acute febrile illness with unknown causes.

Keywords: Arbovirus, Tick, Emerging infectious disease

Abstract No.: ABS0002139

AN EXPERIMENTAL PLATFORM FOR DENGUE RESEARCH

Tomokazu Tamura

Authors: Tomokazu Tamura[1,2,3,4], Takasuke Fukuhara[1,2,3,4,5]

Affiliation:
[1]Department of Microbiology and Immunology, Faculty of Medicine, Hokkaido University, Sapporo, Japan; [2]Institute for Vaccine Research and Development (IVReD), Hokkaido University, Sapporo, Japan; [3]Institute for the Advancement of Higher Education, Hokkaido University, Sapporo, Japan; [4]One Health Research Center, Hokkaido University, Sapporo, Japan; [5]Laboratory of Virus Control, Research Institute for Microbial Diseases, Osaka University, Suita, Japan.

Introduction: Dengue is caused by four genetically distinct viral serotypes, dengue virus (DENV) 1-4. Following transmission by Aedes mosquitoes, DENV can cause a broad spectrum of clinically apparent disease ranging from febrile illness to dengue hemorrhagic fever and dengue shock syndrome. Progress in the understanding of different dengue serotypes and its impact of in detail host-virus interactions has been hampered by scarcity of an experimental model and a toolbox. Here, we aim to establish experimental platform for dengue research.

Methods: We set out to create 20 infectious clones of DENV1-4 originating from the three endemic continents. Using a modified circular polymerase extension reaction, we generated de novo viruses from these sequencing data. Then, we characterized the resulting DENV recombinant viruses in cell culture and in humanized mice, NOD Rag1-/-, IL2rgnull Flk2-/- (NRGF) mice engrafted with components of a human immune system. In addition, we generated the recombinant virus carrying the HiBiT luciferase.

Results: The resulting DENV clones replicate robustly in mammalian cells at levels similar to the parental strains. All DENV strains resulted in viremia in humanized mice but not in non-engrafted NRGF mice. The in vitro replication of the recombinant DENV carrying the HiBiT was comparable to that of the parental virus and the luciferase activity increased in accord with the increase of intracellular viral RNA.

Conclusion: Our data suggest that our de novo generated clones are suitable for studying dengue immunopathogenesis in vivo. In addition, our recombinant DENV carrying the HiBiT is applicable to screening for developing antivirals.

Keywords: Dengue, dengue fever virus, animal model, recombinant virus, reporter assay

Wednesday 13 December 2023

S15: TropMed Tug-of-War Ep 2

15.45-17.15hr

Room D

Wednesday 13 December 2023

S15: TropMed Tug-of-War Ep 2

15.45-17.15hr

Room D

Chairperson:
1. Santi Maneewatchararangsri

Invited speaker:

-

Wednesday 13 December 2023

S16: Travel Medicine Practices in Thai Public Health (Eng Language)

15.45-17.15hr

Room E

Wednesday 13 December 2023

S16: Travel Medicine Practices in Thai Public Health (Eng Language)

15.45-17.15hr

Room E

Chairperson:
1. Parinda Wattanasri
2. Amornsit Chavanayarn

Invited speaker:

1. Travel-related control measures during the COVID-19 pandemic
Ranida Techasuwanna
Other (Department of Disease Control)

2. Travelers' Health at Points of Entry
Bhanasut Hunsajarupan
Faculty of Tropical Medicine, Mahidol University (Hospital for Tropical Diseases)

3. Migration and Border Health
Toonlaya Direkwutthikun
Other (Department of disease control)

Abstract No.: ABS0002250

Travel-related control measures during the COVID-19 pandemic

Ranida Techasuwanna

Authors: Ranida Techasuwanna

Affiliation: Institute for Urban Disease Control and Prevention, Department of Disease Control

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002251

Travelers’ Health at Points of Entry

Bhanasut Hunsajarupan

Authors: Bhanasut Hunsajarupan

Affiliation: Division of International Communicable Disease Control Port Health and Quarantine, Department of Disease Control

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002253

Migration and Border Health

Toonlaya Direkwutthikun

Authors: Toonlaya Direkwutthikun

Affiliation: Office of Disease Prevention and Control Region 2 Phitsanulok, Department of Disease Control

No abstract available

Keyword: No abstract availab

Thursday 14 December 2023

S17: Challenges on Development of New Vaccines/Biological products

08.30-10.00hr

Room A

Thursday 14 December 2023

S17: Challenges on Development of New Vaccines/Biological products

08.30-10.00hr

Room A

Chairperson:
1. Punnee Pitisuttithum
2. Weerapong Phumratanaprapin

Invited speaker:

1. Vaccines in the pipe
Andrew Pollard
Other (University of Oxford)

2. The challenges for developing countries in new vaccine research, development and production
Daniel Rhee
Other (Clinical Development, International Vaccine Institute)

3. Challenges in R&D of new Vaccines for Thailand
NAKORN PREMSRI
Other (Chulalongkorn University)

Abstract No.: ABS0002256

Vaccines in the pipe

Andrew Pollard

Authors: Andrew Pollard

Affiliation: University of Oxford

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002261

The challenges for developing countries in new vaccine research, development and production

Daniel Rhee

Authors: Daniel Chulwoo Rhee

Affiliation: Clinical Development Department, IVI

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002263

Challenges in R&D of new Vaccines for Thailand

NAKORN PREMSRI

Authors: Nakorn Premsri

Affiliation: National Vaccine Institute

No abstract available

Keyword: No abstract available

Thursday 14 December 2023

S18: Emerging Tick-Borne Diseases

08.30-10.00hr

Room B

Thursday 14 December 2023

S18: Emerging Tick-Borne Diseases

08.30-10.00hr

Room B

Chairperson:
1. MAJ Erica Lindroth

Invited speaker:

1. TICK-BORNE DISEASES OF THAILAND AND THE CURRENT STATE OF ACARICIDE RESISTANCE
Ratree Takhampunya
Other (United State Army Medical Directorate-Armed Forces Research Institute of Medical Sciences)

2. Emerging Tick-borne diseases of Mongolia; a growing threat
Michael von Fricken
Other (University of Florida, One Health Center of Excellence)

3. The Expanding Range of Emerging Tick-borne Viruses in Eastern Europe and the Black Sea Region
Koray Ergunay
Other (Walter Reed Biosystematics Unit, Smithsonian Institution, Walter Reed Army Institute of Research)

4. ESTABLISHMENT OF ACARICIDE SUSCEPTIBILITY BIOASSAY USING LARVAL PACKET TEST FOR RHIPECEPHALUS SANGUINEUS TICKS IN THAILAND
Asma Longkunan
Other (Armed Forces Research Institute of Medical Sciences (AFRIMS))

Abstract No.: ABS0002157

TICK-BORNE DISEASES OF THAILAND AND THE CURRENT STATE OF ACARICIDE RESISTANCE

Ratree Takhampunya

Authors: Ratree Takhampunya, Jira Sakolvaree, Wasinee Ngonsawan, Nitima Chanarat, Asma Longkunan Nittayaphon Youngdech, Siriporn, Phasomkusolsil, Bousaraporn Tippayachai, Sommai Promsathaporn, Erica J Lindroth

Affiliation: Department of Entomology, United States Army Medical Directorate - Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand.

Rickettsia spp. are the main tick-borne diseases (TBD) affecting humans in Thailand, though others like Q fever and anaplasmosis impact pets and livestock. Despite many reports, Rickettsia are often ignored as a cause of fever-related diseases. Recent discoveries of Borrelia miyamotoi in ticks and rodents, and its potential human transmission, highlight the importance of TBD as a public health issue. Insecticide usage is the most effective method for controlling and preventing tick bites on domestic animals, but developing resistance in ticks is a concern. This study looks at acaricide resistance across the country and assesses the efficacy of the commonly used insecticide permethrin.

Traditional and next-generation sequencing methods detected bacterial pathogens in ticks. Human exposure was tested using commercial serology kits on local hospitals\' human sera. Acaricide resistance in Rhipicephalus sanguineus ticks from dogs across Thailand was assessed through phenotypic and genotypic assays.

Since the first detection of Rickettsia in Thailand\'s ticks in 1962, various species have been found infecting patients. The discovery of Borrelia miyamotoi in ticks and rodents emphasize concerns of neglected tick-borne diseases, with evidence of transmission via local rodents and ticks. Studies show R. sanguineus ticks in several provinces show a high resistance to permethrin. Genotyping results indicate that most resistant ticks exhibited 1-2 SNPs in the voltage-gated sodium channel gene, with the majority of SNPs occurring in Domain II.

TBD in Thailand affects both human health and animals’, causing economic damage in agriculture and risk to household pets. To address this, implementing strategies such as comprehensive tick

Keywords: Tick-borne disease, permethrin resistance, Rhipecephalus sanguineus, Rickettsia, Borrelia miyamotoi

Abstract No.: ABS0002268

Emerging Tick-borne diseases of Mongolia; a growing threat

Michael von Fricken

Authors: Michael Von Fricken

Affiliation: University of Florida, One Health Center of Excellence

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002275

The Expanding Range of Emerging Tick-borne Viruses in Eastern Europe and the Black Sea Region

Koray Ergunay

Authors: Koray Ergunay

Affiliation: Walter Reed Biosystematics Unit, Smithsonian Institution, Walter Reed Army Institute of Research

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002150

ESTABLISHMENT OF ACARICIDE SUSCEPTIBILITY BIOASSAY USING LARVAL PACKET TEST FOR RHIPECEPHALUS SANGUINEUS TICKS IN THAILAND

Asma Longkunan

Authors: Longkunan A, Takhampunya R, Chanarat N, Sakolvaree J, Tippayachai B, Promsathaporn S, Phasomkusolsil S, Lindroth EJ.

Affiliation: Department of Entomology, United States Army Medical Directorate - Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand.

The brown dog tick, Rhipechephalus sanguineus, is capable of vectoring several pathogens that cause disease in human. The frequent use of permethrin in management of ectoparasites on companion pets and domestic animals has resulted in insecticide resistance worldwide. Currently, acaricide resistance has not been reported among Thai tick populations. To survey the susceptibility or resistance to insecticides in Thai tick populations, bioassays based on the Food and Agricultural Organization (FAO) larval packet test (LPT) was performed determining the lethal concentration (LC) value and resistance ratio (RR) on the susceptible laboratory strain R. sanguineus (OSU-USA) as well as field-collected ticks from five region across Thailand. The mortality following 24 hour exposure to various doses of permethrin was determined. Over 8000 larvae were tested in 4 to 5 concentrations of permethrin. The lethal concentration at 50% mortality (LC50) (% weight/volume) of R. sanguineus collected from Chantaburi, Buengkan, Krabi, Chumphon, and Phetchabun were 4.17%, 1.03%, 3.33%, 5.68%, 2.80%, respectively. The resistance ratio (RR) values of those field collected ticks when comparing with susceptible strain (OSU-USA) range from 62-342. Our results indicate that Thai brown dog tick populations have developed significant resistance to permethrin. The LC calculated here will allow a rapid assessment of permethrin resistance for local ticks. Moreover, our findings may provide useful information for the successful control of ticks in Thailand.

Keywords: larval packet test, insecticide, permethrin resistance, Rhipecephalus sanguineus

Thursday 14 December 2023

S19: Social Epidemiology of Vector Borne Diseases, Prevention and Control

08.30-10.00hr

Room C

Thursday 14 December 2023

S19: Social Epidemiology of Vector Borne Diseases, Prevention and Control

08.30-10.00hr

Room C

Chairperson:
1. Suparat Phuanukoonnon
2. Daniel Parker

Invited speaker:

1. IMPACT OF CONFLICT ON RISING GLOBAL CUTANEOUS AND MUCOCUTANEOUS LEISHMANIASIS INCIDENCE
Maia Tarnas
Other (University of California, Irvine)

2. MIGRATION AND MALARIA: A POTENTIAL RISK FACTOR ANALYSIS OF MALARIA INFECTIONS AMONG MIGRANTS TO A GOLD-MINING SETTLEMENT IN GAMBELLA REGION OF ETHIOPIA.
Natasha Glendening
Other (University of California Irvine)

3. ENHANCING PATIENT ADHERENCE TO 14-DAY PRIMAQUINE TREATMENT IN MALARIA ENDEMIC REGION OF MYANMAR: INSIGHTS FROM STAKEHOLDERS – A QUALITATIVE STUDY
Kyawt Mon Win
Faculty of Tropical Medicine, Mahidol University (Tropical Hygiene)

4. ACCEPTABILITY, FEASIBILITY AND FIDELITY TO EXPNAD THE ROLE OF MYANMAR MALARIA COMMUNITY HEALTH WORKERS: A MIXED-METHOD STUDY
Win Han Oo
Other (Burnet Institute)

Abstract No.: ABS0002167

IMPACT OF CONFLICT ON RISING GLOBAL CUTANEOUS AND MUCOCUTANEOUS LEISHMANIASIS INCIDENCE

Maia Tarnas

Authors: Tarnas MC[1], Abbara A[2,3], Desai AN[4], Parker DM[1]

Affiliation:
1. Department of Population Health and Disease Prevention, University of California Irvine, USA;
2. Department of Infectious Diseases, Imperial College, London, UK;
3. Syria Public Health Network, UK;
4. Division of Infectious Diseases, University of California Davis, Sacramento, USA

Introduction: Conflict creates an ideal environment for leishmaniasis, with poor living conditions, poverty, malnutrition, and displacement. The increase in such settings, in addition to destructive environmental events, may contribute to the increase in cutaneous and mucocutaneous leishmaniasis cases in recent decades. We assess this by measuring the association between cutaneous and mucocutaneous leishmaniasis incidence and conflict intensity between 2005-2020 while controlling for relevant environmental, economic, and demographic factors.

Methods: We pulled annual cases from the WHO for 53 countries that had conflict intensity scores (range: 1-10) from the Bertelsmann Transformation Index. These scores were used to create severity quintiles ranging from Low (scores of 1-3) to Severe (7.5-10). Using remote sensing, we gathered temperature, precipitation, and humidity data, in addition to data on annual population, internal displacement estimates, and GDP. We fit a negative binomial generalized additive model with a random country-level intercept.

Results: Severe conflict was associated with 2.42 times the risk of cutaneous and mucocutaneous leishmaniasis (95% CI: 1.51-3.87, p=0.0002) compared to low conflict. We also identified a curvilinear relationship between mean temperature and disease incidence, with significant increased risk at approximately 18.5-25.1℃. Importantly, the relationship between conflict intensity and disease incidence was heavily mediated by displacement.

Conclusions: Severe conflict marks when conflict turns largely violent, indicating that violence – and the accompanying destruction – may be driving this association. Violent conflict is likely to create environments primed for both the sandfly vector and rapid disease transmission. Understanding conflict\'s impact on disease dynamics is an important component of preparedness and response.

Keywords: leishmaniasis, conflict, displacement, environment, climate change, vector-borne disease

Abstract No.: ABS0002200

MIGRATION AND MALARIA: A POTENTIAL RISK FACTOR ANALYSIS OF MALARIA INFECTIONS AMONG MIGRANTS TO A GOLD-MINING SETTLEMENT IN GAMBELLA REGION OF ETHIOPIA

Natasha Glendening

Authors: Glendening N[1], Haileselassie W[2], Parker DM[1]

Affiliation:[1] Program in Public Health, Department of Population Health and Disease Prevention, University of California, Irvine

Introduction: Lunga is a recently established gold mining settlement in Gambella Region of Ethiopia. Such extractive settlements are often associated with disease transmission and limited healthcare access. We aimed to investigate potential associations between migrants' characteristics and their risk of malaria infections.

Methods: We interviewed participants for demographic information and tested them for malaria.

The primary outcome for analysis was a positive diagnosis of Plasmodium falciparum by RDT or microscopy. Using a logistic regression model with a random household intercept we analyzed the influence of demographic characteristics on malaria infections.

Results: 247 households and 624 individuals participated. Being aged 15-24 was associated with a 56% (95% CI: 0.198 0.987) decreased odds of malaria compared to children 0-4 years. Being 25+ was associated with 58% (95% CI: 0.190 0.987) decreased odds of infection. Having a bed net was associated with 52% decreased odds (95% CI: 0.25 0.93) of a positive infection but this protective effect dampened when controlling for household factors (AOR: 0.54, 95% CI: 0.293 0.995). Living in a household with higher numbers of positive malaria infections was significantly associated with increased infection odds (AOR: 1.18, 95% CI: 1.05-1.33).

Conclusion: Children under 5 in Lunga have increased risk of malaria infections compared to people aged 15+. Bed net usage is low (12%) but when they are used, they are protective against malaria infections. There is also evidence of household clustering of malaria, indicating that future interventions may be effective when targeted at households and should include bed net distribution.

Keyword: Malaria

Abstract No.: ABS0002152

ENHANCING PATIENT ADHERENCE TO 14-DAY PRIMAQUINE TREATMENT IN MALARIA ENDEMIC REGION OF MYANMAR: INSIGHTS FROM STAKEHOLDERS – A QUALITATIVE STUDY

Kyawt Mon Win

Authors: Kyawt Mon Win[1,2], Pyae Linn Aung[3], Zau Ring[4], Nay Yi Yi Linn[2], Myat Phone Kyaw[5], Wang Nguitragool[3,6], Liwang Cui[7], Jetsumon Sattabongkot[3], Saranath Lawpoolsri[1]

Affiliation:
[1]Department of Tropical Hygiene, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand
[2]Department of Public Health, Ministry of Health, NayPyiTaw, Myanmar
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[4]State Public Health Department, Kachin State, Ministry of Health, MyitKyiNa, Myanmar
[5]Myanmar Health Network Organization, Yangon, Myanmar
[6]Department of Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand
[7]Division of Infectious Diseases and International Medicine, Department of Internal Medicine, Morsani College of Medicine, University of South Florida, Tampa, FL, USA

Plasmodium vivax malaria is considered a major threat to malaria elimination. The radical cure for P. vivax malaria requires a 14-day administration of primaquine (PQ) to clear hypnozoites. However, maintaining adherence to PQ treatment is a significant challenge. The study aimed to formulate interventions for promoting patients' commitment to PQ treatment in a malaria-endemic township in Myanmar.

A qualitative study was conducted in Waingmaw Township in Myanmar, where P. vivax malaria is highly endemic. Key stakeholders including public health officers and community members participated in focus group discussions (FGDs) and in-depth interviews (IDIs) in September 2022.

Responsible individuals from different levels of the Myanmar Malaria Program participated in the IDIs. Most reported the increasing trend of P. vivax and the possibility of relapse cases. Workload was a key concern in implementation of intervention and possible interventions, such as implementing directly observed treatment (DOT) by family members, piloting a shorter PQ regimen, expanding the malaria volunteer network, and strengthening health education activities were discussed. FGDs among community members revealed that although people were knowledgeable about malaria symptoms, treatment locations, and the use of bed nets, most of them still preferred to be treated by quack and rarely used nets at worksites. Many often stopped taking prescribed drugs once symptoms disappeared.

Interventions such as implementing family member DOT or shortening PQ regimens should be introduced to enhance the radical cure for the P. vivax infection. Disseminating information about the importance of radical cure and emphasizing the burden of relapse is also essential.

Keywords: Myanmar, Intervention, Plasmodium vivax, Primaquine, Qualitative research, Treatment adherence, Compliance

Abstract No.: ABS0002154

ACCEPTABILITY, FEASIBILITY AND FIDELITY TO EXPNAD THE ROLE OF MYANMAR MALARIA COMMUNITY HEALTH WORKERS: A MIXED-METHOD STUDY

Win Han Oo

Authors: Win Han Oo[1,2*], Ei Phyu Htwe[1], Win Htike[1], Pwint Phyu Phyu[3], May Chan Oo[1], Kaung Myat Thu[1], Aung Khine Zaw[1], Galau Naw Hkawng[1], Nay Yi Yi Linn[4], Kyawt Mon Win[4], Htun Min[3], Julia Cutts[2], Katherine O'Flaherty[2], Paul A. Agius[2,5,6,] Freya J.I. Fowkes[2,5,7]

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1. Health Security Program, Burnet Institute Myanmar, Yangon, Myanmar
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4. National Malaria Control Programme, Ministry of Health, Nay Pyi Taw, Myanmar
5. Department of Epidemiology and Preventive Medicine, Monash University, VIC, Australia
6. Faculty of Health, Deakin University, VIC, Australia
7. Melbourne School of Population and Global Health, the University of Melbourne, VIC, Australia

To maintain the malaria community health workers' (CHW) contribution to malaria elimination program and primary health care sector, the Community-delivered Integrated Malaria Elimination (CIME) Model that provides services for malaria, non-malaria febrile illness, childhood diarrhoea, dengue and tuberculosis, was co-designed and field-implemented in Myanmar. Its acceptability, fidelity and feasibility to implementation were evaluated.

In-depth interviews with community leaders and malaria program stakeholders (n=20), focus group discussions with CHWs (n=36), supervision (n=69), and participatory field observations (n=6) to CHWs, community-based cross-sectional survey with community members (n=643) were conducted in Yangon region of Myanmar between January and June 2022.

Majority of the community members (97.4%, n=626/643) expressed acceptance and willingness to receive the CIME services as the services met their needs (93.0%, n=598/643) and were satisfactory (97.7%, n=628/643) confirmed by the community leaders in the interviews. The CIME model was feasible to implement because of the enthusiasm of the CHWs to work as expanded CHWs and sufficient supply of medicines. The CHWs showed fidelity to the CIME model by correctly performing all steps of malaria RDT testing (95.7%, n=66/69), prescribing paracetamol to the febrile cases (97.1%, n=67/69), providing pre-referral treatment to childhood diarrhoea cases (87%, n=60/69), and reporting data regularly (92.8%, n=64,69).

Overall, the CIME model was acceptable to all types of stakeholders and feasible to implement successfully. With the enthusiasm and fidelity of the CHWs, the expanded CHW model, the CIME model, could be scaled up nationwide to effectively contribute to the malaria elimination and primary health care programs.

Keywords: Acceptability, Community-delivered Integrated Malaria Elimination Model, Feasibility, Fidelity, Malaria elimination

Thursday 14 December 2023

S20: Biology and Interventions against Pre-erythrocytic Malaria (Seattle Children's Research Institute)

08.30-10.00hr

Room D

Thursday 14 December 2023

S20: Biology and Interventions against Pre-erythrocytic Malaria (Seattle Children's Research Institute)

08.30-10.00hr

Room D

Chairperson:
1. Ashley Vaughan
2. Noah Sather

Invited speaker:

1. INTERROGATING ENDOTHELIAL BARRIER REGULATION BY TEMPORALLY RESOLVED KINASE NETWORK GENERATION
Ling Wei
Other (Seattle Children's Research Institute)

2. A SPECIES-TRANSCENDING AND NEUTRALIZING CSP C-TERMINAL ANTIBODY INHIBITS PRE-ERYTHROCYTIC FORMS OF PLASMODIUM VIVAX
Ganesh Ram Visweswaran
Other (Seattle Children’s Research Institute)

3. O-FUCOSYLATION OF CIRCUMSPOROZOITE PROTEIN IS ESSENTIAL FOR SPOROZOITE MOTILITY OF THE HUMAN MALARIA PARASITE PLASMODIUM FALCIPARUM.
Ashley Vaughan
Other (Seattle Children's' Research Institute)

4. TARGETING RELAPSING P. VIVAX INFECTION BY VACCINATION
Noah Sather
Other (Seattle Children's Research Institute)

Abstract No.: ABS0002168

INTERROGATING ENDOTHELIAL BARRIER REGULATION BY TEMPORALLY RESOLVED KINASE NETWORK GENERATION

Ling Wei

Authors: Wei L[1], Dankwa S[1], Vijayan K[1,4], Smith JD[1,2,3], Kaushansky A[1,2,3]

Affiliation: [1]Center for Global Infectious Disease Research, Seattle Children's Research Institute, Seattle, WA 98109, United States; [2]Department of Pediatrics, University of Washington, Seattle, WA 98109, United States; [3]Department of Global Health, University of Washington, Seattle, WA 98109, United States; [4]School of Biology, Indian Institute of Science Education and Research, Thiruvananthapuram 695551, India

Blood-brain barrier dysfunction is triggered by a range of physiological and pathological stimuli and contributes to cerebral malaria (CM) lethality. Thrombin-induced intravascular coagulation and high circulating levels of proinflammatory cytokines, like tumor necrosis factor (TNF), are associated with disruption of brain endothelial barriers in CM. The integrity of endothelial barriers is tightly controlled by cell-cell junctions and focal adhesions, whose functions are regulated by diverse phosphosignaling pathways. Thus, altering these phosphosignaling pathways is a potential approach to intervention against diseases such as CM. To better understand the kinase regulators and underlying barrier regulatory phosphosignaling networks, we developed a novel methodology, Temporally REsolved KInase Network Generation (TREKING), which combines a 28-kinase inhibitor screen with machine learning and network reconstruction to build time-resolved, functional phosphosignaling networks associated with barrier regulation. We demonstrated the utility of TREKING for identifying pathways mediating barrier integrity following thrombin stimulation with or without TNF pre-conditioning in human brain microvascular endothelial cells. Our results predicted that over 150 kinases (~30% of the human kinome) are functional during barrier insult and provide time-resolved molecular insights into the networks that drive barrier disruption and recovery. Specifically, TREKING assigned distinct barrier phenotypes to different mitogen-activated protein kinase (MAPK) pathways, revealed the condition-specific activity of kinases and rewiring of barrier-regulatory pathways in the two inflammatory conditions. TREKING predicted extensive interconnected canonical and noncanonical pathways that control barrier function in the context of thrombin and TNF stimulation and has the potential for dissecting key host regulators and complex phosphosignaling networks involved in CM.

Keywords: Endothelial barrier permeability, thrombin, TNF, kinase regression, phosphosignaling network, MAPK

Abstract No.: ABS0002206

A SPECIES-TRANSCENDING AND NEUTRALIZING CSP C-TERMINAL ANTIBODY INHIBITS PRE-ERYTHROCYTIC FORMS OF PLASMODIUM VIVAX

Ganesh Ram Visweswaran

Authors: Visweswaran GRR[*], Vijayan K, Watson A[*], Schaefer C[*], Raappana A[*], Camargo N, Roobsoong W[#], Reynolds L[*], Vigdorovich V[*], Sattabongkot J[#], Kaushansky A[*], Kappe SHI[*], Sather DN[*]

Affiliation: [*]Center for Global Infectious Disease Research, Seattle Children\'s Research Institute, Seattle, WA 98109, USA; [#]Mahidol Vivax Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand.

Introduction: *P. vivax*, the geographically widespread and one of the predominant human malaria parasites, accounts for 74% of malaria cases in the WHO region of the Americas. The majority (80%) of the vivax cases are resultant of relapse infections originating from the activated hypnozoites, a dormant form of the parasite residing in the liver. Recently, the efficacy data from RTS/S AS01 (13% reduction in malaria-related child mortality rate) and WHO approval of R21 vaccine to P. falciparum malaria mark a giant leap towards malaria vaccine development. On the converse, presently no approved malaria vaccines to prevent P. vivax infections. Circumsporozoite protein (CSP), an abundant protein on the sporozoite cell surface and the chief constituent of the approved P. falciparum vaccines, is also a prime pre-erythrocytic vaccine target for P. vivax malaria.

Methods, Results & Conclusions: Using single cell sorting, we isolated a novel species-transcending CSP monoclonal antibody (aPcCSP-1) from P. cynomolgi CSP-immunized mice. By ELISA, Octet-BLI and IFAs, we showed aPcCSP-1 binds to its cognate antigen, PcCSP and Pc sporozoites. Interestingly, aPcCSP-1 is also bound to PvCSP vk210 and PvCSP vk247 antigens and sporozoites. Using domain truncations of PvCSP and PcCSP antigens, we demonstrate that aPcCSP-1 specifically binds to the TSR region in the C-terminal domain of CSP. By In vitro sporozoite inhibition (ISI), cell traversal and CSP-shedding assays, we showed a dose-dependent inhibition of Pv sporozoites (vk210) by aPcCSP-1 exhibiting species-transcending activity.

Keywords: Malaria vaccine, monoclonal antibody, Plasmodium vivax, Circumsporozoite protein (CSP)

Abstract No.: ABS0002178

O-FUCOSYLATION OF CIRCUMSPOROZOITE PROTEIN IS ESSENTIAL FOR SPOROZOITE MOTILITY OF THE HUMAN MALARIA PARASITE PLASMODIUM FALCIPARUM.

Ashley Vaughan

Authors: Priya Gupta[1], Nastaran Rezakhani[1], Nelly Camargo[1], Lucia Pazzagli1, Kristian Swearingen[2]and Ashley Vaughan[1,3]

Affiliation: [1]Seattle Children's Research Institute, Seattle, Washington, USA; [2]Institute for Systems Biology, Seattle, Washington, USA; [3]Department of Paediatrics, University of Washington, Seattle, Washington, USA

The human malaria parasite Plasmodium falciparum (Pf) expresses ten thrombospondin type-1 repeat domain (TSR) bearing proteins at different stages throughout its life cycle. It has been shown that TSRs can be modified by two types of glycosylation: O-fucosylation at conserved serine and threonine residues, and C-mannosylation at conserved tryptophan residues. In Pf, the major sporozoite surface protein, circumsporozoite protein (CSP), is fucosylated but not mannosylated. Pf CSP possesses a single TSR in which the threonine at amino acid position 337 has been proposed to be fucosylated. Here, we employed site-directed mutagenesis by CRISPR/Cas9 gene editing to generate a CSP TSR glycosylation-null mutant parasite, Pf CSP_T337A. The fitness of this mutant parasite across the life cycle was quantified in comparison to the parental NF54 and a CSP knockout line. As expected, the CSP knockout line failed to produce sporozoites in infected mosquitoes. However, the glycosylation-null parasite, Pf CSP_T337A, did not show defects in gametocytogenesis and transmission to mosquitoes, harbouring normal numbers of sporozoites in both the midgut and the salivary glands. Proteomic analysis of the mutant Pf CSP_T337A line revealed that the amino acid substitution completely abrogated the O-fucosylation of CSP. In addition, immunofluorescence assays and western blot analysis revealed no change in the localization and expression of CSP in the mutant line. However, salivary gland sporozoites isolated from mosquitoes infected with the mutant parasite were impaired in gliding motility. Thus, our results indicate a crucial role for CSP glycosylation in sporozoite motility.

Keywords: malaria; sporozoite; glycosylation; Plasmodium falciparum

Abstract No.: ABS0002216

TARGETING RELAPSING P. VIVAX INFECTION BY VACCINATION

Noah Sather

Authors: D. Noah Sather[1,2]

Affiliation: [1]University of Washington, Department of Pediatrics; [2]Seattle Children\'s Research Institute

Introduction: It is estimated that up to 80% of P. vivax infection is due to relapsing infections from the dormant hypnozoite, and thus, relapse infection is a primary driver of transmission and highly relevant to the development of vaccines against the pre-erythrocytic form of P. vivax. Reducing or preventing the formation of the hypnozoite, the liver form that causes relapsing infection, would reduce the number of active infections, and in turn, reduce the number of transmission events. Here we discuss our current work on pre-erythrocytic vaccine development for P. vivax.

Methods: Recombinant antigens were designed, produced, and studied in vitro. We immunized BALB/c mice to generate both polyclonal and monoclonal antibodies, the latter of which were isolated by single B cell tetramer sorting and cloning techniques, followed by RT-PCR rescue and recombinant production. We evaluated the effect of antibodies against pre-erythrocytic vaccine candidates on primary hepatocyte infection and relapse infection using a combination of in vitro and in vivo humanized mouse models.

Conclusions: We found that anti-CSP antibodies reduce the formation of both schizonts and hypnozoites, and ultimately the number of measured relapses in humanized mouse models, and that infection inhibition is dependent on high affinity interactions with the antigen. Non-CSP antibodies also reduce primary infection of primary hepatocytes, but have a less clear ability to reduce hypnozoite formation. These studies indicate that even in the absence of sterile protection, a partially protective vaccine may be effective in combating transmission by reducing the number or experienced relapses.

Keywords: plasmodium vivax; antibody; vaccine; monoclonal; circumsporozoite protein

Thursday 14 December 2023

S21: Melioidosis: Clinical, Diagnostic and Environmental Aspects

08.30-10.00hr

Room E

Thursday 14 December 2023

S21: Melioidosis: Clinical, Diagnostic and Environmental Aspects

08.30-10.00hr

Room E

Chairperson:
1. Paul J. Brett
2. Assist. Prof. Muthita Vanaporn

Invited speaker:

1. Clinical aspects of melioidosis in Northeast Thailand
Narisara Chantratita
Faculty of Tropical Medicine, Mahidol University (Microbiology and Immunology)

2. DEVELOPMENT OF MELIMO, A COMMERCIAL PCR FOR DIAGNOSIS OF MELIOIDOSIS
Chawitar Noparatvarakorn
Faculty of Tropical Medicine, Mahidol University (Microbiology and Immunology)

3. REGISTRATION AND VALIDATION OF SECOND-GENERATION ICT FOR DIAGNOSIS OF MELIOIDOSIS
Hasyanee Binmaeil
Faculty of Tropical Medicine, Mahidol University (Microbiology and Immunology)

4. ENVIRONMENTAL DISTRIBUTION OF BURKHOLDERIA PSEUDOMALLEI IN THAI-LAO BORDERS
Kamolchanok Rukseree
Other (Department of Medical Science, Amnatcharoen Campus, Mahidol University)

5. Longitudinal dynamics of antibody response in melioidosis
Natnaree Saiprom
Faculty of Tropical Medicine, Mahidol University (Microbiology and Immunology)

Abstract No.: ABS0002277

Clinical aspects of melioidosis in Northeast Thailand

Narisara Chantratita

Authors: Narisara Chantratita[1,2], Rungnapa Phunpang[1,2], Atchara Yarasai[1], Adul Dulsuk[1,2], Thatcha Yimthin[1], Lauren A. Onofrey[3], Taylor D. Coston[3], Ekkachai Thiansukhon[4], Seksan Chaisuksant[5], Kittisak Tanwisaid[6], Somchai Chuananont[6], Chumpol Morakot[7], Narongchai Sangsa[8], Sunee Chayangsu[9], Wirayut Silakun[10], Noppol Buasi[11], Ploenchan Chetchotisakd[12], Nicholas P. J. Day[2,13], Ganjana Lertmemongkolchai1[4,15], T. Eoin West[1,3,16]

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[16]Department of Global Health, University of Washington, Seattle, WA, USA

Melioidosis is a neglected tropical infection caused by the environmental saprophyte Burkholderia pseudomallei. We conducted a prospective, observational study at nine hospitals in northeastern Thailand, a hyperendemic melioidosis zone, to define current characteristics of melioidosis patients and quantify outcomes over one year. 2574 individuals hospitalised with culture-confirmed melioidosis were screened and 1352 patients were analysed. The median age was 55 years, 975 (72%) were male and

951 (70%) had diabetes. 561 (42%) patients presented with lung infection, 1042 (77%) were bacteraemic, 442 (33%) received vasopressors/inotropes and 547 (40%) received mechanical ventilation. 1307 (97%) received an intravenous antibiotic against B. pseudomallei. 335/1354 (25%) patients died within one month and 448/1331 (34%) of patients died within one year. Most patients had risk factors for melioidosis, but patients without identified risk factors did not have a reduced risk of death. Of patients discharged alive, most received oral trimethoprim-sulfamethoxazole, which was associated with decreased risk of post-discharge death; 235/970 (24%) were readmitted, and 874/1015 (86%) survived to one year.

Recurrent infection was detected in 17/1018 patients (2%). Patients with risk factors other than diabetes had increased risk of death and increased risk of hospital readmission. In northeastern Thailand, patients with melioidosis experience high rates of bacteraemia, organ failure and death. Most patients discharged alive survive one year although all-cause readmission is common. Recurrent disease is rare. Strategies that emphasize prevention, rapid diagnosis and intensification of early clinical management are likely to have greatest impact in this and other resource-restricted regions.

Keywords: melioidosis, Northeast Thailand

Abstract No.: ABS0002162

DEVELOPMENT OF MELIMO, A COMMERCIAL PCR FOR DIAGNOSIS OF MELIOIDOSIS

Chawitar Noparatvarakorn

Authors: Noparatvarakorn C[1], Jakkul W[1], Ottiwet O[2], Janon R[3], Chantratita N[1, 4]

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[3]Department of Medicine, Mukdahan Hospital, Mukdahan, Thailand
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Melioidosis is a severe infectious disease caused by Burkholderia pseudomallei. It is a significant health threat in tropical regions. Diverse clinical presentations and the lack of rapid, accurate diagnostics often lead to delayed intervention and fatal outcomes. To improve the laboratory diagnosis, we developed MELIMO, a user-friendly real-time polymerase chain reaction (PCR) kit for accurate B. pseudomallei detection in various clinical samples. MELIMO encompasses the mastermix, specific primers, and a probe for B. pseudomallei detection. It integrates an internal control, positive control, and negative control, ensuring a complete and reliable diagnostic solution. The internal control validates the extraction process and DNA amplification, enhancing accuracy and facilitating immediate error detection and correction, obviating batch retesting. The MELIMO PCR kit demonstrates high sensitivity and specificity, significantly boosting diagnostic speed and accuracy. Its versatility in detecting the target across diverse sample types extends its utility beyond clinical settings, proving valuable for epidemiological studies and research. MELIMO has extensive application in medical institutions, notably high-workload hospitals, academic establishments, and research organizations. Its user-friendly design, featuring color-coded labeling for reagent tubes and internal control, minimizes human error risks during preparation. Additionally, the compact kit size simplifies storage, ensuring ready access to fresh, reliable reagents, optimizing efficiency and convenience. In summary, MELIMO marks a substantial stride in melioidosis diagnostics, offering a reliable, efficient solution. Its potential to elevate patient care and streamline public health efforts emphasizes its crucial role in combatting melioidosis and reducing public health burden, particularly in regions endemic to melioidosis.

Keywords: Burkholderia pseudomallei, melioidosis, PCR, internal control, diagnosis, MELIMO

Abstract No.: ABS0002161

REGISTRATION AND VALIDATION OF SECOND-GENERATION ICT FOR DIAGNOSIS OF MELIOIDOSIS

Hasyanee Binmaeil

Authors: Hasyanee Binmaeil[1], Narisara Chantratita[1], Paul J. Brettb[2], Mary N. Burtnick[2]

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Melioidosis infection affects 165,000 people each year worldwide and causes 89,000 deaths annually. We have developed a rapid Immunochromatography test (ICT) for melioidosis with the sensitivity of 88.3% and specificity of 86.1%. Recently, the second-generation ICT has been developed to improve the sensitivity and specificity of the first-generation ICT test. The objective of this study was to develop the second-generation ICT and evaluate the performance of the ICT test, and validation of product performance in the real clinical settings for regulatory submission. We have developed the second-generation ICT using a hemolysin-coregulated protein as target antigen for melioidosis under ISO 13485. We evaluated the ICT tests using serum, plasma and whole blood samples obtained from 3 groups of human subjects (110 culture-confirmed melioidosis, 110 healthy donors, and 110 patients infected with other organisms). The performance of the ICT tests compared with culture considered as the gold standard. The sensitivity of second-generation ICT when performed on serum, plasma, and whole blood samples were 87.5%, 75%, and 75%, respectively while the specificity was 95%, 95%, and 100%, respectively. At the end of this project, the ICT tests have been up-levelled to TRL 9 and approved by the Thai FDA for medical device. Using serum samples, the ICT tests showed the high sensitivity and specificity. An ongoing study is evaluating the performance of second-generation ICT in Thailand and other countries using stored serum samples. The ICT test is a potential test that provides reliable results in the clinical diagnosis of melioidosis for serological surveillance.

Keywords: *Burkholderia pseudomallei*, immunochromatography test, antibody detection, melioidosis, serological diagnosis

Abstract No.: ABS0002160

ENVIRONMENTAL DISTRIBUTION OF BURKHOLDERIA PSEUDOMALLEI IN THAI-LAO BORDERS

Kamolchanok Rukseree

Authors: Rukseree K[1], Boonyanugomol W[1], Ruangchai W[2], Palittapongarnpim P[2]

Affiliation:[1]Department of Medical Science, Amnatcharoen Campus, Mahidol University; [2]Professor Pornchai Matangkasombut Center for Microbial Genomics, Department of Microbiology, Faculty of Science, Mahidol University

Melioidosis is a life-threatening infection caused by the gram-negative environmental bacterium, Burkholderia pseudomallei. This study aimed to survey the presence of the bacterium in soil collected from each side of the 2 main roads, Route 212 and Route 12, heading to the border checkpoints between Mukdahan, Thailand, and Savannakhet, Lao PD. From the border gate, 4 main sampling sites were set 20 km apart, at which the soil was collected from both sides of the road, At each site, soil was collected from 9 sampling points designated by a 2x 2 grid of square (1 m x 1 m) at the depth of 30 cm. Soil samples were collected twice from Route 212 in December 2014 and December 2016, and from Route 12 in November 2016 and June 2017. Totally, 288 soil samples were collected and cultured using selective media, threonine-basal salt solution plus Colistin and Ashdown agar. Suspected colonies of B. pseudomalle were identified by latex agglutination test, antimicrobial susceptibility test and biochemical test. Thirty-seven (12.85%) of soil samples were culture positive for B. pseudomallei. Using multilocus sequence typing (MLST), 14 sequence types (STs) were identified. The STs among the isolates were ST70 (n=5), ST168 (n=4), ST208 (n=4), ST34 (n=3), ST50 (n=2), ST206 (n=2) and ST492 (n=2), respectively. Other STs, ST48, ST157, ST174, ST306, ST486, ST538 and ST654, were found in only one isolate each. There are still nine isolates that have not yet been identified. This survey showed the wide distribution of B. pseudomallei in northeast Thailand.

Keywords: Melioidosis, Burkholderia pseudomallei, multilocus sequence typing, sequence type

Abstract No.: ABS0002278

Longitudinal dynamics of antibody response in melioidosis

Natnaree Saiprom

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Affiliation: Faculty of Tropical Medicine, Mahidol University

No abstract available

Keyword: No abstract available

Thursday 14 December 2023

S22: Acute Undifferentiated Fever (AUFI): 2023 Update (Faculty of Medicine Siriraj Hospital, Mahidol University)

10.30-12.00hr

Room A

Thursday 14 December 2023

S22: Acute Undifferentiated Fever (AUFI): 2023 Update (Faculty of Medicine Siriraj Hospital, Mahidol University)

10.30-12.00hr

Room A

Chairperson:
1. Yupin Suputtamongkol
2. Napaporn Sriden

Invited speaker:

1. DIAGNOSTIC VALUES OF VIRAL TARGET ENRICHED AND METAGENOMIC NGS AMONG PATIENTS WITH ACUTE UNDIFFERENTIATED FEVER IN THAILAND
Yupin Suputtamongkol
Other (Faculty of Medicine Siriraj Hospital, Mahidol University)

2. Human Scrub Typhus Trends: Northeast, Thailand 2011-2023
Wilawan Thipmontree
Other (Department of Internal Medicine, Maharat Nakhon Ratchasima Hospital Nakhon Ratchasima, Thailand)

3. Ivermectin against chikungunya infection: an experience from compassionate use during the urban outbreak in Southern Thailand
Sarunyou Chusri
Other (Department of Internal Medicine, Faculty of Medicine, Prince of Songkla University)

Abstract No.: ABS0002217

DIAGNOSTIC VALUES OF VIRAL TARGET ENRICHED AND METAGENOMIC NGS AMONG PATIENTS WITH ACUTE UNDIFFERENTIATED FEVER IN THAILAND

Yupin Suputtamongkol

Authors: Suputtamongkol Y[1,2], Berg MG[2,3], Cloherty GA[2,3]

Affiliation: [1]Faculty of Medicine Siriraj Hospital, Mahidol University, Thailand, [2]Abbott Pandemic Defense Coalition (APDC), [3]Abbott Laboratories, Abbott Park, IL USA

Background: Despite extensive laboratory testing, pathogens were detected in approximately 50% of patients hospitalized with acute undifferentiated febrile illness (AUFI). We reported here the diagnostic usefulness of viral target enrichment (Comprehensive Viral Research Panel or CVRP; Twist Biosciences) and metagenomic Next Generation Sequencing (mNGS) for the identification of known and novel pathogens in this population.

Methods: Plasma from 442 patients with AUFI were studied. Reads were taxonomically classified by the SURPI or DiVir pipelines and viral reads were mapped in the CLC Bio Genomics Workbench (Qiagen, Inc).

Results: We identified viruses in 23% of them by CVRP. mNGS has increased viral detection to 26.8% and the overall pathogen detection to 41.8%. Both methods identified relatively prevalent viruses such as Dengue, HIV-1, HBV, HAV and Chikungunya, infrequently detected viruses such as Measles, HHV-6B, CMV, and emerging viruses such as Severe Fever with Thrombocytopenia Syndrome (SFTS) virus. We observed a high degree of correlation between viruses detected and their clinical data. The most frequent bacterial pathogens detected were Rickettsia typhi and R. felis. Other uncommon bacterial pathogens included Capnocytophaga carnimorsus, Salmonella enterica and Leptospira interrogans.

Conclusions: Viral and rickettsial infections were important etiologies for AUFI in Thailand. This data supports the current recommendation of empirical therapy with ceftriaxone and doxycycline or azithromycin in severe or hospitalized AUFI. Thus, it has implications for proper management of AUFI including lower rates of unnecessary testing and antimicrobial use. We highlight the need to improve diagnostics for several pathogens in Thailand, particularly rickettsial infections and

Keywords: acute undifferentiated febrile illness, metagenomic Next Generation Sequencing, Rickettsia, SFTSV

Abstract No.: ABS0002279

Human Scrub Typhus Trends: Northeast, Thailand 2011-2023

Wilawan Thipmontree

Authors: Wilawan Thipmontree

Affiliation: Department of Internal Medicine, Maharat Nakhon Ratchasima Hospital Nakhon Ratchasima, Thailand

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002283

Ivermectin against chikungunya infection: an experience from compassionate use during the urban outbreak in Southern Thailand

Sarunyou Chusri

Authors: Sarunyou Chusri

Affiliation: Department of Internal Medicine, Faculty of Medicine, Prince of Songkla University

No abstract available

Keyword: No abstract available

Thursday 14 December 2023

S23: Recent Advance in Leishmaniasis Research in Thailand

10.30-12.00hr

Room B

Thursday 14 December 2023

S23: Recent Advance in Leishmaniasis Research in Thailand

10.30-12.00hr

Room B

Chairperson:
1. Mathirut Mungthin
2. Sonthaya Tiawsirisup

Invited speaker:

1. EPIDEMIOLOGY OF LEISHMANIASIS IN THAILAND: TRACING THE PAST AND ENVISIONING THE FUTURE
Phunlerd Piyaraj
Other (Phramongkutklao College of Medicine)

2. Promising Evidence Incriminating Culicoides Biting Midges as Important Vectors for Autochthonous Leishmaniasis in Thailand
Padet Siriyasatien
Other (Department of Parasitology, Faculty of Medicine, Chulalongkorn University)

3. DEVELOPMENT OF SIMPLIFIED QUANTITATIVE LAMP ASSAY FOR SCREENING LEISHMANIA INFECTION IN ASYMPTOMATIC PATIENTS WITH HIV
Toon Ruang-areerate
Other ()

4. Omics study of Leishmania species in Thailand
Teerasak E-kobon
Other (Faculty of Science, Kasetsart University)

Abstract No.: ABS0002219

EPIDEMIOLOGY OF LEISHMANIASIS IN THAILAND: TRACING THE PAST AND ENVISIONING THE FUTURE

Phunlerd Piyaraj

Authors: Phunlerd Piyaraj[1], Mathirut Mungthin[1], Saovanee Leelayoova[1], Toon Ruang-Areerate[1], Suradej Siripattanapipong[2]

Affiliation: [1]Department of Parasitology, Phramongkutklao College of Medicine, Bangkok, Thailand, [2]Department of Microbiology, Faculty of Science, Mahidol University, Bangkok, Thailand

Leishmaniasis is a neglected tropical disease that poses a significant health burden, particularly among immunocompromised individuals such as HIV-infected patients. Understanding the prevalence and risk factors of Leishmania infection in specific populations is crucial for effective prevention and control strategies. This study aimed to determine the prevalence of leishmaniasis and identify associated risk factors among HIV-infected patients in Satun Province, one affected area of leishmaniasis in southern Thailand. A cross-sectional study was conducted among 650 HIV-infected individuals at a tertiary-care hospital. Data on demographic characteristics, clinical parameters, and potential risk factors were collected. Individual plasma, buffy coat, and saliva samples were collected. Leishmania infection was determined using the Direct Agglutination Test (DAT) and nested polymerase chain reaction (nPCR) of nPCR-buffy coat and nPCR-saliva. Logistic regression analysis assessed the association between risk factors and Leishmania infection. The prevalence of Leishmania infection was 8.61% (56/650). Species identification was identified among 18 HIV-infected patients as follows: Leishmania orientalis (n = 12), Leishmania martiniquensis (n = 4), and Leishmania donovani complex (n = 2). Each one-year increase in age was associated with 3% higher odds of infection. Intravenous drug users had significantly higher odds of Leishmania infection. Individuals with a CD4 cell count < 500 cells/mm3 and a viral load > 50 copies/mL also had increased odds of infection. Other factors such as sex, education, opportunistic infection, recreational drug use, bed net use, animal raising, and living in a stilt house did not show a significant independent association with Leishmania infection. The prevalence of

Keywords: Leishmania infection, Prevalence, Risk factors, HIV-infected patients, Thailand

Abstract No.: ABS0002204

Promising Evidence Incriminating Culicoides Biting Midges as Important Vectors for Autochthonous Leishmaniasis in Thailand

Padet Siriyasatien

Authors: Siriyasatien P[1]

Affiliation:[1]Center of Excellence in Vector Biology and Vector-Borne Disease, Department of Parasitology, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand

Leishmaniasis is a neglected tropical disease that has been traditionally known to be transmitted by phlebotomine sand flies. In the past, Thailand was regarded as a non-endemic area of this disease. However, autochthonous leishmaniasis has been continuously reported in Thailand since 1996, especially in the northern and southern parts of Thailand. Most autochthonous cases were caused by two Leishmania species in the newly classified Mundinia subgenus, namely L. martiniquensis and L. orientalis. The interesting question is which insect species are responsible for the disease transmission. Importantly, there was experimental evidence demonstrating 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 Mundinia species are most likely to be spread by Culicoides biting midges rather than sand flies. To confirm this, we investigated the species diversity and abundance of Culicoides in the endemic areas of Thailand and also dissected the midgut of the midges to reveal the presence of living Leishmania promastigotes as well as metacyclic colonization at the stomodeal valve. The positive microscopic finding was molecularly confirmed by PCR and sequencing, showing that amplicons belong to L. martiniquensis. In addition, we also explored the host preference of engorged Culicoides and found that some species can feed on humans. Altogether, our field evidence corroborates the former experimental findings, strongly advocating that Culicoides biting midges are most likely to be natural vectors of Mundinia leishmaniasis in Thailand.

Keywords: Culicoides biting midges, Autochthonous leishmaniasis, Leishmania, Mundinia, Vector incrimination

Abstract No.: ABS0002210

DEVELOPMENT OF SIMPLIFIED QUANTITATIVE LAMP ASSAY FOR SCREENING LEISHMANIA INFECTION IN ASYMPTOMATIC PATIENTS WITH HIV

Toon Ruang-areerate

Authors: Toon Ruang-areerate[1], Phunlerd Piyaraj[1], Suradej Siripattanapipong[2], Wijitar Dungchai[3], Panthita Ruang-areerate[4], Saovanee Leelayoova[1] and Mathirut Mungthin[1]

Affiliation: [1]Department of Parasitology, Phramongkutklao College of Medicine, Bangkok, 10400, Thailand; [2]Department of Microbiology, Faculty of Science, Mahidol University, Bangkok, 10400, Thailand; [3]Analytical Chemistry, Department of Chemistry, Faculty of Science, King Mongkut's University of Technology Thonburi, Bangkok, 10140, Thailand; [4]National Omics Center, National Science and Technology Development Agency (NSTDA), Pathum Thani, 12120, Thailand

Asymptomatic visceral leishmaniasis cases have continuously increased, particularly among patients with HIV who are at risk to develop further symptoms of leishmaniasis. A simple, sensitive and reliable diagnosis is crucially needed because risk populations mostly reside in rural communities with limited resources of laboratory equipment. In our study, a highly sensitive and selective determination of Leishmania among asymptomatic patients with Leishmania/HIV co-infection was successfully developed to simultaneously interpret and semi-quantify using 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 3 detection methods were equivalent and had reliable performances achieving as high as 95.5%. Limits of detection were 102 parasites/mL (0.0147 ng/µL) which were 10 times more sensitive than other related studies. This simplified quantitative LAMP assay using dPAD combined with SYBR safe and gold nanoparticle probe is reliably fast, simple, inexpensive and practical for field diagnostics to point-of-care settings in resource-limited areas which can be set up in all levels of healthcare facilities, especially in low to middle income countries, to empower leishmaniasis surveillance as well as prevention and control.

Keywords: Leishmania, LAMP, quantitative, paper device, SYBR safe, gold nanoparticle, probe

Abstract No.: ABS0002286

Omics study of Leishmania species in Thailand

Teerasak E-kobon

Authors: Teerasak E-kobon

Affiliation: Faculty of Science, Kasetsart University

No abstract available

Keyword: No abstract available

Thursday 14 December 2023

S24: Latest Updates on the Top 3 Dengue Vaccines

10.30-12.00hr

Room C

Thursday 14 December 2023

S24: Latest Updates on the Top 3 Dengue Vaccines

10.30-12.00hr

Room C

Chairperson:
1. Chukiat Sirivichayakul
2. Kriengsak Limkittikul

Invited speaker:

1. Optimizing Dengue Vaccine Strategies for Thailand: Aligning Health Policy Perspectives
NAKORN PREMSRI
Other (Chulalongkorn University)

2. TAK-003: LONG-TERM DENGUE PROTECTION WITH A NEXT-GENERATION DENGUE VACCINE - A COMPREHENSIVE UPDATE
Walid Kandeil
Other (Takeda)

3. TV003: A NEW DENGUE VACCINE CANDIDATE
Louis Macareo
Other (MSD)

Abstract No.: ABS0002287

Optimizing Dengue Vaccine Strategies for Thailand: Aligning Health Policy Perspectives

NAKORN PREMSRI

Authors: Nakorn Premsri

Affiliation: National Vaccine Institute

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002170

TAK-003: LONG-TERM DENGUE PROTECTION WITH A NEXT-GENERATION DENGUE VACCINE - A COMPREHENSIVE UPDATE

Walid Kandeil

Authors: Kandeil W, Patel S

Affiliation: Takeda Pharmaceuticals International AG, Zurich, Switzerland

Introduction: QDENGA® (TAK-003) is a live, attenuated tetravalent dengue vaccine, approved for prevention of dengue disease caused by any dengue virus serotype in several countries. The clinical development program has evaluated TAK-003 in Phase I-III trials in dengue-endemic and non-endemic countries, including the ongoing Phase III trial (DEN-301, NCT02747927) which has data up to 4.5 years post-second dose.

Methods: Efficacy, safety and immunogenicity of TAK-003 have been evaluated in 19 trials including 28,175 participants aged 1.5-60 years in 13 countries. In DEN-301, dengue-naïve and -exposed healthy participants aged 4–16 years (n=20,099) were randomized 2:1 to receive two doses of TAK-003 or placebo three months apart in 8 dengue-endemic countries.

Results: Safety and immunogenicity data from Phase I/II trials established the formulation and dosing schedule. In DEN-301, an overall VE of 80.2% (95% CI: 73.3–85.3) against VCD (primary endpoint) was achieved. VE of 90.4% (95% CI: 82.6–94.7) against hospitalized VCD was also demonstrated. Cumulative VE through 54 months post-second dose was 61.2% (95% CI: 56.0–65.8) against VCD and 84.1% (95% CI: 77.8–88.6) against hospitalized VCD. Efficacy varied by serotype and some decline in efficacy was noted in a year-to-year comparison but remained robust against hospitalized VCD. SAEs were low (5.0% TAK-003 and 5.9% placebo); none were vaccine-related.

Conclusions: TAK-003 was efficacious against symptomatic dengue and had sustained long-term efficacy against hospitalized VCD up to 4.5 years post-second dose in both dengue-naïve and -exposed participants. Furthermore, TAK-003 was well-tolerated by participants aged 4-60 years with no important safety risk identified.

Keywords: TAK-003, dengue, vaccine, safety, efficacy, long-term

Abstract No.: ABS0002223

TV003: A NEW DENGUE VACCINE CANDIDATE

Louis Macareo

Authors: Macareo LR[1]

Affiliation: [1]MSD

Introduction: An attenuated live virus quadrivalent dengue vaccine formulation, referred to as TV003, originated at the Laboratory for Infectious Diseases at the National Institute for Allergy and Infectious Disease (NIAID), U.S. National Institutes of Health (NIH). NIH licensed the technology to partners interested in advancing development towards licensure including, but not limited to, Institute Butantan and MSD.

Method: Review of the characteristics of the TV003 vaccine candidate and its development, including key clinical study results.

Result: The TV003 formulation was evaluated in studies conducted by several manufacturers using their own manufacturing processes and product. When given as a single dose, TV003 was demonstrated to be generally safe, producing broad immunogenicity, and field-based efficacy against dengue serotypes 1 and 2 in subjects both seronegative and seropositive to dengue at baseline. Studies to determine efficacy against other serotypes are planned.

Conclusion: The TV003 vaccine candidate formulation is being advanced by multiple manufacturers as a single dose vaccine with the intent to provide efficacy against multiple dengue serotypes in both endemic regions and to travelers in non-endemic regions.

Keywords: dengue, arboviruses, dengue vaccine, MSD, Institute Butantan, NIH, TV003

Thursday 14 December 2023

S25: Progress and Challenges in Eliminating Malaria in Southeast Asia

10.30-12.00hr

Room D

Thursday 14 December 2023

S25: Progress and Challenges in Eliminating Malaria in Southeast Asia

10.30-12.00hr

Room D

Chairperson:
1. CAPT Andrew Letizia
2. LT Huy Nguyen

Invited speaker:

1. CURRENT MALARIA SITUATION IN VIETNAM WITH FOCUS ON ANTIMALARIAL DRUG RESISTANCE TRENDS AND CHALLENGES IN ELIMINATING MALARIA BY 2030
Quang Huynh Hong
Other (Institute of Malariology, Parasitology, and Entomology Quy Nhon, Vietnam)

2. CURRENT MALARIA SITUATION IN MALAYSIA WITH FOCUS ON THE CHALLENGES POSED BY SIMIAN MALARIAS AND THEIR VECTORS
Van Lun Low
Other (Universiti Malaya)

3. CURRENT MALARIA SITUATION AND CHALLENGES TO ACHIEVE ELIMINATION IN LAOS
Moritoshi Iwagami
Other (National Center for Global Health and Medicine (NCGM))

4. Progress and current challenges of eliminating malaria in Thailand
Jetsumon Prachumsri
Faculty of Tropical Medicine, Mahidol University (Mahidol Vivax Research Unit (MVRU))

Abstract No.: ABS0002158

CURRENT MALARIA SITUATION IN VIETNAM WITH FOCUS ON ANTIMALARIAL DRUG RESISTANCE TRENDS AND CHALLENGES IN ELIMINATING MALARIA BY 2030

Quang Huynh Hong

Authors: Huynh Hong Quang[1], Chau Van Khanh[1], Michael D. Edstein[2], Andrew G Letizia[3], Huy Nguyen[3], Marina Chavchich[2]

Affiliation:[1]Institute of Malariology, Parasitology, and Entomology, Quy Nhon, Vietnam; [2]Australian Defence Force Malaria and Infectious Disease Institute, Brisbane, Australia; [3]US Naval Medical Research Unit Indo-Pacific, Sembawang, Singapore.

Introductions: Vietnam has successfully reduced malaria incidence by more than 90% over the past 5 years, and on the way for malaria elimination roadmap. However, the osillating malaria burden resides in high-risk populations of seasonal labors, forest-goers, field-hut sleepers at remote zones in Vietnam.

Methods: Evidence-based data descriptive study.

Results: Especially in 2023, an outbreak of malaria happening in a Coastal Central province of Khanh Hoa. On the other hand, An. minimus, An. dirus vector complexes in the villages, forests, and malaria ecology presents multiple challenges. These are warning red flag, and informing the risk of malaria to increase again, and should not be underestimated. Delayed response and resistance in P. falciparum to artemisinin and partner drugs, and potentially in P. vivax to chloroquine, is one of the biggest challenges in elimination phase. Dihydroartemisinin-piperaquine (DHA-PPQ) was reported being resisted by P. falciparum in provinces border to Cambodia. This led to the change of first-line therapy to artesunate-pyronaridin tetraphospate (Pyramax@). Therefore, therapeutic efficacy study is a must-to-do routine task. In addition, molecular marrkers are needed to track resistance to arrtemisinine and partner drugs as the GMS has confirmed resistance, so delayed clearance is to be expected for all ACTs. Hence, at the same TES/iDES, all dry blood spot (DBS) will be important to look molecular resistance markers in both resistance-confirm and unconfirm zones in line with whole-of-system responses.

Conclusion: With all above risk factors, should be addressed through malaria elimination programmes and rational interventional strategies in Vietnam in the next steps.

Keywords: Malaria trend, antimalarial drug efficacy, molecular markers

Abstract No.: ABS0002146

CURRENT MALARIA SITUATION IN MALAYSIA WITH FOCUS ON THE CHALLENGES POSED BY SIMIAN MALARIAS AND THEIR VECTORS

Van Lun Low

Authors: Van Lun Low[1], Indra Vythilingam[2]

Affiliation:[1]Tropical Infectious Diseases Research & Education Centre, Universiti Malaya, Malaysia; [2]Department of Parasitology, Faculty of Medicine, Universiti Malaya, Malaysia

This talk delves into the evolving malaria landscape in Malaysia, spotlighting the emergence of simian malarias, such as Plasmodium inui and Plasmodium cynomolgi. While Plasmodium knowlesi has been extensively studied, these less familiar simian malaria species are gaining recognition. Recent research has uncovered the potential for Plasmodium inui and Plasmodium cynomolgi to infect humans, heightening concerns about zoonotic transmission. Originally limited to non-human primates, these emerging parasites have demonstrated the capacity to cross species boundaries, resulting human infections. Comprehensive understanding of their epidemiology and vectors is essential for effective malaria control. This talk will delve into the challenges presented by their respective Anopheles vectors and the resultant implications for malaria transmission dynamics. Acknowledging the evolving nature of simian malarias beyond P. knowlesi is vital in the ongoing battle against malaria in Malaysia. The talk also underscores the significance of sustained research, vigilant surveillance, and collaborative efforts to address these emerging challenges in malaria control.

Keywords: simian malaria, infectious diseases, Anopheles, Malaysia

Abstract No.: ABS0002132

CURRENT MALARIA SITUATION AND CHALLENGES TO ACHIEVE ELIMINATION IN LAOS

Moritoshi Iwagami

Authors: Moritoshi Iwagami[1,2]

Affiliation:[1]Institut Pasteur du Laos, Ministry of Health, Vientiane Capital, Lao PDR
[2]National Center for Global Health and Medicine, Tokyo, Japan

Morbidity and mortality of malaria have decreased drastically over the last decade in Lao People's Democratic Republic (PDR). The Lao government and WHO adopted the goal of eliminating falciparum malaria by 2025 and eliminating all other human malaria by 2030. However, several challenges are remaining to achieve this ambitious goal. Artemisinin-based combination therapies (ACTs) are used for the first-line treatment of malaria in Lao PDR. However, prevalence of mutations in K13 gene of Plasmodium falciparum genome which is responsible for artemisinin resistance is increasing in Lao PDR and the neighboring countries. In addition, asymptomatic Plasmodium carriers and low-parasite density infection were found in the several endemic areas in the Greater Mekong Sub-region. Such infections can be a source of malaria transmission by Anopheles mosquito but those infected people will not seek treatment for malaria because they have no signs and symptoms of malaria. Mobile and migrant people are high-risk population for malaria but they are often far from healthcare services including malaria treatment. In 2023, the Lao Ministry of Health and WHO conducted a targeted mass drug administration (tMDA) for malaria in some selected districts in Savannakhet and Attapeu provinces in Lao PDR. Although the tMDA seems to be highly effective in the districts, the tMDA may have a risk of emergence of drug resistant malaria. Therefore, careful monitoring of drug resistance, and detection and treatment for asymptomatic Plasmodium carriers by using a highly sensitive diagnosis, such as LAMP method is needed to accelerate malaria elimination in Lao PDR.

Keywords: Malaria, Lao PDR, artemisinin resistance, asymptomatic Plasmodium carriers, Elimination

Abstract No.: ABS0002289

Progress and current challenges of eliminating malaria in Thailand

Jetsumon Prachumsri

Authors: Jetsumon Prachumsri

Affiliation: Faculty of Tropical Medicine, Mahidol Univeristy

No abstract available

Keyword: No abstract available

Thursday 14 December 2023

S26: Digital Surveillance for Disease Prevention and Control (Thai Language)

10.30-12.00hr

Room E

Thursday 14 December 2023

S26: Digital Surveillance for Disease Prevention and Control (Thai Language)

10.30-12.00hr

Room E

Chairperson:
1. Visal Moolasart

Invited speaker:

1. Digital surveillance
Pawinee Doung-ngern
Other (Division of Epidemiology, Department of Disease Control)

2. Early warning and response system (EWARS) for dengue outbreaks in subdistrict level in Thailand
APINYA NIRAMITSANTIPONG
Other (DEPARTMENT OF DISEASES CONTROL)

3. Revolutionizing Malaria Elimination in Thailand: Unveiling the Cross-Border Surveillance System
Peeriya Watakulsin
Other (Medical physician and Field Epidemiologist at the Office of Disease Prevention and Control 2, Phitsanulok Province)

4. Mpox Mysteries in the Land of Smiles: Navigating Thailand's Encounter with the Risk Population
Theerasak Chaxnum
Other (Veterinarian/Division of Epidemiology)

5. Mpox Mysteries in the Land of Smiles: Navigating Thailand's Encounter with the Risk Population
Krittaecho Siripassorn
Other (Office of the Senior Expert Committee (OSEC), Department of Disease Control)

Abstract No.: ABS0002290

Digital surveillance

Pawinee Doung-ngern

Authors: Pawinee Doung-ngern

Affiliation: Division of Epidemiology, Department of Disease Control

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002291

Early warning and response system (EWARS) for dengue outbreaks in subdistrict level in Thailand

APINYA NIRAMITSANTIPONG

Authors: Apinya Niramitsantipong

Affiliation: Department of Disease Control

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002292

Revolutionizing Malaria Elimination in Thailand: Unveiling the Cross-Border Surveillance System

Peeriya Watakulsin

Authors: Peeriya Watakulsin

Affiliation: Medical physician and Field Epidemiologist at the Office of Disease Prevention and Control 2, Phitsanulok Province

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002315

Mpox Mysteries in the Land of Smiles: Navigating Thailand's Encounter with the Risk Population

Theerasak Chaxnum

Authors: Theerasak Chaxnum

Affiliation: Veterinarian/Division of Epidemiology

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002314

Mpox Mysteries in the Land of Smiles: Navigating Thailand's Encounter with the Risk Population

Krittaecho Siripassorn

Authors: Krittaecho Siripassorn

Affiliation: Office of the Senior Expert Committee (OSEC), Department of Disease Control

No abstract available

Keyword: No abstract available

Thursday 14 December 2023

Tropical Diagnosis Solutions-How to develop Tropical Diseases IVD assay with Raw Materials (Fapon) Biotech

12.00-13.00hr

Room E

Thursday 14 December 2023

Tropical Diagnosis Solutions-How to develop Tropical Diseases IVD assay with Raw Materials (Fapon) Biotech

12.00-13.00hr

Room E

Chairperson:
1. Nitaya Indrawattana

Invited speaker:
1. Tropical Diagnosis Solutions: How to develop Tropical Diseases IVD Research Used Kits with Raw Materials
Sandeep Kumar Vashist
Other (Fapon Biotech Inc.)

Abstract No.: ABS0002285

Tropical Diagnosis Solutions: How to develop Tropical Diseases IVD Research Used Kits with Raw Materials

Sandeep Kumar Vashist

Authors: Sandeep K. Vashist

Affiliation: Fapon Biotech Inc

No abstract available

Keyword: No abstract available

Thursday 14 December 2023

Vaccination Turn the TIDES in Fight Against Dengue: Role of the Vaccine and Recommendation (Takeda)

12.00-13.00hr

Room D

Thursday 14 December 2023

Vaccination Turn the TIDES in Fight Against Dengue: Role of the Vaccine and Recommendation (Takeda)

12.00-13.00hr

Room D

Chairperson:
1. Punnee Pitisuttithum

Invited speaker:

1. Vaccination Turn the TIDES in Fight Against Dengue: Role of the Vaccine and Recommendation
Punnee Pitisuttithum
Faculty of Tropical Medicine, Mahidol University (Clinical Tropical Medicine)

2. Vaccination Turn the TIDES in Fight Against Dengue: Role of the Vaccine and Recommendation
Chukiat Sirivichayakul
Faculty of Tropical Medicine, Mahidol University (Tropical Pediatrics)

Abstract No.: ABS0002282

Vaccination Turn the TIDES in Fight Against Dengue: Role of the Vaccine and Recommendation

Punnee Pitisuttithum

Authors: Punnee Pitisuttithum

Affiliation: Faculty of Tropical Medicine, Mahidol University

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002284

Vaccination Turn the TIDES in Fight Against Dengue: Role of the Vaccine and Recommendation

Chukiat Sirivichayakul

Authors: Chukiat Sirivichayakul

Affiliation: Faculty of Tropical Medicine, Mahidol University

No abstract available

Keyword: No abstract available

Thursday 14 December 2023

S27: Novel Knowledge and Concept in Sustainable Control of Tropical Helminthiases

13.45-15.15hr

Room A

Thursday 14 December 2023

S27: Novel Knowledge and Concept in Sustainable Control of Tropical Helminthiases

13.45-15.15hr

Room A

Chairperson:
1. Dorn Watthanakulpanich
2. Kittipong Chaisiri

Invited speaker:

1. ENHANCED DISCRIMINATION OF PARASITES IN STOOL EXAMINATIONS USING DEEP LEARNING APPROACH
Kaung Myat Naing
Other (College of Advanced Manufacturing Innovation, King Mongkut's Institute of Technology Ladkrabang)

2. A CALL TO ACTION FOR THE SUSTAINABLE CONTROL OF STRONGYLOIDIASIS IN SOUTHEAST ASIA IN THE ERA OF GLOBAL CHANGE
Abigail Hui En Chan
Faculty of Tropical Medicine, Mahidol University (Helminthology)

3. MOLECULAR AND MORPHOLOGICAL INSIGHTS INTO ANGIOSTRONGYLUS CANTONENSIS AND A. MALAYSIENSIS: A STUDY ON MISIDENTIFICATION RATES AND DIFFERENTIATION CHARACTERISTICS
Chanisara Kaenkaew
Faculty of Tropical Medicine, Mahidol University (Helminthology)

4. Lymphatic filariasis management in Thailand
Rawadee Kumlert
Other (Division of Vector Borne Diseases, Department of Disease control, Ministry of Public HealthThailand)

5. CHALLENGES IN DIAGNOSING NON-ENDEMIC HELMINTHIASES IN MALAYSIA
Azlin Muhammad
Other (Medical Faculty, Universiti Kebangsaan Malaysia)

Abstract No.: ABS0002094

ENHANCED DISCRIMINATION OF PARASITES IN STOOL EXAMINATIONS USING DEEP LEARNING APPROACH

Kaung Myat Naing

Authors: Kaung Myat Naing[1], Siridech Boonsang[2], Santhad Chuwongin[1], Veerayuth Kittichai[3], Teerawat Tongloy[1], Samrerng Prommongkol[4], Paron Dekumyoy[5] and Dorn Watthanakulpanich[5]

Affiliation: [1]Center of Industrial Robot and Automation (CiRA), College of Advanced Manufacturing Innovation, King Mongkut's Institute of Technology Ladkrabang, Bangkok, Thailand; [2]Department of Electrical Engineering, School of Engineering, King Mongkut\'s Institute of Technology Ladkrabang, Bangkok, Thailand; [3]Faculty of Medicine, King Mongkut\'s Institute of Technology Ladkrabang, Bangkok, Thailand; [4]Mahidol Bangkok School of Tropical Medicine, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [5]Department of Helminthology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand.

Introduction: Neglected tropical diseases (NTDs) are ancient ailments linked to poverty, imposing a significant human, societal, and economic burden, mainly affecting tropical and subtropical regions. The World Health Organization (WHO) estimates that annually, over 1.7 billion people require targeted prevention and treatment for at least one of these diseases. Stool examination serves as a microscopic diagnostic method to identify NTDs such as intestinal helminthic and protozoan parasite infections. Despite the necessity of diagnostic services for individuals in underdeveloped regions, equipment and trained personnel availability remain challenges. To address this, we introduce a deep learning-based stool examination approach for classifying 34 categories of helminthic and protozoan parasites.

Methods: Our methodology employs a modified direct smear method adapted from the simple direct smear and modified Kato-Katz methods to collect an image dataset through microscopy. This effort produced 1773 varied images, divided into 80% for model training and 20% for testing. For training, we chose the tiny version of You Only Look Once (YOLO) version 7 due to its remarkable accuracy and speed. The model's performance was assessed using an unseen test image dataset, utilizing the non-maximum suppression technique (default parameter of 0.4) and a statistically significant threshold (0.5).

Results: The model-wise evaluation achieved a precision of 93.95%, sensitivity of 92.09%, accuracy of 99.59%, and specificity of 99.82%.

Conclusion: The outcomes of this study demonstrate the effectiveness of our proposed method in discriminating parasites during stool examinations. This approach can serve as an initial stage to aid physicians in identifying parasite-related diseases among patients residing in

Keywords: Intestinal Parasites; Helminths; Protozoa; Stool Examination; Deep Learning; YOLOv4.

Abstract No.: ABS0002099

A CALL TO ACTION FOR THE SUSTAINABLE CONTROL OF STRONGYLOIDIASIS IN SOUTHEAST ASIA IN THE ERA OF GLOBAL CHANGE

Abigail Hui En Chan

Authors: Chan AHE[1], Kusolsuk T[1], Watthanakulpanich D[1], Pakdee W[1], Doanh PN[2], Yasin AM[3], Dekumyoy P[1], Thaenkham U[1]

Affiliation:[1]Department of Helminthology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [2]Institute of Ecology and Biological Resources, Graduate University of Science and Technology, Vietnam Academy of Science and Technology, Hanoi, Vietnam; [3]Department of Parasitology and Medical Entomology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Selangor, Malaysia

Strongyloidiasis, caused by *Strongyloides stercoralis* and *Strongyloides fuelleborni*, is estimated to affect over 600 million individuals worldwide. The disease is endemic in Southeast Asia, where a warm-humid climate and socio-economic conditions maintain the parasite's life cycle and transmission. Climate changes, globalization, and the emergence of zoonoses and infectious diseases in this era all contribute to strongyloidiasis transmission. Current diagnostic methods may not be sufficiently sensitive, suggesting that the true prevalence of strongyloidiasis could be underestimated. Therefore, we aim to determine the prevalence of strongyloidiasis in Southeast Asia through a systematic review, discuss diagnostic approaches, and advocate the need for a One-Health approach for sustainable control. Following PRISMA guidelines, we conducted a systematic literature search in PubMed and Google Scholar to identify studies reporting *Strongyloides* prevalence data in Southeast Asia. A random-effects model was employed to estimate the pooled prevalence of *S. stercoralis* at both regional and country levels. The estimated pooled prevalence of *S. stercoralis* regionally was 12.7% (95% CI: 10.70 – 14.80%), ranging from 0.4% to 24.9% at the country level. Cambodia had the highest pooled prevalence (24.9%, 95% CI: 15.65 – 35.38%), followed by Lao PDR (16.5%, 95% CI: 9.50 – 24.95%). Factors contributing to the strongyloidiasis transmission include the role of animal hosts, impact of global connectivity, and the significance of the co-endemicity of other *Strongyloides* species. Based on these findings, a multi-pronged One-Health approach is essential, especially in this era of global change.

Keywords: Strongyloides; Strongyloidiasis; Southeast Asia; Prevalence; Sustainable control

Abstract No.: ABS0002097

MOLECULAR AND MORPHOLOGICAL INSIGHTS INTO ANGIOSTRONGYLUS CANTONENSIS AND A. MALAYSIENSIS: A STUDY ON MISIDENTIFICATION RATES AND DIFFERENTIATION CHARACTERISTICS

Chanisara Kaenkaew

Authors: Kaenkaew C[1], Chan AHE[1], Saralamba N[2], Ruangsittichai J[3], Chaisiri K[1], Charoennitiwat V[1], Thaenkham U[1]

Affiliation:[1]Department of Helminthology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [2]Department of Molecular Tropical Medicine and Molecular Genetics, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [3]Department of Medical Entomology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

Angiostrongylus cantonensis and *A. malaysiensis*, have been reported to share similar hosts and life cycles. Those two species have reported outbreak of angiostrongyliasis and both *A. cantonensis* and *A. malaysiensis* DNA were present in cerebrospinal fluid of affected patients in Thailand. The morphological similarities, overlapping distribution, and genetic background of these closely related species pose challenges in accurately identifying them. This study aims to evaluate the morphological characters of both *A. cantonensis* and *A. malaysiensis* after confirming their genetics using the mitochondrial cytochrome b gene. Males and females of 257 *Angiostrongylus* spp. adults from 19 different geographical localities in Thailand were first morphologically identified. Molecular identification using the cytochrome b gene was then performed using the species-specific SYBR Green quantitative PCR method. Morphological characters were validated with the species identity obtained after molecular identification. The results revealed that 35.8% were morphologically identified as *A. cantonensis* while 64.2% were *A. malaysiensis*. After confirming genetic background, 42.8% and 57.2% were identified as *A. cantonensis* and *A. malaysiensis*, respectively. Overall, the percentage of misidentification was 14%. The findings indicate that morphological misidentifications frequently occur between these closely related species because they share similar morphological characteristics. Our validation revealed that while certain male characteristics such as body length and width can help distinguish between those species, female traits are difficult for differentiation. Through our findings, we suggest that molecular identification can support accurate species identification for closely related species like *A. cantonensis* and *A. malaysiensis*.

Keywords: *Angiostrongylus cantonensis*; *Angiostrongylus malaysiensis*; Morphological identification; Molecular identification; cytochrome b gene; Thailand

Abstract No.: ABS0002091

Lymphatic filariasis management in Thailand

Rawadee Kumlert

Authors: Kumlert R[1], Sarasan T[1], Prapawicha A[1], Mongkalangoon P[1], Gopinath D[2]

Affiliation: [1]Division of Vector Borne Diseases, Department of Disease Control, Ministry of Public Health, Nonthaburi, Thailand; [2]World Health Organization (WHO), Country Office, Thailand

Introduction: WHO validated the elimination of LF as a public health problem in Thailand in 2017 with a recommendation for continued post validation surveillance (PVS) measures for at least 10 years (2018 to 2027).

Methods: PVS covers 357 sub-villages or implementing units (IUs) in 11 former LF endemic provinces. Human blood surveys target 10% of IUs each year, aiming to achieve 100% coverage by 2027. Vector surveys are conducted in 1% of IUs where human blood surveys are conducted in that year. Blood surveys are conducted among migrants in five provinces that record the highest number of labour migrants registered in the previous year. Surveillance of cats are done in B. malayi IUs that previously recorded > 1.0% Mf rate among cats. LF Morbidity Management and Disability Prevention (MMDP) assessments are conducted every 2 years for chronic LF patients.

Results: Over five years (2018-2022), human blood surveys were conducted in 44.26% of IUs with a total of 27 LF cases detected. Vector surveys detected Mf (all *B. malayi*) in Narathiwat province only. Among domestic/peri-domestic cats in Brugia endemic provinces, the microfilaria positive rate was 0.7%. Among 7,633 unregistered migrants, 12 positive cases were detected in 6 provinces. 76 chronic LF cases remain with MMDP assessments conducted among 34 Health Promoting Hospitals providing care as part of integrated primary healthcare activities.

Conclusion: In 2022, after 5 years of PVS, Thailand has demonstrated on-going transmission in only one province of Narathiwat where Mf prevalence is below the WHO transmission threshold of 1%.

Keywords: Lymphatic filaria management, Post-validation of Lymphatic filariasis, Lymphatic filaria surveillance, Filaria elimination and elephantiasis.

Abstract No.: ABS0002130

CHALLENGES IN DIAGNOSING NON-ENDEMIC HELMINTHIASES IN MALAYSIA

Azlin Muhammad

Authors: Azlin MY[1], NurAthirah AF[1]

Affiliation: Universiti Kebangsaan Malaysia[1]

Introduction: Intestinal nematodes especially soil transmitted helminthiases and lymphatic filariasis are endemic in rural Malaysia. Other helminths especially the cestodes and trematodes are very rarely reported. However, in the past ten years, there is a sharp increase in cases of non-endemic helminthic infections especially tissue nematode, tissue cestode and trematode. This may be due to increase dietary trend and migration of human globally. The patients come from various background which includes local people as well as from foreign people staying in Malaysia. Diagnosing non-endemic helminthiasis can be challenging due to several factors. Non-endemic areas typically lack the infrastructure, limited diagnostic resources and experience in dealing with such infections, making diagnosis and management more difficult. Method: We report case series of patients from different background who presented to the hospital with various non-specific clinical manifestations of helminthic infections. These cases were referred to our department for consultation and confirmatory diagnostic tests. Results: This case series describes the epidemiology, clinical manifestations and diagnostic protocols in four patients warded in general hospitals in Malaysia. The complete laboratory investigations and some radiological imaging tests will be discussed further. Conclusion: To overcome these challenges, healthcare providers in non-endemic regions should be educated about the possibility of helminth infections, especially in individuals with relevant travel histories. Public health efforts should also focus on increasing awareness, improving diagnostic capabilities, and developing guidelines for the management of helminthiases in these regions. Additionally, international collaboration and information sharing can help in addressing these challenges effectively.

Keywords: Challenges, Diagnosis, non-endemic helminths, Malaysia

Thursday 14 December 2023

S28: Clean Air for Sustainable ASEAN

13.45-15.15hr

Room B

Thursday 14 December 2023

S28: Clean Air for Sustainable ASEAN

13.45-15.15hr

Room B

Chairperson:
1. Kiyoung Lee
2. Kraichat Tantrakarnapa

Invited speaker:

1. No title or abstract available
Kiyoung Lee
Other (Seoul National University, Graduate School of Public Health)

2. APPLICATION OF SOURCE APPORTIONMENT IN AIR POLLUTION MANAGEMENT
Seung-Muk Yi
Other (Graduate School of Public Health, Seoul National University)

3. Air quality management in Thailand and neighbouring countries
Kraichat Tantrakarnapa
Faculty of Tropical Medicine, Mahidol University (Social and Environmental Medicine)

Abstract No.: ABS0002293

No title or abstract available

Kiyoung Lee

Authors: Kiyoung Lee

Affiliation: Seoul National University, Graduate School of Public Health

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002212

APPLICATION OF SOURCE APPORTIONMENT IN AIR POLLUTION MANAGEMENT

Seung-Muk Yi

Authors: Seung-Muk Yi, Ilhan Ryoo, Taeyeon Kim, Hyejin Shin, Sujung Han

Affiliation: Graduate School of Public Health, Seoul National University

South Korea is a one of the East Asian countries with severe air pollution such as PM2.5, and the government of South Korea has been implementing several policies to reduce PM2.5. The relevant actions were initiated with the forecasting/warning of fine dust in 2014 and the Comprehensive Action Plan on Fine Dust was implemented in 2017. Additionally, the Seasonal Particulate Matter Management System was introduced in December 2019. Since then, this seasonal management system has been enforced from December through March.

Therefore, the present study aims to identify and apportion the PM2.5 sources in Seoul, Korea using Dispersion Normalized Positive Matrix Factorization (DN-PMF) based on South Korea and China joint research program, and to extensively evaluate the effects of seasonal management policy for South Korea by comparing PM2.5 source contributions of the different periods.

Samples using a three-channel low-volume air sampler in Seoul were collected three times from January to December 2019 (before implementation policy period), and from September 2020 to May 2021 (1st after implementation policy), and from July 2021 to March 2022 (2nd after implementation policy).

The samples were analyzed for fifteen trace elements, two carbonaceous species, and six ionic species. PM2.5 mass concentration and its chemical constituents were applied to DN-PMF for source apportionment. Subsequently, directional analysis of PM2.5 sources was performed using CBPF (Conditional Bivariate Probability Function).

Our results can be used as basic data to establish more effective air pollution control and management policies to reduce PM2.5 in ambient air.

Keywords: PM2.5, Source apportionment, Air pollution management, DN-PMF, Source location

Abstract No.: ABS0002202

Air quality management in Thailand and neighbouring countries

Kraichat Tantrakarnapa

Authors: Kraichat Tantrakarnapa

Affiliation: Department of Social and Environmental Medicine, Faculty of Tropical Medicine, Mahidol University

Introduction: Air pollution especially, particulates cause a spectrum of adverse health effects including respiratory, cardiovascular, neurological, and metabolic system. Millions of premature deaths each year are attributed to exposure to ambient particulate matter (PM).

Method: We collected data on ambient $PM_{2.5}$/PM_{10} concentrations from automatic monitoring stations across Thailand. We analyzed the pattern of haze episodes in different regions. We used historic exposure to $PM_{2.5}$/and PM_{10} to estimate the morbidity and mortality in various provinces from many related diseases.

Results: The patterns of air pollution in terms of haze episodes were different in each region. The Southern haze episode always occurred in the August-September period, whereas the other regions found the haze episode in the transition period from the rainy season to the dry season (December to April). Climatological plays a key role in air pollution in Thailand and neighbouring countries. Other factors also important roles and influence air quality such as biomass burning, traffic, and industrial activities. We calculated 50,019 deaths and 508,918 DALYs in 2016 attributed to long-term $PM_{2.5}$/exposure in Thailand. Based on the VSL, we calculated a cost of US$ 60.9 billion, which represents nearly 15% of Thailand's gross domestic product in 2016.

Conclusion: Many interventions were performed to reduce air pollution and PM exposure in Thailand. We need to conduct the reduction based on the stricter regulatory limits for PM and other air pollutants. These mitigation measures would help prolong life, and delay, or prevent, the onset of related air pollution diseases.

Keywords: Air Pollution, Particulate Matters, Health Impacts, Climatological Factors, Thailand and Neighboring Countries

Thursday 14 December 2023

S29: Free Paper II: Covid-19

13.45-15.15hr

Room C

Thursday 14 December 2023

S29: Free Paper II: Covid-19

13.45-15.15hr

Room C

Chairperson:
1. Pornsawan Leaungwutiwong
2. Viravarn Luvira

Invited speaker:

1. PARENTAL HESITANCY TO VACCINATE THEIR CHILDREN UNDER THE AGE OF 16 AGAINST COVID-19 AMONG FACTORY WORKERS
Kyaw Thiha Aung
Other (Health and Disease Control Unit)

2. INTERLEUKIN-6 PRODUCTION INDUCED BY SARS-COV-2 NUCLEOCAPSID PROTEIN AND BANGLADESHI COVID-19 PATIENTS' SERA
MD ABU HASAN
Other (EVERCARE HOSPITAL DHAKA, BANGLADESH)

3. THE EPIDEMIOLOGICAL CHARACTERISTICS OF COVID-19 AND RISK FACTORS FOR MORTALITY IN LAOS DURING HIGHEST PERIOD OF CASES.
Phonepasith BOUPHA
Other (Master of Philosophy in Applied Epidemiology (MAE) Scholar, Australian National University)

4. Unique Mode of antiviral action of a marine alkaloid and sulfated polysaccharides against Ebola virus and SARS-CoV-2
Yoshinao Kubo
Other (Nagasaki University)

5. Respiratory virus spectrum identified from SAR-CoV-2 negative specimens in Watansoppeng, a bat city in Eastern Indonesia
Fiqry Kleib
Other (EXEINS Health Initiative)

Abstract No.: ABS0001998

PARENTAL HESITANCY TO VACCINATE THEIR CHILDREN UNDER THE AGE OF 16 AGAINST COVID-19 AMONG FACTORY WORKERS

Kyaw Thiha Aung

Authors: Aung KT[1,2], Htun YM[1,2], Htet ZL[1,2], Soe YNM[1,2], Ko PK[1], Oo W[1], Aung MS[3] & Win TT[1]

Affiliation:
[1]Department of Preventive and Social Medicine, Defence Services Medical Academy, Yangon, Myanmar
[2]Department of Prevention and Research Development of Hepatitis, AIDS and Other Viral Diseases, Health and Disease Control Unit, Nay Pyi Taw, Myanmar
[3]Department of Preventive and Social Medicine, University of Medicine (1), Yangon, Myanmar

Introduction: Ongoing COVID-19 pandemic, there are some reasons to parental COVID-19 vaccine hesitancy to their children. This study aimed to identify the factors associated with parental COVID-19 vaccine hesitancy and to explore the reasons of COVID-19 vaccine hesitancy to their children.

Methods: A cross-sectional with sequential mixed-methods study was conducted among 170 parents having children under the age of 16, followed by in-depth interviews with 12 parents in Tri Star tyre factory, Yangon Region, Myanmar from August 2022 to February 2023. The Oxford COVID-19 vaccine hesitancy scale was used as a tool and quantitative data analysis was performed by binary logistic regression. The thematic analysis was executed for the qualitative data.

Results: Among the total, 18.2% of parents were hesitant to get vaccinated their children against COVID-19. There was a statistically significant association of parental COVID-19 vaccine hesitancy with sex (male over female, AOR: 3.04, 95% CI: 1.35-6.84) and previous SARS-CoV-2 infection of parents (no over yes, AOR: 2.66, 95% CI: 1.06-6.70). The main reasons for unwillingness to vaccinate to their children were: too young to get vaccinated, concerns about the safety of the COVID-19 vaccines, uncertainty about the effectiveness of the COVID-19 vaccines, and lack of trust in origin of the COVID-19 vaccines.

Conclusion: Nearly one-fifth of the parents were hesitant to vaccinate to their children against COVID-19. The government and health authorities should promote the literacy about COVID-19 vaccine by health education programs or risk communication in the comprehensive way to minimize the parental hesitancy to COVID-19 vaccination.

Keywords: COVID-19, Hesitancy, Parents, Previous infection, Vaccine

Abstract No.: ABS0002055

INTERLEUKIN-6 PRODUCTION INDUCED BY SARS-COV-2 NUCLEOCAPSID PROTEIN AND BANGLADESHI COVID-19 PATIENTS' SERA

MD ABU HASAN

Authors: Hasan A[1], Rahim R[1], Nakayama EE[2], Uno K[3], Hasan N[1], Rahman M[1,*], and Shioda T[2,*]

Affiliation:[1]EVERCARE HOSPITAL DHAKA; [2]OSAKA UNIVERSITY JAPAN; [3]Louis Pasteur Center for Medical Research, Kyoto

Introduction: Coronavirus disease 2019 (COVID-19) is a respiratory tract infection caused by severe acute respiratory syndrome coronavirus 2 that can have detrimental effects on multiple organs and accelerate patient mortality. Numerous cytokines are associated with rapid disease progression of COVID-19, interleukin-6 (IL-6) is the most prominent among them which regulates cell proliferation, differentiation, apoptosis, and plays a significant role in pathogenesis.

Methods: This study encompassed 130 confirmed COVID-19 patients that were assessed at three different time points (i.e., 3, 7, and 12 days) after the onset of symptoms, investigated IL-6 enhancement induced by viral nucleocapsid (N) protein from a myeloid cell line. Disease severity was categorized as mild, moderate, and severe.

Results: The severe cases were characterized as having significant elevations in serum IL-6, C-reactive protein, D-dimer, ferritin, creatinine, leukocytes, and neutrophil-to-lymphocyte ratio, and decreased hemoglobin, hematocrit, and albumin levels, compared to mild and moderate cases. To evaluate IL-6 inducing activity, heat-inactivated sera from these patients were incubated with and without N protein. The findings showed a progressive increase in IL-6 production in severe cases upon N protein stimulation. There was a strong correlation between anti-N antibody and levels of IL-6 secreted by myeloid cells in the presence of N protein and patients' sera.

Conclusion: Our results indicated the crucial role of the anti-N antibody in inducing IL-6 production from myeloid cells. Since uncontrolled IL-6 production was identified as a pivotal role in disease pathogenesis, exacerbating the severity and fatality, efficiently targeting N protein could potentially be employed as a therapeutic strategy for regulating the immune response

Keywords: COVID-19; SARS-CoV-2; IL-6; N protein; anti-N antibody; Nucleocapsid.

Abstract No.: ABS0002044

THE EPIDEMIOLOGICAL CHARACTERISTICS OF COVID-19 AND RISK FACTORS FOR MORTALITY IN LAOS DURING HIGHEST PERIOD OF CASES.

Phonepasith BOUPHA

Authors: Boupha P[1], Sengkeopraseuth B[2], Houatthongkham S[3], Xangsayarath P[1], Khamphaphongphane B[1], Kelly M[1]

Affiliation: [1]Master of Philosophy in Applied Epidemiology (MAE) Scholar, National Centre for Epidemiology and Population Health, Research School of Population Health, Australian National University; [2]National Center for Laboratory and Epidemiology, Department of Communicable Disease Control, Ministry of Health, Vientiane, Lao PDR

Introduction: Epidemiological characteristics of COVID-19 vary across place and time and include asymptomatic and severe disease. Understanding location specific epidemiological patterns are key for responding and preparing for new outbreaks. To date no such analysis has been carried out for Lao PDR.

Methods: Confirmed COVID-19 cases and deaths between January to July 2022 were extracted from national surveillance system data. Descriptive and multivariable regression analysis described epidemiological characteristics and associations between risk factors and mortality.

Results: In total 99,765 cases (370 deaths) were recorded, 13.6 cases per 1000 population, Case Fatality Rate of 0.37. Male and female proportions were similar (47.6, 52.4%). Mean (SD) age was 32.3 (16.6) years and two-thirds of cases ranged from 20-49 years old. Of cases with symptoms reported, 31.9% were asymptomatic and 64.6% had mild symptoms. Most common were sore throat (35.4%), cough (34.6%), fever (31.7%), running nose (15.8%) and lost smell or taste (4.2%), 3.5% (2,323) were severe. Age 30-39, 40-49 and ≥50 (adjusted odds ratio (aOR), 1.11, 3.16 and 3.48), being male (aOR 1.33), underlying conditions (aOR 43.96), no vaccines (aOR 4.66) and severe symptom/s (aOR 70.74) associated with mortality risk among COVID-19 patients.

Conclusion: Characteristics of patients (age, sex, vaccine status, severity, and underlying conditions) with highest risk for severe disease and mortality identified here will help Lao PDR understand health system needs and public healthcare policy in response to COVID-19.

Keywords: COVID-19 in Laos, Epidemiological characteristics of COVID-19, Mortality risk among COVID-19 patients

Abstract No.: ABS0002033

Unique Mode of antiviral action of a marine alkaloid and sulfated polysaccharides against Ebola virus and SARS-CoV-2

Yoshinao Kubo

Authors: Yoshinao Kubo[1], Mai Izumida[1], Osamu Kotani[2], Hideki Hayashi[1], Chris Smith[1], Tsutomu Fukuda[3], Koushirou Suga[4], Masatomo Iwao[3], Fumito Ishibashi[4], Hironori Sato[2]

Affiliation:[1]Institute of Tropical Medicine, Nagasaki University, Japan; [2]National Institute of Infectious Diseases, Japan; [3]Graduate School of Engineering, Nagasaki University, Japan; [4]Graduate School of Fisheries, Nagasaki University, Japan

Introduction: Lamellarin alpha 20-sulfate is a cell-impenetrable marine alkaloid that can suppress HIV-1 infection. We explored the antiviral action and mechanisms of this sulfated alkaloid and other sulfated polysaccharides against Ebola virus and SARS-CoV-2.

Methods: Effects of the marine alkaloid and sulfated polysaccharides including fucoidan, heparin, dextran sulfate, and chondroitin sulfate on infection by HIV-1 vector pseudotyped with glycoprotein (GP) of Ebola virus or SARS-CoV-2 were analyzed. Interaction between the vector particles and target cells were measured by p24 ELISA.

Results: The alkaloid inhibited the infection by HIV-1 vector pseudotyped with Ebola virus or SARS-CoV-2. The antiviral effects were independent of the HIV-1 Gag-Pol proteins. Although heparin and dextran sulfate suppressed the vector binding to target cells, lamellarin did not. In silico structural analysis of the Ebola virus GP disclosed that the lamellarin-binding site is near the NPC1-binding site and fusion loop of the Ebola virus GP, whereas those for heparin and dextran sulfate were dispersed across the GP. It was calculated that the binding of lamellarin to GP is enhanced by acidification.

Discussion: These results suggest that the action of lamellarin against Ebola virus is specific to events following endocytosis, possibly during conformational changes of GP in acidic endosomes. Our finding highlight the unique biological and physicochemical feature of lamellarin and should lead to the further use of broadly reactive antivirals.

Keywords: Ebola virus, SARS-CoV-2, lamellarin alpha 20-sulfate, heparin, fucoidan, Dextran sulfate, chondroitin sulfate

Abstract No.: ABS0002014

Respiratory virus spectrum identified from SAR-CoV-2 negative specimens in Watansoppeng, a bat city in Eastern Indonesia

Fiqry Kleib

Authors: Fiqry Kleib[1], Irfan Idris[2], Ungke Antonjaya[3], Edison Johar[1], Ida Yus Sriyani[1], Aghnianditya Kresno Dewantari[1], Oderna[4], Mustakin[4], Fatmawati[4], Frilasita Aisyah Yudhaputri[1], Iswa Wahid[2], Khin S. Myint[1]

Affiliation:
[1]Exeins Health Initiative, Jakarta, Indonesia
[2]Faculty of Medicine, Universitas Hasanuddin, Makassar, Indonesia
[3]Oxford University Clinical Research Unit Indonesia, Jakarta, Indonesia
[4]Soppeng District Health Office, Makassar, Indonesia

Respiratory infections account for millions of hospital admissions worldwide. Non-COVID-19 specimens in Soppeng Regency, South Sulawesi, a natural habitat for more than 12,500 fruit bats were analyzed to study the spectrum. Understanding the etiology will reinforce the management and preventive strategies to reduce morbidity and mortality. Between March 2020 to July 2021, 288 negative nasopharyngeal specimens for COVID-19 by RT-PCR were collected from COVID-19-suspected patients having fever >38oC and respiratory symptoms from Lalabata and Donri-Donri Districts by Soppeng Public Health Offices and the District Hospital. The specimens were tested for Coronaviridae, Paramyxoviruses, Herpesviridae, Adenoviridae for family; and for Influenza (Influenza A and B), Pneumovirus (Respiratory Syncytial Virus (RSV) and Human metapneumovirus (hMPV)), Enterovirus (Rhinovirus, Coxsackievirus) and Bocavirus for genus identifications. From 288 specimens, 19 specimens tested positive for 10 virus species: RSV A (n=2), RSV B (n=1), Parainfluenza virus 1 (n=2), Parainfluenza virus 2 (n=1), Rhinovirus A (n=3), Rhinovirus B (n=2), Rhinovirus C (n=3), hMPV (n=2), Influenza virus A (n=3), Coxsackievirus A6 (n=1), and 1 sample was positive for both Rhinovirus A and hMPV. However, 91.7% of the samples remained unidentified. Important bat-borne viruses including SARS-CoV, MERS-CoV, Avian influenza, Nipah and Hendra viruses, were not detected, notably Nipah virus which is endemic in Indonesian bats. Indonesia is a high-risk area due to its biodiversity; the respiratory surveillance studies in strategic areas like Watansoppeng having appropriate conditions for viral spillover could provide critical insight to identify novel respiratory pathogens that can pose a significant threat to humans.

Keywords: respiratory viruses, COVID-19, bats, Watansoppeng, Indonesia

Thursday 14 December 2023

S30: Triple Artemisinin-Based combination Therapies for Malaria: Progress and Challenges

13.45-15.15hr

Room D

Thursday 14 December 2023

S30: Triple Artemisinin-Based combination Therapies for Malaria: Progress and Challenges

13.45-15.15hr

Room D

Chairperson:
1. Arjen Dondorp
2. Chanaki Amaratunga

Invited speaker:

1. The Development of Triple Artemisinin-based Combination Therapies (DeTACT) project
Chanaki Amaratunga
Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

2. Safety, tolerability and efficacy of triple artemisinin-based combination therapies in Africa and Asia
Mehul Dhorda
Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

3. EVOLUTION OF MULTI DRUG-RESISTANT MALARIA: IMPLICATIONS ON DEPLOYMENT OF TRIPLE ARTEMISININ-BASED COMBINATION THERAPIES
Mallika Imwong
Faculty of Tropical Medicine, Mahidol University (Molecular Tropical Medicine and Genetics)

4. Modeling the epidemiological benefits of triple artemisinin-based combination therapies in Rwanda and Uganda
Maciej Boni
Other (Department of Biology, Penn State University, USA)

5. DEVELOPMENT OF ANTIMALARIAL - ARTEMETHER, LUMEFANTRINE, AMODIAQUINE FIXED DOSE COMBINATION (ALAQ FDC)
Yanjie Xiong
Other (Shanghai Fosun Pharmaceutical (Group) Co., Ltd.)

Abstract No.: ABS0002294

The Development of Triple Artemisinin-based Combination Therapies (DeTACT) project

Chanaki Amaratunga

Authors: Chanaki Amaratunga

Affiliation: Mahidol Oxford Tropical Medicine Research Unit, Thailand

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002295

Safety, tolerability and efficacy of triple artemisinin-based combination therapies in Africa and Asia

Mehul Dhorda

Authors: Mehul Dhorda

Affiliation: Mahidol Oxford Tropical Medicine Research Unit, Thailand

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002135

EVOLUTION OF MULTI DRUG-RESISTANT MALARIA: IMPLICATIONS ON DEPLOYMENT OF TRIPLE ARTEMISININ-BASED COMBINATION THERAPIES

Mallika Imwong

Authors: Imwong M[1,2]*, Suwannasin K[2], Srisutham S[3], Vongpromek R[4], Promnarate C[4], Saejeng A[5], Phyo AP[6], Proux S[7], Pongvongsa T[8], Nguon C[9], Miotto O[2,10,11], Tripura R[2,11], Chau NH1[2], Lek D[9], Trung NHD[12], Peto T J[2,11], Callery JJ[2], Pluijm RW[2], Amaratunga C[2,11], Mukaka M[2,11], Seidlein L[2,11], Mayxay M[11,13,14], Thuy-Nhien NT[12], Newton PN[11], Day NPJ[2,11] , Ashley EA[11,14], Nosten FH[7,11], Smithuis FM[6,11], Dhorda M[2,3,11], White NJ[2,11], Dondorp AM[2,11]

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[12]Oxford University Clinical Research Unit, Hospital for Tropical Diseases, Ho Chi Minh City, Vietnam

[13]Institute of Research and Education Development, University of Health Sciences, Ministry of Health, Vientiane, Lao PDR

[14]Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit, Microbiology Laboratory, Mahosot Hospital, Vientiane, Lao PDR

Increasing resistance in Plasmodium falciparum to artemisinins and their artemisinin combination therapy (ACT) partner drugs jeopardizes effective antimalarial treatment. Resistance is worst in the Greater Mekong subregion. Monitoring genetic markers of resistance can help to guide antimalarial

therapy. Markers of resistance to artemisinins (PfKelch mutations), mefloquine (amplification of P. falciparum multidrug resistance-1 [PfMDR1]), and piperaquine (PfPlasmepsin2/3 amplification and specific P. falciparum chloroquine resistance transporter [PfCRT] mutations) were assessed in 6,722 P. falciparum samples from Vietnam, Lao People\'s Democratic Republic (PDR), Cambodia, Thailand, and Myanmar between 2007 and 2019. Against a high background prevalence of PfKelch mutations, PfMDR1 and PfPlasmepsin2/3 amplification closely followed regional drug pressures over time. PfPlasmepsin2/3 amplification preceded piperaquine resistance-associated PfCRT mutations in Cambodia and reached a peak prevalence of 23/28 (82%) in 2015. This declined to 57/156 (38%) after first-line treatment was changed from dihydroartemisinin-piperaquine to artesunate-mefloquine (ASMQ) between 2014 and 2017. The frequency of PfMDR1 amplification increased from 0/293 (0%) between 2012 and 2017 to 12/156 (8%) in 2019. Amplification of PfMDR1 and PfPlasmepsin2/3 in the same parasites was extremely rare (4/6,722 [0.06%]) and was dispersed over time. The mechanisms conferring mefloquine and piperaquine resistance may be counterbalancing. This supports the development of ASMQ plus piperaquine as a triple artemisinin combination therapy.

Keywords: Greater Mekong subregion; Plasmodium falciparum; genetic resistance markers

Abstract No.: ABS0002296

Modeling the epidemiological benefits of triple artemisinin-based combination therapies in Rwanda and Uganda

Maciej Boni

Authors: Maciej Boni

Affiliation: Department of Biology, Penn State University, USA

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002133

DEVELOPMENT OF ANTIMALARIAL - ARTEMETHER, LUMEFANTRINE, AMODIAQUINE FIXED DOSE COMBINATION (ALAQ FDC)

Yanjie Xiong

Authors: Michelle Xiong

Affiliation: Shanghai Fosun Pharmaceutical (Group) Co.,, Ltd.

Artemisinin-based combination therapies (ACTs) are globally the first-line treatments for uncomplicated Plasmodium falciparum malaria, and there are currently no alternatives available. Artemisinin partial resistance, observed widely in the Greater Mekong Subregion and recently in Rwanda and Uganda, facilitates the emergence and spread of resistance to the ACT partner drugs, resulting in treatment failure. One important approach to overcome this problem is the development of Triple Artemisinin-based Combination Therapies (TACTs), where the artemisinin derivative is combined with two partner drugs.

Fosun Pharma is under development of one adult formulation and one paediatric formulation of ALAQ-FDC.

Keywords: Triple Artemisinin-based Combination Therapies (TACTs)

Thursday 14 December 2023

S31: Collaborative Innovations in Tropical Medicine: A Thai-UK Partnership for Global Impact

15.45-17.15hr

Room E

Thursday 14 December 2023

S31: Collaborative Innovations in Tropical Medicine: A Thai-UK Partnership for Global Impact

15.45-17.15hr

Room E

Chairperson:
1. Narisara Chantratita
2. James Spencer

Invited speaker:

1. Opening pathways to address health challenges in Tropical Medicine through Thai-UK World Class University Consortium
Narisara Chantratita
Faculty of Tropical Medicine, Mahidol University (Microbiology and Immunology)

2. COLLABORATION TO DEVELOP AND EVALUATE AFFORDABLE INFECTION DISEASE DIAGNOSTIC TECHNOLOGY, INCLUDING DENGUE IMMUNOASSAYS AND RAPID ANTIBIOTIC SUSCEPTIBILITY TESTS
Alexander Edwards
Other (University of Southampton)

3. Moving rapid antibiotic susceptibility testing to the clinic: the role of mass-manufacturing microfluidics in generating clinical data
Sarah Needs
Other (University of Reading)

4. Carbapenem-hydrolyzing board spectrum activity of β-lactamase form bacteria
James Spencer
Other (School of Cellular and Molecular Medicine, University of Bristol, U.K.)

5. Southeast Asia initiative to combat SARS-CoV-2 variants (SEACOVARIANTS), 2022-2025
Susanna Dunachie
Other ()

6. LONGITUDINAL ANALYSIS OF NEUTRALIZING ANTIBODY RESPONSES TO SARS-COV-2 VARIANTS IN COVID-19 PATIENTS
Prapassorn Poolchanuan
Faculty of Tropical Medicine, Mahidol University (Microbiology and Immunology)

Abstract No.: ABS0002297

Opening pathways to address health challenges in Tropical Medicine through Thai-UK World Class University Consortium

Narisara Chantratita

Authors: Narisara Chantratita[1,2]

Affiliation: [1]Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

[2]Mahidol-Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

The Thai-UK World Class University Consortium, stands as a beacon of collaborative innovation between seven Thai institutions and their UK counterparts, supported by the British Council in partnership with the Office of the Permanent Secretary, Ministry of Higher Education, Science, Research and Innovation (MHESI). Focused on cutting-edge research and advancements in Life Sciences, one consortium, led by Prof. Narisara Chantratita (Mahidol University), Prof. Jeremy Tavaré (University of Bristol), Prof. James Spencer (University of Bristol), Assoc. Prof. Alexander Edwards (University of Reading), Prof. Susanna Dunachie (University of Oxford) and Dr Trevor Lawley (Wellcome Trust Sanger Institute) has successfully united several programs in Research from Thai and leading UK universities. The consortium's achievements span a diverse range, including sharing resources, fostering cross-cultural understanding of health challenges, and making a global impact on tropical diseases. Its capacity-building initiatives, research and innovation endeavors, and preparations for epidemic responses have garnered international recognition. The success criteria, ranging from organized meetings, student exchanges, to collaborative grant writing and scientific publications. This presentation will demonstrate the consortium's commitment to achieving tangible outcomes.

Keywords: Thai-UK World Class University Consortium

Abstract No.: ABS0002151

COLLABORATION TO DEVELOP AND EVALUATE AFFORDABLE INFECTION DISEASE DIAGNOSTIC TECHNOLOGY, INCLUDING DENGUE IMMUNOASSAYS AND RAPID ANTIBIOTIC SUSCEPTIBILITY TESTS

Alexander Edwards

Authors: Needs SH[1], Noparatvarakorn C[2], Avirutnan P[2], Puttikhunt C[3], Chantratita N[2] and Edwards AD[1,4]

Affiliation: [1]University of Reading, [2]Mahidol University, [3]BIOTEC, [4]University of Southampton

The need for better diagnostic products using the latest bioassay technologies has never been clearer. To bridge the gap between proof-of-concept ideas, and real-world products in widespread use, close international collaboration is essential. Building on expertise across UK-Thailand partnerships, we developed and evaluated two microfluidic rapid and portable testing concepts for infectious disease diagnostics. Firstly, we co-developed serotype-specific multiplex immunoassay devices that detect dengue virus NS1 protein. This culminated in a 250 sample validation study that showed, for the first time, the performance of microcapillary immunoassays is similar to microplate ELISA, but with rapid assay times and multiplexing. Secondly, we are currently exploring global health applications of low-cost, portable antibiotic susceptibility tests. These may be useful for tropical diseases (e.g. Burkholdia pseudomaleii), or infections that affect all populations (e.g. urinary tract infection). For both examples, being able to rapidly make thousands of devices allows us to extensively optimise assay conditions. We also use inexpensive readers (typically

Keywords: diagnostics, dengue, microbiology, microfluidics

Abstract No.: ABS0002148

Moving rapid antibiotic susceptibility testing to the clinic: the role of mass-manufacturing microfluidics in generating clinical data

Sarah Needs

Authors: Sarah Needs[1], Jessica Hayward[1], Stephen P. Kidd[2] and Alexander Edwards[1,3]

Affiliation:[1]University of Reading, UK
[2]Hampshire Hospitals NHS Foundation Trust, UK
[3]Electronics and Computer Science, University of Southampton, UK

Whilst new technologies offer the promise of faster more accessible antibiotic susceptibility testing – vital to combat antimicrobial resistance – we have limited evidence of their performance. Many emerging technologies change three critical parameters of antimicrobial susceptibility tests (AST): 1) microfluidics miniaturize the sample volume; 2) susceptibility or resistance are scored at earlier time points; 3) clinical samples (such as urine) are directly tested rather than pure isolates taken from overnight agar culture.

Mass-manufactured melt-extruded capillary film offers 10 parallel 270 µm diameter capillaries, is produced in 500 m reels, providing us with thousands of disposable microfluidic devices used to systematically study miniaturized analytical microbiology. Greater than 3000 by 17 mm long individual test strips can be produced per batch. Test strips are arranged in holders containing 12 strips to interact with standard 96 well plates. This has allowed us to systematically study >29 000 conditions, across a comprehensive range of pathogen/antibiotic combinations.

From 3 sites in the UK, Spain and Thailand we have tested 367 pure cultured isolates from clinical samples against 8-17 different antibiotics, establishing for many antibiotics >90% accuracy when compared with clinical reference standard methods.

Keywords: Antibiotic resistance, Diagnsotics

Abstract No.: ABS0002298

Carbapenem-hydrolyzing board spectrum activity of β-lactamase form bacteria

James Spencer

Authors: James Spencer

Affiliation: School of Cellular and Molecular Medicine, University of Bristol, UK

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002299

Southeast Asia initiative to combat SARS-CoV-2 variants (SEACOVARIANTS), 2022-2025

Susanna Dunachie

Authors: Susanna Dunachie

Affiliation: Nuffield Department of Clinical Medicine, University of Oxford, UK

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002209

LONGITUDINAL ANALYSIS OF NEUTRALIZING ANTIBODY RESPONSES TO SARS-COV-2 VARIANTS IN COVID-19 PATIENTS

Prapassorn Poolchanuan

Authors: Prapassorn Poolchanuan[1,] Vichapon Tiacharoen[1], Adul Dulsuk[1], Rungnapa Phunpang[1], Tanaya Siripoon[2], Watcharapong Piyaphanee[2,3], Le Van Tan[4], Susanna Dunachie[5,6], Chee Wah Tan[7], Wasun Chantratita[8,9], Viravarn Luvira[2], Narisara Chantratita[1,6],*

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[1]Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University
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[3]Thai Travel Clinic, Hospital for Tropical Diseases, Faculty of Tropical Medicine, Mahidol University
[4]Oxford University Clinical Research Unit, Hospital for Tropical Diseases, Ho Chi Minh City, Vietnam
[5]Nuffield Department of Clinical Medicine, University of Oxford, Oxford, United Kingdom
[6]Mahidol-Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University
[7]Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
[8]Department of Pathology, Faculty of Medicine Ramathibodi Hospital, Mahidol University, Thailand
[9]Center for Medical Genomics, Faculty of Medicine Ramathibodi Hospital, Mahidol University

New variants of SARS-CoV-2 with the ability to evade the immune response continue to emerge. Antibodies, whether acquired through natural infection or vaccination, tend to wane over time. Consequently, the durability and effectiveness of circulating neutralizing antibodies (Nabs) against SARS-CoV-2 variants remain crucial, as antibodies play a pivotal role in the viral clearance process. We prospectively recruited 111 COVID-19 patients, including those who were either unvaccinated or vaccinated with homologous/heterologous vaccine regimens (inactivated, viral vector, or mRNA vaccines). Nabs levels against SARS-CoV-2 variants in participants were measured using the Multiplex Surrogate Virus Neutralization Test (sVNT). On day 14, all patients exhibited Nabs levels approximately 85.2% inhibition against all variants, except for the omicron variant, which exhibited 48.3% inhibition. Nabs levels significantly declined at 1 year post-infection ($P < 0.05$). Breakthrough patients ($n = 94$) had shorter hospital stays (8 days vs 10 days, $P = 0.0061$) and higher Nabs levels against omicron variants ($P < 0.05$) than those without vaccination ($n = 17$). Breakthrough patients with omicron infection exhibited higher Nabs levels against omicron variants than those breakthrough with delta infection ($P < 0.0001$). The heterologous vaccine (combining different vaccine types) demonstrated increased Nabs levels against BA.1 and BA.2 variants compared to the homologous inactivated vaccine ($P < 0.05$). The homologous mRNA vaccine exhibited higher Nabs levels against omicron variants than the homologous inactivated vaccine and the homologous viral vector vaccine ($P < 0.05$). These results suggest the role of the vaccine in protecting against severe disease and reducing hospitalization.**Keywords:** COVID-19; neutralizing antibody; SARS-CoV-2 variants; natural infection; vaccination

Thursday 14 December 2023

S32: IT-driven Disease Surveillance and Predictive Models

15.45-17.15hr

Room A

Thursday 14 December 2023

S32: IT-driven Disease Surveillance and Predictive Models

15.45-17.15hr

Room A

Chairperson:
1. Saranath Lawpoolsri Niyom
2. Myat Su Yin Muang

Invited speaker:

1. HIGH RESOLUTION MAPPING OF URBAN AEDES AEGYPTI IMMATURE ABUNDANCE THROUGH BREEDING SITE DETECTION BASED ON SATELLITE AND STREET VIEW IMAGERY
Stefen Knoblauch
Other (Heidelberg University)

2. WEB AND MOBILE APPLICATION TO ASSIST DENGUE INVESTIGATION
Jennifer Horstmann
Other (University of Bremen)

3. Climate-Based Malaria Modelling for Vector Surveillance and Control in Ghana
EDMUND ILIMOAN YAMBA
Other (Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana)

4. Internet of Things for Monitoring the Human Exposome: An Overview
Anna Foerster
Other (University of Bremen)

Abstract No.: ABS0002176

HIGH RESOLUTION MAPPING OF URBAN AEDES AEGYPTI IMMATURE ABUNDANCE THROUGH BREEDING SITE DETECTION BASED ON SATELLITE AND STREET VIEW IMAGERY

Stefen Knoblauch

Authors: Knoblauch S[1], Yin MS[2], Chatrinan K[2], Haddawy P[2], Lautenbach S[1], Zipf A[1]

Affiliation:[1]Heidelberg University; [2]Mahidol University

Identification of Aedes aegypti breeding hotspots is essential for the implementation of targeted vector control strategies and thus the prevention of several infectious disease worldwide. The combination of increasingly collected big spatial data and novel object detection models provides a large potential in this context, especially for the high-resolution mapping of urban mosquito habitat suitability.

In this study, we evaluated the relationship between the density of common breeding containers and Aedes aegypti infestation by applying object detection models on satellite and street view imagery. Univariate negative binomial regression models were fitted using monthly collected entomological surveillance data for the city of Rio de Janeiro between 2019 to 2022 on Aedes aegypti immature stages for validation.

The results showed that all microhabitat proxies generated through object detection in this study had a significant impact on model performance, enabling an explanation of the high spatial variance in Aedes aegypti populations on an urban scale. The density of water tanks, old car tires, plastic bags, potted plants, and storm drains showed a positive association with Aedes aegypti egg and larva counts, whereas dumpsters, small trash bins, and large trash bins exhibited a negative association.

The object detection of urban Aedes aegypti breeding habitats using complementary data sources such as satellite and street view imagery has the potential to significantly optimize vector control strategies. It opens the pathway for high-resolution interpolation of entomological surveillance data and therefore supports the mitigation of diseases transmitted by Aedes aegypti, such as dengue, chikungunya, and Zika.

Keywords: Aedes aegypti, Breeding Containers, Street View, Satellite Imagery, Rio de Janeiro, Dengue

Abstract No.: ABS0002166

WEB AND MOBILE APPLICATION TO ASSIST DENGUE INVESTIGATION

Jennifer Horstmann

Authors: Horstmann J[1], Lawpoolsri S[2], Berg C[1], Barkowsky T[1], Haddawy P[1,2]

Affiliation:[1]University of Bremen; [2]Mahidol University

Dengue case investigation proves to be one of the most effective ways to prevent severe dengue outbreaks. Since dengue is a notifiable disease in Thailand, every case has to be reported from the diagnosing instances up to the Ministry of Public Health using a standardized form. However, between these instances the communication about dengue cases is often informal and combines paper-based and digital workflows. This limits not only the potential of timely measures for the case investigation but also of standardized and high quality reporting.

This project aims to develop a mobile application and a web dashboard to support dengue case investigation. The system assists with the communication on local levels between the District Health Offices and Health Centers. It includes analysis of the data as well as reporting to superordinate authorities. Moreover we evaluate the user experience and the satisfaction towards the system.

In order to meet the special needs of the target users, we employ user centered design (UCD). For this, we gathered user requirements and delivered working prototypes of both parts of the system, i.e. a mobile app and a web dashboard at an early stage in the process. These are used to evaluate the user experience and satisfaction towards the application. The results are the base for further adjustments of the applications. In this way, the users are involved throughout the process and we ensure that the system not only meets their needs but adapts to their workflows and increases the efficacy of their work.

Keywords: Dengue Fever, Dengue Case Investigation, Dengue Vector Control, Digital Public Health

Abstract No.: ABS0002300

Climate-Based Malaria Modelling for Vector Surveillance and Control in Ghana

EDMUND ILIMOAN YAMBA

Authors: EDMUND ILIMOAN YAMBA

Affiliation: Kwame Nkrumah University of Science and Technology, Ghana

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002184

Internet of Things for Monitoring the Human Exposome: An Overview

Anna Foerster

Authors: Anna Foerster

Affiliation: University of Bremen

The Internet of Things is a relatively new technology that allows a fine-grained real-time monitoring of various processes and properties. In this talk, we will explore how this technology can be used to monitor the exposome of people in urban and rural environments and how this monitoring can contribute to a better understanding and better management of our environment. We will discuss technological and social challenges and will explore sample applications around the world.

Keywords: internet of things, exposome monitoring, environmental monitoring, public health

Thursday 14 December 2023

S33: Sustainable Prevention of Helminth Infection Risk Using Innovative Strategies

15.45-17.15hr

Room B

Thursday 14 December 2023

S33: Sustainable Prevention of Helminth Infection Risk Using Innovative Strategies

15.45-17.15hr

Room B

Chairperson:
1. Teera Kusolsuk
2. Marcelo Otake Sato

Invited speaker:

1. ECOEPIDEMIOLOGY OF OPISTHORCHIASIS IN SAVANNAKHET-LAO PDR USING THE EDNA APPROACH
Megumi Sato
Other ()

2. THE USE OF ENVIRONMENTAL APPROACHES IN NTDS: SCHISTOSOMIASIS AND STH
Marcello Otake Sato
Other (Division of Global Environment Parasitology/Niigata University of Pharmacy and Medical and Life Sciences)

3. Prevalence of helminthic infections and associated factors among pregnant women in Lao PDR
Sengdavy Xaypadith
Other (Ministry of Health, Department of Health Personnel)

4. DESIGN THINKING OF PREVENTING SOIL-TRANSMITTED HELMINTHS: FROM PAIN POINTS TO THE PRE-PROTOTYPE DEVELOPMENT
Sivapong Sungpradit
Other (Faculty of Veterinary Science, Mahidol University)

Abstract No.: ABS0002102

ECOEPIDEMIOLOGY OF OPISTHORCHIASIS IN SAVANNAKHET-LAO PDR USING THE EDNA APPROACH

Megumi Sato

Authors: Megumi Sato[1], Marcello Otake Sato[2], Toshifumi Minamoto[3], Riko Matsuo[3,4], Yanin Limpanont[5] & Poom Adisakwattana[4]

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Opisthorchiasis, is a neglected foodborne disease caused by the liver fluke Opisthorchis viverrini (Ov). It is endemic in Southeast Asian countries infecting more than 10 million people in the lower Mekong River Basin and constitutes a major health problem once chronic infection by Ov increases the risk of cholangiocarcinoma. Despite the efforts on treatment of infected people there is no consistent reducing on the prevalence of the disease in endemic areas. The prophylactic measures include reducing human ingestion of fish with metacercaria. However, it is difficult to detect metacercaria in fish, thus there is a lack of tests for monitoring the infection risk by ingesting fish. To overcome this issue, we develop an environmental DNA approach, detecting hosts and parasite DNA from the water and soil in the environment, it is possible to better understand the habitat of O. viverrini and the dynamics of infection with high accuracy, and sensitivity. With Eco epidemiological eDNA data it is possible to determine hotspots of environmental contamination by the parasite and predict active transmission sites. In this report we will show our advances in a prospective study in Savannakhet, Lao-PDR with the application of the eDNA technique for Ov and its hosts.

Keywords: opisthorchiasis, environmental DNA, Lao-PDR

Abstract No.: ABS0002103

THE USE OF ENVIRONMENTAL APPROACHES IN NTDS: SCHISTOSOMIASIS AND STH

Marcello Otake Sato

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Neglected tropical diseases (NTDs) are a group of 20 illnesses. Practically absent from the global health agenda, NTDs are mainly prevalent in tropical areas, affecting more than 1 billion people, especially the less empowered and in a situation of social vulnerability. Schistosomiasis, also known as bilharzia, is caused by a group of blood flukes called schistosomes. An estimated over 230 million people are infected by schistosomes and nearly 700 million people are at risk of infection. Soil-transmitted helminth (STH) a group formed by ascariasis, trichuriasis and hookworm infections are among the most common infections worldwide, with an estimated infection rate of 24% (1.5 billion) of the world's population. The control of Schistosomiasis and STH is complex and directly related to environmental conditions. The presence of animal reservoirs and lack of health education and sanitation infrastructure make their public-health control challenging. Besides the diagnosis of infected hosts, an "ecologic diagnosis" of the disease is an important step towards the design of sustainable control strategies. We are working on the development and improvement of tools to detect the factors associated with human infection in the environment using the environmental DNA approach. We will present our findings and insights in the use of geographical information and environmental DNA in different prevalence scenarios, and how we are improving these tools turning laboratory bench tests into POC tests, to help surveillance and control programs of endemic areas.

Keywords: one-health, ecohealth, environmental DNA, helminths

Abstract No.: ABS0002125

Prevalence of helminthic infections and associated factors among pregnant women in Lao PDR

Sengdavy Xaypadith

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Intestinal helminthic infections are a major health concern in developing countries. Infections during pregnancy can have serious consequences for maternal and fetal well-being.

Five hospitals were undertaken for eight months to assess the prevalence of infection and associated factors. The pregnant women visiting the antenatal care (ANC) unit (N=300) were recruited. Stool samples were screened using Kato's thick smear technique. Descriptive statistics and logistic regression were used for data analysis.

The prevalence of intestinal parasites was 17.7%. Ascaris was the most prevalent (19 cases, 43.9%), followed by Strongyloides (8 cases, 22.0%), Hookworm (8 cases, 17.1%), Opisthorchis (3 cases, 7.3%), Trichuris (3 cases, 7.3%), and Taenia spp. (1 case, 2.4%). Eating uncooked food (33%), increased the odds of infection (OR: 3.71, CI: 2.01-6.85). Eating fresh vegetables (73%) also increased the risk of infection (OR: 2.93, CI: 1.20-7.14). Taking anthelminthic drugs once a year was significantly associated with a reduced infection (OR: 0.47, CI: 0.22-0.99).

In conclusion, a significant prevalence of intestinal helminth infections was observed among pregnant women. Therefore, all pregnant women who visit ANC unit must be screened and treated these infections timely.

Keywords: helminthic infections, pregnant women, Lao PDR

Abstract No.: ABS0002104

DESIGN THINKING OF PREVENTING SOIL-TRANSMITTED HELMINTHS: FROM PAIN POINTS TO THE PRE-PROTOTYPE DEVELOPMENT

Sivapong Sungpradit

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Introduction: Soil-transmitted helminth (STH) parasites affect more than one third of the world’s population and cause substantial disease and disability. This neglected disease affects humans, animals and the environmental.

Methods: Based on the One Health approach, information on soil-transmitted helminths, and design thinking principles and activities, the pre-prototype was selected and approved by the in vitro experiment. The ethanol extractions of a star fruit (Averrhoa carambola, or Ma-Fuang in Thai), the great elephant apple fruit (Dillenia aurea, or Ba-San in Thai), and the Siam weed or Sab-Suea leaf (*Chromolaena odorata* L.) were prepared. Each in vitro reaction was composed of herb compounds and Parascaris egg-containing larvae or dividing cells. Regarding the in vitro results, the combination of herb extractions as the spray pre-protype was sent for in vitro skin irritation analysis.

Results: The results showed that the ethanol extracted from the star fruit and Siam weed leaf, with the lowest LC50 of 6.86 mg/ml affected the parasite eggshell and larvae. However, the result of the skin irritation test revealed that the herb hand spray decreased tissue viability (mean 22.01%, SD **8.582), which indicates an irritant effect.**

Conclusion: The selected pre-prototype was the herbal hand spray, from which a useable pre-prototype will further be developed—to protect local communities from helminth infective eggs. This design thinking and One Health approach model can be used by other communities affected by STHs worldwide.

Keywords: Design thinking, soil-transmitted helminth, herb

Thursday 14 December 2023

S34: Free Paper III: Global Health

15.45-17.15hr

Room B

Wednesday 14 December 2023

S34: Free Paper III: Global Health

15.45-17.15hr

Room B

Chairperson:
1. Thitinan Kitisin
2. Panita Looareesuwan

Invited speaker:

1. IMPACT OF 10-VALENT PNEUMOCOCCAL CONJUGATE VACCINE ON HOSPITAL ADMITTION DUE TO PNEUMONIA AMONG CHILDREN IN NEPAL
Yumiko Hayashi
Other (School of Tropical Medicine and Global Health, Nagasaki University, Japan)

2. BACTERIAL ETIOLOGIES OF DIARRHEA IN CHILDREN UNDER 5 YEARS FROM MUKURU INFORMAL SETTLEMENT AND THEIR ANTIMICROBIAL SENSITIVITY PROFILES.
Susan Kiiru
Other (KENYA)

3. ASSOCIATION OF RENEWED BLOOD PRESSURE CATEGORY WITH PRETERM BIRTH IN KWALE COUNTY, KENYA
Mami HITACHI
Other (Nagasaki University)

4. ESTABLISHING THE SPATIAL DISTRIBUTION OF CIRCULATING ARBOVIRUSES IN URBAN AND RURAL LIBERIA
Albert To
Other (Department of Tropical Medicine, University of Hawaii/Chulalongkorn University)

5. THE USE OF ZIEHL-NEELSEN AND NAOH CONCENTRATION TECHNIQUES IN THE DETECTION OF PARAGONIMUS OVA IN SPUTUM
Rupert Stephen Charles Chua
Other (University of the Philippines Neglected Tropical Diseases Study Group)

6. Detection of GB Virus C in a Child Presenting with Dengue-like Illness
Edison Johar
Other (Exeins Health Initiative)

Abstract No.: ABS0002071

IMPACT OF 10-VALENT PNEUMOCOCCAL CONJUGATE VACCINE ON HOSPITAL ADMITTION DUE TO PNEUMONIA AMONG CHILDREN IN NEPAL

Yumiko Hayashi

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Introduction: Pneumococcus is the most common pathogen to cause pneumonia. The government of Nepal has introduced 10-valent pneumococcal vaccine (PCV10) since 2015. The impact of PCV10 is not conclusive by the previous study findings in Nepal. We aim to assess impact before and after the introduction of PCV10 among hospital admitted children due to chest x-ray confirmed pneumonia.

Methods: We implemented a retrospective cross-sectional study as a hospital surveillance in Siddhi Memorial Hospital (SMH), which is the only one general pediatric hospital in Bhaktapur, Nepal. We assessed the impact of PCV10 on proportion of chest x-ray confirmed pneumonia as a cause of hospital admission before and after introduction of PCV10 using log-binomial regression model. Adjusted prevalence ratio (APR) was calculated in each year of post-PCV10 period (2016 to 2020) by comparing the prevalence of the pre-PCV10 period (2014 and 2015). APR was adjusted by age, sex, and month of admission.

Results: Out of 8,119 admission cases, 989 had chest x-ray confirmed pneumonia. The prevalence of pneumonia in total admission was 18.5% (379/2039) in the pre-PCV10 period and 10.0% (610/6080) in the post-PCV10 period. The overall APR was 0.70 (95%CI: 0.60-0.81) in 2019 and 0.45 (95%CI: 0.34-0.60) in 2020. Especially, in the age group under 2 years old, the APR showed 80% reduction (APR: 0.20, 95%CI: 0.07-0.58).

Conclusion: The prevalence of hospital admission cases due to pneumonia decreased in post-PCV10 period from 2016 to 2019. The introduction of PCV10 is one of the effective measures to prevent from hospital admission due to pneumonia among Nepali children.

Keywords: Children, Nepal, 10-valent Pneumococcal conjugate vaccine, pneumonia, Streptococcus pneumoniae

Abstract No.: ABS0001988

BACTERIAL ETIOLOGIES OF DIARRHEA IN CHILDREN UNDER 5 YEARS FROM MUKURU INFORMAL SETTLEMENT AND THEIR ANTIMICROBIAL SENSITIVITY PROFILES.

Susan Kiiru

Authors: Authors: Susan Kiiru[1,2], John Maina1, John Mwaniki[1], Edinah Songoro[2], Samuel Kariuki[1]

Affiliation: [1]; Center for Microbiology Research, Kenya Medical Research Institute, Kenya.
[2]; Jomo Kenyatta University of Agriculture and Technology, JKUAT, Kenya.

Background: In Kenya, diarrhoeal disease is the third leading cause of child mortality after Malaria and Pneumonia, accounting for nearly 100 deaths daily. We conducted a cross-sectional study in Mukuru informal settlements to determine the diarrhoea-causing bacteria and their ASTs.

Methods: 219 Diarrheagenic children (≤ 5 years) were recruited from outpatient clinics of Municipal City Council, Mukuru kwa Reuben, Mary Mother Mission, and Mama Lucy Kibaki Hospital, Nairobi. Stool culture was done on MacConkey and Salmonella Shigella Agar, while the recovered bacteria were identified using VITEK®2GNID and PCR, and Antibiotic Susceptibility Testing (AST) was done using VITEK®2AST-GN83.

Results: At least one bacterial organism was recovered from each of the 213 (97%) participants. The most dominant bacteria recovered included; Escherichia coli (35.5%), Enterobacter spp (27.8%), Klebsiella spp (11%), and Citrobacter spp (4.7%). Potentially pathogenic isolates such as Salmonella 7 (2%), Proteus mirabilis 16 (6%), Providencia alcalifaciens 1 (0.3 %), and Shigella 16 (4.7%) were also detected. Rarely reported but implicated with diarrhoeal disease, Isolates such as Pantoea spp 0.67% (2), Raoultella planticola 0.33% (1), and Kluyvera 2% (6) were also recovered. Ampicillin (64%), cefazolin (57%), and sulfamethoxazole-trimethoprim (55%) were the least effective antimicrobials, while meropenem (99%), amikacin (99%), tazobactam piperacillin (96%), and cefepime (95%) were the most effective. Overall33(21%) of all enterics recovered were multidrug-resistant (MDR).

Conclusion: Infection with diarrhoeagenic bacteria is prevalent in children in the Mukuru settlement. The strains were resistant to the commonly used antibiotics, thus narrowing the treatment options for diarrheal disease.

Keywords: Bacterial enterics, diarrhea, and AMR.

Abstract No.: ABS0002063

ASSOCIATION OF RENEWED BLOOD PRESSURE CATEGORY WITH PRETERM BIRTH IN KWALE COUNTY, KENYA

Mami HITACHI

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Introduction: Hypertension in pregnancy serves to screen high risk women of preterm birth. Redefined lower diagnostic threshold does not apply to pregnant women. This study aimed to evaluate the association between renewed blood pressure categories and preterm delivery.

Methods: This was a retrospective study used electronic records of the Maternal and Child Health Handbook registered by the Women and Infant Registration System. All women who had at least one antenatal care visit and delivery between January 2017 and April 2020 and between May and December 2022 were included in the study. A birth of less than 37 weeks was defined as preterm delivery. The maximum blood pressure across all antenatal care visits was classified based on the newly recommended criteria. A generalized linear model with binomial distribution and logit link function was used to evaluate the association between new blood pressure categories and preterm birth by health facility level.

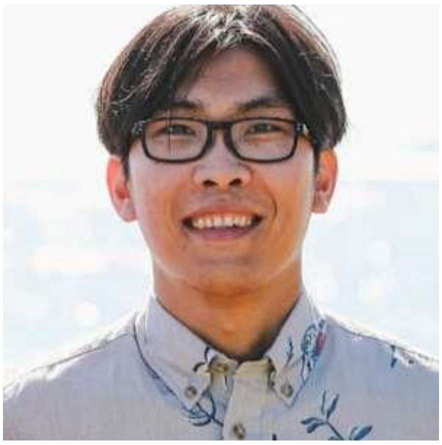
Results: A total of 825 women were analysed. Of these, elevated blood pressure was 13.7%, stage 1 hypertension was 15.2%, non-severe stage 2 hypertension was 4.5% and severe stage 2 hypertension was 1.2%. A significant association was identified between severe stage 2 hypertension and preterm delivery in higher-level facilities (AO R:10.94; 95% CI:1.08-110.93; P=0.04). There was no association between the refined category and preterm delivery in the lower-level facilities.

Conclusions: This study showed no association between the lower blood pressure thresholds and preterm delivery. However, previous studies in well-resourced countries with larger sample sizes also reported a significant association. Therefore, further investigations are required.

Keywords: hypertension, pregnancy, preterm birth, low-resource setting

Abstract No.: ABS0002051

ESTABLISHING THE SPATIAL DISTRIBUTION OF CIRCULATING ARBOVIRUSES IN URBAN AND RURAL LIBERIA



Albert To

Authors: Albert To[1], Varney M. Kamara[1,2], Davidetta M. Tekah[2], Mohammed A. Jalloh[2], Salematu B. Kamara[2], Teri Ann S. Wong[1], Aquena H. Ball[1], Ludwig Mayerlen[1], Kyle Ishikawa[3], Hyeong Ahn[3], Bode Shobayo[4], Julius Teahton[4], Brien K. Haun[1,5], Wei-Kung Wang[1], John M. Berestecky[1,2,6], Peter S. Humphrey[2], Vivek R. Nerurkar[1], Axel T. Lehrer[1]

Affiliation:[1]Department of Tropical Medicine, Medical Microbiology and Pharmacology, University of Hawai‘i, [2]Department of Biological Sciences, Medical Science TJR Faulkner College of Science and Technology, University of Liberia, [3]Department of Quantitative Health Sciences, University of Hawai‘i, [4]National Public Health Institute of Liberia, [5]Cell and Molecular Biology Graduate Program, University of Hawai‘i, [6]Math & Science Department, Kapiolani Community College, University of Hawai‘i

Given the high number of arbovirus outbreaks in West African nations, as well as Central Africa, it is implied that mosquito- and tick-borne viruses account for a large proportion of non-malaria febrile illnesses in Liberia. Such etiologies are severely under-reported as they are frequently undiagnosed, misdiagnosed, or not recognized (if asymptomatic). The primary goal of this study is to establish a spatiotemporal baseline of arbovirus exposure in Liberia.

A rapid, sample-sparing, and high-throughput bead-based multiplex immunoassay based on high-quality, immunodominant antigens was developed for field testing in a mobile laboratory. Approximately 600 human serum samples collected throughout the country, from communities with varying levels of urbanization, were analyzed for IgG reactive to nine common flavi-, alpha-, and bunyaviruses detected elsewhere in West Africa.

Preliminary data indicate a relatively moderate-high seroprevalence of CHIKV and, to a lesser extent, WNV in Liberia. Serological evidence of DENV, ZIKV and YFV were also detected but not as prevalent. A low seroprevalence of RVFV and CCHFV were observed.

Results: generated through this study will help establish a baseline of infection which can be used to guide government policy in resource allocation and animal husbandry practices. Additionally, the success of this testing platform in generating accurate and reliable data validates the use of our thermotolerant immunoassay in emergency situations where use of PCR or ELISA tests is not possible, especially in the field as part of a mobile laboratory.

Keywords: Arboviruses, Mosquito-borne viruses, Viral antigen, Multiplex Immunoassay, Serosurveillance, Liberia, West Africa

Abstract No.: ABS0002001

THE USE OF ZIEHL-NEELSEN AND NAOH CONCENTRATION TECHNIQUES IN THE DETECTION OF PARAGONIMUS OVA IN SPUTUM

Rupert Stephen Charles Chua

Authors: Chua RS[1], de Guzman LC[1], Sambo JG[1], Siao TG[1], Mistica MS[2], Belleza MB[2], Folgo NB[3], Tomimbang M[4], Belizario VY[1,2]

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Introduction: Pulmonary paragonimiasis is a parasitic disease with signs and symptoms that mimic pulmonary tuberculosis (PTB). Current laboratory methods for diagnosis of paragonimiasis rely on ova detection by microscopy through sodium hydroxide (NaOH) concentration technique, but studies have shown that the Paragonimus ova can also be seen using the Ziehl-Neelsen (ZN) staining technique for acid fast bacilli. This study aimed to revisit the use of both ZN and NaOH concentration techniques in the diagnosis of paragonimiasis and compare their detection rates.

Methods: Sputum samples were collected from patients exhibiting signs and symptoms of PTB and were processed and examined using both ZN and NaOH techniques by trained microscopists.

Results: A total number of 479 patients were included in this study. Paragonimus ova was seen in 14.2% of the patients by ZN technique, 7.5% by NaOH technique, 19.2% by either technique, and 2.5% were positive by both techniques. Coinfection with PTB was seen in 0.4% of the patients. Using positivity for any one technique as reference standard, sensitivity for ZN technique and NaOH concentration technique were 73.9% and 39.1%, respectively.

Conclusion: ZN technique shows a higher sensitivity (73.9%) than NaOH concentration technique (39.1%). In known co-endemic areas, using the ZN technique offers the benefit of screening for both PTB and paragonimiasis at the same time.

Keywords: Paragonimiasis, Ziehl-Neelsen, sodium hydroxide concentration

Abstract No.: ABS0002009

Detection of GB Virus C in a Child Presenting with Dengue-like Illness

Edison Johar

Authors: Johar E[1], Witari NPD[2], Sriyani IY[1], Dewi YP[1], Antonjaya U[3], Yudhaputri FA[1], Ledermann J[4], Powers A[4], Masyeni S[2], and Myint KSA[1]

Affiliation:[1]Exeins Health Initiative, Jakarta, Indonesia; [2]Faculty of Medicine and Health Sciences, Universitas Warmadewa, Bali, Indonesia; [3]Oxford University Clinical Research Unit Indonesia, Jakarta, Indonesia; [4]Centers for Disease Control, Fort Collins, Colorado, USA

GB virus C (GBV-C) or hepatitis virus G, is a +ssRNA virus from the Flaviviridae family. The virus is often associated with post-blood-transfusion hepatitis, and frequently found in patients infected with HIV-1, HBV, or HCV. The virus causes a mild disease with non-specific symptoms, but its association with acute and chronic liver disease is not well understood. A 3-year-old male, with no prior history of blood transfusion, was admitted with high fever, malaise and bleeding to Tabanan General Hospital, Bali, Indonesia in November, 2017. Blood counts, including platelets, were normal. The provisional diagnosis was dengue infection, but a dengue NS1 rapid test was negative. Blood serum was negative by Alphavirus and Flavivirus genus-specific RT-PCR. Further investigation using metagenomic NGS recovered a complete coding genome of GBV-C with an average depth of 144.8 reads. No HIV-1 and Hepatitis A to E viruses reads were recovered. The study isolate belonged to genotype VI, and the closest isolate was from Japan collected before 1997 with 91.9% genome similarity. This study highlights the importance of metagenomic NGS when routine diagnostic panels are negative or inconclusive. GBV-C should be considered in febrile patients presenting with bleeding and a normal blood count when typical viral hemorrhagic fevers test negative.

Keywords: GB virus C, Hepatitis G, Pediatric, Dengue-like Illness, Metagenomic, NGS

Advancing Knowledge of Cryptic Intraerythrocytic Infections in Plasmodium vivax Malaria

15.45-17.15hr

Room C

Thursday 13 December 2023

S34: Advancing Knowledge of Cryptic Intraerythrocytic Infections in Plasmodium vivax Malaria

15.45-17.15hr

Room C

Chairperson:
1. Wanlapa Roobsoong

Invited speaker:

1. PLASMODIUM VIVAX CRYPTIC ERYTHROCYTIC INFECTIONS
Hernando del Portillo
Other (Institute for Global Health (ISGlobal), Hospital Clínic - Universitat de Barcelona, Barcelona, Spain)

2. MECHANISTIC INSIGHTS AND FUNCTIONAL STUDIES OF PLASMODIUM VIVAX INTRASPLENIC INFECTIONS
Carmen Fernández
Other (Institute for Global Health (ISGlobal), Hospital Clínic - Universitat de Barcelona, Barcelona, Spain)

3. 3D PRINTED BONE-MARROW-ON-A-CHIP AND BLOOD RHEOLOGY CHALLENGES
Aurora Hernandez-Machado
Other (Institute of Nanoscience and Nanotechnology (IN2UB), University of Barcelona)

4. TOWARDS AN ENGINEERED VASCULARIZED BONE-MARROW-ON-CHIP TO UNDERSTAND PLASMODIUM VIVAX CRYPTIC NICHES: PRELIMINARY RESULTS ON DEVICE ASSEMBLY
Cristina C. Barrias
Other (i3S - Instituto de Investigação e Inovação em Saúde, Universidade do Porto)

Abstract No.: ABS0002266

PLASMODIUM VIVAX CRYPTIC ERYTHROCYTIC INFECTIONS

Hernando del Portillo

Authors: Hernando del Portillo

Affiliation: Institute for Global Health (ISGlobal), Hospital Clínic - Universitat de Barcelona, Barcelona, Spain

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002267

MECHANISTIC INSIGHTS AND FUNCTIONAL STUDIES OF PLASMODIUM VIVAX INTRASPLENIC INFECTIONS

Carmen Fernández

Authors: Carmen Fernández

Affiliation: Institute for Global Health (ISGlobal), Hospital Clínic - Universitat de Barcelona, Barcelona, Spain

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002269

3D PRINTED BONE-MARROW-ON-A-CHIP AND BLOOD RHEOLOGY CHALLENGES

Aurora Hernandez-Machado

Authors: Aurora Hernandez-Machado

Affiliation: Institute of Nanoscience and Nanotechnology (IN2UB), University of Barcelona

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002270

TOWARDS AN ENGINEERED VASCULARIZED BONE-MARROW-ON-CHIP TO UNDERSTAND PLASMODIUM VIVAX CRYPTIC NICHES: PRELIMINARY RESULTS ON DEVICE ASSEMBLY

Cristina C. Barrias

Authors: Cristina C. Barrias

Affiliation: i3S - Instituto de Investigação e Inovação em Saúde, Universidade do Porto

No abstract available

Keyword: No abstract available

Thursday 14 December 2023

S35: Update on Human Infection Models in Thailand

15.45-17.15hr

Room D

Thursday 14 December 2023

S35: Update on Human Infection Models in Thailand

15.45-17.15hr

Room D

Chairperson:
1. Jetsumon Pachumsri
2. Phaik Yeong Cheah

Invited speaker:

1. Malaria Infection Studies in Thailand
Jetsumon Prachumsri
Faculty of Tropical Medicine, Mahidol University (Mahidol Vivax Research Unit (MVRU))

2. Dengue Infection Studies in Thailand
Oranich Navanukroh
Other (Siriraj Hospital)

3. Dengue Infection Studies in Thailand
Panisadee Avirutnan
Other (Faculty of Medicine Siriraj Hospital)

4. PUBLIC ENGAGEMENT FOR DENGUE HUMAN INFECTION STUDIES
Woraphat Ratta-apha
Other (Faculty of Medicine Siriraj Hospital, Mahidol University)

5. Malaria Infection Studies in Thailand – perspective of volunteer 1
Khanayot Bunnak
Other (MORU)

6. Malaria Infection Studies in Thailand – perspective of volunteer 2
Praparat Junyaphongsatorn
Other (MORU)

Abstract No.: ABS0002301

Malaria Infection Studies in Thailand

Jetsumon Prachumsri

Authors: Jetsumon Prachumsri

Affiliation: Mahidol Vivax Research Unit, Faculty of Tropical Medicine, Mahidol University

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002303

Dengue Infection Studies in Thailand

Oranich Navanukroh

Authors: Oranich Navanukroh

Affiliation: Siriraj Hospital

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002302

Dengue Infection Studies in Thailand

Panisadee Avirutnan

Authors: Panisadee Avirutnan

Affiliation: Siriraj Hospital

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002224

PUBLIC ENGAGEMENT FOR DENGUE HUMAN INFECTION STUDIES

Woraphat Ratta-apha

Authors: Ratta-apha W.

Affiliation: Faculty of Medicine Siriraj Hospital, Mahidol University

Introduction: Community engagement is a critical component when implementing human challenge infection models (CHIMs) in research. This study aims to study opinion and community engagement for controlled human dengue infection in Thailand (DHIT) among personnel in a hospital where DHIT will be conducted.

Methods: Participants are personnel who currently working at Siriraj Hospital. The participants received study information, such as a link to information and a video regarding DHIT, and answered paper-based or online questionnaire. Using the interest to participate in the DHIT study, the data were classified into two groups: the participants who were interested in participating in the DHIT study and those who were not. The t-test, chi-square test, or Mann-Whitney U test were conducted to compare the differences in characteristics between the two groups.

Results: Out of 343 participants who answered the questionnaire, 75 (21.8%) were interested in the DHIT. Compared to the opinions of the participants who were interested in the DHIT and those who were not, the reasons for the project's interest ($p < 0.001$), benefit to participants ($P < 0.001$), and benefit to society (p 0.02) were significantly different. They agreed to support conducting the study ($P < 0.001$) and thought that this study would be assured of safety if approved by the institutional review board of faculty (P 0.001). However, the non-interested group agreed to have an alternative way to conduct the research (P 0.04).

Conclusion: Organizing community engagement activities helps to reflect community opinions, understand the community, and is an important part of successful research.

Keywords: Controlled human challenge models (CHIM); Community engagement; Dengue infection

Abstract No.: ABS0002239

Malaria Infection Studies in Thailand – perspective of volunteer 1

Khanayot Bunnak

Authors: Khanayot Bunnak

Affiliation: Malaria Infection Study Thailand Participant (CHIM study)

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002240

Malaria Infection Studies in Thailand – perspective of volunteer 2

Praparat Junyaphongsatorn

Authors: Praparat Junyaphongsatorn

Affiliation: Malaria Infection Study in Thailand Programme participant

No abstract available

Keyword: No abstract available

Thursday 14 December 2023

S36: Novel Tools to Aid the Management of Febrile Illness in Southeast Asia

15.45-17.15hr

Room E

Thursday 14 December 2023

S36: Novel Tools to Aid the Management of Febrile Illness in Southeast Asia

15.45-17.15hr

Room E

Chairperson:
1. Kesinee Chotivanich
2. Arjen Dondorp

Invited speaker:

1. The feasibility of novel point-of-care diagnostics for febrile illnesses at health centres in Southeast Asia: a mixed-methods study
James Callery
Other (MORU/University of Oxford)

2. Glucose - 6 - Phosphate Dehydrogenase (G6PD) measurement using biosensors by community-based village malaria workers and hospital laboratory staff in Cambodia: a quantitative study
Bipin Adhikari
Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

3. EXPANDING THE ROLES OF COMMUNITY HEALTH WORKERS TO SUSTAIN PROGRAMMES DURING MALARIA ELIMINATION: OPERATIONAL RESEARCH IN SOUTHEAST ASIA
Thomas Peto
Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

Abstract No.: ABS0002172

The feasibility of novel point-of-care diagnostics for febrile illnesses at health centres in Southeast Asia: a mixed-methods study

James Callery

Authors: Fidelis Jacklyn Adella, Moul Vanna, Bipin Adhikari, Sam Ol, Rupam Tripura, Chan Davoeung, James J. Callery, Yok Sovann, Arjun Chandna, Voeunrung Bunreth, Carina Asnong, Lorenz von Seidlein, Arjen M. Dondorp, Richard J. Maude, Yoel Lubell, Bridget Wills, Dysoley Lek, and Thomas J. Peto

Affiliation: Mahidol-Oxford Tropical Medicine Research Unit (MORU)

The decline of malaria in Southeast Asia means other causes of fever are increasingly relevant, but often undiagnosed. The objective of this study was to assess the feasibility of point-of-care tests to diagnose acute febrile illnesses in primary care settings.

Methods: A mixed-methods study was conducted at nine rural health centres in western Cambodia. Workshops introduced health workers to the STANDARD(TM) Q Dengue Duo, STANDARD(TM) Q Malaria/CRP Duo and a multiplex biosensor detecting antibodies and/or antigens of eight pathogens. Sixteen structured observation checklists assessed users' performances and nine focus group discussions explored their opinions.

Results: All three point-of-care tests were performed well under assessment, but sample collection was difficult for the dengue test. Respondents expressed that the diagnostics were useful and could be integrated into routine clinical care, but were not as convenient to perform as standard malaria rapid tests. Health workers recommended that the most valued point-of-care tests would directly inform clinical management (e.g. a decision to refer a patient or to provide/withhold antibiotics).

Conclusions: Deployment of new point-of-care tests to health centres could be feasible and acceptable if they are user-friendly, selected for locally circulating pathogens and are accompanied by disease-specific education and simple management algorithms.

Keywords: point-of-care diagnostics, health centres, Southeast Asia

Abstract No.: ABS0002153

Glucose - 6 - Phosphate Dehydrogenase (G6PD) measurement using biosensors by community-based village malaria workers and hospital laboratory staff in Cambodia: a quantitative study

Bipin Adhikari

Authors: Bipin Adhikari[1,2]*, Rupam Tripura[1,2], Lek Dysoley[3], Thomas J Peto[1,2], James J Callery[1,2], Chhoeun Heng1, Thy Vanda1, Ou Simvieng1, Sarah Cassidy-Seyoum4, Kamala Thriemer4, Arjen M Dondorp[1,2], Benedikt Ley[4] and Lorenz von Seidlein[1,2]

Affiliation:

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[2] Centre for Tropical Medicine and Global Health, Nuffield Department of Clinical Medicine, University of Oxford, Oxford, UK

[3] C.N.M National Center for Parasitology, Entomology and Malaria Control, Phnom Penh, Cambodia

[4] Global and Tropical Health Division, Menzies School of Health Research and Charles Darwin University, Darwin, Australia

Introduction: Radical cure for vivax malaria can prevent relapses but requires measurement of glucose-6-phosphate dehydrogenase enzyme (G6PD) activity. The objectives of this study were to 1. compare the G6PD activity readings using biosensor by Village malaria workers and hospital laboratory technicians; and 2. compare the G6PD deficiency categorization with the manufacturer based on adjusted male median.

Methods: Each of the 28 VMWs and five LTs received a Biosensor and standardized training on its use. G6PD activities of febrile patients identified in the community were measured by VMW; in a subset a second reading was done by LTs. All participants were tested for malaria by rapid diagnostic test (RDT). The adjusted male median (AMM) was calculated from all RDT negative participants and defined as 100% G6PD activity.

Results: VMWs measured activities in 1,344 participants, 1,327 (98.7%) readings were included in the analysis, 68 of these had a positive RDT result. 100% activity was calculated as 6.4U/gHb (interquartile range: 4.5 to 7.8); 9.9% (124/1259) of RDT negative participants had G6PD activities below 30%, 15.2% (191/1259) had activities between 30% and 70%; and 75.0% (944/1259) had G6PD activities >70%. Repeat measurements among 114 participants showed a significant correlation of G6PD readings (rs=0.784, p

Conclusions: G6PD measurements by VMWs and LTs were similar. Manufacturer recommendations of G6PD categories differed significantly and thus require a revision.

Keywords: Village malaria worker; biosensor; vivax malaria; G6PD; primaquine; radical cure; Southeast Asia

Abstract No.: ABS0002215

EXPANDING THE ROLES OF COMMUNITY HEALTH WORKERS TO SUSTAIN PROGRAMMES DURING MALARIA ELIMINATION: OPERATIONAL RESEARCH IN SOUTHEAST ASIA

Thomas Peto

Authors: Lek Dysoley[1,2,] James J Callery[3,4,] Voeurng Bunreth[5,] Moul Vanna[6,] Chan Davoeung[5,] Yok Sovann[7,] Sles You[5,] Sam Ol[6,] Rupam Tripura[3,4,] Rusheng Chew[3,4,8,] Arjun Chandna[4,9,] Céline Christiansen-Jucht[10,] Jayme Hughes[12,] Nguon Sokomar[13, 14, 15,] Top Sophornarann1[3,14,15,] Jeanne Rideout[13,14,15,] Tat Veyvath[5], Oum Sarith[7,] Thaung Puthy[5,] Hay Sothearoth5, Sen Sam An[13,14,15,] Sazid Ibna Zaman[3,] Lorenz von Seidlein[3,4,] Lim Vanthy[6,] Preap Sodavuth[16,] Chrun Vannak[16,] Arjen M Dondorp[3,4,] Yoel Lubell[3,4,] Richard J Maude[3,4,17,] **Thomas J Peto**[3,4,] Bipin Adhikari[3,4]

Affiliation:
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5: Provincial Health Department, Battambang, Cambodia
6: Action for Health Development, Battambang, Cambodia
7: Provincial Health Department, Pailin, Cambodia
8: Faculty of Medicine, University of Queensland, Brisbane, Australia
9: Cambodia Oxford Medical Research Unit, Angkor Hospital for Children, Siem Reap, Cambodia
10: World Health Organization, Phnom Penh, Cambodia
11: President's Malaria Initiative, Phnom Penh, Cambodia
12: Clinton Health Access Initiative, Phnom Penh Cambodia
13: Cambodia Malaria Elimination Project 2, Phnom Penh, Cambodia
14: University Research Company Ltd., Phnom Penh, Cambodia
15: USAID, Phnom Penh, Cambodia
16: United Nations Office for Project Services, Phnom Penh, Cambodia
17: The Open University, Milton Keynes, UK

Introduction: In Southeast Asia malaria elimination is targeted by 2030. Cambodia aims to achieve this by 2025, driven in large part by the urgent need to control the spread of artemisinin-resistant falciparum infections. Rapid elimination depends on sustaining early access to diagnosis and effective treatment. In much of Cambodia, rapid elimination will rely on a village malaria worker (VMW) network. Yet as malaria declines and is no longer a common cause of febrile illness, VMWs may become less popular with febrile patients, as VMWs do not diagnose or treat other conditions at present. There is a

risk that VMWs become inactive and malaria rebounds before the complete interruption of transmission is achieved.

Methods: During 2021-23 a large-scale operational research study was conducted in western Cambodia to explore how a VMW network could be sustained by including health activities that cover non-malarial illnesses to encourage febrile patients to continue to attend.

Results: 105 VMWs received new rapid diagnostic tests (including dengue antigen-antibody and combined malaria/C-reactive protein tests), were trained in electronic data collection, and attended health education packages on hygiene and sanitation, disease surveillance and first aid, management of mild illness, and vaccination and antenatal care.

Conclusion: In August 2023 the National Malaria Control Programme of Cambodia convened a stakeholder meeting in Battambang, Cambodia. Findings from the study were reviewed in the context of current malaria elimination strategies. The discussions inform policy options to sustain the relevance of the VMW network in Cambodia, and the potential for its integration with other health worker networks. This

Keywords: Community health workers, village malaria workers, malaria elimination

Friday 15 December 2023

S37: Free Paper IV: Global Health 2

08.30-10.00hr

Room A

Friday 15 December 2023

S37: Free Paper IV: Global Health 2

08.30-10.00hr

Room A

Chairperson:
1. Yoel Lubell
2. Yanin Limpanont

Invited speaker:

1. THE ROLE OF TYPR VI SECRETION SYSTEM ACCESSORY PROTEIN TAGAB-5 IN HUMAN MICROGLIA

Sanisa Lohitthai
Faculty of Tropical Medicine, Mahidol University (Microbiology and Immunology)

2. NEGLECTED TROPICAL DISEASES: AN OUTBREAK OF LEISHMANIASIS AMONG HOUSEHOLD MEMBERS IN AN URBAN AREA OF NAKHON SI THAMMARAT PROVINCE, THAILAND

Kalita Wareewanit
Other (The Office of Disease Prevention and Control region 11, Department of Disease Control)

3. FLY ON FACE: COMPARATIVE ANALYSIS OF KAP SURVEYS AMONG THE TWO SOCIAL GROUPS IN AN ENDEMIC AREA IN SRI LANKA.

Mayumi Manamperi
Other (Ministry of Health, Nutrition and Indigenous Sciences)

4. N-CLEAVED GALECTIN-9 IS A SURROGATE MARKER OF A CLIMATE CHANGE-INDUCED DISEASE

Toshio Hattori
Other (KIBI International University)

5. DETECTION OF TICK-BORNE INFECTIOUS AGENTS IN WILDLIFE FROM NORTHERN TAIWAN

Jing-Syuan Huang
Other (environmental and occupational health science)

6. SPATIO-TEMPORAL OCCURRENCE, BURDEN, RISK FACTORS AND MODELLING METHODS FOR ESTIMATING SCRUB TYPHUS BURDEN: A SYSTEMATIC REVIEW

Qian Wang
Other (MORU)

Abstract No.: ABS0002188

THE ROLE OF TYPR VI SECRETION SYSTEM ACCESSORY PROTEIN TAGAB-5 IN HUMAN MICROGLIA

Sanisa Lohitthai

Authors: Sanisa Lohitthai[1], Amporn Rungruengkitkun[1], Niramol Jitprasutwit[2], Thida Kongngoen[1], , Sarunporn Tandhavanant[1,3], Passanesh Sukphopetch[1], Narisara Chantratita[1,4], Nitaya Indrawattana1, and Pornpan Pumirat[1]

Affiliation: [1]Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand; [2]Center for Vaccine Development, Institute of Molecular Biosciences, Mahidol University, Nakhon Pathom 73170, Thailand;

Burkholderia pseudomallei is a Gram-negative pathogen that responsible for melioidosis, a potentially fatal disease that endemic in tropical region. A person can be infected by *B. pseudomallei* via percutaneous inoculation, inhalation, and ingestion. Disease manifestations of melioidosis can range from being mild infection to more severe illness, depending on the infected organs. Melioidosis can affect any organ system, nevertheless melioidosis of the central nervous system (CNS) can be rapidly fatal even in well-resourced settings. Type VI secretion system (T6SS) is a major virulence determinant in *B. pseudomallei*. Recently, T6SS accessory protein TagAB-5 was found to promote *B. pseudomallei* intracellular survival and virulence. In present study, we aim to elucidate the pathogenesis and virulence of *B. pseudomallei* TagAB-5 in human microglia, a residence of immune cells in CNS. We constructed *B. pseudomallei* tagAB-5 mutant and complement strains. The effects of TagAB-5 deletion on the pathogenicity of *B. pseudomallei* were studied by co-culture assays of bacteria with HMC3 cells. Compared with the wild-type, the tagAB-5 mutant exhibited defective pathogenic abilities in intracellular replication, multinucleated giant cell formation, and induction of cell damage. Additionally, infection by the tagAB-5 mutant elicited a decreased production of interleukin 8 (IL-8) in HMC3, suggesting that efficient pathogenicity of *B. pseudomallei* is required for IL-8 production in microglia. Collectively, this study indicated that microglia might be an important intracellular niche for *B. pseudomallei*, particularly in CNS infection, and TagAB-5 confers *B. pseudomallei* pathogenicity in these cells.

Keywords: *Burkholderia pseudomallei*; neuropathogenesis; type VI secretion system

Abstract No.: ABS0002049

NEGLECTED TROPICAL DISEASES: AN OUTBREAK OF LEISHMANIASIS AMONG HOUSEHOLD MEMBERS IN AN URBAN AREA OF NAKHON SI THAMMARAT PROVINCE, THAILAND

Kalita Wareewanit

Authors: Wareewanit K[1] Saengsuwan L[1] Thongkhaw K[1]

Affiliation: [1]The Office of Disease Prevention and Control Region 11, Department of Disease Control

Leishmaniasis is a parasitic disease that is classified as a neglected tropical disease (NTD). On 22 Sep 2018, a patient was confirmed having leishmaniasis from Nakhon Si Thammarat Province, case was reported to The Office of Disease Prevention and Control, Region 11. An investigation was conducted to identify reservoirs and vectors. Blood and Saliva samples were collected from humans, domestic mammals and rodents' blood specimens were collected, and sandfly trapping was implemented by light traps. All samples were tested by PCR technique.

Two cases were confirmed with Leishmania martiniquensis infection by PCR, both lived in household. The Residence is located in an urban area. The first case, a 46-year-old younger who is a van driver has a history of drug addiction, living with HIV. The patient presented with chronic fever, weight loss of 9 kg. in a month, right leg rash but no pain and Hepatosplenomegaly. Physician has diagnosed Visceral and Cutaneous leishmaniasis and treated the case with amphotericin B 60 mg., and died during treatment. The second case, a 64 years old older Brother who is trader with no symptoms. 49 sandfly traps were found, 85.71% were Sergentomyia iyengari. Leishmania martiniquensis was identified in 2 samples. All samples from domestic mammals and rodents were negative. Deltamethrin fogging was done to control the vectors.

Leishmaniasis was confirmed as an outbreak in household setting. Awareness of leishmaniasis among immunocompromised people should be raised for timely appropriate medical attention and specific vector control for sandflies in the area should be implemented.

Keywords: Leishmaniasis, L. martiniquensis, urban, Neglected Tropical Diseases, Nakhon Si Thammarat Province

Abstract No.: ABS0002029

FLY ON FACE: COMPARATIVE ANALYSIS OF KAP SURVEYS AMONG THE TWO SOCIAL GROUPS IN AN ENDEMIC AREA IN SRI LANKA.

Mayumi Manamperi

Authors: Manamperi M [1,2] , Wijegunawardana NDAD [2] ,Kandegedara P [2]

Affiliation:[1] Ministry of Health, Nutrition, and Indigenous Sciences, Sri Lanka; [2] Rajarata University of Sri Lanka.

The good old trial-and-error control strategy and limited awareness have led to an increase in leishmaniasis disease incidences in Sri Lanka. Studies indicate that a lack of focus on relevant social groups is the main reason for low awareness among the population. The study aimed to investigate the knowledge, attitudes, and practices regarding leishmaniasis between two social groups in the same endemic area to determine the most effective group for awareness.

The study used a cross-sectional design involving two different social groups living in an endemic area of the Anuradhapura district. A cohort of students aged 12-14 years (n=203) and residents aged 18-80 years (n=277) participated in this study. This study was conducted from December 2022 to August 2023.

The chi-square test reveals that there is a significant difference in existing knowledge about the disease symptoms (p=0.008), vector (p=0.000), and attitude (p=0.000) in the two social groups with respect to age. Knowledge sources are significantly different in the two social groups with respect to the number of family members (p=0.000). Students obtain their knowledge from social media. Adults obtain their knowledge from mass media. The Mann-Whitney U and Kruskal Wallis H tests were applied to compare the values of each area with different demographic factors. Considering $p < 0.05$ as statistically significant, there was a difference between the mean knowledge about the symptoms (p=0.000), vectors (p=0.002), and practices (p=0.000) scores of the different ages.

The present study indicates on existing disease control programs through community engagements should be more age-specific.

Keywords: Awareness, KAP Surveys, Leishmaniasis

Abstract No.: ABS0002035

N-CLEAVED GALECTIN-9 IS A SURROGATE MARKER OF A CLIMATE CHANGE-INDUCED DISEASE

Toshio Hattori

Authors: Toshio Hattori[1] Hiroko Iwaski Hozumi[1] Toshiro Niki[2] Yugo Ashino[3]

Affiliation:[1]Kibi International University; [2] Kagwa University; [3]Sendai City Hospital

Introduction: After the great East Japan earthquake, we had 10 consecutive seminars on disaster-related infectious diseases and the most talked about RNA viruses (doi.org/10.3390/reports5010007).

These viruses become an epidemic due to recent climate change. Galcetin-9 (Gal-9) was first identified as a Dengue virus disease severity marker. We recently measured plasma N-cleaved Gal9 levels and evaluated if it could reflect the severity of COVID-19, another climate change-induced disease (CCID). We also asked if the levels could reflect the therapeutic effect of tocilizumab (TCZ) because we previously reported the double-edged sword effect of TCZ (doi.org/10.3390/reports3040029;doi.org/10.3390/reports5020024). We additionally examined if the levels on admission predict the duration of hospitalization in COVID-19.

Methods: This study was a cross-sectional analytical study and the patients were recruited in Sendai City Hospital (SCH). Twenty-three patients with mild clinical symptoms (CV) and 32 patients associated with pneumonia (CP) were diagnosed. Patients' EDTA plasma was obtained. The N-cleaved-Gal9 levels were calculated by subtracting the concentration measured by full-length-Gal9 ELISA from that measured by truncated-Gal9 ELISA.

Results: Increased levels of plasma N-cleaved-Gal9 were associated with the severity of COVID-19. MMP-9 may involve the generation of N-cleaved-Gal9 and sIL-2R. A decrease in plasma N-cleaved-Gal9 was associated with the suppression of inflammation during TCZ treatment. Plasma N-cleaved-Gal9 levels on admission were positively associated with duration of hospitalization. The levels on admission efficiently discriminated the patients with longer hospitalization from those with shorter hospitalization.

Conclusion: Our results shed new light on the relevance of proteolytic products of Gal-9 in the pathophysiology and clinical management of COVID-19 and other CCIDs.

Keywords: COVID-19, Galectin-9, N-cleaved-Gal9, surrogate marker

Abstract No.: ABS0002060

DETECTION OF TICK-BORNE INFECTIOUS AGENTS IN WILDLIFE FROM NORTHERN TAIWAN

Jing-Syuan Huang

Authors: Jing-Syuan Huang[1], Pin-Huan Yu[2],, and Kun-Hsien Tsai[1,3]

Affiliation:

[1] Institute of Environmental and Occupational Health Sciences, National Taiwan University, Taipei, Taiwan；

[2] Institute of Veterinary Clinical Science, School of Veterinary Medicine, National Taiwan University, Taipei, Taiwan；

[3] Department of Public Health, College of Public Health, National Taiwan University, Taipei, Taiwan

Introduction: Ticks are the primary ectoparasites of animals and serve as vectors for multiple bacteria which make threats to human's and animals' health. Various wildlife species are the principal reservoir hosts for zoonotic Babesia species. The study reported the infection rates of Babesia spp., tick species on wildlife animals and other tick-borne pathogens in ticks and host bloods collected in northern Taiwan.

Methods: Ticks were identified by morphological and molecular methods. Gene primers of 16S genes were applied for tick species identification, Anaplasma and Ehrlichia spp. detection. For rickettsia detection, genes of gltA, OmpA, were amplified to perform the gene diversity and prevalence rate of Rickettsia spp. Gene of 18S were applied for Babesia spp. detection.

Results: Samples were collected from northern Taiwan, including 21 ticks and 30 host bloods from 2022 to 2023. Host blood specimens including 19 Melogale moschata, 7 Paguma larvata taivana, 2 Viverricula indica pallida and 2 Bubalus bubalis. The prevalence rate of Rickettsia spp. was 0%. Ehrlichia spp. was found in 1 tick and 1 host blood. Anaplasma spp. was found in 1 tick. Babesia spp was found in 1 tick and 14 host blood.

Conclusion: This study indicated 3 tick-borne pathogens in northern Taiwan. Base on the genes of 18S, Babesia spp. found in this study showed 100% gene sequence similarity to Babesia hongkongensis (JQ867356.1). Whether it can be transmitted by tick for further chances to infect humans or not are unknown. There should be continuous monitoring to ensure the health and safety of both humans and animals in Taiwan.

Keywords: Wildlife, Babesia, Tick, Taiwan.

Abstract No.: ABS0002084

SPATIO-TEMPORAL OCCURRENCE, BURDEN, RISK FACTORS AND MODELLING METHODS FOR ESTIMATING SCRUB TYPHUS BURDEN: A SYSTEMATIC REVIEW

Qian Wang

Authors: Qian Wang[1,2], Tian Ma[3], Benn Sartorius[4], Nicholas Philip John Day[1,2], Richard James Maude[1,2]

Affiliation:[1] Mahidol University; [2] University of Oxford; [3] Chinese Academy of Sciences; [4] The **University of Queensland**

Introduction: Previously considered endemic to tropical regions, scrub typhus is gaining recognition as a global health concern, yet its prevalence, impact, and risk factors remain underexplored. Our systematic review aims to fill this knowledge gap.

Methods: We did a comprehensive search on peer-reviewed studies and grey literature. We extracted data on scrub typhus prevalence, incidence and mortality and extracted median value. The long-term reported incidence was generated from included studies and national surveillance system. Exposure for scrub typhus were evaluated using a random-effects meta-analysis. Environmental variables and predictive models were also summarized.

Results: Among 227 studies across 20 countries, median reported seroprevalence was 8.90% in healthy individuals and 19.18% in febrile patients. Females and older individuals showed higher prevalence rates. China reported the highest case number (26,675 in 2018), while South Korea and Thailand exhibited the highest incidence. The median mortality ranged from 2.17% to 6.70%, depending on the patient group. Predominant risk factors included agricultural work, suitable vegetation exposure, bad personal health habits, and environmental factors like temperature and humidity. ARIMA and DLNM were commonly used for temporal and risk factor analysis, while BRT dominated spatial risk prediction.

Conclusion: The high seroprevalence in certain countries, even among healthy populations, along with the diverse mortality, highlights the global significance of scrub typhus and the need for targeted interventions and standardized diagnostics. Our review provides a foundation for the deepened understanding and into scrub typhus and underscores the urgency for further research.

Keywords: systematic review, scrub typhus, prevalence, incidence, mortality, risk factor, model

Friday 15 December 2023

S38: Young Investigator Awards 1

08.30-10.00hr

Room B4

Friday 15 December 2023

S38: Young Investigator Awards 1

08.30-10.00hr

Room B

Chairperson:
1. Kriengsak Limkittikul
2. Wirichada Pan-ngum

Invited speaker:

1. POPULATION PHARMACOKINETICS OF PRIMAQUINE IN LACTATING WOMEN AND BREASTFED INFANTS
Thanaporn Wattanakul
Other ()

2. COMPREHENSIVE EVALUATION OF MALARIA REACTIVE SURVEILLANCE AND RESPONSE STRATEGIES IN LAO PEOPLE DEMOCRATIC REPUBLIC: A MIXED-METHODS STUDY
Win Htike
Other (Burnet Institute)

3. REVISITING RODENT-BORNE RICKETTSIOSES IN THE PHILIPPINES THROUGH MOLECULAR DETECTION
Jan Clyden Tenorio
Other (Tropical Medicine Graduate Program, Faculty of Medicine, Khon Kaen University, Thailand)

4. MOLECULAR DETECTION OF PATHOGENIC LEPTOSPIRA AND HELICOBACTER PYLORI IN ENVIRONMENTAL SPECIMENS FROM THE OPISTHORCHIASIS ENDEMIC AREAS AT KHON KAEN, THAILAND
Shih Keng Loong
Other (Tropical Infectious Diseases Research & Education Centre, Universiti Malaya)

5. DIVERSITY AND DISTRIBUTION OF ANOPHELINE SPECIES IN SOUTHWEST INDIA
DEBATTAM MAZUMDAR
Other (ICMR NATIONAL INSTITUTE OF MALARIA RESEARCH)

Abstract No.: ABS0002073

POPULATION PHARMACOKINETICS OF PRIMAQUINE IN LACTATING WOMEN AND BREASTFED INFANTS

Thanaporn Wattanakul

Authors: Thanaporn Wattanakul[1], Mary Ellen Gilder[2], Rose McGready[2,3], Warunee Hanpithakphong[1], Nicholas P. J. Day[1,3], Nicholas J. White[1,3], François Nosten[2,3], Joel Tarning[1,3], Richard M. Hoglund[1,3]

Affiliation: [1]Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [2]Shoklo Malaria Research Unit, Mahidol Oxford Tropical Medicine Research Unit, Mahidol University, Mae Sot, Thailand; [3]Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, Oxford University, Oxford, UK.

Introduction: Primaquine is an essential drug for the radical cure of vivax malaria. However, lactating women are excluded from this treatment due to the unknown risk of haemolysis in breastfed infants with glucose-6-phosphate dehydrogenase (G6PD) deficiency.

Methods: Twenty-one lactating women were included in this analysis, and received a standard daily dose of primaquine (30mg/day) for 14 days. Primaquine and its metabolite (carboxyprimaquine) concentrations were measured in plasma, capillary blood, and breast milk. Population pharmacokinetic analysis was performed using nonlinear mixed-effects modelling. A mother-to-infant model, mimicking the observed feeding pattern in the studied population, was developed to predict infant drug exposure. The maternal exposure after a single low dose of primaquine (0.25mg/kg) served as a reference dose that does not cause clinically significant haemolysis in G6PD-deficient individuals.

Results: The final model consisted of one-compartment disposition models for both parent and metabolite, and accurately described the measured drug concentration-time data. Primaquine absorption was described by a transit absorption model with first-pass metabolism. Primaquine and its metabolite were excreted into breastmilk, but the estimated infant dose was

Conclusion: Modelling and simulations demonstrated negligible infant drug exposure. The predicted primaquine dose in infants was

Keywords: primaquine, pharmacokinetics, lactating women, vivax malaria

Abstract No.: ABS0002000

COMPREHENSIVE EVALUATION OF MALARIA REACTIVE SURVEILLANCE AND RESPONSE STRATEGIES IN LAO PEOPLE DEMOCRATIC REPUBLIC: A MIXED-METHODS STUDY

Win Htike

Authors: Win Htike[1,2], Win Han Oo[1,3], Nilar Aye Tun[4], Boualam Khamlome[5], Phoutnalong Vilay[5], Thet Lynn[6], Sanya Vathanakoune[6], May Chan Oo[1], Ei Phyu Htwe[1], Aung Khine Zaw[1], Kaung Myat Thu[1], Galau Naw Hkawng[1], Kaung Myat Khant[3], Paul A. Agius[2,3,7], Katherine O'Flaherty[3], Ellen A. Kearney[3,7], Julia C. Cutts[3], Freya J. I. Fowkes[3,4,7]

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Introduction: Lao People's Democratic Republic (Lao PDR) has made a significant progress in reducing malaria burden and aims to eliminate malaria by 2030. To achieve this goal, Lao PDR adopted the 1-3-7 reactive surveillance and response (RASR) strategy. It is important to evaluate the RASR strategy so that it may be improved to better contribute towards the goal of malaria elimination.

Methods: A mixed-methods study of secondary data analysis, quantitative surveys, and qualitative discussions was conducted between September and October 2022. Outcomes of interest were timeliness of RASR activities; knowledge, attitude, and practice of malaria program stakeholders and service providers on RASR strategies; and acceptability and feasibility of implementing RASR strategies in Lao PDR. Quantitative and qualitative data were analysed descriptively and thematically.

Results: In 2022, timeliness of case notification and case investigation were 98.0% and 98.6%, respectively. Malaria program stakeholders and service providers had a good knowledge of RASR; however, mobile and migrant populations were not well aware of these activities. Implementation of RASR in Lao PDR was acceptable and feasible to implement. Nevertheless, issues such as low level of community awareness of RASR activities, a high level of migration, and limitations in health system capacity need to be addressed to improve the performance of RASR.

Conclusion: Overall, the implementation of RASR strategy was satisfactory and acceptable. However, this study highlighted some key issues and ways for improving the effectiveness of RASR strategy and accelerating Lao PDR's progress towards malaria elimination.

Keywords: Lao People’s Democratic Republic, malaria elimination, reactive surveillance and response strategy

Abstract No.: ABS0001991

REVISITING RODENT-BORNE RICKETTSIOSES IN THE PHILIPPINES THROUGH MOLECULAR DETECTION

Jan Clyden Tenorio

Authors: Jan Clyden B. Tenorio[1,2], Mark Jaypee C. Gonzales[3], Rey Anthony D. Galo[4], Kristina Andrea C. Sandalo[5], Saubel Ezrael A. Salamat[5], Remil L. Galay[5]

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Introduction: Rodent-borne rickettsioses, including those caused by *Rickettsia typhi* and *Orientia tsutsugamushi*, cause significant febrile infections in Southeast Asia, but are often misdiagnosed. Both pathogens were previously reported in the Philippines about half a century ago, but there had been no recent epidemiological data. In this study, we conducted detection of these pathogens in field rats from different regions of the country using polymerase chain reaction (PCR) assays and assessed the trombiculid mites infesting the field rats that may serve as vectors.

Methods: A total of 153 spleen samples were collected from field rats trapped in different provinces in the Philippines. Trombiculid mites were collected from the ears and were morphologically identified using taxonomic keys. Nested PCR targeting the *56-kDa* tsa gene of O. tsutsugamushi, and quantitative PCR and nested PCR targeting the *gltA* gene of Rickettsia spp. were performed to detect the pathogens in rat spleens.

Results: None of the spleen samples were found positive for *O. tsutsugamushi*. Meanwhile, *Rickettsia* spp. was detected in 49 (32%) field rat samples. Of these, Northern Samar Province had the highest prevalence at 81.3%. This is followed by Cotabato Province (32%), Agusan del Sur (16.7%), and Camarines Sur (10%). Trombiculid mites were found in 67 field rats distributed in all provinces covered, except in Camarines Sur. These mites were morphologically identified as *Ascoshoengastia indica* and *Blankaartia acuscutellaris*, with the latter being the most common.

Conclusion: The results indicate that field rats from different parts of the country carry *Rickettsia* spp. that may cause significant human infections.

Keywords: Rickettsia, One Health, Vector-borne Diseases, Zoonoses

Abstract No.: ABS0002012

MOLECULAR DETECTION OF PATHOGENIC LEPTOSPIRA AND HELICOBACTER PYLORI IN ENVIRONMENTAL SPECIMENS FROM THE OPISTHORCHIASIS ENDEMIC AREAS AT KHON KAEN, THAILAND

Shih Keng Loong

Authors: Loong SK[1,2], Sripa M[2], Wannachart S[2], Phumipheng L[2], Saykaew T[2], Liu Y[2,3], Tangkawattana S[2,4], Sripa B[2,5]

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Introduction: Opisthorchiasis is a foodborne trematodiasis common in Thailand. Interestingly, opisthorchiasis endemic areas were found to have substantial incidences of leptospirosis as well as *Helicobacter pylori* infection. The parasite causing opisthorchiasis (*Opisthorchis viverrini*) has a complex life cycle involving different intermediate hosts before maturing into the infective metacercariae stage and infecting humans through ingestion of mainly raw fish. *O. viverrini* infection is the main risk factor for cholangiocarcinoma in humans. Since *O. viverrini*, *Leptospira* spp. and *H. pylori* are present in various aquatic environments, we attempted to elucidate the relationships of these pathogens at the opisthorchiasis endemic areas around the Lawa Lake region at Khon Kaen, Thailand.

Methods: Specimens were collected from ten study sites around the Lawa Lake region at Khon Kaen. Mud, water, snail and fish mucus were collected from the study sites. One metacercariae specimen was also included in the study. DNA extracted from the specimens were subjected to PCR assays targeting the *lipL32* (pathogenic *Leptospira*) and *cagA* (*H. pylori*) genes. PCR positive products were sequenced and compared using the BLAST database for identification.

Results: Sequencing of the PCR positive products revealed that the mud, fish mucus and metacercariae specimens were positive for the presence of *H. pylori*. Remarkably, the same mud specimens that were positive for *H. pylori* were also positive for the presence of pathogenic *Leptospira*, suggesting co-localization of these two pathogens at the same site.

Conclusion: Our findings suggest that *H. pylori* and pathogenic *Leptospira* are prevalent in opisthorchiasis endemic areas at Khon Kaen, Thailand.

Keywords: Bacteria, infection, liver fluke, trematode, tropical disease

Abstract No.: ABS0002030

DIVERSITY AND DISTRIBUTION OF ANOPHELINE SPECIES IN SOUTHWEST INDIA

DEBATTAM MAZUMDAR

Authors: Mazumdar D[1], Govekar A[1], Singh V[2], Anvikar A[2], Rathod P[3], Patrapuvich R[4], Mohanty AK[1]

Affiliation:[1]ICMR-National Institute of Malaria Research, Field Unit, Goa, India;[2]ICMR-National Institute of Malaria Research, New Delhi, India;[3]Department of Chemistry, University of Washington, Seattle, WA, USA; [4]Drug Research Unit for Malaria, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

Introduction: Urbanization, high-frequency human activities, considerable environmental changes and population migration possibly alter disease vector community structure, distribution, and infection dynamics. Entomological surveillance was carried out to understand the current distribution of Anopheline species and the rate of malaria parasite infection in the context of human-induced environmental changes in the Goa state.

Method: Mosquitoes were collected using CDC light traps from different habitat types in different seasons throughout the year. Malaria parasite infection was detected using PCR. The Shannon diversity index was used to calculate species diversity and richness. The Bayesian method was used to construct the phylogenetic tree.

Results: With 432 traps, a total of 29,418 mosquitoes belonging to 48 species and 9 genera were captured from 9 study sites. Of these, a total of 2,735 female Anophelines belonging to 15 species were captured. The per trap density of *Anopheles jamesii* was found highest among the Anopheline species. *Anopheles stephensi* and *Anopheles subpictus* are the two recognized malaria vectors and they were significantly (P*An. stephensi* was found highest in developmental sites as compared to the residential areas. This study found differences in mosquito species richness between study sites. The variation in parasite infection level was observed in vector species.

Conclusion: This study suggests that Anopheline species abundance, diversity and parasite infection rate in different endemic areas varied according to the season. This information will be helpful in formulating efficient vector control interventions.

Keywords: Keywords: Goa, *Anopheles stephensi*, *Anopheles subpictus*, Malaria vectors, Plasmodium infection, Urbanization

Friday 15 December 2023

S39: Antimicrobial Resistance in a One Health Spectrum

08.30-10.00hr

Room C

Friday 15 December 2023

S39: Antimicrobial Resistance in a One Health Spectrum by MAJ Dan Boudreaux

08.30-10.00hr

Room C

Chairperson:
1. MAJ Dan Boudreaux

Invited speaker:

1. Using Water Surveillance to understand the transmission of Antimicrobial Resistance
Daniel Boudreaux
Other (United States Army Medical Directorate - Armed Forces Institute of Medical Sciences)

2. THAILAND\'S INTEGRATED AMR WITH ONE HEALTH APPROACH GUIDELINE
Watcharaporn Kamjumphol
Other (National Institute of Health, Department of Medical Sciences, Ministry of Public Health)

3. Antimicrobial resistance in animals
Arshnee Moodley
Other (International Livestock Research Institute)

4. Antimicrobial Stewardship in Human Health: The Thailand Experience
Anucha Apisarnthanarak
Other (Antimicrobial Stewardship in Human Health: The Thailand Experience)

5. Complexities of tracking AMR at the One Health Interface
Paul Plummer
Other (Iowa State University)

Abstract No.: ABS0002252

Using Water Surveillance to understand the transmission of Antimicrobial Resistance

Daniel Boudreaux

Authors: Dutsadee Peerapongpaisarn[1], Chatchadaporn Thamnurak[1], Wilawan Oransathit[1], Wirote Oransathit[1], Paksathorn Kietsiri[1], Chantida Pradipol[1], Kirakarn Kirativanich[1], Sirigade Ruekit[1], Paphavee Ketwalha[1], Passara Wongthai[2], Pimwan Thongdee[2], Pongthorn Narongroeknawin[2], Sirachat Nitchaphanit[2], Tanit Boonsiri[2], Nonlawat Boonyalai[1], Nattaya Ruamsap[1], **Daniel M. Boudreaux**[1], Jeffery R. Livezey[1]

Affiliation: [1]Department of Bacterial and Parasitic Diseases, Armed Forces Research Institute of Medical Sciences (AFRIMS), Bangkok, Thailand; [2]Department of Microbiology, Phramongkutklao College of Medicine, Bangkok, Thailand

Understanding how and where antimicrobial resistance (AMR) is spread to humans can build support for preventive measures which improve public health. While it is thought that AMR bacteria are primarily spread from person-to-person or from contaminated surfaces to a person in either community or healthcare settings, the One Health concept suggests that either food, animal, vector, soil, or water-borne transmission may also play a significant role in transmission. Interestingly, water can serve as a medium to propagate AMR, transmit it to humans or animals, and carry AMR away in waste. The CoVID-19 pandemic advanced the utility of surveying wastewater to predict infections within a community. By leveraging methods used during the pandemic, water surveillance is now being used to understand the AMR threat. Water is being periodically sampled from wastewater treatment plants, surface waters, hospital effluents, drinking water, and agricultural runoffs. Samples are tested using either conventional bacterial culture, antimicrobial susceptibility, targeted polymerase chain reactions, or by metagenomic-based methods. Our team has gained insights into the benefits of different methods. Through this experience we’ve identified clinically relevant bacteria with colistin, carbapenem, and cephalosporin resistance. We are currently developing plans to correlate AMR trends in water with human infections by using our ongoing surveillance of antimicrobial resistance in hospitals, to ultimately use water as an early warning indicator for human infections. Together this work will help bolster support for AMR research and inform public health decisions both locally and wordwide.

Keywords: Water Surveillance, Antimicrobial Resistance

Abstract No.: ABS0002144

THAILAND\'S INTEGRATED AMR WITH ONE HEALTH APPROACH GUIDELINE

Watcharaporn Kamjumphol

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Affiliation: [1]National Institute of Health, Department of Medical Sciences, Ministry of Public Health

Antimicrobial resistance (AMR) is the major issue posing a serious health threat that affects all countries. The Global Action Plan on antimicrobial resistance and the United Nations Political Declaration on antimicrobial resistance set standards for countries to resolve antimicrobial resistance challenges under the One Health approach. Thailand has developed a national strategic plan on antimicrobial resistance (NSP-AMR) 2017-2022, which is Thailand's first strategic plan addressing AMR issue, and endorsed by the Cabinet in 2016. The NSP-AMR plan included a set of ambitious goals together with six strategies. Strategy 1 was to establish an antimicrobial resistance surveillance system under the One Health approach. AMR surveillance is an essential tool for monitoring AMR trends and evaluating the outcomes of NSP-AMR implementation. After 5 years of the strategic plan's implementation, a Thailand\'s integrated AMR with One Health Approach Guideline was developed by the 'One Health' tripartite partners from human, animal, agricultural, and environmental sectors and technical experts in various fields. The aim of this guideline is to provide a framework for the development of antimicrobial resistance surveillance systems in Thailand. This will be achieved through collaborative thinking and practices, focusing on the objectives and priorities defined in the NSP-AMR. Additionally, it considers the capabilities of relevant agencies and available resources. In the next stage, stakeholders\' engagement and ownership of the strategies will support effective implementation of this guideline in three main areas: human, animal (food chain), and the environment. Effective implementation requires evidence, cross-sectoral capacities, and sustained political commitment.

Keywords: Antimicrobial resistance, Surveillance, One Health approach

Abstract No.: ABS0002254

Antimicrobial resistance in animals

Arshnee Moodley

Authors: Arshnee Moodley

Affiliation: International Livestock Research Institute

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002257

Antimicrobial Stewardship in Human Health: The Thailand Experience

Anucha Apisarnthanarak

Authors: Anucha Apisarnthanarak

Affiliation: Thammasat University Hospital

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002258

Complexities of tracking AMR at the One Health Interface

Paul Plummer

Authors: Paul Plummer

Affiliation: Iowa State University

No abstract available

Keyword: No abstract available

Friday 15 December 2023

S40: Update on Ivermectin, Malaria Transmission and Antimalarial Activities

08.30-10.00hr

Room D

Friday 15 December 2023

S40: Update on Ivermectin, Malaria Transmission and Antimalarial Activities by

08.30-10.00hr

Room D

Chairperson:
1. Kesinee Chotivanich
2. Joel Tarning

Invited speaker:

1. IVERMECTIN STRUCTURES, MOSQUITO-LETHAL EFFECT, AND CHANNEL INTERACTIONS
Pattarapon Khemrattrakool
Other (Mahidol-Oxford Tropical Medicine Research Unit)

2. PHARMACOKINETIC AND MOSQUITO-MORTALITY MODELLING OF IVERMECTIN AND ITS METABOLITES
Joel Tarning
Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

3. Activity of ivermectin and its metabolites on Plasmodium falciparum
Achaporn Yipsirimetee
Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

4. Activity of ivermectin and its metabolites on Plasmodium falciparum liver stages
Pradeep Annamalai Subramani
Other (University of South Florida)

5. SUMBA LIVESTOCK IVERMECTIN FOR MALARIA (SLIM) PROJECT
Kevin Kobylinski
Other (Armed Forces Research Institute of Medical Sciences)

Abstract No.: ABS0002196

IVERMECTIN STRUCTURES, MOSQUITO-LETHAL EFFECT, AND CHANNEL INTERACTIONS

Pattarapon Khemrattrakool

Authors: Pattarapon Khemrattrakool[1], Thitipong Hongsuwong[1], Patchara Sriwichai[2], Borimas Hanboonkunupakarn[3], Podjanee Jittamala[4], Joel Tarning[1,5], Kevin Kobylinski[1]

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Introduction: Ivermectin is a novel vector control tool wherein 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. Protein crystallography has elucidated several ivermectin binding points to the GluCl channel in the transmembrane helixes, but it is thought the primary effect is derived by binding to the extracellular GluCl M2-M3, which occurs on the primary sugar ring and lactone structure. However, Anopheles GluCl channel and ivermectin interactions have not been adequately characterized.

Methods: The two primary Southeast Asian malaria vectors, Anopheles dirus and Anopheles minimus, are the most ivermectin-tolerant and -susceptible vectors worldwide. Three ivermectin structures were blood-fed to these to species across a range of concentrations. The structures were: ivermectin parent compound (contains both primary and secondary sugar rings), monosaccharide (contains only primary sugar ring), and aglycone (missing both sugar rings).

Results: Interestingly, compared to ivermectin parent compound, ivermectin monosaccharide and ivermectin aglycone structures impart only partial and no mosquito-lethal effect, respectively.

Conclusions: This suggests that there are potentially novel binding interactions with the second ivermectin sugar ring and Anopheles GluCl channel that were not observed with nematode GluCl-ivermectin wet-lab work performed previously. Future directions include classical and next long-read sequencing to determine the GluCl sequences of An. dirus and An. minimus to support 3-D in silico docking models of Anopheles GluCl-ivermectin, -monosaccharide, -aglycone interactions to characterize how ivermectin binds to the GluCl channel.

Keywords: Anopheles, malaria, ivermectin, glutamate-gated chloride ion channel

Abstract No.: ABS0002180

PHARMACOKINETIC AND MOSQUITO-MORTALITY MODELLING OF IVERMECTIN AND ITS METABOLITES

Joel Tarning

Authors: Joel Tarning[1,2], Kevin Kobylinski[1,3], Podjanee Jittamala[1,4], Borimas Hanboonkunupakarn[1,5], Narenrit Wamaket[3,6], Patchara Sriwichai[7], Siriporn Phasomkusolsil[3], Nicholas P.J. Day[1,2], Nicholas J. White[1,2], Richard M. Hoglund[1,2]

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Introduction: Ivermectin is an antiparasitic drug, but it also has mosquito-lethal properties. This is a highly useful quality during mass drug administration campaigns 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 metabolites and mosquito mortality.

Methods: 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.

Results: 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, using the sum of ivermectin and metabolite concentrations to drive the effect. An. minimus mosquitoes was substantially more sensitive to ivermectin and its metabolites compared to An. dirus.

Conclusion: 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

Keyword: to guide malaria elimination campaigns.

Keywords: ivermectin; malaria; pharmacokinetics; pharmacodynamics; pharmacometrics; mosquito-mortality

Abstract No.: ABS0002190

Activity of ivermectin and its metabolites on Plasmodium falciparum

Achaporn Yipsirimetee

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Introduction: Ivermectin is an endectocide and is widely used to treat parasitic diseases. It has potent mosquito-killing activity and has been introduced to mass drug administration for malaria transmission control. The field trials showed a significant reduction in Anopheles mosquito survival and human malaria incidence. However, the effect of ivermectin and its metabolites on the asexual blood stage of the parasite is unclear. The study aims to evaluate the effects of ivermectin and its metabolites and assess the drug combination effects of ivermectin with artemisinin and its partner drugs on asexual blood-stage Plasmodium falciparum.

Methods: The susceptibility of P. falciparum parasite isolates to ivermectin and its metabolites (M1, M3, M6 and ivermectin-B1a-aglycone, ivermectin-monosaccharide) were investigated using SYBR green-I based assay. Percentage of growth and half maximal inhibitory concentration (IC50) were evaluated. The drug combination effect of ivermectin and antimalarial drugs was measured by checkerboard analysis and determined the impact by isobologram and fractional inhibitory concentration (FIC).

Results: The mean IC50s of ivermectin was 0.81 µM and no significant difference (P=0.574) between artemisinin-sensitive and artemisinin-resistant P. falciparum. The ivermectin metabolites M1, M3 and M6 were 2-fold to 4-fold less active than the ivermectin parent compound (P

Conclusion: Ivermectin and its metabolites did not show clinically relevant parasite inhibition effects on the asexual blood stage of P. falciparum. Ivermectin also did not alter the antimalarial activity of antimalarial drugs in vitro. Further investigation is needed to evaluate the effects of ivermectin on other

Keyword: stages of parasite development such as gametocytes.

Keywords: Malaria, Plasmodium falciparum, Antimalarial drug, Ivermectin

Abstract No.: ABS0002211

Activity of ivermectin and its metabolites on Plasmodium falciparum liver stages

Pradeep Annamalai Subramani

Authors: Pradeep Annamalai Subramani[1], Phornpimon Tipthara[2], Surendra Kumar Kolli[1], Justin Nicholas[1], Samantha J. Barnes[1], Madison M. Ogbondah[1], Kevin C. Kobylinski[2,4], Joel Tarning[2,3], John H. Adams[1]

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Malaria remains a major global public health threat due to prevalence of drug-resistances, failure to frontline antimalarial therapy hindering the global efforts to control and eliminate the disease. Almost none of the available antimalarial drugs are efficacious against the liver stage of Plasmodium falciparum, which is the initial stage of infection that leads to disease causing blood stage infection. The 8-aminoquinolines are the only FDA-approved class of drug capable of eliminating Plasmodium liver stage parasites however, this drug class has its own limitation due to potential hemolytic activity in people with favism and therefore not suitable for mass drug administration. There is a critical need for safer and more efficacious drugs that can prevent liver stage development of malaria parasites. Ivermectin is an approved broad spectrum antiparasitic drug that has been proposed as a novel malaria transmission control tool to kill mosquito vectors that transmit malaria and aid malaria elimination. Recent studies have demonstrated the activity of ivermectin against the liver-stage development of rodent malaria parasite, P. berghei and the primate malaria parasites, P. cynomologi suggesting this drug may be an effective antimalarial drug. Ivermectin is known to be metabolized by cytochrome P450 3A4 enzyme, which exhibits polymorphism among different individuals to potentially alter the efficacy against Plasmodium, emphasizing the importance of understanding the metabolism of ivermectin and its metabolites. We established a robust in vitro liver assay to study the liver stage development of human malaria parasites in primary human hepatocytes that can be used to evaluate the potential

Keywords: impact of these metabolic differences on ivermectin’s anti-liver stage efficacy. This model can be used to evaluate the metabolism of ivermectin in hepatocytes from different donors and its efficacy against P. falciparum liver stages.

Abstract No.: ABS0002201

SUMBA LIVESTOCK IVERMECTIN FOR MALARIA (SLIM) PROJECT

Kevin Kobylinski

Authors: Kevin Kobylinski[a], Tri Baskoro T. Satoto[b], Wisnu Nurcahyo[b], Vincentius Arca Testamenti[b], Diana Timoria[c], Mary Chambers[c,d], Joel Tarning[a,d], Lorenz von Seidlein[a,d], Claus Bøgh[e]

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[d]University of Oxford
[e]The Sumba Foundation

Introduction: Sumba Island has some of the highest diversity of *Anopheles* species in Indonesia, contributing to its high malaria incidence. Southwestern Sumba, the area with highest malaria burden, has small livestock holder systems. *Anopheles* mosquitoes frequently blood-feed on livestock providing an opportunity for vector control by treating the animals with insecticides. Ivermectin is a systemic endectocide used to control helminth and ectoparasites in livestock, and ivermectin-treated hosts are lethal to *Anopheles* vectors.

Methods: Both standard (Ivomec®) and long-lasting (Ivergen® Platinum) commercial formulations of ivermectin were investigated in cattle and buffalo in this study. Treated animals were placed in net traps and blood-fed *Anopheles* were captured, transported to an insectary, where their survival was monitored for ten days post-capture.

Results: Ten Anopheles species were frequently collected including: *An. aconitus, An. annularis, An. barbirostris, An. flavirostris, An. kochi, An. maculatus, An. subpictus, An. sundaicus, An. tessellatus,* and *An. vagus*. Cattle and buffalo treated with standard ivermectin were lethal to all *Anopheles* species for 16 and 8 days post-treatment, respectively. While cattle and buffalo treated with long-lasting ivermectin were lethal to all *Anopheles* species for 72 and 56 days post-treatment, respectively.

Conclusions: This is the first time a commercially available, long-lasting ivermectin formulation has been evaluated against Anopheles survival, and the first time this potential vector control measure has been evaluated in buffalo. Long-lasting ivermectin provides superior mosquito-lethal effect to wild blood-feeding *Anopheles* compared to standard ivermectin and could be considered for mass deployment as a malaria control intervention.

Keywords: *Anopheles*, malaria, ivermectin, long-lasting, cattle, buffalo

Friday 15 December 2023

S41: Melioidosis: Vaccines and Immunology

08.30-10.00hr

Room E

Friday 15 December 2023

S41: Melioidosis: Vaccines and Immunology

08.30-10.00hr

Room E

Chairperson:
1. Narisara Chantratita
2. Pornpan Pumirat

Invited speaker:

1. THE DEVELOPMENT OF THE HOST IMMUNE RESPONSE TO MELIOIDOSIS IN CHILDREN
Shelton Wright
Other (University of Washington)

2. IDENTIFICATION AND FUNCTION OF A NOVEL HUMAN MEMORY-LIKE NK CELL POPULATION EXPRESSING CD160 IN MELIOIDOSIS
Anucha Preechanukul
Faculty of Tropical Medicine, Mahidol University (Microbiology and Immunology)

3. INFLUENCE OF ADJUVANTS ON MELIOIDOSIS SUBUNIT VACCINES
Sarah Weiby
Other (University of Nevada, Reno)

4. RAPID PRODUCTION OF MONOCLONAL ANTIBODIES AGAINST BURKHOLDERIA PSEUDOMALLEI ANTIGENS
Sineenart Sengyee
Other (University of Nevada)

5. DEFINING CORRELATES OF IMMUNITY AGAINST INHALATIONAL MELIOIDOSIS
PAUL BRETT
Other (University of Nevada, Reno School of Medicine)

Abstract No.: ABS0002207

THE DEVELOPMENT OF THE HOST IMMUNE RESPONSE TO MELIOIDOSIS IN CHILDREN

Shelton Wright

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Introduction: The clinical epidemiology of many lower respiratory tract infections differs between children and adults, including melioidosis. Whether the pediatric pulmonary host immune response during pulmonary melioidosis is distinct compared to adults is unknown. We hypothesized that juvenile mice develop a unique pulmonary neutrophil response in a mouse model of pulmonary melioidosis.

Methods: Facility-bred juvenile (3-4 weeks of age) and adult (8-12 weeks of age) mice were infected with a lethal dose of aerosolized Burkholderia thailandensis (Bt) and subsequently assessed for 1) survival, 2) bacterial load by lung and spleen culture, 3) airway neutrophils by bronchoalveolar lavage with cytospin and 4) lung immune cell populations by flow cytometry.

Results: Adult mice have significantly worse survival compared to juveniles after Bt infection (P

Conclusion: Despite similar inoculum, juvenile mice have improved survival and enhanced bacterial clearance compared to adults in a lethal mouse model of melioidosis. However, juvenile mice have decreased neutrophil recruitment but enrichment of innate-like lymphocytes in the lung, independent of bacterial load. Further studies will seek to elucidate the functional mechanisms related to inflammatory regulation in juveniles which may serve a protective function during severe pneumonia.

Keywords: pediatric melioidosis, neutrophils, innate-like lymphocytes

Abstract No.: ABS0002149

IDENTIFICATION AND FUNCTION OF A NOVEL HUMAN MEMORY-LIKE NK CELL POPULATION EXPRESSING CD160 IN MELIOIDOSIS

Anucha Preechanukul

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Affiliation: [1]Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [2]Peter Medawar Building for Pathogen Research, Nuffield Department of Clinical Medicine, University of Oxford, Oxford, UK; [3]Centre for Global Health Research, Nuffield Department of Clinical Medicine, University of Oxford, Oxford, UK; [4]Department of Medical Technology and Clinical pathology, Mukdahan Hospital, Mukdahan, Thailand; [5]Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [6]Mahidol-Oxford Tropical Medicine Research Unit, Mahidol University, Bangkok, Thailand; [7]Department of Medicine, Mukdahan Hospital, Mukdahan, Thailand; [8]Oxford University Hospitals NHS Foundation Trust, Oxford, UK

Keywords: *Burkholderia pseudomallei*, Melioidosis, NK cell, NK cell memory

Abstract No.: ABS0002155

INFLUENCE OF ADJUVANTS ON MELIOIDOSIS SUBUNIT VACCINES

Sarah Weiby

Authors: Sarah B. Weiby[1], Sineenart Sengyee[1], Sergei S. Biryukov[2], Christopher P. Klimko[2], Nathaniel O. Rill[2] , Christopher K. Cote[2], David DeShazer[2], Mary N. Burtnick[1,3] and Paul J. Brett[1,3]

Affiliation:

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Burkholderia pseudomallei, the etiologic agent of melioidosis, causes severe disease in humans and animals. Several studies have shown that this CDC Tier 1 select agent expresses a variety of structurally conserved protective antigens that include cell-surface polysaccharides, cell-associated and secreted proteins. Based on this, such antigens have become important components of the subunit vaccine candidates that our lab is developing. In this study, the 6-deoxyheptan capsular polysaccharide (CPS) was purified from *Burkholderia thailandensis* E555, chemically activated and covalently linked to recombinant CRM197 diphtheria toxin mutant to produce CPS-CRM197. Additionally, affinity chromatography techniques were used to prepare highly purified, tag-less *B. pseudomallei* hemolysin co-regulated protein 1 (Hcp1) from *E. coli*. Immunization of C57BL/6 mice with CPS-CRM197 plus Hcp1 formulated with Alhydrogel and ODN 2006 resulted in high-titer IgG responses against CPS as well as high-titer IgG and robust IFN-γ secreting T cell responses against Hcp1. When the same vaccine antigens were formulated with Adju-Phos and ODN 2006, however, only high-titer IgG responses against CPS were detected. Additionally, immunization of mice with the vaccine antigens formulated with Alhydrogel alone resulted high-titer IgG responses against both CPS and Hcp1 but very low IFN-γ secreting T cell responses against Hcp1. Interestingly, this decreased T cell response correlated with a lack of protection when the mice were challenged with a lethal inhalational dose of *B. pseudomallei* K96243. Collectively, these studies highlight the influence of different adjuvant systems on our vaccine antigens and provide important insights towards the development of a safe and effective melioidosis vaccine.

Keywords: *Burkholderia pseudomallei*, melioidosis, subunit vaccine, CPS, Hcp1, adjuvants

Abstract No.: ABS0002156

RAPID PRODUCTION OF MONOCLONAL ANTIBODIES AGAINST BURKHOLDERIA PSEUDOMALLEI ANTIGENS

Sineenart Sengyee

Authors: Sineenart Sengyee[1], Caitlyn E. Orne[1], Paul J. Brett[1,2] and Mary N. Burtnick[1,2]

Affiliation:[1]Department of Microbiology and Immunology, University of Nevada, Reno School of Medicine, Reno, NV, USA; [2]Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

Burkholderia pseudomallei is a Gram-negative bacterium that causes melioidosis, a severe and life-threatening disease in both humans and animals. Rapid and accurate detection of this bacterial pathogen is critical for diagnosis and treatment. Monoclonal antibodies (mAbs) have emerged as important tools for the development of diagnostic assays and immunotherapeutics. Single-cell RNA sequencing (scRNA-seq) is a powerful approach that can provide antibody sequences from individual B cells. In this study, we used scRNA-seq technology to facilitate the rapid production of mAbs against a known protective antigen expressed by *B. pseudomallei*. Activated B cells were isolated from lymph nodes of mice immunized with three doses of *B. pseudomallei* 6-deoxyheptan capsular polysaccharide (CPS) covalently linked to the carrier protein CRM197. These cells were then subjected to 10x Genomics-based scRNA-seq. Recombinant IgG1, IgG2a, and IgG2c mAbs were generated based on the expression of paired-heavy and light chain sequences in Chinese hamster ovary cells. The antigen-binding efficiencies of the recombinant mAbs were confirmed using endpoint ELISAs. Functional activities associated with the recombinant mAbs were evaluated using opsonophagocytosis and complement deposition assays. The recombinant IgG1, IgG2a, and IgG2c mAbs exhibited high purity and demonstrated strong reactivity against purified CPS. While all three mAbs promoted opsonophagocytosis, only IgG2a and IgG2c showed enhanced deposition of complement on bacterial surfaces compared to negative controls. Collectively, our findings demonstrate that scRNA-seq technology is a promising strategy for rapidly producing recombinant mAbs to help develop novel diagnostics and immunotherapeutics to combat disease caused by *B. pseudomallei*.

Keywords: *Burkholderia pseudomallei*, melioidosis, CPS, single cell sequencing, B cell, monoclonal antibody

Abstract No.: ABS0002159

DEFINING CORRELATES OF IMMUNITY AGAINST INHALATIONAL MELIOIDOSIS

PAUL BRETT

Authors: Weiby SB[1], Sengyee S[1], Biryukov SS[2], Klimko CP[2], Rill NO[2], Cote CK[2], DeShazer D[2], Burtnick MN[1,3], **Brett PJ[1,3]**

Affiliation: [1]Department of Microbiology and Immunology, University of Nevada, Reno School of Medicine, Reno, NV, USA; [2]United States Army Medical Research Institute of Infectious Diseases, Frederick, MD, USA; [3]Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

Burkholderia pseudomallei, the etiologic agent of melioidosis, causes severe disease in humans and animals. Diagnosis and treatment of melioidosis is challenging and no licensed vaccines currently exist. The 6-deoxyheptan capsular polysaccharide (CPS) expressed by this bacterial pathogen is both a virulence factor and a protective antigen. In this study, we investigated the protective capacity of CPS-specific polyclonal antibodies and monoclonal antibodies (mAbs) in the presence or absence of trimethoprim/sulfamethoxazole (TMP/SMX). Purified CPS from *Burkholderia thailandensis* E555 was chemically activated and covalently linked to recombinant CRM197 diphtheria toxin mutant (CRM197) to produce the glycoconjugate, CPS-CRM197. 10x Genomics single cell RNA-sequencing was used to produce recombinant CPS-specific mAbs following the isolation of activated B cells from CPS-CRM197 immunized mice. C57BL/6 mice were immunized with CPS-CRM197 or CPS-specific mAbs in the presence or absence of TMP/SMX. Following lethal inhalational challenges with *B. pseudomallei* K96243, 70% of the actively immunized animals were still alive upon termination of the study at day 70. In addition, the majority of tissues from the survivors were found to be sterile when assessed for bacterial loads. In contrast, only 10% of the passively immunized animals survived the same timeframe. While administration of TMP/SMX alone as a control in these studies resulted in low levels of protection, high survival rates were observed for actively and passively immunized mice that also received the antibiotic. Collectively, these studies demonstrate important role(s) for CPS-specific antibodies in combatting disease caused by *B. pseudomallei* and provide valuable insights towards the development of novel combination therapies.

Keywords: *Burkholderia pseudomallei*, melioidosis, CPS, polyclonal antibodies, monoclonal antibody, antibiotics

Friday 15 December 2023

S42: Smart Mosquito Detection and Control: Application of Machine Learning Techniques

10.30-12.00hr

Room A

Friday 15 December 2023

S42: Smart Mosquito Detection and Control: Application of Machine Learning Techniques

10.30-12.00hr

Room A

Chairperson:
1. Peter Haddawy
2. Saranath Lawpoolsri Niyom

Invited speaker:

1. MosquitoSong Sensors: Bio-acoustic IoT sensors for mosquito surveillance
Myat Su Yin
Other (Faculty of ICT, Mahidol university)

2. Advances in optical methods for differentiation of mixed populations of free-flying mosquito vectors
Michael Weber
Other (Biogents AG)

3. Self-Supervised Learning Improves Mosquito Classification
Santhad Chuwongin
Other (College of Advanced Manufacturing Innovation, KMITL)

4. A low-cost TinyML model for Mosquito Detection in Resource-Constrained Environments
Gibson Kimutai
Other (Department of Mathematics, Physics and Computing)

Abstract No.: ABS0002205

MosquitoSong Sensors: Bio-acoustic IoT sensors for mosquito surveillance

Myat Su Yin

Authors: Su Yin M[1], Haddawy P[1,2], Apisitpuwakul N[1], Kumnerdpun P[1], Jirapatmaneechot T[1]

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Traditional mosquito population monitoring methods are labor-intensive and unsuitable for large-scale use. Previous studies have explored employing species-specific wingbeat acoustic signatures for population surveys. The most accurate methods employ machine learning models, requiring extensive, time-consuming data collection, typically conducted in laboratory settings. Importantly, datasets collected in laboratories frequently lack crucial biodiversity information. Our MosquitoSongSense IoT platform, integrated with the Biogents BG-Counter 2 mosquito trap, automates the process of wingbeat audio data collection. However, the absence of labels on collected audio data requires a suitable classification model training strategy. Leveraging MosquitoSong models trained in controlled lab environments, we assign pseudo-labels to recorded wingbeat audio, developing semi-supervised classification models. Results indicate good performance, achieving 85% accuracy with as few as 50 labeled samples. A single pseudo-labeling iteration significantly enhances accuracy, suggesting the feasibility of classifying new mosquito species with minimal labeled data.

Keywords: Mosquitoes surveillance, Wingbeats, Data Collection, Deep learning, Semi-supervise models, Pseudo-labeling, Species and Sex classification

Abstract No.: ABS0002218

Advances in optical methods for differentiation of mixed populations of free-flying mosquito vectors

Michael Weber

Authors: Michael Weber[2] Brian J. Johnson[1] Hasan Mohammad Al-Amin[1], Martin Geier[2,] Gregor J. Devine[1]

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In recent years, invasive mosquito species have extended their range and outbreaks of vector-borne disease are increasing worldwide, even in "rich" countries with local outbreaks of dengue and West Nile Virus in Europe and malaria and dengue in the United States.

However, resource-poor countries remain the most threatened:
- in the Horn of Africa, urban malaria transmission by invasive *Anopheles stephensi;*
- in Africa and Asia, even with wide use of insecticide-treated bed nets, malaria stabilizing at high levels due to pesticide resistance and shifts in vectors and behavior;
- in Southeast Asia and elsewhere, *Aedes aegypti* continuing to cause large dengue outbreaks.

Mitigation utilizing IPM methods and disease models requires increased levels of mosquito surveillance for higher data density in space and time; that need can only be achieved with autonomous surveillance traps capable of differentiating between vectors and other insects.

These require sensitive, affordable sensors for identifying species and sex of captured mosquitoes using AI and machine learning. At the same time, these sensors have to be robust and reliable in the field and compatible with traps highly effective in attracting the vector species. We are designing our sensors to also leverage remote communication with the cloud-based system and the infrastructure for manufacturing, deployment and maintenance we have already created for mosquito counters (several thousand units shipped world-wide).

We will report on the progress proceeding from the lab to a semi-field environment and on new learnings informing the next stages of development.

Keywords: mosquito vector surveillance, smart traps, species ID, sex ID, AI, ML, malaria, dengue, disease modeling

Abstract No.: ABS0002259

Self-Supervised Learning Improves Mosquito Classification

Santhad Chuwongin

Authors: Santhad Chuwongin

Affiliation: College of Advanced Manufacturing Innovation, King Mongkut’s Institute of Technology

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002260

A low-cost TinyML model for Mosquito Detection in Resource-Constrained Environments

Gibson Kimutai

Authors: Gibson Kimutai

Affiliation: Mathematics, Physics and Computing, Moi University, Kenya

Yearly, more than 200 million malaria cases are recorded worldwide. Most of these cases are witnessed in less developed countries as the environments are not well-maintained, which forms breeding places for mosquitoes. Female mosquito-anopheles is responsible for malaria infection, dengue, chikungunya, and zika. Developing countries struggle to fight diseases; malaria still claims more than 400,000 lives annually. One current way to keep away anopheles mosquitoes is using commercially available electric liquid mosquito repellents, which can adversely affect the human body when used for extended periods. Furthermore, energy and sprays are wasted as they constantly work even without the presence of anopheles mosquitoes. We propose a low-cost IoT-based TinyML model that intelligently discharges the mosquito repellent when an anopheles mosquito is in the room. First, we prove the concept by exploring two lightweight deep learners with a 1D Convolution Neural Network (1D-CNN) and 2D Convolution Neural Network (2D-CNN) to classify raw sounds from mosquito wingbeats. We adopted a Leaky ReLU in building the 1D-CNN to speed up training and improve classification performance. Furthermore, we adopted batch normalization to avoid degradation and vanishing gradient problems. We implemented the experiments in an Edge impulse platform. Each of the CNN models recorded stable classification performance during the proof of concept study, while the 1D-CNN took less time and computing resources in training, validation, and testing. As we aimed to propose a low-cost solution, we evaluated the performance of the 1D-CNN-based prototype in the actual deployment by playing mosquito wingbeat sounds on a laptop which

Keywords: we placed next to it in intervals of 0.5, 1.0, 1.5, 2.0, 2.5, and 3 meters. The model showed promising results across distances and thus could be used to chase away mosquitoes in a room of small to medium size.

Friday 15 December 2023

S43: Young Investigator Awards 2

10.30-12.00hr

Room B

Friday 15 December 2023

S43: Young Investigator Awards 2

10.30-12.00hr

Room B

Chairperson:
1. Kriengsak Limkittikul
2. Wirichada Pan-ngum

Invited speaker:

1. PROSPECTS FOR PRIMARY CARE INTERVENTIONS TO IMPROVE QUALITY OF CASE AND STRENGTHEN LINKAGES WITH COMMUNITY HEALTH WORKERS IN THAILAND
Monnaphat Jongdeepaisal
Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

2. THE EFFECTIVENESS OF AN EXPANDED ROLE FOR COMMUNITY HEALTH WORKERS ON MALARIA ELIMINATION IN MYANMAR: A STEPPED-WEDGE CLUSTER RANDOMISED CONTROLLED TRIAL
Win Han Oo
Other (Burnet Institute)

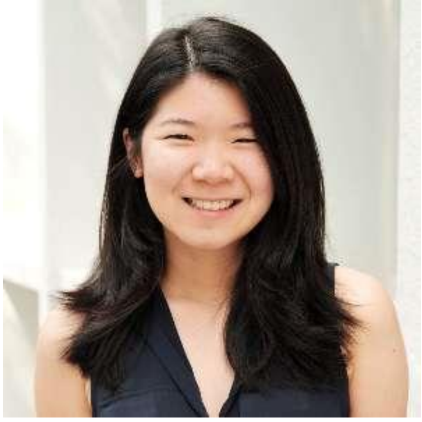
3. HIGH LEVELS OF HEAT STRESS AND HEAT-RELATED SYMPTOMS AMONG SUGARCANE WORKERS IN THAILAND
Tadpong Tantipanjaporn
Other (University of Manchester, The United Kingdom)

4. DEFINING IMMUNE ESCAPE POLYMORPHISMS IN PLASMODIUM VIVAX: INSIGHTS FROM THE GENOMIC ANALYSIS OF 16 ANTIGEN VACCINE CANDIDATES
ALISON PAOLO BARENG
Other (Deakin University)

5. MOLECULAR MECHANISM OF NEROLIDOL, A SESQUITERPENE BY MODULATING HEPATIC CARBOHYDRATE METABOLIC ENZYME AND GLYCOGEN CONTENT IN HIGH FAT DIET AND LOW DOSE STREPTOZOTOCIN INDUCED TYPE2 DIABETIC C57BL/6J MICE
Paari Ellappan
Other (Annamalai University)

Abstract No.: ABS0002041

PROSPECTS FOR PRIMARY CARE INTERVENTIONS TO IMPROVE QUALITY OF CASE AND STRENGTHEN LINKAGES WITH COMMUNITY HEALTH WORKERS IN THAILAND



Monnaphat Jongdeepaisal

Authors: Jongdeepaisal M[1], Ekkapongpisit M[1], Kanthawang N[1], Prasert O[1], Maneenate S[1], Yangsup K[1], Projanaprasert C[2], Pell C[3], Chareonsuk I[4], Intrawalan D[5], Sopa P[6], Perrone C[1], Lubell Y[1], Maude RJ[1]

Affiliation:[1]Mahidol-Oxford Tropical Medicine Research Unit; [2]Faculty of Tropical Medicine; [3]Amsterdam Institute for Global Health and Development; [4]Buntharik hospital; [5]Chiangrai Regional Hospital; [6]Ubon Ratchathani Provincial Health Office

Introduction: In resource-limited settings, primary health care is a key strategy to ensure accessible and equitable public health services. Although well established, overcrowding, inadequate human, financial, and technological resources hinders the provision of quality care. This study explores the prospects for leveraging new point-of-care technologies at primary care units (PCUs) in Ubon Ratchathani and Chiang Rai, Thailand.

Methods: Data were collected through online survey (n=273) and interviews (n=28) with health workers. Interview respondents were purposively drawn from PCUs in urban and border areas; surveys subsequently were distributed to a wider group

Results: Across the PCUs, staff were primarily preoccupied with disease screening, surveillance, and chronic condition management; prioritized preventative and rehabilitative health programs ranged from local disease burdens (diabetes, hypertension, dengue, tuberculosis) to emerging public health issues (eldercare, mental illnesses). Health workers were familiar with available medical equipment (blood pressure monitor, fetal doppler); however, many reported having insufficient life-saving equipment and skills (automated external defibrillator, cardiopulmonary resuscitation). Although novel technological devices have been introduced to a limited degree at the primary level, new point-of-care devices for tuberculosis and febrile illnesses were suggested to mitigate delayed medical care and lessen the workload at PCUs. Benefits were also perceived in healthcare innovations enabling a stronger patient referral system, particularly for home-based care, mental health assessment, and cross-border health services.

Conclusion: Future adoption of novel (and existing) health interventions requires fine-tuning based on local needs and resources, while strengthening the digital skills of local health workers, ideally with the support of community hospitals and medical professionals.

Keywords: Primary health care, point of care testing, community health workers

Abstract No.: ABS0001980

THE EFFECTIVENESS OF AN EXPANDED ROLE FOR COMMUNITY HEALTH WORKERS ON MALARIA ELIMINATION IN MYANMAR: A STEPPED-WEDGE CLUSTER RANDOMISED CONTROLLED TRIAL

Win Han Oo

Authors: Win Han Oo[1,2], Win Htike[2,3], May Chan Oo[2], Pwint Phyu Phyu[4], Kyawt Mon Win[5], Nay Yi Yi Linn[5], Ei Phyu Htwe[2], Aung Khine Zaw[2], Kaung Myat Thu[2], Galau Naw Hkawng[2], Julia C. Cutts[1], Nick Scott[1], Katherine O’Flaherty[1], Nilar Aye Tun[6], Paul A. Agius[1,3,7], Freya J.I. Fowkes[1,2,6,7]

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6. Centre for Epidemiology and Biostatistics, Melbourne School of Population and Global Health, University of Melbourne, Melbourne, VIC, Australia;
7. Department of Epidemiology and Preventive Medicine, Monash University, Melbourne, VIC, Australia

As Mekong countries approach malaria elimination, the motivation and social role of community health workers, and malaria testing rates, have declined in parallel with decreasing malaria burden. To address this issue, a health system model which expanded the role for community health workers (The Community-delivered Integrated Malaria Elimination (CIME) model) in malaria elimination, dengue, tuberculosis, childhood diarrhoea and non-malaria fever management was developed from an evidence-base and field-tested in Myanmar.

An open stepped-wedge cluster-randomised controlled trial randomised at the village level was conducted in 72 villages in Yangon Region from 1 November 2021 to 17 April 2022 to evaluate the CIME model’s effectiveness and cost-effectiveness compared to the existing integrated community malaria volunteer model. One-off and continuous implementation costs of the models were calculated.

Compared to the existing volunteer model, the introduction of an expanded role for community health workers, the CIME model, resulted in a 23% relative increase in village weekly rapid diagnostic testing for malaria, the primary outcome, (adjusted incidence rate ratio = 1.23, 95%CI = 1.01, 1.49, p=0.042), adjusting for time and season. The total cost per worker per five-year period was USD 14,794 for the CIME model and USD 5,816 for the existing volunteer model.

Although the CIME model is associated with additional costs for providing health services for common tropical diseases, it is effective in increasing the annual blood examination rate required for malaria elimination accreditation compared to the existing volunteer model.

Keywords: The Community-delivered Integrated Malaria Elimination model, Myanmar, effectiveness, cost-effectiveness

Abstract No.: ABS0001997

HIGH LEVELS OF HEAT STRESS AND HEAT-RELATED SYMPTOMS AMONG SUGARCANE WORKERS IN THAILAND

Tadpong Tantipanjaporn

Authors: Tantipanjaporn T[1,4], Povey A[2], Shiels H[3], van Tongeren M[2]

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[3]Division of Cardiovascular Sciences, School of Medical Sciences, Faculty of Biology, Medicine and Health, University of Manchester, The United Kingdom;

[4]Division of Occupational Health and Safety, Faculty of Public Health, Naresuan University, Phitsanulok City, Thailand

Introduction: In continued global warming, the effects of elevated temperatures on the health of agricultural workers are a practical concern. This study investigates heat stress and heat-related symptoms in the past 7 days in Thai sugarcane workers.

Methods: Data was collected from participants during the cooler months (n = 152 participants) and hotter months (n = 148) using a questionnaire. Heat stress was measured using Wet Bulb Globe Temperature (WBGT) instruments in the sugarcane fields for a full work shift. Workloads were estimated following American Conference of Governmental Industrial Hygienists (ACGIH) guidelines.

Results: After adjusting for the participants' clothing, the one-hour time-weighted average (TWA) effective WBGT was high in both seasons, although somewhat higher in the hotter months (a peak effective TWA-WBGT1hr of 33.9 °C), compared to the cooler months (31.3 °C). The measured WBGT, wet-bulb temperature, dry-bulb temperature, globe temperature, relative humidity, and wind velocity were all significantly higher in the hotter months. Using ACGIH guidelines, sugarcane harvesting activities were assessed as heavy work, and the harvesters' heat stress in both seasons exceeded the ACGIH Threshold Limit Values for the majority of the work shift. 98% of participants experienced one or more heat-related symptoms, with the top five being heavy sweating (85.9%), weakness/fatigue (71.5%), thirst (65.9%), elevated body temperature (58.4%), and rapid pulse (45.2%).

Conclusion: Thai sugarcane workers are at high risk of developing heat stress-related health effects, and further measures are needed to reduce heat stress levels in both seasons.

Keywords: Global warming, Heat stress, Wet bulb globe temperature, Heat-related symptoms, Sugarcane workers, Harvesting

Abstract No.: ABS0002056

DEFINING IMMUNE ESCAPE POLYMORPHISMS IN PLASMODIUM VIVAX: INSIGHTS FROM THE GENOMIC ANALYSIS OF 16 ANTIGEN VACCINE CANDIDATES

ALISON PAOLO BARENG

Authors: Bareng APN[1,2] , Naung N[1,3], Razook Z[1,2], Arnott A[3], Brewster J[3], Lin E[4], Kiniboro B[4], Laman M[4], Robinson LJ[2], Mueller I[3], Barry AE[1,2]

Affiliation:[1]Centre for Innovation in Infectious Disease and Immunology Research (CIIDIR), The Institute for Mental and Physical Health and Clinical Translation (IMPACT), School of Medicine, Deakin University; Geelong, Victoria, Australia; [2]Life Sciences Discipline, Burnet Institute, Melbourne, Victoria, Australia; [3]Division of Population Health and Immunity, The Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria, Australia; [4]Vector Borne Diseases Unit, Papua New Guinea Institute of Medical Research, Madang, Madang Province, Papua New Guinea

Malaria continues to be a huge public health burden worldwide, with Plasmodium vivax (Pv) standing out as a significant contributor. Developing a vaccine against Pv is imperative to drive down this burden; however, the extensive genetic diversity of vaccine candidate antigens reduces the effectiveness of vaccines as polymorphisms may be maintained by immune selection pressure. This study aimed to pinpoint polymorphisms associated with immune escape for 16 Pv vaccine candidate antigens. With the use of isolates from clinical and asymptomatic infections from a longitudinal cohort of children in Papua New Guinea, we compared variation between gene sequences from successive infections within and between hosts. The data comprised of sequences from 600 infections, from 127 children, generated using multiplexed-long read amplicon sequencing. Data processing included stringent allele calling to account for multiple infections, and direct sequence comparisons to identify polymorphisms between infections. We then measured the rate of allelic turnover driven by within host factors, to the rate of turnover between hosts as a measure of background population genetic diversity. Analysis reveals allele changes within the antigens that are potentially associated with immune evasion in addition to those that may be selected for by host genetic factors. Haplotypes comprised 'immune escape' polymorphisms were also used to predict serotypes that could be combined in a multivalent vaccine to cover antigenic diversity. These findings not only provide insights into the complex relationship between parasites and human hosts but also offer researchers a rational basis for the development of broadly effective vaccine against Pv.

Keywords: Plasmodium vivax; immune escape polymorphisms; vaccine candidate antigens; antigenic diversity

Abstract No.: ABS0002038

MOLECULAR MECHANISM OF NEROLIDOL, A SESQUITERPENE BY MODULATING HEPATIC CARBOHYDRATE METABOLIC ENZYME AND GLYCOGEN CONTENT IN HIGH FAT DIET AND LOW DOSE STREPTOZOTOCIN INDUCED TYPE2 DIABETIC C57BL/6J MICE

Paari Ellappan

Authors: Paari E[1], Manoharan S[1]

Affiliation:[1]Department of Biochemistry and Biotechnology, Annamalai University, Annamalainagar-608002, Tamilnadu, INDIA

Introduction: The study was designed to evaluate the antihyperglycemic effects of nerolidol, a natural sesquiterpenes is found in the essential oils found in many plants such as Baccharis dracunculifolia, Amaranthus retroflexus and Canarium schweinfurthii and is also present in flowers, like neroli, jasmine, ginger lavender, and tea tree, has shown significant biological effects of antioxidants, antiinflammatory and anticarcinogenic activities. So, we attempted to determine whether nerolidol would be protective against hyperglycemia in high fat diet and low dose streptozotocin induced type2 diabetic C57BL/6J mice.

Methods: 36 nos. of male C57BL/6J mice (body weight 20g to 22 g) were segregated into 6 groups with 6 mice each and used for the study. Animals were purchased from Biogene animal laboratories , Bangalore. Studies were carried out in accordance with Indian National Law on Animal Care and Use and were approved by the Institutional ethical committee (Proposal no. AU-IAEC/PR/1334/7/22) of Rajah Muthiah Medical College and Hospital, Annamalai University, India

Results: Diabetic mice exhibited an increase in glucose and HbA1c with a significant fall in insulin and hemoglobin levels. Aberrations in carbohydrate metabolic enzymes were noticed in liver and kidney of type2 diabetic C57BL/6J mice. A fall in liver and skeletal muscle glycogen with alterations in glycogen synthase and phosphorylase activities was also observed. Oral administration of nerolidol in dose dependent manner and metformin 25mg/kg b.w.)

Conclusion: The insulinotropic effect of nerolidol was supported by performing the various biochemical parameters, histomorphological changes and immunohistochemical studies. we concluded that administration of nerolidol has benefcial effects.

Keywords: Nerolidol, High fat diet, streptozotocin, metformin, Carbohydrate metabolic enzymes.

Friday 15 December 2023

S44: Global Movement on Antimicrobial Resistance (Faculty of Medicine, Chulalongkorn University)

10.30-12.00hr

Room C

Friday 15 December 2023

S44: Global Movement on Antimicrobial Resistance (Faculty of Medicine, Chulalongkorn University)

10.30-12.00hr

Room C

Chairperson:
1. Viroj Tangcharoensathien

Invited speaker:

1. Antimicrobial Resistance: Accelerating National and Global Responses
Viroj Tangcharoensathien
Other (International Health Policy Program)

2. Policy and National Movement of AMR in Global (Animal) Health
Rungtip Chuanchuen
Other (Faculty of Veterinary Science, Chulalongkorn University)

3. AMR in Hospital-acquired Infections
Tanittha Chatsuwan
Other (Department of Microbiology, Faculty of Medicine, Chulalongkorn University, Thailand)

Abstract No.: ABS0002262

Antimicrobial Resistance: Accelerating National and Global Responses

Viroj Tangcharoensathien

Authors: Viroj Tangcharoensathien

Affiliation: Senior Advisor, International Health Policy Program (IHPP) Ministry of Public Health, Thailand

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002264

Policy and National Movement of AMR in Global (Animal) Health

Rungtip Chuanchuen

Authors: Rungtip Chuanchuen

Affiliation: "FAO Reference Center for Anti-microbial Resistance, Faculty of Veterinary Science, Chulalongkorn University, Thailand"

Due to the global rise of antimicrobial resistance (AMR), there is an urgent need for policy interventions to address the challenge. Unified intersectoral collaboration of national and international agencies is required to coordinate One Health global responses to AMR. The "Global Action Plan" was endorsed by the World Health Assembly in 2015 with the goal to ensure continuation of successful treatment and prevention of infectious diseases with effective and safe medications. Since that year, WOAH has gathered data on the use of antimicrobials in animals and annually published a report to offer access to the data. Later, WHO Guidelines on use of medically important antimicrobials in food-producing animals has been released with primary aim to help preserve the effectiveness of medically important antimicrobials. FAO Action Plan on AMR 2021-2025 has been released and set out five key objectives to increase stakeholder awareness and engagement, strengthen surveillance and research, enable good practices, promote responsible antimicrobial use, and strengthen governance. Thailand has announced the first national strategic plan (NAP) on AMR 2017-2022 with six strategies encompassing human and animal sectors. The significant output in food-producing animals was the reduction of antimicrobial 36% from the baseline in 2017. In particular, the Department of Livestock Development simultaneously issues the strategic management plan of AMR for the livestock sector in accordance with the NAP. Integrated AMR Surveillance with One Health Approach Guideline has been recently released. Policies and regulation to minimize AMU in food animals in Thailand is emphasized.

Keywords: AMR, global health

Abstract No.: ABS0002265

AMR in Hospital-acquired Infections

Tanittha Chatsuwan

Authors: Tanittha Chatsuwan

Affiliation: Department of Microbiology, Faculty of Medicine, Chulalongkorn University, Thailand

No abstract available

Keyword: No abstract available

Friday 15 December 2023

S45: Free Paper V: Dengue

10.30-12.00hr

Room D

Friday 15 December 2023

S45: Free Paper V: Dengue

10.30-12.00hr

Room D

Chairperson:
1. Parnpen Viriyavejakul
2. Hisham Imad

Invited speaker:

1. GENETIC REGIONS AFFECTING THE REPLICATION AND PATHOGENICITY OF DENGUE VIRUS TYPE 2
Yoshihiro Samune
Other (Osaka university)

2. GENETIC ANALYSIS OF DENGUE VIRUS IN SEVERE AND NON-SEVERE CASES IN DHAKA, BANGLADESH, IN 2018–2022
MST RUMMANA RAHIM
Other (EVERCARE HOSPITAL DHAKA, BANGLADESH)

3. ANTI-DENGUE ACTIVITY OF ANDROGRAPANIN COMPOUND AGAINST DENGUE VECTOR, AEDES AEGYPTI AND DENGUE VIRUS
Kalimuthu Kovendan
Other (Annamalai University)

4. Identification of an effective fraction from Lagerstroemia speciosa with anti-dengue virus activities in vitro and in vivo
Paulpandi Manickam
Other (Bharathiar University, India)

5. PHYTOCHEMICAL PROFILE AND ANTI-DENGUE POTENTIAL OF ASSYRIAN PLUM (CORDIA MYXA L.) UNRIPE FRUIT EXTRACT: AN IN-VITRO APPROACH
RAJAPANDIAN RAJAGANESH
Other (BHARATHIAR UNIVERSITY)

6. Sera of rats fed with baicalein showed effective against dengue virus replication
Pouya Hassandarvish
Other (Tropical Infectious Diseases Research & Education Centre)

Abstract No.: ABS0002072

GENETIC REGIONS AFFECTING THE REPLICATION AND PATHOGENICITY OF DENGUE VIRUS TYPE 2

Yoshihiro Samune

Authors: Yoshihiro Samune1, Akatsuki Saito2, Tadahiro Sasaki1, Ritsuko Koketsu1, Narinee Srimark3, Juthamas Phadungsombat1, Masaru Yokoyama4, Osamu Kotani4, Hironori Sato4, Atsushi Yamanaka3, Saori Haga5, Toru Okamoto5, Takeshi Kurosu6, Emi E Nakayama1, Tatsuo Shioda1

Affiliation:

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2 Department of Veterinary Science, Faculty of Agriculture, University of Miyazaki.

3 Thailand-Japan Research Collaboration Center on Emerging and Re-emerging Infections, Research Institute for Microbial Diseases, Osaka University.

4 Pathogen Genomics Center, National Institute of Infectious Diseases

5 Institute for Advanced Co-Creation Studies, Research Institute for Microbial Diseases, Osaka University.

6 Department of Virology I, National Institute of Infectious Diseases

Introduction: Genome sequencing of the recent DENV2 strains in Thailand showed that Cosmopolitan genotype cocirculated with Asian-I genotype. A focus forming assay (FFA) of these clinical isolates showed that Cosmopolitan viruses grew faster than Asian-I viruses. We identified the genetic regions that affect viral proliferative and infectious potential by generating recombinant viruses between these phenotypically different strains. The present study aimed to further narrow down the responsible regions within E protein.

Methods: By using both in vitro and in vivo experimental approaches, we identified relevant regions and performed functional and structural analysis.

Results: The focus size was larger when the structural proteins and/or non-structural NS1-NS2B proteins were derived from the Cosmopolitan virus. The infectious titers were consistent with the focus sizes. Single-round infectious particle assay confirmed that the chimeric viruses with Cosmopolitan structural proteins, particularly prM/E, had significantly increased luciferase activity. Replicon assay showed that Cosmopolitan NS1-NS2B proteins also increased reporter gene expression levels. Furthermore, in interferon-receptor knock-out mice, viruses with Cosmopolitan structural and NS1-NS2B proteins had higher titers in the blood, and caused critical disease courses. Molecular modeling of these E proteins showed that five of the amino acid substitutions between Asian-I and Cosmopolitan were located near the interface between two E protein dimers. Mutational analyses of these five amino acid residues are now ongoing.

Conclusion: These and preliminary mutational analysis results suggested that the region responsible for proliferation of DENV2 Cosmopolitan viruses is the five amino acid residues in E protein.

Keywords: Dengue virus, Asian-I genotype, Cosmopolitan genotype, in silico structure analysis

Abstract No.: ABS0002054

GENETIC ANALYSIS OF DENGUE VIRUS IN SEVERE AND NON-SEVERE CASES IN DHAKA, BANGLADESH, IN 2018–2022

MST RUMMANA RAHIM

Authors: Rahim R[1], Hasan A[1], Phadungsombat J[2], Hasan N[1], Ara N[1], Biswas SM[1], Nakayama EE[2], Rahman M[1,*] and Shioda T[2,*]

Affiliation:[1]EVERCARE HOSPITAL DHAKA; [2]OSAKA UNIVERSITY JAPAN

Introduction: Dengue virus (DENV) infections have unpredictable clinical outcomes, ranging from asymptomatic or minor febrile illness to severe and fatal disease. The severity of dengue infection is at least partly related to the replacement of circulating DENV serotypes and/or genotypes.

Methods: To describe clinical profiles of patients and the viral sequence diversity corresponding to non-severe and severe cases, we collected patient samples from 2018 to 2022 at Evercare Hospital Dhaka, Bangladesh. Real time PCR method was used for serotype detection and sequencing of E region was done for phylogenetic analysis of DENV serotypes.

Results: Serotyping of 495 cases and sequencing of 179 cases showed that the dominant serotype of DENV shifted from DENV2 in 2017 and 2018 to DENV3 in 2019. DENV3 persisted as the only representative serotype until 2022. Co-circulation of clades B and C of the DENV2 cosmopolitan genotype in 2017 was replaced by circulation of clade C alone in 2018 with all clones disappearing thereafter. DENV3 genotype I was first detected in 2017 and was the only genotype in circulation until 2022. We observed a high incidence of severe cases in 2019 when the DENV3 genotype I became the only virus in circulation. Phylogenetic analysis revealed clusters of severe cases in several different subclades of DENV3 genotype I.

Conclusion: A high incidence of severe cases was found in 2019 when the DENV3 genotype I became the only virus in circulation. Thus, these serotype and genotype changes in dengue virus may explain the large dengue outbreaks and increased severity of the disease.

Keywords: DENV; Bangladesh; serotypes; phylogenetic tree; clades

Abstract No.: ABS0002005

ANTI-DENGUE ACTIVITY OF ANDROGRAPANIN COMPOUND AGAINST DENGUE VECTOR, AEDES AEGYPTI AND DENGUE VIRUS

Kalimuthu Kovendan

Authors: Kalimuthu Kovendan[1*], Arulsamy Jebanesan[1], Savariar Vincent[2]

Affiliation:[1]Division of Vector Biology and Control, Department of Zoology, Faculty of Science, Annamalai University, Annamalainagar – 608 002, Tamil Nadu, India.

[2]P.G. and Research Department of Advanced Zoology & Biotechnology, Loyola College, Nungambakkam, Chennai – 600 034, Tamil Nadu, India.

Introduction: Dengue virus is mainly transmitted by female mosquitoes of Aedes aegypti and Aedes albopictus, it comprises four distinct serotypes (DENV-1, DENV-2, DENV-3, and DENV-4). Due to the presence of various phytochemical compounds in botanicals to killing the mosquito eggs, larvae and adult. The aim of the present study to evaluate the mosquitocidal activity and antiviral effect of Andrograpanin compound against Aedes aegypti and dengue viral protein NS5 methyltransferase were assessed by both in-vitro and in-silico approach.

Methods: The toxicity assays of dengue vector, *Ae. aegypti* larvae and adults using standard methods (WHO 2005; WHO 1981), slightly modification (Kovendan et al., 2013). In-vitro anti-dengue activity of DENV-2 (Sujitha et al., 2015), in-silico anti-dengue activity of Andrograpanin against NS5 methyltransferase (1L9K) (Chanprapaph et al., 2005).

Results: The larval and adult mortality was recorded after 24 h of exposure. Our findings showed that the Andrograpanin compound has higher larvicidal activity (100 percentages at 10 µg/mL) and adult mortality occurred 90 percent at 10 µg/mL, respectively. The cytotoxicity assay percentage of vero cell viability and the reduction in DENV-2 viral yield post treatment Andrograpanin at different time intervals (12, 24 and 48 hrs), values of 10 to 79 PFU/ml, respectively. Moreover, we perform the andrograpanin compound were docked against the receptor protein NS5 methyltransferase, the mol dock score was -5.08 (kcal/mol), respectively.

Conclusion: The andrograpanin compound proved strong effective against dengue vector, *Ae. aegypti* and NS5 virus. Therefore, this study was found the novel drug molecules as anti-dengue compound using the structure drug design techniques.

Keywords: Andrograpanin, anti-dengue, Aedes aegypti, In-vitro, In-silico, DENV-2

Abstract No.: ABS0001992

Identification of an effective fraction from Lagerstroemia speciosa with anti-dengue virus activities in vitro and in vivo

Paulpandi Manickam

Authors: Manickam Paulpandi[1], Krishnamoorthy Kavithaa[2],

Affiliation:
[1]Department of Zoology, Bharathiar University, Coimbatore, Tamilnadu, India
[2]Department of Biotechnology, Hindusthan college of Arts and Science, Coimbatore, Tamilnadu, India

Background: Without efficient therapeutic measures, dengue virus (DENV) infection is a major public health problem on a global scale. In both the prevention and treatment of infectious disorders, Lagerstroemia speciosa (LS), a traditional Indian medication for removing heat and detoxifying, has been utilized extensively. The study's goal is to investigate the anti-DENV properties of the LS fraction both in vitro and in vivo.

Materials and methods: The antiviral properties of LS were investigated in kidney fibroblast BHK-21 cells from baby hamsters, ICR. Results: 25 chemicals, including flavonoids, phenols, anthraquinones, alkaloids, and other kinds, were tentatively characterized from LS based on GC/MS analysis. By preventing DENV-2 from adhering to BHK-21 cells, LS reduced the cytotoxic effect, the generation of offspring virus, and the synthesis of viral RNA and proteins. Furthermore, in DENV-infected ICR suckling mice, AR-1 markedly reduced clinical ratings, slowed weight loss, and lengthened survival. Importantly, after AR-1 treatment, the degenerative alterations in the brain and kidney tissues were dramatically reduced. Additional research using AG129 mice revealed that AR-1 significantly lowered pathological lesions brought on by DENV. It also clearly improved clinical symptoms and survival rates.

Conclusion: Overall, this is the first publication to show that LS has anti-DENV effects both in vitro and in vivo, which raises the possibility that LS could be developed as a therapeutic candidate for DENV infection.

Keywords: Antiviral, In vivo, Cell culture, Lagerstroemia speciosa

Abstract No.: ABS0001982

PHYTOCHEMICAL PROFILE AND ANTI-DENGUE POTENTIAL OF ASSYRIAN PLUM (CORDIA MYXA L.) UNRIPE FRUIT EXTRACT: AN IN-VITRO APPROACH

RAJAPANDIAN RAJAGANESH

Authors: Rajapandian Rajaganesh[1] and Kadarkarai Murugan[1]

Affiliation:[1]Division of Entomology, Department of Zoology, School of Life Sciences, Bharathiar University, Coimbatore-641 046, Tamil Nadu, India.

Introduction: Neglected tropical diseases (NTDs) have become a major public health concern around the world, particularly the potentially fatal dengue hemorrhagic fever transmitted by the Aedes aegypti mosquito. To address Aedes-borne diseases, mosquito vector control strategies remain critical in public health vector surveillance and control. *Cordia myxa* (Assyrian plum) is a common tree in some Asian and African regions. *C. myxa tree,* leaves, and fruit have vital usage in various communities, and the fruit is noted for its therapeutic properties. Although there has been little published study on *C. myxa*.

Methods: Phytochmeicals analysis of *C. myxa* unripe fruit extract by (Shwaish and Al-Imarah, 2017), toxicity assays of *Ae. aegypti* larvae and eggs (3rd instar) using conventional techniques and methods (Rajaganesh et al., 2016). Anti-dengue activity in-vitro (Sujitha et al., 2015); in-silico research (Murugan et al., 2022).

Results: A total of 20 volatile compounds was identified in the extract using GC-MS analysis. C. myxa unripe fruit extract has good mortality at very low concentrations (µg/mL) in ovicidal and larvicidal toxicity experiments. *C. myxa* unripe fruit had minimum IC50 values for the dengue viral protein NS5 respectively in *in-vitro* condition.

Conclusion: *C. myxa* unripe fruit extract revealed potent anti-dengue and mosquitocidal properties against both the NS2 virus and the dengue vector. As a result, this study was the first to report on first-hand scientific data on unripe fruit extract had dual preventative capabilities for the dengue virus and vector borne disease management.

Keywords: Unripe fruit, Mosquitocidal, Anti-dengue, in-vitro, Phytochemicals

Abstract No.: ABS0002118

Sera of rats fed with baicalein showed effective against dengue virus replication

Pouya Hassandarvish

Authors: Ehsan Moghaddam [1], Rafidah Lani [2], Didi Erwandi[3], Zamri Chik[4], Sazaly AbuBakar[1]* , Pouya Hassandarvish[1],*and Keivan Zandi [1, 5]

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Dengue virus (DENV) is a member of the Flaviviridae family and is responsible for the most common mosquito-borne human disease. Currently, there are no available antiviral drugs to treat DENV infections. However, certain flavonoids, including baicalein and baicalin, have demon-strated significant anti-DENV effects in vitro. This study aimed to assess the bioavailability of baicalein and its metabolite, baicalin, in the blood serum of Albino Wistar rats using the Liquid Chromatography with tandem mass spectrometry (LC/MS/MS) method. The in vitro activity of sera obtained from rats administered baicalein was evaluated for its anti-DENV properties using quantitative RT-PCR and the Foci Forming Reduction Assay (FFRA). The results obtained through LC/MS/MS analysis indicated that the bioavailability of baicalin in rat blood serum reached 44.20 µg/ml one hour after oral administration of baicalein. Furthermore, the sera collected from rats given baicalein exhibited a significant 78.26% inhibition of DENV-2 replication when tested against Dengue-2 using both quantitative RT-PCR and FFRA. These findings suggest that baicalein and baicalin hold promise as potential therapeutic candidates for further investigation in the development of treatments against DENV infections.

Keywords: Infectious Diseases; Arboviruses; Dengue Virus; Baicalin; B

Friday 15 December 2023

S46: Extracellular Vesicles in Healthscience and Technology Innovations

10.30-12.00hr

Room E

Friday 15 December 2023

S46: Extracellular Vesicles in Healthscience and Technology Innovations

10.30-12.00hr

Room E

Chairperson:
1. Wittaya Panvongsa

Invited speaker:

1. APPLICATIONS OF EXTRACELLULAR VESICLES IN HEALTHSCIENCE
Kovit Pattanapanyasat
Other (Faculty of Medicine Siriraj Hospital, Mahidol University)

2. DIAGNOSTIC AND PROGNOSTIC POTENTIAL USING EVS IN CANCER DISEASE
Wittaya Panvongsa
Faculty of Tropical Medicine, Mahidol University (Tropical Nutrition and Food Science)

3. PLANT-DERIVED NANOVESICLES AND TECHNOLOGY INNOVATION
ARTHIT CHAIROUNGDUA
Other (Department of Physiology, Faculty of Science, Mahidol University)

Abstract No.: ABS0002128

APPLICATIONS OF EXTRACELLULAR VESICLES IN HEALTHSCIENCE

Kovit Pattanapanyasat

Authors: Chaichompoo P[1], Atipimonpat A[2], Subsoontorn P[2], Kumphune S[3], Kheansaard W[1], Klaihmon P[1], Svasti S[1], Khowawisetsut L[1], **Pattanapanyasat K[1]**

Affiliation:
[1]Center of Excellence for Microparticle and Exosome in Diseases, Department of Research, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok 10700, Thailand; [2]Department of Biochemistry, Faculty of Medical Science, Naresuan University, Phitsanulok 65000, Thailand; [3]Biomedical Engineering Center, Chiang Mai University, Chiang Mai 50200, Thailand

Extracellular vesicles (EVs) are bioactive, submicron-sized particles released from almost all cell types upon activation, stress or apoptosis. EVs are abundantly found in biofluids, and broadly classified into exosomes, microvesicles and apoptotic bodies depending on their mode of biogenesis. EVs have emerged as important mediators of cell-to-cell communication. Availability of EVs in the body fluids make them highly attractive as potential diagnostic and prognostic biomarkers. The rich diversity of EVs can also be used as therapies to prevent or reverse disease. In the past two decades, we have been working on effect of EVs on thromboembolic complications and cardiomyopathy in β-thalassemia/HbE patients, an inherited hemoglobin disorder caused by a decrease or complete deficiency of β-globin chain synthesis. A significant increase in the levels of circulating EVs originated mainly from activated platelets and red blood cells. These EVs contain proteins related to high levels of reactive oxygen species that potentiate thromboembolic events and endothelial cell activation. We also tested the hypothesis that specific molecules in EVs such as iron form ferritin and degraded heme based on iron overload commonly found in thalassemia patients potentially induce higher cardiomyocyte proliferation. Our current research addresses engineering of exosomes for precise targeting drug delivery for neuronal and cardiovascular diseases. We have designed and constructed two collections of plasmid vectors, namely exosome guiding and exosome loading collection. These exosomes will be used for downstream in vitro and in vivo experiments. Some of our previous and recent findings will be discussed in this communication.

Keywords: Biomarkers, cardiovascular diseases, extracellular vesicles, stroke, thalassemia

Abstract No.: ABS0002197

DIAGNOSTIC AND PROGNOSTIC POTENTIAL USING EVS IN CANCER DISEASE

Wittaya Panvongsa

Authors: Wittaya Panvongsa[1,2,9] Teerada Siripoon[3] Wittawin Worakitchanon[2,4] Lalida Arsa[5] Narumol Trachu[6], Natini Jinawath[7,8] Nuttapong Ngamphaiboon [2], Arthit Chairoungdua[2,4,9]

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[3]Division of Medical Oncology, Department of Medicine, Faculty of Medicine Ramathibodi Hospital, Mahidol University;
[4]Department of Physiology, Faculty of Science, Mahidol University;
[5]Molecular Histopathology Laboratory, Department of Pathology, Faculty of Medicine Ramathibodi Hospital, Mahidol University;
[6]Research Center, Faculty of Medicine Ramathibodi Hospital, Mahidol University;
[7]Program in Translational Medicine, Faculty of Medicine Ramathibodi Hospital, Mahidol University;
[8]Integrative Computational BioScience Center (ICBS), Mahidol University;

Poor survival of patients with locally advanced head and neck squamous cell carcinoma (HNSCC) is partly due to early diagnosis difficulties and the lack of reliable biomarkers for predicting treatment outcomes. Extracellular vesicles (EVs) are released by most cell types, playing crucial roles in tumor progression. In this study, an EV-miRNA was identified as a potential blood-based diagnostic and prognostic biomarker for HNSCC. In the discovery cohort, plasma-derived EVs from HNSCC patients and healthy volunteers were used for miRNA profiling. Ten EV-associated miRNAs were differentially expressed between HNSCC patients and healthy volunteers. Subsequently, the results were validated in the individual discovery and additional cases by qRT-PCR. Among 10 EV-miRNAs, four (miR-27b-3p, miR-491-5p, miR-1910-5p, and miR-630) were significantly dysregulated in HNSCC patients compared with healthy volunteers. The miRNA prediction models were developed to discriminate HNSCC patients from healthy volunteers. The model using miR-491-5p was selected as a diagnostic biomarker for HNSCC with a sensitivity and specificity of 46.6% and 100%, respectively. The dynamic changes of miRNA model score (ΔmiRNAs) were determined using scores pre- and post-definitive treatment further to investigate the prognostic value of miRNA prediction models. The univariate and multivariate analyses indicated that ΔmiR-491-5p was the most powerful and independent prognostic indicator for overall survival (hazard ratio [HR] 5.66) and disease-free survival (HR 2.82) of HNSCC patients. In summary, the miR-491-5p prediction model could serve as a blood-based diagnostic marker for HNSCC. Moreover, ΔmiR-491-5p could be a potential monitoring prognostic marker to reflect the survival of HNSCC patients.

Keywords: biomarker, extracellular vesicle, head and neck squamous cell carcinoma, miRNA

Abstract No.: ABS0002213

PLANT-DERIVED NANOVESICLES AND TECHNOLOGY INNOVATION

ARTHIT CHAIROUNGDUA

Authors: Nittaya Boonmuen[1], Wittaya Panvongsa[2] and Arthit Chairoungdua[1,3,4]

Affiliation:

[1]Department of Physiology, Faculty of Science, Mahidol University, Bangkok, Thailand

[2]Department of Tropical Nutrition and Food Science, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

[3]Toxicology Graduate Program, Faculty of Science, Mahidol University, Bangkok, Thailand
[4]Excellent Center of Drug Discovery (ECDD), Mahidol University, Bangkok, Thailand

Extracellular vesicles (EVs) are nano-sized phospholipid membrane vesicles actively released from all cell types into their surroundings. EVs play critical roles in intercellular communication by transferring a wide range of functional proteins, lipids, nucleic acids, and metabolites. In mammalian cells, these bioactive components are unique and often reflect the disease state. Therefore, EVs are regarded as promising biomarkers for disease diagnosis and emerging therapeutic nanoparticles. Plant-derived nanovesicles (PNVs) have been recently characterized; however, the information relating to their pharmacological activity is in infancy. Our group investigates the anticancer applications of fingerroot-derived nanovesicles (FDNVs). Although numerous pharmacological activities of compounds from fingerroot have been documented, the characterization and activity of FDNVs have yet to be shown. The isolated FDNVs showed round-shaped vesicles with an average size of approximately 100 nm. FDNVs were internalized and exhibited selective anticancer activity in colorectal cancer cell lines but not the normal colon epithelial cells. Mechanistically, FDNVs disrupt intracellular redox homeostasis and induce apoptosis in cancer cells. We also evaluated the anticancer activity of FDNVs in two brain tumor cell lines: atypical teratoid rhabdoid tumor (BT12) and diffuse intrinsic pontine glioma (SF8628). FDNVs uptake into these brain tumor cells and induced apoptosis. FDNVs significantly suppressed migration and invasion of BT12 and SF8628 cells at non-toxic doses. Interestingly, the toxicity of FDNVs was not observed in microglia cells. These studies highlight the therapeutic applications of nanovesicles from fingerroot and possibly from other sources. The continuing exploration of the functions of PNVs will promote their clinical translation and

Keywords: Extracellular vesicles, PNVs, anticancer

Friday 15 December 2023

S47: Anti-Aging and Regenerative Medicine

13.00-14.30hr

Room A

Friday 15 December 2023

S47: Anti-Aging and Regenerative Medicine

13.00-14.30hr

Room A

Chairperson:
1. Richard Kaszynski
2. Kampon Sriwatanakul

Invited speaker:

1. IMMUNOTHERAPY FOR CANCER USING iNKT CELL AND NEXT GENERATION NKT THERAPY WITH DRUG DELIVERY SYSTEM
Taehun Hong
Other (Tokyo Medical University)

2. Nicotinamide Mononucleotide (NMN) reverse Kidney function
Richard Kaszynski
Other (Stanford Solutions, Stanford Medical School)

3. Updates on Stem cell therapy
Kampon Sriwatanakul
Other (President, Thailand Charter of Health)

4. Measurement of the Telomere Length as an Aging Marker using Flow-FISH technology
Pongrama Ramasoota
Faculty of Tropical Medicine, Mahidol University (Social and Environmental Medicine)

5. Potential of Aquatic Animal Stem Cells in Regenerative Medicine
Chee Wee Lee
Other (Aquaculture Innovation Centre)

Abstract No.: ABS0002169

IMMUNOTHERAPY FOR CANCER USING iNKT CELL AND NEXT GENERATION NKT THERAPY WITH DRUG DELIVERY SYSTEM

Taehun Hong

Authors: Hong T[1, 2], Igarashi K[1], Li S[1], Matsuda K[1], Cabral H[1]

Affiliation: [1]University of Tokyo; [2]Tokyo Medical University

Introduction: Among the numerous challenges associated with aging, carcinogenesis stands out as one of the most devastating and fearsome issues. Despite the development of various antitumor drugs, many patients still lack a complete cure, while others suffer from severe side effects. Immunotherapy using immune checkpoint inhibitors (ICIs) has emerged as a promising approach for cancer treatment in recent years due to its low toxicity and ability to engage autoimmune cells in self-cure. However, the instability of treatment effects in individual patients has hindered the achievement of satisfactory outcomes in many cases. In this study, we propose a novel immunotherapy approach based on the activation of NKT cells, independent of cancer type and patient characteristics.

Methods & Results: To implement this approach, we utilized a Drug Delivery System (DDS) to create a nano-carrier that effectively delivers RK-163 to dendritic cells in the lymph nodes adjacent to the tumor. This delivery mechanism activates the NKT cells and enhances the immune system\'s ability to attack cancer cells. Our method demonstrated successful suppression of 4T1 breast cancer growth, even in cases which showed resistance to conventional ICIs. Furthermore, it prolonged the survival of 4T1 tumor-bearing mice by five-fold.

Conclusion: By implementing DDS into the NKT activation method we aimed to inhibit cancer growth in a cost-effective and simple manner for those cancers that cannot be effectively treated with traditional immuno-cancer therapies.

Keywords: Immunotherapy for cancer; NKT cell activation; RK-163; Drug Delivery System; Immune checkpoint inhibitors.

Abstract No.: ABS0002271

Nicotinamide Mononucleotide (NMN) reverse Kidney function

Richard Kaszynski

Authors: Richard Kaszynski

Affiliation: Stanford Solution, Stanford University, USA

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002272

Updates on Stem cell therapy

Kampon Sriwatanakul

Authors: Kampon Sriwatanakul

Affiliation: President, Thailand Charter of Health

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002273

Measurement of the Telomere Length as an Aging Marker using Flow-FISH technology

Pongrama Ramasoota

Authors: Pongrama Ramasoota

Affiliation: Faculty of Tropical Medicine, Mahidol University

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002191

Potential of Aquatic Animal Stem Cells in Regenerative Medicine

Chee Wee Lee

Authors: Chee-Wee LEE

Affiliation: Aquaculture Innovation Centre, Temasek Polytechnic, Singapore; and School of Chemistry, Chemical Engineering and Biotechnology, Nanyang Technological University, Singapore

Regenerative medicine has emerged as a groundbreaking field, offering the promise of addressing a wide spectrum of medical conditions through the replacement or repair of damaged or degenerated tissues. While terrestrial organisms have been extensively scrutinized for their regenerative potential, aquatic animals, with their diverse and often astonishing regenerative abilities, represent an underexplored resource.

Our preliminary investigation underscores the potential of harnessing stem cells derived from a tropical fish species for regenerative applications. The immediate advantages stem from the uncomplicated cultivation and scalability of these cells, which could translate into cost-effective production processes. Notable cost-related benefits include:

1. Rapid Proliferation: These cells exhibit swift replication, enabling the generation of a substantial quantity of stem cells and differentiated cell types within a shorter timeframe, thereby reducing production costs associated with cell expansion.

2. Reduced Maintenance Costs: These cells demonstrate robustness and may not necessitate CO2 and serum, making them less dependent on environmental variables such as pH, salinity, and temperature.

3. Scalability: These cells can be readily scaled up for large-scale production due to their rapid replication and easy maintenance, a critical factor for clinical applications.

4. Lower Contamination Risk: These cells, when cultivated in controlled environments, are less vulnerable to certain types of contamination (e.g., pathogens or endotoxins) that can affect mammalian cell cultures.

In conclusion, aquatic animal stem cells and tissues present a captivating avenue for regenerative medicine. Their regenerative capabilities, plasticity, and suitability for mass production make them invaluable resources for addressing a wide array of medical conditions.

Keywords: Aquatic Animal, Stem Cells, Regenerative Medicine

Friday 15 December 2023

S48: New Perspectives for Vector Controls

13.00-14.30hr

Room B

Friday 15 December 2023

S48: New Perspectives for Vector Controls

13.00-14.30hr

Room B

Chairperson:
1. Suchada Sumruayphol
2. Suparat Phuanukoonnon.

Invited speaker:

1. XYbank: sharing images online as a tool for the taxonomic use of geometric morphometrics
Sebastien Dujardin
Other (DujardinS)

2. Household larval survey tool: application for effective control practices
Suparat Phuanukoonnon
Faculty of Tropical Medicine, Mahidol University (Social and Environmental Medicine)

3. Bioefficacy effect on Temephos coated product under contacted and non-contacted conditions
Sungsit Sungvornyothin
Faculty of Tropical Medicine, Mahidol University (Medical Entomology)

Abstract No.: ABS0002186

XYbank: sharing images online as a tool for the taxonomic use of geometric morphometrics

Sebastien Dujardin

Authors: Sebastien Dujardin[1], Jean-Pierre Dujardin[2]

Affiliation:[1]DujardinS, Montpellier, France; [2] INTERTRYP, University of Montpellier, CIRAD, IRD, F-34398, Montpellier, France

In an entomological surveillance program the need for species identification remains constant over time and may vary unpredictably depending on the geographic location.
The Geometric Morphometrics (GM) has been suggested as a possible way to handle such a challenge. The GM method is based on coordinates of anatomical points (landmarks).

Can we use the coordinates of another person in order to identify its own images ?
Normally we cannot due to the inter user measurement error. One of the solution to this problem could be the use of collaborative landmarks

What are collaborative landmarks?
When we digitize an image, we add plots to the image, which are landmarks represented by a series of coordinates (x, y) used by GM statistical tools. Actually, landmarks are data collected by a single user from multiple images; these are referred to as single-user landmarks.

Due to measurement errors, the single-user landmarks are only valid for that particular user.
How can multi-user landmarks be made useful for everyone? We propose a solution to this question by introducing **collaborative landmarks. Collaborative landmarks** are landmarks performed by various users on the same images. They allow us to compute the average or median coordinates of various users, which are theoretically the most accurate landmarks to be derived from a single image.

In order to use **collaborative landmarks** we need modern **web/cloud** tools such as:

a web application with user friendly interfaces; highly available and scalable databases for images and metadata

This web tool is presented during the session.

Keywords: Geometric Morphometrics, collaborative landmarks, web, cloud, xybank

Abstract No.: ABS0002198

Household larval survey tool: application for effective control practices

Suparat Phuanukoonnon

Authors: Soe Htet Aung [1], Patchara Sriwichai [2], **Suparat Phuanukoonnon [3]**

Affiliation:
[1]Department of Tropical Hygiene, Faculty of Tropical Medicine, Mahidol University, Thailand.
[2]Department of Medical Entomology, Faculty of Tropical Medicine, Mahidol University, Thailand.
[3]Department of Social and Environmental Medicine, Faculty of Tropical Medicine, Mahidol University, Thailand.

Dengue is a major public health concern in South-east Asia. Two cross-sectional studies were carried out to identify key containers for Aedes larval infestation in household water storage containers and evaluate the efficacy of larval control activities such as the use of the larvicide, temephos, covering the containers with lids and weekly cleaning on the presence of Aedes aegypti larvae in these water-storage containers so as to improve entomological surveillance under the current dengue control program. The larval survey form was developed for the survey in rural and urban Khon Kaen Thailand in 2002, and in peri-urban of Yangon, Myanmar in 2018-2019. This larval survey form collects data on each water storage container, the presence of Aedes aegypti larvae, location- inside or outside the house, water storage purposes (drinking, washing, bathing, flushing the toilet, gardening, and recreation), and control practices applied (single or multiple measures). The results showed key container identification and the effective control measures which can be applied for those containers. Both studies found a complex interaction between household water use, container characteristics, and larval control practices. The results from both studies pointed out that larval control strategies will require ongoing entomological surveillance and the importance of identification of key breeding sources and optimal control methods.

Keywords: Dengue, larval control, household, control measures

Abstract No.: ABS0002274

Bioefficacy effect on Temephos coated product under contacted and non-contacted conditions

Sungsit Sungvornyothin

Authors: Sungsit Sungvornyothin

Affiliation: Faculty of Tropical Medicine, Mahidol University

No abstract available

Keyword: No abstract available

Friday 15 December 2023

S49: Srub Typhus (MORU)

13.00-14.30hr

Room C

Friday 15 December 2023

S49: Srub Typhus (MORU)

13.00-14.30hr

Room C

Chairperson:
1. Nicholas Day
2. Qian Wang

Invited speaker:

1. Estimating the global burden of scrub typhus
Qian Wang
Other (MORU)

2. IS SCRUB TYPHUS A GLOBAL DISEASE?
Ivo Elliott
Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

3. Scrub typhus: behaviour, prevention and community engagement
Carlo Perrone
Other (MORU)

4. Spatial Transcriptomics in Orientia tsutsugamushi to Reveal Bacterial-Host Interactions in Vitro and in Vivo
Chitrasak Kullapanich
Faculty of Tropical Medicine, Mahidol University (Microbiology and Immunology)

5. Innovations in Rickettsial Diagnostics
Jantana Wongsantichon
Other (Mahidol-Oxford Tropical Medicine Research Unit (MORU))

Abstract No.: ABS0002276

Estimating the global burden of scrub typhus

Ms. Qian Wang

Authors: Qian Wang, Qian Wang

Affiliation: Mahidol Oxford Tropical Medicine Research Unit (MORU)

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002221

IS SCRUB TYPHUS A GLOBAL DISEASE?

Ivo Elliott

Authors: Elliott I[1,2]

Affiliation:
1. Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand
2. Centre for Tropical Medicine & Global Health, University of Oxford, Oxford, United Kingdom

Scrub typhus is a major cause of febrile illness across the Asia-Pacific. Up to 20% of fever presenting to hospital is due to scrub typhus and seroprevalence can reach 50% with an untreated mortality of ~6%. Scrub typhus is caused by Orientia species and is transmitted by larval Trombiculid mites, which are in turn primarily hosted by small mammals. The Tsutsugamushi triangle has been considered the endemic region for scrub typhus since the 1950s. This 8 million km2 region covers Pakistan in the west, the Russian Far East in the north, Japan in the East and northern Australia to the south, putting half the world's population potentially at risk of infection. Prior to 2006, there were 3 possible reports of infection from Africa. In 2006 the first case of scrub typhus was reported from Chile, followed by a case from the UAE in 2010. Orientia species have now been identified in Trombiculid mites on all continents except Antarctica. Emerging serological data suggests exposure to Orientia occurs across Africa, S & C America. However outside Chile, the clinical syndrome is unknown. Scrub typhus appears to have a heterogeneous distribution governed by a complex interaction of factors: virulence, vector and host species, habitat, climate and human behaviour. Over the next decade our understanding of this pathogen as a global disease will transform. An accurate disease burden will be established and impacts of changing climate and land use better understood. This will drive urgently needed research into this poorly understood neglected tropical disease.

Keywords: scrub typhus, Orientia, epidemiology, ecology

Abstract No.: ABS0002280

Scrub typhus: behaviour, prevention and community engagement

Carlo Perrone

Authors: Carlo Perrone

Affiliation: Mahidol Oxford Tropical Medicine Research Unit (MORU)

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002281

Spatial Transcriptomics in Orientia tsutsugamushi to Reveal Bacterial-Host Interactions in Vitro and in Vivo

Chitrasak Kullapanich

Authors: Chitrasak Kullapanich

Affiliation: Mahidol Oxford Tropical Medicine Research Unit (MORU)

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002307

Innovations in Rickettsial Diagnostics

Jantana Wongsantichon

Authors: Jantana Wongsantichon

Affiliation: Mahidol Oxford Tropical Medicine Research Unit (MORU)

No abstract available

Keyword: No abstract available

Friday 15 December 2023

S50: Free Paper VI: Global Health 3

13.00-14.30hr

Room D

Friday 15 December 2023

S50: Free Paper VI: Global Health 3

13.00-14.30hr

Room D

Chairperson:
1. Arjen Dondorp
2. Sirasate Bantuchai

Invited speaker:

1. BLOOD CULTURE NEGATIVE INFECTIVE ENDOCARDITIS: AN UPDATED REVIEW OF THE LITERATURE
Natasha Vaselli
Other (University of Liverpool)

2. AUTOMATED CLASSIFICATION OF ZOONOTIC TRYPANOSOMA EVANSI USING SELF-SUPERVISED LEARNING APPROACH
Supasuta Busayakanon
Other (King Mongkut's Institute of Technology Ladkrabang)

3. DEVELOPMENT OF RECOMBINASE POLYMERASE AMPLIFICATION FOR THE DETECTION OF HUMAN ROTAVIRUS AND VIRAL ACUTE ENCEPHALITIS (HEPATITIS A)
Michael Kim JR Mendoza
Other (University of the Philippines)

4. UTILIZATION OF A RECOMBINASE POLYMERASE AMPLIFICATION (RPA) ASSAY FOR THE DETECTION OF ENTERIC HUMAN ADENOVIRUS IN FRESH PRODUCE
ELCHIN JUANICO
Other (NATURAL SCIENCES RESEARCH INSTITUTE UP DILIMAN)

5. The R&D Landscape of Vaccines and Drugs for Tropical Diseases
Guanqiao Li
Other (Faculty of Vanke School of Public Health, Tsinghua University)

Abstract No.: ABS0001984

BLOOD CULTURE NEGATIVE INFECTIVE ENDOCARDITIS: AN UPDATED REVIEW OF THE LITERATURE

Natasha Vaselli

Authors: Frazer Kirk[1&2], Natasha Marcella Vaselli[1,3&4]

Affiliation:
1. Gold Coast University Hospital, Southport, Queensland, Australia.
2. School of Medicine and Dentistry, Griffith University, Gold Coast, Queensland Australia
3. Institute of Infection, Veterinary & Ecological Sciences, University of Liverpool, Liverpool, UK
4. NIHR HPRU in Gastrointestinal Infections at the University of Liverpool, Liverpool, United Kingdom

Background: Blood culture negative endocarditis (BCNE) is an important disease carrying significant morbidity and mortality. Studies show it accounts up to 30% of cases of infective endocarditis. Current guidelines recommend a multimodal approach to diagnosis using serology, molecular and imaging techniques. The purpose of this review is to highlight areas for improvement and modification of current guidelines.

Methods: We performed an updated review of the literature. We searched the databases Web of Science, MEDLINE, EMBASE, and SCOPUS for the latest clinical guidelines and literature on BCNE. We provide a narrative synthesis of the clinical guidelines and literature on BCNE.

Results: BCNE is associated with higher rates of recurrence and reoperation as well as higher risk of death at 1 year. The Modified Duke's criteria has diminished sensitivity when used for BCNE and doesn't include the advances in molecular testing. The addition of the St Thomas' minor criteria allows a more definitive diagnosis among BCNE. Although the Duke's criteria has been updated to include serology for Coxiella, it still needs to be updated to reflect the aetiology of BCNE, such as serology for Bartonella. Despite the European Society of Cardiology having a separate BCNE investigation pathway it still includes the modified Duke's criteria, and thus does not circumvent the insensitivity in detecting BCNE initially.

Conclusion: Despite evolving technology improving the identification of infective organism, the Modified Dukes Criteria for diagnosis of IE remains insensitive for detection of BCNE and current guidelines do not reflect these changes. Updates to current diagnostic criteria

Keywords: Infective endocarditis; blood culture negative endocarditis; cardiac surgery; prosthetic valve endocarditis; native valve endocarditis

Abstract No.: ABS0001993

AUTOMATED CLASSIFICATION OF ZOONOTIC TRYPANOSOMA EVANSI USING SELF-SUPERVISED LEARNING APPROACH

Supasuta Busayakanon

Authors: Supasuta Busayakanon[1], Veerayuth Kittichai[2], Natchapon Pinetsuksai[3], Siridech Boonsang[4]

Affiliation:[1]Faculty of Medicine, King Mongkut's Institute of Technology Ladkrabang, Bangkok, Thailand; [2]Faculty of Medicine, King Mongkut's Institute of Technology Ladkrabang, Bangkok, Thailand; [3]College of Advanced Manufacturing Innovation, King Mongkut's Institute of Technology Ladkrabang, Bangkok, Thailand; [4]Department of Electrical Engineering, School of Engineering, King Mongkut's Institute of Technology Ladkrabang, Bangkok, Thailand

Trypanosoma evansi, known for causing the Surra disease in animals worldwide, has demonstrated the potential for zoonotic transmission as evidenced by human cases in areas akin to Thailand. Although the route of transmission is uncertain, there remains a risk to residents. Within Thailand, water buffaloes are reported as reservoir hosts of *T. evansi*. This establishes the capacity for parasite transmission from animals to humans in the local setting. Thus, the development of innovative tools to support active surveillance becomes necessary. Deep learning has proven to become a practical technique for the automatic identification of parasites. This approach overcomes gold-standard microscopic observation in terms of time-consuming, high-facility costs, and the need for specialized skills, making it suitable for remote areas. We introduced a classification model utilizing Bootstrap Your Own Latent (BYOL), a novel self-supervised learning (SSL) approach that requires a fraction of data labels for model training. During SSL pretraining and finetuning processes, three ResNet models; ResNet50, ResNet101, and ResNet152 - were compared to determine the most suitable model for identifying the appropriate fraction of class labels comparable to the baseline. Using the ResNet50, the proposed approach achieved an accuracy of 94.17% and an AUC of 100% with merely 10% labelled data. Finally, our BYOL-trained model demonstrates effective classification of *T. evansi* even when confronted with limited data. This reduction in the need for the amount of data not only alleviates the workload but also enhances the efficiency of Artificial intelligence in parasite classification, which may contribute to further control programs.

Keywords: *Trypanosoma evansi*, Classification, Self-supervised learning, Fine-tuning, Label fraction

Abstract No.: ABS0002025

DEVELOPMENT OF RECOMBINASE POLYMERASE AMPLIFICATION FOR THE DETECTION OF HUMAN ROTAVIRUS AND VIRAL ACUTE ENCEPHALITIS (HEPATITIS A)

Michael Kim JR Mendoza

Authors: Mendoza MKJ[1,2], De Jesus E[1] & Santos JA[1]

Affiliation:
[1]Biological Research and Services Laboratory, Natural Sciences Research Institute, University of the Philippines Diliman, Diliman Quezon City Philippines 1101
[2]Department of Biochemistry and Molecular Biology, College of Medicine, University of the Philippines Manila, Ermita Manila Philippines

Rotavirus (RV) and Hepatitis A (HaV) are two of the common Food and Waterborne Diseases reported to the Epidemic-Prone Disease Case Surveillance System (ECSC) in the Philippines. Burden and epidemiology have not been well-documented properly in the country since the laboratory tests are not routinely performed. The study aims to develop a point-of-care detection kit for RV and HaV by the utility of the Recombinase Polymerase Amplification (RPA). The assay development was performed by doing primer design, primer Screening using SYBR green-qPCR and optimization of RPA conditions. Twenty-three 23 primer combinations from the UTR area were utilized for HaV, whereas 9 primer combinations for RV targeting the NSP 3 region were screened.

RPA assays for HaV and RV can be completed in as little as 10 minutes and can be downsized into half reaction volumes of 25 uL. Improved sensitivity can be carried out using 37ºC for 30 minutes for both targets. The sensitivity of HaV is determined at 10^3 while 10^2 viral DNA copy for RaV. The technology enables quick and easy detection of the two targets and can be utilized for point of care detection of the enteric viruses. The assays can be used as a replacement for the conventional PCR and culture methods. Future plans involve the utility of paper-based technology for the visualization of RPA amplicons which is currently being developed.

Keywords: Hepatitis A; Rotavirus; RPA; qPCR

Abstract No.: ABS0002023

UTILIZATION OF A RECOMBINASE POLYMERASE AMPLIFICATION (RPA) ASSAY FOR THE DETECTION OF ENTERIC HUMAN ADENOVIRUS IN FRESH PRODUCE

ELCHIN JUANICO

Authors: Elchin Juanico[1] and Joy Ann P. Santos[1]

Affiliation: [1]Biological Research and Services Laboratory, Natural Sciences Research Institute, University of the Philippines Diliman, Diliman Quezon City Philippines 1101

Recently, the need for healthful meals free of chemical additives has led to an increase in consumption of fresh produce. However, this scenario also lead to an increase in foodborne outbreaks. Enteric virus contamination of food is a serious issue since the viruses have a low infectious dose and a high level of environmental persistence causing infections. Among the enteric viruses, human adenovirus (HAdV) has been suggested as a reliable indicator of food faecal contamination. In this study, a recombinase polymerase amplification (RPA) assay was developed for the detection of human adenovirus from naturally contaminated fresh produce found in wet market, mall and farms. All samples collected were subjected to both quantitative PCR (qPCR) and RPA assays. Out of the 150 samples (lettuce, cucumber, spring onion, tomato and strawberry), 83 were positive in qPCR and 72 by RPA; in both methods, HadV was found to be prevalent in malls and wet market, which most likely happened during handling and transit. The entire RPA amplification process can be completed in the isothermal condition of 35ºC for 40 minutes which was remarkably superior to qPCR with an accuracy of 77.89% to 90.02%, specificity up to 87.80%, and sensitivity up to 96%. Furthermore, the assay was statistically relevant to qPCR performance avoiding sophisticated thermal cyclers with simple operation. The assay can efficiently be used in the detection of HAdV in fresh produce, making it a reliable, point-of-care HAdV diagnostics tool, an alternative to qPCR.

Keywords: Keywords: Human Adenovirus (HadV), Quantitative polymerase chain reaction (qPCR), and Recombinase Polymerase Amplification (RPA) assay

Abstract No.: ABS0002194

The R&D Landscape of Vaccines and Drugs for Tropical Diseases

Guanqiao Li

Authors: Guanqiao Li

Affiliation: Vanke School of Public Health, Tsinghua University, Beijing, China

Introduction: Tropical diseases have gained prominence due to their considerable health and economic impact. This study investigates the research and development (R&D) landscape for tropical disease drugs and vaccines, emphasizing recent advances critical for global health improvement.

Methods: Our analysis focused on candidates for tropical disease prevention and treatment, including those in clinical or preclinical phases, as of October 2023, curated from clinical trial registries, academic literature, and company announcements. A total of 669 candidates were included. We also explored the correlation between the number of candidates and disability-adjusted life years (DALYs) to gauge unmet medical needs.

Results: The global R&D landscape for tropical diseases comprises 320 candidate vaccines and 325 drugs. Malaria (45.63%), rabies (28.13%), and dengue fever (11.25%) are the primary diseases in vaccine development, while malaria (44.00%), dengue fever (10.46%), and rabies (8.92%) lead in drug development. The United States, Europe, and China are the primary regions for R&D. Private companies and industry contribute 77.88%, while academic and non-profit organizations contribute 22.12%. Malaria carries the highest DALYs burden, with the most vaccines (146) and drugs candidates (143). Dengue fever follows, with 36 vaccines and 34 drugs. Neglected tropical diseases, like schistosomiasis and lymphatic filariasis, receive insufficient attention and resources in R&D.

Conclusion: Sustained R&D support is crucial for future breakthroughs. While diseases like malaria and dengue fever have received deserved attention, rectifying the imbalance and expanding research into neglected tropical diseases with substantial burdens is pivotal for future R&D in tropical diseases.

Keywords: Tropical diseases, malaria, dengue, vaccines, drugs, research and development

Friday 15 December 2023

S51: Artificial Intelligence (AI) for Disease Control (Thai Language)

13.00-14.30hr

Room E

Friday 15 December 2023

S51: Artificial Intelligence (AI) for Disease Control (Thai Language)

13.00-14.30hr

Room E

Chairperson:
1. Darin Areechokchai

Invited speaker:

1. Innovations for screening and diagnosing liver fluke and other helminths with Artificial Intelligence (AI)
Thidarut Boonmars
Other (Department of Parasitology KhonKaen University)

2. Innovations for screening and diagnosing liver fluke and other helminths with Artificial Intelligence (AI)
Sanparith Marukatat
Other (National Electronics and Computer Technology Center (NECTEC))

3. Innovations for screening and diagnosing liver fluke and other helminths with Artificial Intelligence (AI)
Ampas Wisetmora
Other (department of diseases control)

4. AI for ensuring the chemical droplets sizing measurement and verifying the effectiveness of PH sprayers
pongsakorn sadakorn
Other (Bureau of Vector Borne Disease)

5. Advances in diagnosis of Tuberculosis: leveraging artificial intelligence for chest x-ray interpretation
Phalin Kamolwat
Other (Division of Tuberculosis, Department of Disease Control, Ministry of Public Health, Thailand)

6. Advances in diagnosis of Tuberculosis: leveraging artificial intelligence for chest x-ray interpretation
Ekapol Chuangsuwanich
Other (Computer Engineering Department, Faculty of Engineering, Chulalongkorn University)

Abstract No.: ABS0002229

Innovations for screening and diagnosing liver fluke and other helminths with Artificial Intelligence (AI)

Thidarut Boonmars

Authors: Thidarut Boonmars

Affiliation: Department of Parasitology KhonKaen University

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002230

Innovations for screening and diagnosing liver fluke and other helminths with Artificial Intelligence (AI)

Sanparith Marukatat

Authors: Sanparith Marukatat

Affiliation: National Electronics and Computer Technology Center (NECTEC)

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002231

Innovations for screening and diagnosing liver fluke and other helminths with Artificial Intelligence (AI)

Ampas Wisetmora

Authors: Ampas Wisetmora

Affiliation: Division of Communicable Diseases, Department of Disease Control

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002232

AI for ensuring the chemical droplets sizing measurement and verifying the effectiveness of PH sprayers

Mr. pongsakorn sadakorn

Authors: Pongsakorn Sadakorn

Affiliation: Division of Vector Borne Disease, Department of Disease Control

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002233

Advances in diagnosis of Tuberculosis: leveraging artificial intelligence for chest x-ray interpretation

Phalin Kamolwat

Authors: Phalin Kamolwat

Affiliation: Division of Tuberculosis Thailand

No abstract available

Keyword: No abstract available

Abstract No.: ABS0002228

Advances in diagnosis of Tuberculosis: leveraging artificial intelligence for chest x-ray interpretation

Ekapol Chuangsuwanich

Authors: Ekapol Chuangsuwanich

Affiliation: Computer Engineering Department, Faculty of Engineering, Chulalongkorn University

No abstract available

Keyword: No abstract available

Friday 15 December 2023

S52: Closing Ceremony Awards (Young Investigator, Poster, etc.)

15.00-16.00hr

Friday 15 December 2023

S52: Closing Ceremony Awards (Young Investigator, Poster, etc.)

15.00-16.00hr

Closing Keynote Address
"Applying System Thinking to Bring Innovation to Tropical Diseases Control and Elimination"
by Carlos J. Cuellar

Closing Remarks by
Jetsumon Prachumsri/ Weerapong Phumratanaprapin

Chairperson: -

Invited speaker:

1. **Applying System Thinking to Bring Innovation to Tropical Diseases Control and Elimination**
   Carlos Cuellar
   Other (University Research Co. (URC))

Abstract No.: ABS0002305

Applying System Thinking to Bring Innovation to Tropical Diseases Control and Elimination

Carlos Cuellar

Authors: Carlos J. Cuéllar

Affiliation: University Research Co., LLC

No abstract available

Keyword: No abstract available

Wednesday 13 – 15 December 2023

Poster Sessions

13.00-13.45hr

Wednesday 13 – 15 December 2023

Poster Sessions

13.00-13.45hr

Chairperson: -

Invited speaker:

1. REINTEGRATING PARAGONIMIASIS WITH TUBERCULOSIS SURVEILLANCE IN CO-ENDEMIC AREAS IN THE TIME OF GENEXPERT
Jenelle Sambo
Other (University of the Philippines Manila)

2. TETANUS IN CHILD WITH DENTAL CARIES INFECTION: A CASE REPORT
Elvira Rosana Muslimin
Other (Department of Child Health, Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada/Dr Sardjito General Hospital, Yogyakarta, Indonesia)

3. EVALUATION OF BOOSTING ALGORITHM MODELS TO PREDICT ANTIMICROBIAL RESISTANCE IN Escherichia coli
Pierangeli Vital
Other (Natural Sciences Research Institute, University of the Philippines Diliman)

4. A FOUR-YEARS SURVEY OF ANTIMICROBIAL RESISTANT ESKAPEE PATHOGENS ISOLATED IN A TERTIARY REFERRAL MEDICAL CENTER IN CHONBURI, THAILAND
Wilawan Oransathit
Other (AFRIMS)

5. DISTRIBUTION OF ANTIMICROBIAL RESISTANT ESKAPEE PATHOGENS ASSOCIATED WITH HOSPITAL-ACQUIRED INFECTIONS IN BATTAMBANG, CAMBODIA
Wirote Oransathid
Other (AFRIMS)

6. BlaOXA-48 VARIATION AMONG CARBAPENEM-RESISTANT ENTEROBACTERALES ISOLATED FROM PRAPOKKLAO HOSPITAL, CHANTHABURI PROVINCE, THAILAND
Witawat Tunyong
Faculty of Tropical Medicine, Mahidol University (Microbiology and Immunology)

7. ANTIMICROBIAL RESISTANCE PROFILE OF Escherichia coli ISOLATED FROM RAW CHICKEN MEAT IN A SELECTED WET MARKET IN MANILA CITY, PHILIPPINES
Maria Margarita Lota
Other (Faculty, Department of Medical Microbiology, College of Public Health, University of the Philippines Manila)

8. Application of LAMP Methods for Detecting Malaria Parasite DNA in RDT-Negative Blood Samples in Lao PDR
Kanako Komaki-Yasuda
Other (National Center for Global Health and Medicine)

9. PERFORMANCE EVALUATION OF AUTOMATED HEMATOLOGY ANALYZER XN-31 PROTOTYPE FOR MALARIA PARASITES DETECTION AT MAHIDOL UNIVERSITY\'S OUTPATIENT CLINIC IN BANGKOK, THAILAND
Miki Kawaguchi
Other (Sysmex Corporation)

10. DEVELOPMENT OF RAPID MOLECULAR DIAGNOSTICS FOR GLUCOSE-6-PHOSPHATE DEHYDROGENASE DEFICIENCY
Beatriz Aira Jacob
Faculty of Tropical Medicine, Mahidol University (Molecular Tropical Medicine and Genetics)

11. COSTS AND HEALTH OUTCOMES OF A NEW RAPID TEST FOR MELIOIDOSIS IN THAILAND
Puttarin Kulchaitanaroaj
Other (Mahidol-Oxford Tropical Medicine Research Unit)

12. DETECTION OF THE V1016G MUTATION IN THE VOLTAGE-GATED SODIUM CHANNEL GENE OF AEDES AEGYPTI IN DENGUE-RISK AREAS IN THAILAND BY ALLELE-SPECIFIC REAL-TIME PCR ASSAY
Jakkrawarn Chompoosri
Other (National Institute of Health, Department of Medical Sciences)

13. A HIGH-THROUGHPUT CELL-BASED SCREEN FOR THE DISCOVERY OF NOVEL PAN-FLAVIVIRUS SMALL MOLECULES
Supaksorn Chattagul
Other (Walter Reed Army Institute Of Research)

14. APPLICABILITY OF THE LOCALLY DEVELOPED QUASR-LAMP ASSAY TO DETECT ENTERIC HUMAN ADENOVIRUSES IN WATER ENVIRONMENTS FOR SURVEILLANCE
Joy Ann Santos
Other (Natural Sciences Research Institute, University of the Philippines Diliman)

15. Targeted Sequencing Solution for DENV Virus Genome Surveillance
Cavin Ker
Other (MGI Tech)

16. AN EVALUATION OF ANTIMALARIAL RESISTANCE MARKERS OF RETROSPECTIVE MALARIA SAMPLES COLLECTED DURING 1998-2001 IN THAILAND BY TaqMan Array Card (TAC)
Sasikanya Thaloengsok
Other (AFRIMS)

17. SUBCLINICAL MALARIA AND ANEMIA AMONG RURAL PREGNANT WOMEN: A COMMUNITY-BASED LONGITUDINAL STUDY IN MYANMAR
Poe Poe Aung
Other (Maastricht University, Netherlands)

18. DETECTION OF SUB-PATENT MALARIA INFECTIONS AMONG FEBRILE MIGRATORY POPULATION: A STRATEGY TO ACCELERATE EFFORTS TOWARDS MALARIA ELIMINATION
Abhishek Mewara
Other (Department of Medical Parasitology, Postgraduate Institute of Medical Education and Research (PGIMER), Chandigarh, India)

19. Climate zones are a key component of the heterogeneous presentation of malaria and should be added as a malariometric for the planning of malaria elimination
Rajit Mullick
Other (ICMR-National Institute of Malaria Research)

20. First year Evaluation of Long Term Sub-District Dengue Management activity in Thailand (2022-2024)
Apinya Prapawicha
Other (Division of Vector Borne Diseases, Department of Disease control, Ministry of Public Health,Thailand)

21. MAPPING MALARIA TRANSMISSION FOCI IN NORTHEAST THAILAND FROM 2011-2021: APPROACHING ELIMINATION IN A HYPOENDEMIC AREA
Kulchada Pongsoipetch
Other (Mahidol Oxford Tropical Medicine Research Unit)

22. Asymptomatic Malaria and its Treatment Effectiveness in Gia Lai and Phu Yen Provinces of Vietnam for the Malaria Elimination Roadmap
Marina Chavchich
Other (ADFMIDI)

23. Resurgence of malaria in Thailand-Myanmar border
Aung Myint Thu
Other (Mahidol Oxford Research Unit)

24. ENCHANCING ONE HEALTH PROGRAM: SURVEILLANCE OF ZOONOTIC INFLUENZA VIRUSES IN ANIMAL AND HUMAN IN THAILAND
Arasa Suttana
Other (Armed Force Research Institute of Medical Sciences)

25. STR polymorphism in the promoter region of Cyclophilin 19B drives its transcriptional upregulation contributing to drug resistance in Plasmodium falciparum
Michal Kucharski
Other (School of Biological Sciences, Nanyang Technological University, Singapore / Division of Global Health, Academic Medical Centers, University of Amsterdam, Amsterdam, The Netherlands)

26. EXPLORING PROGNOSTIC BIOMARKERS FOR PULMONARY EDEMA IN SEVERE FALCIPARUM MALARIA
Haruhiko Ishioka
Other (Division of Infectious Diseases, Jichi Medical University)

27. Molecular biomarker identification in seasonal cardiovascular comorbid diseases (SCCD) using network metanalysis
Apoorv Gupta
Other (Amity Institute of Pharmacy, Amity University, Manesar, Haryana)

28. INFECTION OF IMMUNOSUPPRESSED RHESUS MACAQUES WITH ATTENUATED CHIKUNGUNYA VIRUS STRAIN 181/CLONE 25
Piyanate Sunyakumthorn
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Somchai Pinlaor
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Other (Centre for Medical Laboratory Technology Studies, Faculty of Health Sciences, Puncak Alam Campus, Universiti Teknologi MARA, Bandar Puncak Alam 42300, Malaysia)

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Azlin Muhammad
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Wallop Pakdee
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Pavadee Chuaicharoen
Faculty of Tropical Medicine, Mahidol University (Tropical Hygiene)

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Ruchuorn Wongpirom
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Punyisa Asawapaithulsert
Faculty of Tropical Medicine, Mahidol University (Clinical Tropical Medicine)

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Thitipong Hongsuwong
Other (Mahidol Oxford Tropical Medicine Research Unit)

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Noppadon Tangpukdee
Faculty of Tropical Medicine, Mahidol University (Clinical Tropical Medicine)

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Songpol Eiamsam-Ang
Faculty of Tropical Medicine, Mahidol University (Medical Entomology)

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Punyavee Srikirin
Other (Bamrasnaradura Infectious Disease Institute)

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Tipawan Ammarit
Faculty of Tropical Medicine, Mahidol University (Medical Entomology)

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Tassapon Kertsook
Other (Armed Forces Research Institute of Medical Sciences (AFRIMS))

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Worawaran Kallayanasit
Other (Department of disease control)

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Cindy Agitha Batti
Other (Department of Child Health, Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada/Dr Sardjito General Hospital, Yogyakarta)

63. INCIDENCE AND RISK FACTORS OF FATTY LIVER IN HUMAN IMMUNODEFICIENCY VIRUS PATIENTS ON ANTIRETROVIRAL TREATMENT
Daniel Aditya
Other (Faculty of Medicine, Sam Ratulangi University, Manado)

64. PREVALENCE AND ANTIMICROBIAL SUSCEPTIBILITY OF NEISSERIA GONORRHOEAE AND CHLAMYDIA TRACHOMATIS AMONG HIGH-RISK PEOPLE IN PATTAYA, THAILAND
Dutsadee Peerapongpaisarn
Other (USAMD-AFRIMS)

65. Mitigating Malaria Resurgence: Enhancing Surveillance through Primary Health Care in Vulnerable Pha Phueng Sub-Village
Sataphorn Rodkum
Faculty of Tropical Medicine, Mahidol University (Mahidol Vivax Research Unit (MVRU))

66. Changing mosquito vector population structure during construction of Mae Sot Reservoir
Panuwat Youndkome
Faculty of Tropical Medicine, Mahidol University (Mahidol Vivax Research Unit (MVRU))

67. Malaria Resurgence in Phop Phra Noi Village: Risk Factors and Strategies beyond 1-3-7
Banchong Bokkaew
Other ()

Abstract No.: ABS0002008

REINTEGRATING PARAGONIMIASIS WITH TUBERCULOSIS SURVEILLANCE IN CO-ENDEMIC AREAS IN THE TIME OF GENEXPERT

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Introduction. Paragonimiasis, a foodborne trematode infection acquired through consumption of raw or undercooked crustaceans, may often be misdiagnosed as pulmonary tuberculosis (TB) in co-endemic areas due to their similar signs and symptoms. An integrated TB-paragonimiasis surveillance protocol was developed with smear microscopy as the recommended screening tool for both. However, with the increasing use of GeneXpert in TB screening, missed or delayed diagnosis of paragonimiasis or co-infection may lead to insufficient or delayed treatment. This study aimed to revisit, modify, and test the integrated TB-paragonimiasis surveillance protocol with GeneXpert as the recommended diagnostic tool for TB.

Methods. The existing protocol was modified based on current global and national guidelines on the diagnosis of TB and paragonimiasis. Sputum specimens from symptomatic patients were processed and examined using smear microscopy and GeneXpert. Testing of the proposed surveillance protocol was conducted in known endemic communities in combination with capacity building and active surveillance activities.

Results. TB and paragonimiasis were found to be co-endemic with considerably high prevalence in the selected barangays (villages), with 1 case of co-infection detected. Among symptomatic GeneXpert-negative cases, 12.8% (6 out of 47) were found to have paragonimiasis using smear microscopy by either Ziehl-Neelsen or NaOH (sodium hydroxide) concentration techniques.

Conclusions. Re-integrating smear microscopy with GeneXpert is recommended to avoid missed or delayed diagnosis of paragonimiasis in co-endemic areas. Continued capacity building of medical technologists using the proposed surveillance protocol is also recommended to enhance case finding and treatment for both TB and paragonimiasis.

Keywords: foodborne trematode infection, neglected tropical disease, paragonimiasis, pulmonary tuberculosis, surveillance

Abstract No.: ABS0002028

TETANUS IN CHILD WITH DENTAL CARIES INFECTION: A CASE REPORT

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Introduction: Although the incidence of tetanus has been declining over the past two decades due to immunization programs, it remains a health problem in developing countries.

Method: Case report study.

Results: A 6 years 5-month-old boy resident in Yogyakarta, was admitted to our hospital on July 2023 with tetanus. The patient had experienced a slight fever and general malaise for one week before developing muscle tightness. The patient thereafter experienced trouble opening the mouth and dysphagia. He was sent to a district hospital, and because his spasms weren\'t getting better, he was sent to our hospital. At that time of presentation, he was alert but showed signs of trismus and muscle rigidity. Together with the lack of immunization and dental caries, this led to the suspicion of a generalized tetanus infection. After sedation, passive immunization, and continuation of antimicrobial treatment, he was transferred to a pediatric intensive care unit (PICU) for further treatment. He continued to experience paroxysmal muscle spasms throughout his time in the PICU. Patient being admitted, he was successfully weaned off of sedatives five days later, at which point he was moved to the ward. The condition fully recuperating, then the patient was discharged with arrangements made for outpatient dentistry and catch-up immunization care.

Conclusion: Tetanus infection remains to occur in developing countries. Tetanus should always be considered in non-immunized patients with an acute onset of dysphagia and muscle rigidity together with the risk factor of dental caries.

Keywords: Tetanus, dental caries, non-immunized, children

Abstract No.: ABS0002034

EVALUATION OF BOOSTING ALGORITHM MODELS TO PREDICT ANTIMICROBIAL RESISTANCE IN *Escherichia coli*

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Boosting is an algorithm used in predictive modelling to reduce errors and improve performance. In this study, two boosting algorithm models: Adaptive Boosting (AB) and Extreme Gradient Boosting (XGB) were used to predict antimicrobial susceptibility results of *Escherichia coli*. Six antibiotics, namely ampicillin, ciprofloxacin, nalidixic acid, trimethoprim-sulfamethoxazole, streptomycin and tetracycline were utilized. To construct the models, meta-data *E. coli* isolates were retrieved from the NCBI database and *E. coli* isolates from urban gardens in Quezon City, Philippines were used as experimental data. The FASTQ files were aligned to the NCBI Reference Gene Catalog using DIAMOND, an accelerated version of BLASTX to detect antimicrobial resistance genes (ARGs). The models were built using R Studio with corresponding predictive modelling packages. Variables for construction of the models included their antibiogram profiles and ARGs. Area Under the ROC Curve (AUC) score was used as an evaluation parameter for the performance of the models. Results showed that AB models have slightly higher performance than XGB models, with AUC of 0.95 in ciprofloxacin, 0.90 in nalidixic acid, 0.98 in streptomycin, and 0.94 in trimethoprim-sulfamethoxazole. XGB showed more potential in ampicillin and tetracycline. Models showed satisfactory results when applied to experimental data. In conclusion, boosting algorithms helps the models to have greater accuracy, thereby allowing ease of predicting antimicrobial resistance.

Keywords: adaptive boosting, antimicrobial resistance, boosting algorithm, *Escherichia coli*, extreme gradient boosting, predictive modelling

Abstract No.: ABS0002059

A FOUR-YEARS SURVEY OF ANTIMICROBIAL RESISTANT ESKAPEE PATHOGENS ISOLATED IN A TERTIARY REFERRAL MEDICAL CENTER IN CHONBURI, THAILAND

Wilawan Oransathit

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Introduction: The prevalence of antimicrobial resistance in ESKAPEE pathogens continues to grow and is spreading rapidly throughout the regions of the world. In this study, we determined the distribution of ESKAPEE pathogens and their antimicrobial resistant patterns over four year in the Queen Sirikit Naval Hospital in Chonburi, Thailand.

Methods: ESKAPEE pathogens isolated from patients were phenotypically characterized and tested antimicrobial susceptibility using the BD Phoenix™ M50 automated microbiology system.

Results: A total of 1,537 ESKAPEE pathogens were isolated from clinical specimens between September 2019 and June 2023. Overall, 76.3% of isolates were found to be multi-drug resistant (MDR) and 18.7% were extensively drug resistant (XDR). Among the 1,173 MDR isolates, E. coli was the most frequent microorganism (43.5%), followed by A. baumannii (24%), K. pneumoniae (18.2%), P. aeruginosa (11%), E. cloacae (1.5%), S. aureus (1.2%), and Enterococcus spp. (0.6%). In addition, A. baumannii (53.7%) and P. aeruginosa (30.3%) were the predominant XDR pathogens, while K. pneumoniae (63%) was the most frequent pathogen exhibiting colistin resistance. Almost one-third (31.1%) of S. aureus isolates were found to be methicillin resistant. Among the ESKAPEE isolates, 46.7%, 38.8%, and 1.2% were identified as carbapenemase, extended-spectrumbeta-lactamases (ESBL), both carbapenemase and ESBL producers, respectively.

Conclusion: Our data demonstrated that carbapenem and colistin resistant ESKAPEE isolates remains a major concern associated with hospital-acquired infection in healthcare settings in Thailand. Our findings contribute to the awareness of emerging antimicrobial resistance and emphasize the need of controlling the spread of those MDR isolates in this country.

Keywords: Antimicrobial resistance, ESKAPEE, multi-drug resistance (MDR), extensively drug resistance (XDR), colistin

Abstract No.: ABS0002070

DISTRIBUTION OF ANTIMICROBIAL RESISTANT ESKAPEE PATHOGENS ASSOCIATED WITH HOSPITAL-ACQUIRED INFECTIONS IN BATTAMBANG, CAMBODIA

Wirote Oransathid

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Introduction: ESKAPEE pathogens pose a health risk due to the emergence of multidrug-resistance, particularly in low-income countries. This study, we determined prevalence and antimicrobial resistance of ESKAPEE pathogens in Cambodia.

Methods: During November 2019-April 2023, ESKAPEE (n=1,713) were isolated from various clinical specimens among patients attending the Battambang Refferal Hospital, Cambodia. The BD Phoenix™ M50 automated system was used to identify bacterial species and test antimicrobial susceptibility.

Results: The results showed that a majority of ESKAPEE were from pus (1034/1,173, 60%). Of all isolates, E. coli (43.7%) and S. aureus (32.6%) were the two main predominant microorganisms, followed by K. pneumoniae (10.9%), P. aeruginosa (5.3%), Enterococcus spp. (3.4%), A. baumannii (2.4%), and E. cloacae (1.7%). E. coli showed high rate of ESBL producers (60%; 449/748), but low rate of colistin resistance (0.8%; 6/748) and carbapenemase producers (3.9%; 29/748). Notably, ESBL producing E. coli were highly resistant to the third- and fourth-generation cephalosporins ceftriaxone (98.9%), cefepime (82%), and ceftazidime (48.1%), and a large percentage were co-resistant to all three drugs (47.4%). For S. aureus, 40.3% (225/558) were methicillin-resistant (MRSA). Among the MRSA isolates, 89.8% (202/225) was found to have methicillin resistance mediated by mecA, but vancomycin resistance was not observed. There are increasing trends of MRSA and cabapenem-resistant E. coli over time.

Conclusion: Our findings demonstrate high antibiotic resistance rates in hospital-acquired ESKAPEE infections in Cambodia, as a representative low-income country in Southeast Asia. This crucial data highlights the need to strengthen local surveillance and antibiotic stewardship interventions in healthcare systems.

Keywords ESKAPEE, E. coli, ESBL, methicillin-resistant S. aureus (MRSA), Cambodia

Abstract No.: ABS0002090

BlaOXA-48 VARIATION AMONG CARBAPENEM-RESISTANT ENTEROBACTERALES ISOLATED FROM PRAPOKKLAO HOSPITAL, CHANTHABURI PROVINCE, THAILAND

Witawat Tunyong

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Introduction: The global spread of carbapenem-resistant *Enterobacterales* is one of the most severe threats to human health and serious infections resulting in an increased mortality rate in healthcare facilities globally. The presence of Carbapenemase enzymes alongside other resistance mechanisms controlled by blaOXA-48-like can confers high levels of carbapenem resistance among the agents. This study aimed to investigate the prevalence of Carbapenemase-producing strains and blaoxa-48 variation among CRE isolated from Prapokklao Hospital, Chanthaburi Province, Thailand during 2016-2017.

Methods: Carbapenem resistant *Enterobacterales* were recovered from stock and reconfirmed species by conventional technique. Multidrug-resistant (MDR) bacteria were determined by the disc diffusion method and minimum inhibitory concentration (MIC) test strips. The Carbapenemase production was determined by using the modified carbapenem inactivation method and the modified Hodge test. The bla_{OXA}-48 gene was detected by PCR and confirmed by Sanger sequencing.

Results: A representative of 123 CRE isolates were included in this study. Investigation of carbapenemase production by phenotypic tests and determination of carbapenem MICs. Of the 123 isolates, 118 (95.93%) were modified Hodge test (MHT)-positive, and 94 (76.42%) were modified carbapenem inactivation method (mCIM)-positive. Carbapenem MICs interpreted using CLSI criteria presented resistance to ertapenem and meropenem in 97.7% and 83.1%, respectively.

Conclusion: The results of this study provide evidence of the Carbapenemase-producing phenotype and genetic mutation of OXA-48-like-ß-lactamase among the CRE isolates which have reported. Effective control measures and active surveillance of drug resistance in nosocomial pathogens are crucial for controlling diseases associated with difficult-to-treat bacteria.

Keywords: Carbapenem-Resistant Enterobacterales; Carbapenemase; mCIM; *bla*$_{\text{OXA-48}}$ variation

Abstract No.: ABS0002093

ANTIMICROBIAL RESISTANCE PROFILE OF Escherichia coli ISOLATED FROM RAW CHICKEN MEAT IN A SELECTED WET MARKET IN MANILA CITY, PHILIPPINES

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Background: In the Philippines, drug-resistant *E. coli* have been isolated from common food animals, increasing the risk of cross-contamination between humans, animals, and the environment. However, there is a lack of data on the distribution in chicken meat in public wet markets. This study aims to describe the AMR profile of *E. coli* in raw chicken meat from retail stalls in a selected wet market in Manila City.

Methods: This quantitative descriptive study characterized the AMR profile of *E. coli* isolated from 25 raw chicken meat samples from a wet market in Manila City. Antimicrobial susceptibility was determined through disk diffusion method against 23 antimicrobial agents in 16 antimicrobial classes. MDR E. coli were identified based on the resistance patterns. ESBL- and carbapenemase-producing capacities of the bacteria were tested through double disk synergy test and modified carbapenem inactivation method, respectively.

Results: Twenty-four out of 25 (96%) chicken samples contained E. coli isolates. Of these, 23 (96%) were classified as MDR. High resistance rates were observed against ampicillin (92%), tetracycline (88%), trimethoprim-sulfamethoxazole (83%), chloramphenicol (79%), ampicillin-sulbactam (75%), amoxicillin-clavulanic acid (67%), fosfomycin (67%), and streptomycin (54%).

Conclusion: The high rates of AMR E. coli isolated in isolated in this study suggest that chickens in wet markets can potentially serve as reservoir hosts for drug resistant genes which could transfer to other bacteria and contaminate, animals and the environment within the food and supply chain. These findings emphasize the need for AMR surveillance and strategies to combat AMR in the Philippines through the One Health approach.

Keywords: Antimicrobial resistance, *E. coli*, One Health Approach

Abstract No.: ABS0002036

Application of LAMP Methods for Detecting Malaria Parasite DNA in RDT-Negative Blood Samples in Lao PDR

Kanako Komaki-Yasuda

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Introduction: Within Laos, the prevalence of low-density parasite infections with *Plasmodium falciparum* (Pf) and *P. vivax* (Pv) has been reported. This study endeavors to assess the performance of parasite detection using the loop-mediated isothermal amplification (LAMP) method among patients tested negative by rapid diagnostic tests (RDTs) in Laos.

Method: Dried blood samples were collected from individuals presenting symptoms such as fever who sought medical assistance in Sekong prefecture, Laos, in 2017. A total of 750 RDT-negative samples were randomly selected, and subsequently, the parasite DNA was extracted using the PURE method (EIKEN). LAMP was performed using three different kits from EIKEN: *Plasmodium spp*. (Pan)-LAMP, Pf-LAMP, and Pv-LAMP and then turbidity was measured. The Polymerase Chain Reaction (PCR) tests were also conducted to confirm the presence of Pf and Pv DNA.

Results: The Pf-LAMP outcomes exhibited negativity across all 750 samples. Among these, 26 samples were both Pan-LAMP(+)and Pv-LAMP(+), of which 23 were identified as Pv-positive and three as negative by PCR. One sample was Pan-LAMP(-) but Pv-LAMP(+), aligning with negative PCR. Six samples were Pan-LAMP(+) and Pv-LAMP(-), with negative PCR. The remaining 717 samples were Pan-LAMP(-) and Pv-LAMP(-), of which 57 were arbitrarily selected and tested by PCR to show negative results.

Conclusion: The study underscored higher sensitive results of LAMP than those of PCR and consequently highlighted the prospective capacity of LAMP in detecting low-density Pv parasite carriers with negative RDTs. The study's findings suggest the need for a potential shift towards integrating LAMP-based detection strategies alongside conventional diagnostic methods.

Keywords: malaria, low-density parasite carriers, RDT, LAMP, *Plasmodium vivax,* Laos

Abstract No.: ABS0002077

PERFORMANCE EVALUATION OF AUTOMATED HEMATOLOGY ANALYZER XN-31 PROTOTYPE FOR MALARIA PARASITES DETECTION AT MAHIDOL UNIVERSITY\'S OUTPATIENT CLINIC IN BANGKOK, THAILAND

Miki Kawaguchi

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Introduction: The objective of this study is to demonstrate the efficacy of Automated Hematology Analyzer XN-31 prototype (XN-31p) in detecting malaria parasites in clinical settings in Thailand, where there is a high prevalence of Plasmodium (P.) falciparum and P. vivax. Using the flowcytometry principle, XN-31p analyzes whole blood samples without pretreatment and provides a complete blood count (CBC), the number and rate of “malaria-infected red blood cells (MI-RBC)” and identification of Plasmodium species in about one minute.

Method: A cohort of 350 patients with suspected malaria infections was enrolled at the Hospital for Tropical Medicine, Mahidol University, Bangkok, spanning from November 2019 to June 2022. The performance of XN-31p was assessed against established diagnostic methods including microscopy, rapid diagnostic tests (RDTs) and PCR assays.

Result: Comparative analysis with microscopy and PCR demonstrated that XN-31p exhibited sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) all surpassing 96.0%. In contrast, when evaluated against RDTs, XN-31p showcased comparable sensitivity (96.5%) and NPV (98.1%), albeit with slightly lower specificity (93.3%) and PPV (88.0%). The concordance of Plasmodium species identification between XN-31p and PCR or microscopy was 95.7%, while agreement between XN-31p and RDTs was 87.1%.

Conclusion: The findings from this study underscore the parity in performance between XN-31p, microscopy and PCR. In fact, XN-31 outperformed RDTs, offering potential as a valuable aid for rapid and accurate malaria diagnosis within Thai clinical settings. These results imply a pivotal role for XN-31p in the broader global campaign for malaria elimination.

Keywords: Malaria, Automated Hematology Analyzer XN-31 prototype, Diagnosis, Plasmodium falciparum, Plasmodium vivax

Abstract No.: ABS0002107

DEVELOPMENT OF RAPID MOLECULAR DIAGNOSTICS FOR GLUCOSE-6-PHOSPHATE DEHYDROGENASE DEFICIENCY

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Introduction: Glucose-6-phosphate dehydrogenase (G6PD) deficiency is the most common enzymopathy worldwide, caused by inherited mutations in the *G6PD* gene. This disorder may lead to hemolytic anemia triggered by exogenous agents, such as 8-aminoquinolines utilized for *Plasmodium vivax* radical cure. Thus, G6PD deficiency diagnosis is critical to avoid drug-induced hemolysis. Recently, growing evidence supports the integration of genetic testing with phenotyping in the accurate assessment of G6PD deficiency status. Recombinase polymerase amplification (RPA) is an emerging technique for point-of-care genotyping, which allows allelic discrimination at constant temperature within a short detection period. The study aimed to develop RPA towards the detection of four common *G6PD* variants in Thailand: *G6PD* Viangchan, *G6PD* Mahidol, *G6PD* Canton, and *G6PD* Gaohe.

Methods: Primers were designed and screened to determine the pair displaying high discrimination between each variant and the wild-type. Probes were also constructed to enable lateral flow dipstick detection. The method was developed such that a single control line will indicate the absence of the *G6PD* mutation and the presence of both test and control lines will confirm the detection of the *G6PD* mutation. The assay was validated using DNA samples containing the corresponding mutations.

Results and Conclusion: RPA was able to discriminate between each *G6PD* variant and wild-type, as visualized on lateral flow dipsticks.

Keywords: G6PD deficiency, molecular diagnostics, recombinase polymerase amplification

Abstract No.: ABS0002122

COSTS AND HEALTH OUTCOMES OF A NEW RAPID TEST FOR MELIOIDOSIS IN THAILAND

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Introduction: Melioidosis is a deadly bacterial infection prevalent in South-East Asia. Bacterial culture tests have poor sensitivity (60%) and take 2-4 days. A novel rapid test, hemolysin co-regulated protein 1- immunochromatography (Hcp1-ICT), with 88.3% sensitivity and 91.8% specificity, was introduced at a secondary hospital. Outcomes including use of melioidosis treatment (i.e. ceftazidime or meropenem) on the first day of admission, length of stay (LOS), survival, and costs were compared when using culture and Hcp1-ICT with culture in Thailand.

Methods: Non-randomized clinical trials with pre (2019-2020)-post (2020-2022) design provided the sample with suspected symptoms of melioidosis at Mukdahan hospital. Costs of diagnostic tools, antimicrobial agents, and hospitalization stay were included. Changes in the outcomes were evaluated by multiple regression models, adjusted for diabetes and symptom onset.

Results: The culture group (N = 94) and the Hcp1-ICT with culture group (N = 140) did not differ in the number of patients with diabetes and onset of symptoms at baseline. Hcp1-ICT might indicate the trend in increasing use of melioidosis treatment toward melioidosis patients by 6% (92.3% vs. 86.1%; p = 0.45) although not statistically significant. Hcp1-ICT may reduce total costs by 4,012.83 baht (USD 112.12) (p = 0.09) and lower LOS by 2.6 days (p = 0.054). However, it may not benefit survival (84% vs. 94%; p = 0.25).

Conclusions: Hcp1-ICT may help reduce direct medical costs and LOS among suspected melioidosis patients at a secondary hospital; however, further analysis at a primary care setting is warranted to evaluate benefits such as survival.

Keywords: melioidosis, rapid tests, diagnosis, costs, clinical outcomes, Thailand

Abstract No.: ABS0002126

DETECTION OF THE V1016G MUTATION IN THE VOLTAGE-GATED SODIUM CHANNEL GENE OF AEDES AEGYPTI IN DENGUE-RISK AREAS IN THAILAND BY ALLELE-SPECIFIC REAL-TIME PCR ASSAY

Jakkrawarn Chompoosri

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Introduction: Resistance to pyrethroid insecticides in Aedes aegypti, the principal vector of dengue, is reported across Thailand. A point mutation at position 1016 in domain II, segment 6 of the VGSC gene in Ae. aegypti leads to a valine-to-glycine substitution (V1016G) that confers resistance to pyrethroids. This study aimed to detect the V1016G mutation in VGSC gene in Ae. aegypti in dengue-risk areas in Thailand by allele-specific real-time PCR assay.

Methods: Six study areas located in Chanthaburi, Chumphon, Kanchanaburi, Nakhon Ratchasima, Nakhon Pathom, and Phitsanulok provinces, were chosen for the collection of Ae. aegypti in July and August 2023 based on the dengue case report between 2018 and 2022 and the report of insecticide resistance in Ae. aegypti. The mosquito larvae were collected by droppers in 15-30% of the total households per study area. Thirty F0 Ae. aegypti females from each province were extracted for genomic DNA and then subjected to allele-specific real-time PCR assay to detect the V1016G **mutation.**

Results: The results revealed that only the heterozygous genotype (V/G) was detected in the F0 Ae. aegypti females from all six study provinces. The frequencies of V1016G mutation obtained from the mosquitoes in Nakhon Ratchasima, Kanchanaburi, Nakhon Pathom, Phitsanulok, Chumphon, and Chanthaburi provinces were (3/30), 0.17 (5/30), 0.2 (6/30), 0.27 (8/30), 0.27 (8/30), and 0.3 (9/30), respectively.

Conclusions: In conclusion, the V1016G mutation in VGSC gene was indeed detected in Ae. aegypti in dengue-risk areas in Thailand by allele-specific real-time PCR assay. It causes a critical failure in vector control by pyrethroids.

Keywords: V1016G mutation, VGSC gene, Aedes aegypti, dengue-risk areas, allele-specific real-time PCR assay

Abstract No.: ABS0002127

A HIGH-THROUGHPUT CELL-BASED SCREEN FOR THE DISCOVERY OF NOVEL PAN-FLAVIVIRUS SMALL MOLECULES

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Introduction: Arthropod-borne flaviviruses are significant human pathogens and include viruses such as dengue virus (DENV), yellow fever virus (YFV), and Zika virus (ZIKV). No approved therapeutics drug against flaviviruses are currently available and the effective vaccines coverage remain a challenge. To effectively combat emerging and re-emerging flaviviruses, innovative broad-spectrum antivirals are urgently needed.

Methods: To identify pan-flavivirus inhibitors, two strategies of target-based and a phenotypic screen were employed simultaneously. NGI-1 and 35 analogs synthesized in-house were selected as target-based screen. Additionally, two small molecule libraries (11,200 total compounds) were selected for use in a phenotypic screen. Furthermore, an in silico artificial neural network was performed to virtually screen >30,000 compounds where the highest ranked predicted compounds were selected for evaluation. Using an in vitro cell-based assay with robotic liquid handling and high-content imaging, the antiviral activity of each drug was initially tested in a single-point screen. Hit compounds were subsequently evaluated using the MTT test to determine the CC50 and the EC50 against DENV serotypes 1-4, ZIKV, and YFV.

Results: DENV serotypes 1-4 were inhibited by NGI-1 parent with EC50 ranges of 0.70 to 4.39 µM and a CC50 >100 µM. With EC50 values ranging from 0.52 to 3.18 µM, three of the NGI-1 analogs were the most effective in reducing viral replication. To address undesired profiles, more optimization is being done.

Conclusion: NGI-1 and its effective analogs were identified inhibitors toward DENV serotypes. To find potential pan-flavivirus inhibitors, future research will evaluate these molecules and novel therapeutic candidates against flaviviruses.

Keywords: high-throughput screening, flavivirus, target-based screen, phenotypic screen

Abstract No.: ABS0002002

APPLICABILITY OF THE LOCALLY DEVELOPED QUASR-LAMP ASSAY TO DETECT ENTERIC HUMAN ADENOVIRUSES IN WATER ENVIRONMENTS FOR SURVEILLANCE

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The human adenovirus (HAdV) has shown greater environmental persistence, more water treatment resistance, and cause infection even at low concentrations. HAdV causes gastrointestinal illnesses and is abundant in various environmental. The detection of these pathogens calls for a more practical and affordable approach.

A recent technology based on the quenching of unincorporated amplification signal reporters (QUASR) was adapted for the detection of human adenoviruses. This technology allows for non-inhibitory, single-step DNA detection in a closed tube. The QUASR-LAMP assay was tested for its applicability to detect enteric HAdV in two areas where people gets exposed to contaminated water. A total of 203 water samples were collected and tested using both real-time PCR and QUASR-LAMP assays. Results showed a higher positivity rate of 78.82% (160/203) for QUASR-LAMP compared to qPCR with only 58.62% (119/203). The sensitivity and specificity rates for QUASR-LAMP were calculated at 86.55% and 32.14%, respectively when compared to PCR.

The specificity of the QUASR-LAMP assay was lower due to samples that were positive in PCR but negative in the assay. This characteristic does not diminish its utility as a valuable tool for detection. In fact, this attribute enhances its advantages in limited space and instrumentation requirements, making it suitable for rapid surveillance of important viruses. Its ability to discriminate a positive sample from a negative sample at a defined endpoint is very useful for laboratory technicians with limited molecular biology training and/or experience. The QUASR-LAMP platform has demonstrated its usefulness for surveillance of enteric adenoviruses in water sources.

Keywords: QUASR-LAMP, isothermal, human adenoviruses

Abstract No.: ABS0002183

Targeted Sequencing Solution for DENV Virus Genome Surveillance

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Introduction: Dengue infection is a significant public health concern, exacerbated by factors like international travel, urban expansion, and climate change, which contribute to increased DENV transmission. Massively parallel sequencing (MPS) offers an effective tool for monitoring DENV outbreaks. However, challenges remain in implementing MPS for DENV sequencing. Here, we have developed a targeted sequencing method utilizing the ATOPlex platform to comprehensively cover the genomes of DENV types 1-4, providing a solution for DENV virus genome surveillance.

Methods: We designed 423 amplicons for DENV1-4 using the ATOPlex platform and sequenced 10 clinical samples with known RT-qPCR results. Library preparation employed the ATOPlex kit, and sequencing was on the DNBSEQ-G99 platform (PE100). Data analysis utilized an adaptable MGI pipeline. Sample to report process were completed within 16hours.

Results: All 10 samples were successfully sequenced, with 9 samples identified as DENV1 and 1 sample as DENV2, consistent with RT-qPCR results. For the 9 DENV1 genomes, a consensus sequence yielded an average genome coverage of 96.5%±4.4% when compared to NC_001477.1, while the 1 DENV2 genome consensus achieved 97.3% genome coverage against NC_001474.2. The percentage of DENV reads count against spike-in reads count showed a strong correlation with the ct value ($R2=0.96$), demonstrating that ATOPlex can reliably relative quantify virus loads.

Conclusion: In conclusion, we present a comprehensive solution for the rapid capture of the full-length DENV genome. This approach allows for the simultaneous detection and quantification of DENV, serving as a valuable tool for monitoring emerging outbreaks and enhancing global public health control efforts.

Keywords: Dengue virus; Massively parallel sequencing

Abstract No.: ABS0002045

AN EVALUATION OF ANTIMALARIAL RESISTANCE MARKERS OF RETROSPECTIVE MALARIA SAMPLES COLLECTED DURING 1998-2001 IN THAILAND BY TaqMan Array Card (TAC)

Sasikanya Thaloengsok

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One of the obstacles faced by malaria elimination effort is the development of drug resistance by *P. falciparum* as a result of long term usage of the first-line of treatment. This study reports antimalarial resistance markers of retrospective samples collected during 1998-2001. The standard treatment for uncomplicated *P. falciparum* was mefloquine alone or in combination with sulfadoxine/pyrimethemine (S/P), but it was replaced by artesunate combination in a later year due to the increasing resistance to mefloquine. TaqMan Array Card (TAC) malaria panel was used to evaluate retrospective samples. A total of 696 samples were evaluated and all were confirmed to be malaria species. Mutation at positions N86Y, Y184F, and N1042D of PfMDR that confer mefloquine resistance were detected. More than 99% of the samples had a double mutation of PfDHFR while the majority of PfDHPS had multiple mutations, both of which are associated with resistance to S/P. Mutation of K13 at C580Y which confers resistance to artemisinin was not detected but Y493H and R539T mutations were detected at low level. In a separate surveillance (Chaisatit, 2021), a high prevalence of K13 mutation at C580Y (44.11%, 24/57) from Trat was detected. These results indicate that antimalarial resistance in *P. falciparum* evolves with the treatment as the constant use places a constant pressure on *P. falciparum* to develop drug resistance for survival. This indicates that a continuous surveillance of antimalarial resistance is essential for the tracking of resistant molecular markers which are important information for malaria control and elimination program.

Keywords: TaqMan Array Card (TAC), antimalarial resistance markers, *Plasmodium falciparum*

Abstract No.: ABS0002047

SUBCLINICAL MALARIA AND ANEMIA AMONG RURAL PREGNANT WOMEN: A COMMUNITY-BASED LONGITUDINAL STUDY IN MYANMAR

Poe Poe Aung

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Introduction: The prevalence of clinical malaria is 1-2 % among pregnant women in Myanmar. This study assessed the prevalence of subclinical malaria and helminth co-infections among pregnant women, and the adverse outcomes of pregnancy in the presence of infection.

Methods: A prospective longitudinal study was conducted in 12 villages in two townships in Myanmar between 2013 to 2015. A total of 752 pregnant women, with mean age of 27 years, were enrolled and followed up once a month, until six weeks after the delivery.

Results: About 84% of women were asymptomatic and 40% were primigravid at the time of enrolment. The prevalence of subclinical malaria as measured by nested PCR was 5.7% for either P. falciparum or P. vivax (2.7% P. falciparum only and 2.8% P. vivax only). Helminth infections were prevalent in 17% of women. The burden of anemia was high, with an overall prevalence of 37% with or without helminth infection. Eleven abnormal pregnancy outcomes (7 stillbirth, 2 premature, 2 twins) were identified. Poisson regression showed that women in their first trimester had a 2.9 times higher rate of subclinical malaria compared to women in the third trimester (p=0.019), women enrolled during the wet season were 2.5 times more likely to be malaria positive than women enrolled in the dry season (p=0.008), and the malaria positivity rate decreased by 5% when increased in one year of woman’s age (p=0.02).

Conclusions: The low prevalence of heterogenous subclinical malaria among pregnant women should not be neglected when targeting malaria elimination.

Keywords: subclinical malaria, pregnant women, anemia and co-infections, longitudinal study, Myanmar

Abstract No.: ABS0002052

DETECTION OF SUB-PATENT MALARIA INFECTIONS AMONG FEBRILE MIGRATORY POPULATION: A STRATEGY TO ACCELERATE EFFORTS TOWARDS MALARIA ELIMINATION

Abhishek Mewara

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Introduction: Imported malaria in migratory population is a threat to malaria elimination. Case Investigation (CI) with Reactive Active Case Detection strategy (RACD) is a widely used intervention in low transmission settings for the detection of malaria around the index cases. The aim of this study was to identify sub-patent malaria cases around index cases in Punjab state of India which has annual parasite index (API) ≤1 and qualifies for malaria elimination as per the National Framework for Malaria Elimination (NFME), 2016-2030.

Methods: CI with RACD was conducted among migratory population from April to October, 2022 in four districts of Punjab, India. All febrile patients were screened by peripheral blood smear (PBF) microscopy, rapid diagnostic test kits (RDT) and nested polymerase chain reaction (nPCR). G6PD activity was also determined in P. vivax positive patients.

Results: A total of 54 P. vivax migratory index cases were recorded. CI and RACD was initiated for 28 index cases. Through active surveillance, 168 finger prick samples were collected from febrile migratory population around the index cases, of which a total of eight active cases were detected by PBF microscopy, RDT and PCR. All had parasite density

Conclusions: The findings demonstrate the importance of RACD around index cases of migratory populations for early detection and treatment of sub-patent malaria in this population and to reduce the risk of transmission among the local population.

Keywords: Malaria, elimination, RACD, index case, migratory population

Abstract No.: ABS0002068

Climate zones are a key component of the heterogeneous presentation of malaria and should be added as a malariometric for the planning of malaria elimination

Rajit Mullick

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Introduction: Different climatic conditions affect the propagation of malaria vectors thereby influencing malaria incidence. The present study was undertaken to delineate malaria distribution across different climate types and sub-types in India and assess its significance

Methods: All Indian districts were classified into three major climatic zones (Tropical, Temperate and others(Arid, Cold, and Polar)based on the Köppen-Geiger climate classification system. The Annual Parasite Incidence(API) of malaria was analysed in these climatic zones using the Kruskal-Wallis test, and a post hoc comparison was done using the rank-sum test with an adjusted p-value for the level of significance. Further logistic regression was used to investigate the association of these climatic zones with high malaria incidence(i.e.,API>1).The majority of Indian districts fall in Temperate(N= 270/692(39.0%))andTropical(N=260/692(37.6%))regions,followedbyArid(N=140/692(20.2%)),Polar(N = 13/692(1.9%)) and Cold(N= 9/692(1.3%))regions. Arid, Pola, and Cold were similar in terms of malaria incidence over the years and thus were grouped into one.

Results: It was found that the tropical and temperate zones display a significantly higher burden of malaria as compared to others for the studied years(2016–2021).Future projections suggest a significant expansion of tropical monsoon climate towards central and northern India ,along with a growing footprint of tropical wet savannah climate in the northeast of India by 2100, which could increase the risk of malaria transmission.

Conclusion: The heterogeneous climatic zones of India play an important role in malaria transmission and can be used as a malario-metric for the stratification of districts destined for malaria elimination.

Keywords: Malaria, India, Climate Change, Malaria Parasite, Rain, Temperate Regions,Tropical Regions, Summer

Abstract No.: ABS0002082

First year Evaluation of Long Term Sub-District Dengue Management activity in Thailand (2022-2024)

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Introduction: Dengue fever is the arbovirus borne epidemic in Thailand. Successful factors and gaps in Dengue management are important for improvement. The evaluation of long-term in sub-district level is the priority Dengue management system in the community.

Methods: The questionnaires were created based on 5 factors (surveillance, control, diagnosis and treatment, risk communication and networking) which are used for evaluation. The data were based on literature review from publications related to Dengue management and scoring methods. The evaluation surveys were approved by the project committee and public relations of regional government officers. The questionnaire was available for sub-districts who were interested. The dengue management program is from 2022 to 2024 and currently in 2022 the data collection of self-assessment was collected and divided into 4 levels (honorable mention, fair, good and very good). All the participants who took part in this study will receive their certificates after September 2023.

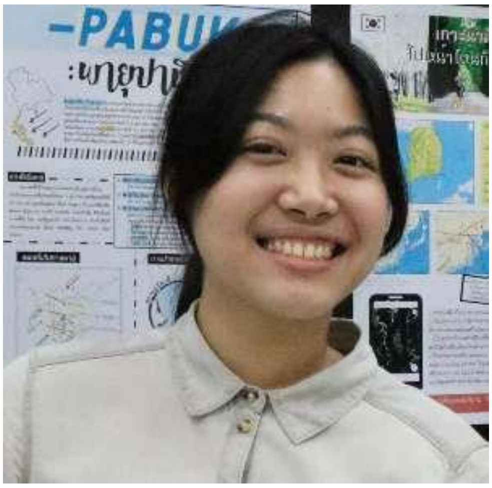
Results: One-hundred and nine sub-districts, 42 districts from 18 provinces participated. The results were 90, 10, 5 and 4 sub-districts had very good, good, fair and honorable mention levels respectively. The average scores of each section were 86.31, 86.21, 90.09, 82.71 and 85.20 respectively.

Conclusion: Most of the participants were high scores and lowest scores shown in the risk communication section. Technology is good support for reporting systems. The suggestions in this project are Covid-19 pandemic affects the Dengue management in communities and the lack of keeping some documents. However, the complete first year evaluation will include committee consideration.

Keywords: Dengue management, Dengue management evaluation, Dengue activity, Dengue management reward and Dengue sub-districts operation

Abstract No.: ABS0002083

MAPPING MALARIA TRANSMISSION FOCI IN NORTHEAST THAILAND FROM 2011-2021: APPROACHING ELIMINATION IN A HYPOENDEMIC AREA



Kulchada Pongsoipetch

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Introduction: Thailand is approaching local elimination in the eastern provinces, but there are persisting transmission hotspots in and around the forest. We used data from the malaria surveillance system to describe spatiotemporal trends of malaria in Northeast Thailand and fine-scale patterns in locally transmitted cases between 2011 and 2021.

Methods: Case data was stratified based on likely location of infection and parasite species. Annual Parasite Index (API) was calculated for different categories. Clusters of high and low API were identified using Getis-Ord Gi* statistic, and the stability of those hotspots compared by case type.

Results: The number of confirmed cases experienced a non-linear decline by 96.6%, from 1,061 in 2011 to 36 in 2021. The proportion of cases classified increased over the study period. There was a large outbreak in Ubon Ratchathani in 2014-2016 which had a high proportion of *P. falciparum*. There has been a decline in *P. vivax* and *P. falciparum* case numbers. There were stable hotspots of indigenous and imported cases in the south of Si Sa Ket and southeast of Ubon Ratchathani.

Conclusions: There has been a large, non-linear decline in the number of cases and an increasing proportion of cases are classed as indigenous to the patient's village of residence. Stable hotspots of transmission in the forested border areas were identified, with transmission likely persisting because of remote location and high-risk forest-going behaviours. Future efforts should include cross-border collaboration and continued targeting of high-risk behaviours to reduce the risk of imported cases seeding local transmission.

Keywords: Malaria, Surveillance, Thailand, Hotspot, Elimination

Abstract No.: ABS0002106

Asymptomatic Malaria and its Treatment Effectiveness in Gia Lai and Phu Yen Provinces of Vietnam for the Malaria Elimination Roadmap

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Introduction: Gaining an understanding of the prevalence, distribution and persistence of asymptomatic malaria, a hidden reservoir for malaria transmission, will help design intervention strategies to accelerate malaria elimination.

Methods: Between June 2022 and February 2023, we screened 1,200 asymptomatic people, residing in Krong Pa district, Gia Lai province and Song Hinh district, Phu Yen province in Central Vietnam. Of these, 400 people (cohort 1) were living in close proximity to the previous year's symptomatic malaria cases and 800 people (cohort 2) were close contacts of the recently diagnosed "index" symptomatic malaria cases. Finger prick blood samples were collected and parasites were detected by rapid diagnostic tests (RDTs), blood film microscopy and one-step RT-qPCR targeting 18S ribosomal RNA transcripts.

Results: All subjects were malaria negative by RDT and microscopy. Of the 1,200 subjects, 77 (6.4%, CI 95%: 5.2-7.9%) were positive for malaria parasites by RT-qPCR, with 73 (94.8%) cases infected with P. falciparum and four cases of unknown speciation. The prevalence of asymptomatic malaria in cohort 1 of 1.8% (CI 95% 0.9%-3.6%) was significantly lower (P

Conclusion: This information will inform the National Malaria Control and Elimination Programme of Vietnam on strategies to accelerate malaria elimination in Vietnam.

Keywords: Asymptomatic malaria, elimination, RT-qPCR detection

Abstract No.: ABS0002111

Resurgence of malaria in Thailand-Myanmar border

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In the Greater Mekong Subregion, malaria is aimed to be eliminated by 2030. However, a recent humanitarian crisis in Myanmar, along with the subsequent disruption of the healthcare system and mass population displacement, has led to an unprecedented increase in malaria cases within the country. In 2022 alone, over 36,688 malaria cases were diagnosed in 4 townships located in Kayin State Myanmar, which shares a lengthy border with the western part of Thailand. More than 90% of these cases were identified as P. vivax malaria. The border between the two regions is extensive, and porous, and experiences a significant amount of cross-border migration. Similarly, the number of malaria cases in the western Thai border province, Tak province surged by 602% from 1,089 cases in 2020 to 6,391 cases in 2022, thus posing a challenge to the regional malaria elimination efforts. This analysis aims to inform the spatial distribution and magnitude of the recent malaria resurgence along the Thai-Myanmar border.

Keywords: malaria, resurgence, thai-myanmar border

Abstract No.: ABS0002115

ENCHANCING ONE HEALTH PROGRAM: SURVEILLANCE OF ZOONOTIC INFLUENZA VIRUSES IN ANIMAL AND HUMAN IN THAILAND

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More than 60% of human emerging infectious diseases are zoonotic, causing a billion illnesses. A "One Health" approach is crucial to tackle these threats by considering human, animal, and environmental well-being. Pigs are important hosts for influenza A, and a new G4 EA H1N1 swine influenza virus in China raises global health concerns. Avian influenza virus also poses a persistent threat, with H5Nx lineages demonstrating zoonotic spread potential. Poor biosecurity in Southeast Asian backyard farms increases the risk of cross-species transmission.

Here we conducted a surveillance study of influenza A using a "One-Health" approach in backyard farms across border areas of Thailand. This study aims to assess the potential risk of an influenza pandemic originating from backyard animals.

The prevalence of influenza A virus in pig (478 samples), poultry (10 samples from chickens, ducks, and turkeys), and humans (52 samples) collected from 39 sites across 8 provinces was determined by serological (microneutralization assay) and molecular assays (qRT-PCR). Seropositivity of 55% (5 of 9) of Pig was detected on the farm in Mae-Ai, Chiangmai province, suggesting a history of influenza A exposure; however, the pig farmer tested negative for the influenza antibody. Influenza A was not detected in any environmental samples in this study. Understanding how pigs are exposed to influenza viruses is crucial for enhancing public health, improving disease surveillance, and implementing prevention measures.

Our surveillance program continues to expand, covering a wider range of areas across Thailand, and aiming to enhance the effectiveness and preparedness against this potential threat.

Keywords: One health, zoonosis, influenza virus, backyard farm, swine, poultry, animals

Abstract No.: ABS0002225

STR polymorphism in the promoter region of Cyclophilin 19B drives its transcriptional upregulation contributing to drug resistance in Plasmodium falciparum

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Introduction: The prevalence of artemisinin resistance in Plasmodium falciparum is now firmly established in Southeast Asia and gradually emerging in Sub-Saharan Africa. While nonsynonymous SNPs in the pfk13 Kelch-repeat propeller (KREP) domain are clearly associated with artemisinin resistance, their functional relevance requires cooperation with other genetic factors and alterations of the P. falciparum genome, collectively referred to as genetic background. Here we explored the potential contribution of these factors using cyclophilin 19B (PfCYP19B) as one of the examples.

Methods: We utilized transcriptome and genome analysis tools on samples from TRACI and TRACII trials to identify perturbations in the PfCYP19B promoter region in artemisinin-resistant parasites. Field-derived findings were validated in vitro using a laboratory model strain episomally expressing PfCYP19B.

Results: PfCYP19B overexpression contributes to resistance against both artemisinin and piperaquine. We showed that PfCYP19B acts as a negative regulator of the integrated stress response (ISR) pathway by modulating levels of phosphorylated eIF2α (eIF2α-P). Curiously, artemisinin and piperaquine affect eIF2α-P in an inverse direction that in both cases can be modulated by PfCYP19B towards resistance. The upregulation of PfCYP19B in drug-resistant parasites is sustained by a short tandem AT-rich repeat (SRT) sequence polymorphism in the gene's promoter region.

Conclusion: This study sheds light on the complex genetic traits contributing to artemisinin resistance, with PfCYP19B identified as a potential key player. The upregulation of PfCYP19B, influenced by a short tandem repeat sequence polymorphism in its promoter region, highlights the multifaceted nature of drug resistance mechanisms in malaria parasites.

Keyword: Artemisinin resistance, piperaquine resistance, Plasmodium falciparum, genetic background, pfk13, cyclophilin 19B, integrated stress response, eIF2α, short tandem repeat, promoter polymorphism.

Abstract No.: ABS0002062

EXPLORING PROGNOSTIC BIOMARKERS FOR PULMONARY EDEMA IN SEVERE FALCIPARUM MALARIA

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Introduction: Pulmonary edema is an unpredictable complication of severe malaria. Pro-inflammatory mediators are thought to play a central role in its pathogenesis.

Methods: An exploratory study was conducted to evaluate candidate biomarkers to predict the development of pulmonary edema in severe malaria in Bangladesh. We measured plasma concentrations of cytokines including interleukin-6, interleukin-8, tumor necrosing factor alpha, and soluble receptor of advanced glycation end-products, and the lung biomarkers, surfactant protein D, Clara cell 16, and KL-6. The correlation between biomarker concentrations and changes in SpO2/FiO2 ratio after admission were evaluated.

Results: A total of 106 patients with falciparum malaria were studied, of whom 56 had severe malaria, and 16 died. The plasma concentrations of four cytokines were higher in patients with severe malaria, compared to patients with uncomplicated malaria, but concentrations of lung biomarkers were not. In patients with severe malaria, SpO2/FiO2 ratio on admission was similar between survivors and patients with a fatal outcome (median [Interquartile range] 452 [448, 462] vs. 441 [423, 462]; P = .098), whereas there was a difference in the decline in SpO2/FiO2 ratio in the first 24 hours between the 2 groups (0 [-10, 10] vs. -203[-264, -10]; P = .002). None of the biomarkers were prognostic for the decline in SpO2/FiO2 ratio.

Conclusions: A decline in SpO2/FiO2 ratio is a strong indicator for pulmonary complications and death in adults with severe malaria and the SpO2/FiO2 ratio should be monitored. The development of pulmonary edema is not predicted by the assessed biomarkers.

Keywords: severe malaria; Plasmodium falciparum; pulmonary edema; cytokine; biomarker; prognostic factor

Abstract No.: ABS0002074

Molecular biomarker identification in seasonal cardiovascular comorbid diseases (SCCD) using network metanalysis

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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.

Keywords: Seasonal; Network-metalysis; Cardiovascular Diseases

Abstract No.: ABS0002110

INFECTION OF IMMUNOSUPPRESSED RHESUS MACAQUES WITH ATTENUATED CHIKUNGUNYA VIRUS STRAIN 181/CLONE 25

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Chikungunya is a mosquito-borne infection caused by Chikungunya virus (CHIKV), which is transmitted to humans by the bite of infected mosquitos. CHIKV induces a rapid-onset febrile disease characterized by fever, headache, lethargy, arthralgia, muscle pain, and rash. An attenuated form of CHIKV known as CHIKV 181/clone 25 was developed for human live vaccine production in 1986 using the CHIKV 15561 strain from Thailand. While it provided significant protection and high antibody titers in animal trials, it was withdrawn due to 8% of Phase II human trial volunteers experiencing transient arthralgia. This study examined CHIKV 181/25\'s impact on rhesus macaques immune suppressed with cyclophosphamide and dexamethasone. All monkeys displayed asymptomatic infection after being inoculated with 107 PFU of CHIKV 181/25, with no core temperature changes, joint swelling, or lymph node enlargement. There was no histopathologic evidence of joint inflammation. Blood cell counts remained stable post-infection. Viral RNA was detectable in circulation from day 1, with prolonged bacteremia in one immunosuppressed monkey. Anti-CHIKV IgM and IgG appeared by day 4, along with cellular immune responses during days 7 to 14 post-infection. Cytokine profiles differed between immunosuppressed and control groups. Viral RNA dissemination was found predominantly in lymph nodes and spleen with greater level in the immunosuppressed group. These results suggest that developing immunosuppressed models could serve as valuable tools for drug testing and vaccine development for CHIKV. However, it should be noted that symptomatic CHIKV illness may require longer immunosuppression treatment.

Keywords: Chikungunya, virus, immunosuppressed model, rhesus macaques, monkeys

Abstract No.: ABS0002124

Validation of cloning methodology for artemisinin resistant Plasmodium falciparum gametocyte-producing strains

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Artemisinin resistance in Plasmodium falciparum malaria parasite is a significant concern for strategic plans toward malaria elimination and global health. The ability to clone artemisinin-resistant strains, especially those producing gametocytes, is essential for research in its transmissibility, and resistance mechanisms, providing the transmission-blocking drug testing platform.

We set up a valid cloning and validation workflow in order to enhance the establishment of artemisinin-resistant P. falciparum gametocyte-producing strains. Using the modified limiting dilution method, four gametocyte-producing P. falciparum clinical isolates (wild-type, G449A, R539T and C580Y of Kelch13) from Thailand were successfully cloned. The clones of wild-type, G449A and R539T lines were further validated including the percentage of gametocytaemia (%G), exflagellation of male gametocytes (%Exf), artemisinin susceptibility and mosquito infectivity. Those parasites produce gametocytes consistently (3.583±0.771 %G, over 8 passages), and show 0.188±0.065 %Exf that could be used for the viability assay to test novel transmission-blocking drugs. Using Standard Membrane Feeding Assay (SMFA), those clones showed positive infectivity to Anopheles dirus. Whole genome sequencing data show that the parasites are singly clonal. The susceptibility to artemisinin resistance of cloned parasite strains was also observed over multiple passages (IC50 2.126±1.560 ng/mL).

The results of this study confirm the cloning methodology's effectiveness and reliability. This technique is useful for research focusing on malaria transmission, enhancing our ability to develop effective plans for malaria elimination.

Keywords: Plasmodium falciparum, Limiting Dilution Cloning, Gametocyte

Abstract No.: ABS0002175

Opisthorchiasis causes kidney injury through gut dysbiosis and increased proteins involved in leaky gut and inflammation in hamsters-fed high-fat/high-fructose diet

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Introduction: Opisthorchis viverrini (Ov) infection and consumption of high-fat and high-fructose (HFF) diets exacerbate liver and kidney disease. Here, we aimed to investigate the effects of a combination of O. viverrini infection and HFF diet on kidney pathology via changes in the gut microbiome and host proteome in hamsters.

Methods: Twenty animals were divided into four equal groups namely normal, HFF, Ov, and HFFOv groups. Fecal samples were extracted and the V3–V4 region of the 16S rRNA gene was sequenced on an Illumina Miseq sequencing platform. In addition, LC/MS-MS analysis was performed. Histopathological studies and biochemical assays were also conducted.

Results: The results indicated that the HFFOv group exhibited the most severe kidney injury, manifested by increased KIM-1 expression and accumulation of fibrosis in kidney tissue. The microbiome of the HFFOv group was more diverse than that of the HFF group: there were increased numbers of Ruminococaceae, Lachospiraceae, Desulfovibrionaceae and Akkermansiaceae, but fewer Eggerthellaceae. A total of 243 significant host proteomes were identified in all groups. Increased number of host proteins involved in leaky gut and inflammation were associated with the development of kidney disease. Among host proteins, TGF-beta, involved in fibrogenesis, was significantly increased in the HFFOv group.

Conclusion: The combination of HFF diet and O. viverrini infection promotes kidney injury through gut dysbiosis and increased proteins involved in leaky gut and inflammation that contribute to kidney abnormalities. This information could provide an effective strategy to prevent kidney disease.

Keywords: Opisthorchis viverrini, non-alcoholic fatty liver disease, chronic kidney disease, next generation sequencing, mass spectrophotometer

Abstract No.: ABS0002011

Effect of Isopropyl Β-D-1-Thiogalactopyranoside (IPTG) Concentration to Expression of Recombinant Protein From Sarcoptes scabiei Tropomyosin Gene

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Introduction: Scabies is a skin disease caused by infestation of the ectoparasite Sarcoptes scabiei mite, and it is grouped as neglected tropical disease with a high burden of disease in poor or developing countries. Currently there are no uniform diagnostic procedure for diagnosing scabies. This research optimizes the expression of recombinant protein from exon 5 tropomyosin gene of S. scabiei as a candidate antigen for scabies diagnostic test.

Methods: An exon with a length of 533 base pairs of the Sarcoptes scabiei tropomyosin gene was cloned using plasmid pLATE-51, a ligation-independent cloning vector. Overexpression was carried out using competent bacteria Eschericia coli BL21(DE3) incubated 20°C overnight (16 hours). Induction was carried out by adding isopropyl β-D-1-thiogalactopyranoside (IPTG) various concentration: 0.1, 0.5, 0.75, 1.0, and 2.0 mM. Analysis of the overexpression results was carried out using SDS-PAGE and nanodrop spectrophotometer at a wavelength of 280 nm to determine the concentration of the protein.

Results: The overexpression results analyzed by SDS-PAGE showed a thicker band on the pellet compared to the supernatant. Induction of overexpression using 0.1 mM of IPTG showed thickest band in SDS-PAGE electrophoresis. Total protein concentrations measured by nanodrop spectrophotometer showed highest concentration using 0.1 mM IPTG as induction agent, with concentration of 2.7 mg/ml and 30.94 mg/ml in supernatant and pellet respectively.

Conclusion: Protein overexpression with 0.1 mM IPTG induction resulted in highest total protein yield. Further confirmation with Western blot is needed to determine the approximate size of the resulting recombinant protein.

Keywords: Scabies, tropomyosin, protein overexpression

Abstract No.: ABS0002021

ASSESSING ACANTHAMOEBA CYTOTOXICITY: T4 AND T9 AS A PATHOGEN-RICH GENOTYPES

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Introduction: Free-living amoebae of the genus Acanthamoeba are causative agents of keratitis and amoebic encephalitis. The global distribution, amphizoic properties and the severity of the disease caused by Acanthamoeba motivate researchers to focus on the isolation of this parasite as well as demonstrating direct and indirect factors that could indicate a possible pathogenic potential. Therefore, this study was performed to characterize the pathogenic potential of Acanthamoeba isolated from recreational lakes in Peninsular Malaysia.

Methods: Thermo- and osmo-tolerance, the secretion of proteases and the effect of trophozoites over HaCaT cell monolayer were analyzed by different methodologies. Additionally, the in vitro cytopathogenicity of these isolates was assessed using the LDH-release assay.

Results: A total of eight Acanthamoeba isolates were classified as thermo- and osmo-tolerant and had presence of serine proteases with a molecular weight of 33–254 kDa. Acanthamoeba genotypes T4 and T9 showed the presence of serine-type proteases of 33 kDa and 133 kDa, respectively. Moreover, three Acanthamoeba T4 and one T9 achieved a cytopathic effect in the range of 41.8–82.5% (intermediate to high cytotoxicity level) when tested in HaCaT cell monolayer. Apart from that, the LDH release assay revealed that three T4 isolates (B4, K8 and SA10) and one T9 isolate (K1) showed higher toxicity (>40%) compared to other isolates.

Conclusion: The presence of Acanthamoeba T4 and T9 genotypes with significant pathogenic potential in samples such as those tested in this study reaffirms the need to reevaluate the role of other genotypes that have been previously considered as non-pathogenic.

Keywords: Acanthamoeba; cytopathic effect; HaCaT cells; pathogenic potential; protease

Abstract No.: ABS0002043

SELECTION OF KINASE INHIBITING SMALL MOLECULE, ALTIRATINIB, FOR THE ANTI-TOXOPLASMA DRUG OF BRAIN-CYST FORMING STRAIN IN VITRO

Howoo Nam

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Toxoplasma gondii has two forms of infection such as acute toxoplasmosis by tachyzoites and chronic one by bradyzoites to make brain-cyst. This study aims to select a drug against bradyzoite stage (Me49) of T. gondii, which is a reactivated form from the ruptured brain-cyst, among the 6 kinase-inhibiting small molecules confirmed already to block the growth of tachyzoite stage (RH) of T. gondii. Bradyzoites were obtained from the mouse brain cyst, cultured in ARPE19 cells, and treated with HER2/HER4 inhibitors Afatinib, Neratinib, VEGFR-2 inhibitors ACTB-1003, Regorafenib, and c-MET inhibitors Altratinib, Forentinib, respectively. Effect to the growth of T. gondii was analyzed by western blot and immunofluorescence. All the inhibitors were effective to block the growth of bradyzoite as well as to tachyzoite, Afatinib showed less effect and Neratinib enhanced more chronic form of bradyzoites. Changes in the host cell side were analyzed by cell viability, apoptosis, necroptosis, and autophagy with specific markers. Bradyzoite infection and drug treatments did not affect the survival of host cells significantly, whereas Afatinib enhanced the autophagy signals and ACTB-1003 and Neratinib affected the mitochondrial biosynthesis and mitophagy. Altiratinib was selected to exhibit anti-bradyzoite effect at the lowest concentration and minimize the impact on the host cells through Apoptosis/Necrosis assay. Altiratinib is selected as an effective small molecule in suppressing immunity and blocking the reactivation of brain-cyst in immunodeficiency patients not only in acute but also in bradyzoite.

Keywords: Toxoplasma gondii, brain-cyst, bradyzoite, Altiratinib, apoptosis, necroptosis, autophagy

Abstract No.: ABS0002046

IN VITRO HIGH-THROUGHPUT ASSAYS USING CRE-LOXP SYSTEM FOR EXAMINATION OF GENE MANIPULATION AND ANTI-ACANTHAMOEBA COMPOUNDS

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Introduction: The Acanthamoeba are causative agents for Acanthamoeba keratitis and granulomatous amoebic encephalitis. There is no single drug that shows uniformly effective and the available drugs have potential toxic side effects, non-specific and have pro-long treatment scheme. Insufficient resources were available for anti-parasitic drug discovery and therefore inexpensive and in vitro high-throughput assays to screen potential new drugs and existing compound libraries are essential. In this work, we described the development and validation of improved methods to evaluate anti-Acanthamoeba compounds in vitro using Acanthamoeba cell lines expressing the tomato fluorescent protein (tdTomato).

Materials and Methods: The tdTomato was introduced by gene replacement construct consists of loxP sequences on both sides of the neomycin resistance cassette flanked by UTR regions of the polyubiquitin gene to allow insertion by homologous recombination. Neo cassettes was removed by Cre recombinase expression. Homologous recombination of UTR region and deletion of neo sequence were established using PCR, and tdTomato expression was screened using a confocal microscope.

Results: The tdTomato gene was successfully integrated into Acanthamoeba genome and expression can be found in the cytosol of Acanthamoeba. Removal of neomycin-resistant gene by cre recombinase was also confirmed by PCR, demonstrating the expression of cre in Acanthamoeba and induced accurate recombination at two loxP sequences.

Conclusion: This is the first experimental demonstration of homologous recombination in Acanthamoeba and will be a valuable means for a generation of single or multiple mutants. This method should also be feasible broader and should construct higher-throughput screening programs for identifying potential treatment of Acanthamoeba infection.

Keywords: Acanthamoeba, Cre-loxP recombinase, Homologous recombination

Abstract No.: ABS0002058

URBAN PUBLIC PARKS AS HOTSPOTS FOR CHIGGER MITE INFESTATIONS AND POTENTIAL SCRUB TYPHUS TRANSMISSION

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Chigger mites are vectors of scrub typhus, an illness caused by the bacteria Orientia tsutsugamushi. The chigger mites occur naturally on various rodent species, and humans become infected when present in places where rodents are common and infected mites crawl onto and bite humans. In metropolitan areas, urban public parks could serve as locations where animals and humans come into contact, potentially leading to the transmission of zoonotic pathogens. However, an understanding of urban scrub typhus' ecological and epidemiological aspects in Thailand remains limited. We captured and assessed small mammals for chigger infestations in urban public parks throughout metropolitan Bangkok, Thailand. We found a notably high occurrence of infestations (76.8%), yet with unexpectedly low species diversity. Through morphological features and molecular confirmation, we identified two chigger species, namely Leptotrombidium deliense and Ascoschoengastia indica. The abundance of chigger infestations was explained by a generalized linear model which considered intrinsic host variables (such as body mass index), along with extrinsic factors such as host density, habitat composition, and open spaces. Polymerase Chain Reaction testing for O. tsutsugamushi bacteria using pooled chigger samples (90 samples) or the spleen samples of animal hosts (164 samples) were all negative. Nevertheless, the abundant presence of chigger vectors suggests a need for the Bangkok

Metropolitan Administration and public health authorities to establish a comprehensive strategy for monitoring and preventing scrub typhus in the parks and nearby communities.

Keywords: Chigger mites, urban parks, scrub typhus

Abstract No.: ABS0002076

LEVEL OF KNOWLEDGE AND ADHERENCE ON SCHISTOSOMIASIS CONTROL AND ELIMINATION PROGRAM OF THE SELECTED RESIDENTS IN AGUSAN DEL SUR

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Introduction: The Schistosomiasis Control and Elimination Program has been implemented in the Philippines for quite some time now and despite it, Schistosomiasis cases still remain as a public health concern in the Philippines. Research on how knowledgeable and adherent Filipinos are to the Schistosomiasis Control and Elimination Program is very minimal.

Methods: This study is a descriptive analytical analysis through quantitative observational and cross-sectional type of research, which aims to know the level of knowledge and adherence on Schistosomiasis Control and Elimination Program in Agusan Del Sur, where 350 residents were selected through a purposive sampling technique. This study used an adapted survey-questionnaire and a validated self-made questionnaire to assess the respondents' level of knowledge and adherence in the disease prevention method of Schistosomiasis respectively.

Results: Results show that most of the residents were aged between 20 and 30 years old (33.4%), female (61.11%), attained secondary education (43.1%), resided in Purok -Upper (22.0%), and 89.7% have household monthly income of less than 10,000. There are 73.4% of respondents have knowledge about the government's Schistosomiasis program. While the respondents' adherence to the program shows a 3.71 mean average which is done often.

Conclusion: The study reveals a significant relationship between resident's knowledge of schistosomiasis and their adherence to the control and elimination program. The level of adherence of the respondents to the program shows no significant relationship to their knowledge of any interventions; such as proper excretal disposal system, avoidance of wadding in irrigation canals, wearing of boots while farming, and medication compliance.

Keywords: Schistosomiasis Control and Elimination Program, Agusan del Sur, Descriptive analytical correlational analysis

Abstract No.: ABS0002085

SOCIO-CULTURAL CONTEXTS OF CAPILLARIASIS AND PARAGONIMIASIS: IMPLICATIONS FOR DISEASE PREVENTION AND CONTROL IN THE PHILIPPINES

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Introduction: This study aimed to describe the social determinants of capillariasis and paragonimiasis to contribute to the enhancement of health promotion and education for the prevention and control of capillariasis and paragonimiasis, with consideration of local sociocultural contexts. Methods. Key Informant Interviews and Focus Group Discussions were utilized to gather data on the sociocultural factors affecting food safety, consumption, sanitation practices, and health-seeking behavior in selected sites in Mindanao, the Philippines. Results. Current strategies for prevention and control of capillariasis and paragonimiasis rely mainly on diagnosis of suspected cases through passive case finding, treatment of confirmed cases, and promotion of Zero Open Defecation, while health promotion and education, and active surveillance need to be prioritized. “Kilaw” is a common method of food preparation where fish and crustaceans are soaked in vinegar and spices and consumed raw. Freshwater fish and crustaceans harbor the infective stage of Capillaria philippinensis and Paragonimus westermani, respectively. The use of cultural explanatory models for disease causation such as “binat”, “kulam” and “pasma” was documented in the study sites, may affect health-seeking behavior of community members. Conclusions. The integration of control measures with related health programs, such as the Integrated Helminth Control Program for capillariasis due to the similarity of the diagnostic technique, and the National TB control Program for paragonimiasis due to the similarity of disease manifestation, may be considered. Health communication may consider explanatory models of disease causation.

Keywords: foodborne helminths, capillariasis, paragonimiasis, social determinants, One Health approach

Abstract No.: ABS0002096

A CLUSTER OF JAPANESE SPOTTED FEVER CASES ASSOCIATED WITH CEMETERY VISITS IN WAKAYAMA CITY, JAPAN

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Introduction: Japanese spotted fever (JSF) is a tick-borne rickettsiosis caused by Rickettsia japonica. Although the number of JSF cases has been increasing, exceeding 300 per year since 2017, clusters of cases are rare. We encountered the first non-familial cluster of the disease documented in the Japanese literature and describe the management of the outbreak through prompt investigation and control-and-prevention measures.

Methods: Patient information was obtained from notification forms submitted to the local health center. JSF was diagnosed from skin and whole blood samples sent to local public health institute. Ticks were collected in a field survey of a cemetery where the case in the cluster were presumed to have been infected.

Results: All seven cases in the cluster had visited the cemetery in September or October of 2019. R. japonica was detected in whole-blood and/or skin samples from six patients and in the larvae of Haemaphysalis hystricis collected in a field survey. This cluster of cases was thought to have been caused by an increase in the number of cemetery visits during a Buddhist event scheduled over a short period of time just when the infections larvae in the cemetery were increased by hatching (vertical transmission from infected females).

Conclusions: Delays in the treatment of JSF can lead to severe manifestations. Early interventions through collaborative efforts among members from the clinical, laboratory, and public health fields are important for controlling outbreaks, raising the awareness of the public, and diagnosing and treating patients.

Keywords: Japanese spotted fever (JSF), vertical transmission, cemetery, Wakayama City

Abstract No.: ABS0002098

NEW INSIGHT ON MICROSPORIDIASIS AMONG MALAY SCHOOL CHILDREN IN RURAL TERENGGANU, MALAYSIA

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Introduction: Microsporidia are single-celled intracellular parasite which causes an emerging opportunistic infection associated with a wide range of clinical syndromes in humans. Most studies of this parasite focus on the immunocompromised patients. Thus, there is a lack of information on microsporidiosis in healthy people worldwide.

Objective: This study was conducted to determine the prevalence and risk factors associated with intestinal microsporidiosis among Malay school children in Besut District, Terengganu, Malaysia.

Methods: Stool samples were collected from 250 school children (age 9 – 11 years old) after consent were given by their parents. Samples were stained with Gram-chromotrope Kinyoun and examined microscopically to detect the spores. Confirmation by PCR were done. Demographic, socioeconomic, environmental and personal hygiene information using a pre-tested questionnaire were also completed.

Results: Ninety of the children (36%) was positive for microsporidia. PCR confirmed 67 of these as Enterocytozoon bieneusi and the others are unknown. Univariate and multivariate analyses showed being male ($p = 0.026$), bathing in warm spring nearby ($p = 0.014$), drinking pipe water ($p= 0.012$) and living in lower household income ($p = 0.001$) were all significantly associated with microsporidiosis.

Conclusion: Microsporidiosis have never been reported in Malay school children. Our findings suggest intestinal microsporidiosis is common in the study population and control measures need to be implemented. Future research needs to investigate the source of the infection and accurate identification of microsporidian species by molecular technique since this will determine the best treatment for the study population.

Keywords: microsporidiosis, immunocompetent, malay children, Malaysia

Abstract No.: ABS0002101

PARASITE COMMUNITIES IN GREY MULLETS: A COMPARATIVE STUDY BETWEEN THE ANDAMAN SEA AND GULF OF THAILAND COASTAL WATERS

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The Andaman Sea and the Gulf of Thailand (GOT) are separated by a land barrier and differ in sea surface currents. We hypothesized that the differences in the environmental conditions of Thailand's two sea areas affect parasite diversity and host–parasite assemblages. This study aimed to compare the prevalence, intensity, species richness and diversity of parasites infecting mullets in the Andaman Sea and the GOT. Additionally, host–parasite assemblage between the mullets and their parasites were analyzed. The study encompassed four mullet species (Crenimugil buchanani, Liza subviridis, Liza vaigiensis, and Mugil cephalus) that were harvested from eight coastal locations. Parasites were extracted and morphologically identified. Subsequently, their diversity and host specificity were assessed. The results highlighted that monogenean ectoparasites exhibited great species diversity and host specificity. Other identified parasites included digeneans, acanthocephalans, nematodes, and copepods. However, they were not host-specific. Notably, the Andaman Sea recorded significantly higher parasite intensity than the GOT, underscoring the role of ecosystem conditions in shaping parasitic diversity and assemblies. Additionally, this study advocates using host-specific monogeneans as a biodiversity indicator, valuable for gauging ecological differences between regions.

Keywords: Andaman sea; Gulf of Thailand; mullet; parasites; host-parasite diversity; host-parasite assemblage

Abstract No.: ABS0002109

A TIME-COURSE KINETIC STUDY OF IMMUNOPATHOLOGICAL RESPONSE IN A RHESUS MACAQUE MODEL (MACACA MULATTA) OF SCRUB TYPHUS

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Scrub typhus, a mite-borne rickettsial disease caused by Orientia tsutsugamushi, is a significant cause of acute undifferentiated febrile illness in tropical regions. Infection can cause a spectrum of symptoms ranging from mild to severe and is potentially fatal. Given the initial non-specific symptoms, diagnosis can be challenging, and no vaccine is currently available. A thorough understanding of the pathogen-host interaction is critical to develop effective countermeasures.

In this study, rhesus macaques (N=12) were intradermally infected with 107.8 murine infection units (MuID50) of O. tsutsugamushi (Karp). Infected macaques were monitored for clinical and immune responses until experimental endpoints at 6, 12, or 18 days post-inoculation (dpi). At euthanasia, major organs were collected for histopathology, quantification of bacterial load, and immunoassays.

During the initial infection stage (6 dpi), the highest bacterial load was found in the inoculation site eschar and draining lymph node, and the serum concentration of IFN-gamma was significantly elevated. The dissemination phase (12 dpi) was characterized by the development of a pronounced inoculation site eschar as well as pathologic lesions and detectable O. tsutsugamushi in multiple organs. The immune response peaked by the final endpoint (18 dpi) while eschar lesions and clinical signs were nearly resolved.

The findings in this study provide insight into the kinetics of bacterial dissemination of O. tsutsugamushi, as well as resulting histopathological lesions and immune responses, which are useful for future translational studies and preclinical evaluation of medical countermeasures against scrub typhus.

Keywords: Immunohistopathology, Vector-borne rickettsiosis, Non-human primate model, rhesus macaques, scrub typhus, Orientia tsutsugamushi

Abstract No.: ABS0002119

IDENTIFICATION OF BLASTOCYSTIS IN TOADS (RHINELLA MARINA) AND COCKROACHES (PERIPLANETA AMERICANA) IN QUEZON CITY, PHILIPPINES

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Blastocystis is a commonly encountered gut protozoan found in humans and animals including poikilotherms. There are currently 38 *Blastocystis* subtypes (STs) found in endotherms (mammals and birds) and 8 non-mammalian and avian subtypes (NMASTs). There is considerable interest on the host specificity of these STs and NMASTs because their host ranges sometimes overlap. In this study, cane toad (*Rhinella marina*) stool samples and cockroach (*Periplaneta americana*) gut contents were inoculated in biphasic medium with horse serum to observe for growth of *Blastocystis*. *Blastocystis* NMAST I was identified in 11 of 93 (11.83%) cane toads while NMAST VI was identified in 1 of 127 (0.79%) cockroaches. Two (2) other cockroach samples were positive for *Blastocystis* using culture and PCR but the sequences had mixed chromatograms indicating possible mixed ST or NMAST cultures. NMAST I is commonly encountered in amphibians and reptiles while NMAST VI is commonly found in cockroaches. Previous studies in the Philippines also show that *Blastocystis* NMAST I has also been identified in duck, Philippine macaque, and box turtle (*Terrapene carolina*) indicating possible identification of NMASTs in mammals and birds. This shows that NMASTs may have wider host ranges than previously expected. It is also recommended to include poikilotherms such as amphibians, reptiles, insects, and fish when sampling for *Blastocystis* to further elucidate host ranges and ST or NMAST-host specificity.

Keywords: Blastocystis, subtypes, host specificity

Abstract No.: ABS0002121

OPTIMAL CONTROL STRATEGIES FOR SOIL-TRANSMITTED HELMINTHS (STH) ELIMINATION IN THAILAND USING MATHEMATICAL MODEL

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Soil-transmitted helminths (STH) infections are considered neglected tropical diseases (NTDs). In Thailand, a school-based mass drug administration (MDA) program has been implemented as part of the controlling helminth program targeting school age children (SAC) in remote areas under Department of Disease Control, Thai Ministry of Public Health. The goal of this program is to eliminate STH, defined as a prevalence below 5%, by 2026. Although the prevalence has significantly declined, one challenge we are now facing in term of achieving the target goal is the persistence of prevalence around the 5% in many focused areas. In this study, we developed an age-structured transmission dynamic model for STH to assess the impacts of control strategies for STH infections and transmission control. The validated model is applied to explore new interventions and some outputs including mean worm and prevalence are estimated and compared. These findings are useful guidance to develop the optimal strategies for controlling and eliminating STH infections in Thailand.

Keywords: Soil-transmitted helminths (STH), Transmission dynamic model, Mass drug administration (MDA)

Abstract No.: ABS0002171

ACCURATE PREDICTION AND OPTIMIZATION OF PARASITIC PROTEIN STRUCTURES

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Introduction: Although artificial intelligence-based structure modeling such as Alpha-Fold and RoseTTAFold have been introduced recently, they require big data of biological sequences and experimentally determined structures. Thus, protein structure prediction still remains challenging for pathogens including parasites, bacteria and viruses. We have tried to find a solution for accurate prediction and optimization of protein structure in trematode.

Methods: Several well-established protein predictors were used according to each basic stage; Swiss-model suite and LOMETS for homology modeling, I-TASSER for threading-based modeling, and AlphaFold and trRosetta for artificial intelligence (AI)-based modeling. Refinement was performed using FG-MD, ModRefiner and Energy-minimization. Parastie-specific customized methods were designed based on the sequence properties of a target protein.

Results: Homology modeling using good templates with more than 85% showed great performance. Since several parasite proteins showed longer sequences at N-/C-terminal regions, this affected their quality control (QC) values. In particular, the disordered region should be removed to get higher QC results albeit its importance of biological function. Single or successive refinements can be helpful for improving their QC values. Differently predicted protein structures of MF6p/host defense molecules (HDMs) were reported but one can be determined using evolutionary homologue-based comparative modeling. This strategy can be applied to another target showing evolutionarily conservation. Parasite-specific tegumental proteins need customized combined methods.

Conclusion: In conclusion, our strategy can be applied to various cases because we successfully improved parasitic protein structures.

Keywords: Trematode, Protein structure prediction, Refinement, Evolutionary homologue, AI-based modeling

Abstract No.: ABS0002004

ENVIRONMENTAL FACTORS IMPACT ON RAT INFESTATION IN HOUSEHOLD: A SYSTEMATIC REVIEW AND THEMATIC SYNSTESIS OF QUALITATIVE RESEARCH

Budsakorn Chommueang

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Objectives: To critically assess the published literature detailing the environmental factors influencing rat infestation in communities.

Design Systematic review and qualitative thematic synthesis.

Methods: Searches MEDLINE, Web of Science, Scopus, PubMed, and Thai Journals Online. Search keywords were combined for qualitative research, environmental factors and rat habitation and were supplemented by searches of reference lists and citations. Study selection was conducted by using selection criteria. Data extraction and quality assessment using the Critical Appraisal Skills tool for appraisal of qualitative research.

Results: Thirty-eight articles reporting on 35 cross-sectional studies, of which 3 were cohort studies and one were quasi-experimental research. Eleven descriptive themes were interpreted, embedded in 3 analytical constructs: environment (flooding, housing conditions, areas) human behaviours: (population, knowledge, attitude, and practice (KAP), Rodent-borne disease) rodent control: (Integrated Pest Management (IPM), model). Factors and rat habitation were described within these themes.

Conclusions: Environmental factors and rat infestation in house have been identified for environment providing repeated flooding that increases the risk for rat habitation in communities. Moreover, human behavior of lacking for housing sanitation are caused to rat abundance, as well as highlighting the need for rat infestation prediction model for rodent control. A comprehensive understanding of these finding factors is essential to eliminate the risk of rat infection and improve the quality of housing sanitation.

Keywords: Environmental factors, Rat infestation, Household, Rodent control, Integrated pest management

Abstract No.: ABS0002042

Prevalence of stress, anxiety, depression and associated risk factors in graduate students in Faculty of Tropical Medicine, Mahidol University

Natefa Rukmanee

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This prospective repeated cross-sectional study aimed to provide information on mental health problems, stress anxiety and depression and their risk factors during studying period among the post-graduate students in Faculty of Tropical Medicine, facilities supporting the improvement of the students' mental health. Self-administrated web-based questionnaire was developed based on the DASS-21 questionnaire and sent to all post-graduate students two times 6 months apart and the 2nd survey was to pick up those missing out from the 1st survey. The study was conducted in 2019 to 2020. After the survey completed, In-depth interview (IDI) was carried out with 9 students. The survey data was analysed using descriptive analysis based on the DASS ranking scores. The in-depth interview data was analysed using thematic analysis.

Total of 54 responses (38 at 1st round, 16 at 2nd round), 51.9% was Ph.D. (Trop.Med.) for and 31.5% was M.Sc. (Trop.Med.). Forty-one percent was international students, 64.8% were female and 81.5% aged range 24-48, with mean age of 31, and mode 29 years old. The data highlighted the high level of depression, anxiety and stress among students as the DASS 21 scored revealed high warrant of all parameters 1) Depression, 31.5% at moderate, 11.1% at severe and 16.7% at extremely severe levels; 2) Anxiety, 18.5% at moderate, 22.2 at severe and 31.5% at extremely severe levels; 3) Stress, 16.7% at moderate, 3.7% at severe and 13% at extremely severe stress levels. From interviews, almost all students had stress from the limit of study time, the needs.

Keywords: stress, anxiety, depression

Abstract No.: ABS0002061

PREVALENCE AND FACTORS ASSOCIATED WITH MUSCULOSKELETAL DISORDERS AMONG AUTOMOTIVE MECHANICS IN MUEANG PHITSANULOK DISTRICT, PHITSANULOK PROVINCE

Yuwadee Tongmee

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The field of automotive mechanics presents various ergonomic hazards such as awkward postures, repetitive motions, and exposure to vibrations that can impact health and well-being. The objectives of this study were to investigate the prevalence and factors associated with musculoskeletal disorders among automotive mechanics. The data were collected from 180 automotive mechanics. Collected data were divided into 4 parts: 1) Personal demographic 2) Work information 3) Ergonomics risk information 4) The Nordic Musculoskeletal Questionnaire (NMQ). The factors associated with musculoskeletal disorders were analyzed by the Chi-square test.

The study results showed that the subjects had the most musculoskeletal disorders in the past 7 days, followed by lower back (21.7%), upper back (15.6%) and neck (14.4%) respectively. In the past 12 months, It was found that most of them had musculoskeletal disorders, which were lower back (33.3%), neck (27.2%), and upper back (22.2%), respectively. The analyzes of the data showed smoking, over time, heavy lifting, exertion in work, material handling, awkward posture, wrist twists, not enough working space, and hard or slip-to-hold materials were associated with musculoskeletal disorders in the past 7 days (P – value

Therefore, there should be a promotion of knowledge on occupational safety, such as training appropriate posture for work and use to automated tools and design workstations for anthropometry of workers.

Keywords: Musculoskeletal Disorders, Work-related Musculoskeletal Disorders, Ergonomics, Automotive mechanic

Abstract No.: ABS0002089

Evaluation of Three Health Facility Levels training to Strengthen Knowledge of Arthropod Borne Diseases of public health importance of Thailand

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Introduction: Although a significant health problem in tropical countries, knowledge of epidemiology, transmission, and management of arthropod borne diseases (ABD), among public health personnel is not given sufficient attention. This article describes an effort to improve through structured training, the management of ABD. The training includes an integrated approach for surveillance, prevention and control of ABD for three public health facility levels in Thailand-village health volunteer (VHV), sub-district primary health care (PHC) and provincial public health staff (PHO) and regional levels (ODPC).

Methods: Five-day training conducted in May 2023, involving 184 persons (96 on-site and 88 virtual) comprised of 20 VHV, 23 PHC, 56 PHO and 85 ODPC. Content included lectures on arthropods of public importance, surveillance, and reporting, practical on field collection, pathogen detection and vector management techniques. Pre and a post-test were done comprising 30 multiple choice questions. Participants who achieved a post-test score ≥70% were eligible to receive certificate. Participant satisfaction with the training methodology and content was assessed through questionnaire with 17 graded choice and 2 open ended questions.

Result: 54% (n=150) and 93.41% (n=91) of participants passed pre and post-test scores, respectively (Comparative score increased by 39.41%). food source of mosquito -larvae and lymphatic filariasis vector question showed lowest and highest increase, 2.04% and 39.91% respectively. 61.54% (n=56) of participants were very satisfied, 36.26% (n=33) satisfied and 2.20% (n=2) least satisfied with training.

Conclusion: An integrated ABD training involving health staffs showed increased in participants knowledge and good satisfaction with the training content and methodology.

Keywords: Vector borne diseases, Neglected vector borne diseases, Knowledge assessments, Vector borne diseases health literacy, Vector borne diseases training

Abstract No.: ABS0002113

Effectiveness the Community Care Model for Multi-Drug Resistant of Tuberculosis (CCM for MDR-TB) patient in Responsibility Area of the Office of Disease Prevention and Control Region 10th Ubon Ratchathani

Thossaphong Buraman

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The aimed of this research was to evaluate the effectiveness of the CCM for MDR-TB patient. The study areas were 36 sub-districts where found MDR-TB patient in the responsibility area of ODPC 10th. Target group were 53 of MDR-TB patients, 53 of Health volunteers or care givers, and 36 of the community leaders. The tools were CCM for MDR-TB patient which was implemrnt for 12 months and the questionnaires for evaluation the model. The data was analysis by descriptive and Paired T-Test.

More than half of MDR-TB patient were male (74.5%), education at primary school (64.74%), no career (41.2%) and age average 50.55years. Most of care giver were female (77.4%), farmer (79.2%), education at primary school (43.4%), and age average 50.42 years. Most of the community leader were male (61.71), farmer (68.1%), education at secondary school (36.2%) and age average 50.66 years. The effectiveness when compared before and after implementing the model were as followed; It was found significantly (p-value 0.05) in aspect of the social support and ability to care of MDR-TB patient of care giver and community leader and knowledge of community leader. And was found non-significant in aspects of stigma of three groups (MDR-TB patient, community leader and care giver). And was found non-significant in aspect of the knowledge of MDR-TB patient and care giver. Treatment outcome was found success at 88 % and the community performance to prevention MDR-TB distribution in the community was 100 %

Keywords: Model, Community Care, MDR-TB

Abstract No.: ABS0002114

An Evaluation of Health Literacy in Mosquito-Borne Diseases Control and Prevention in Ubon Ratchathani and Mukdahan Province.

Ruchuorn Wongpirom

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Introduction: Thailand has adopted a policy of prevention and control against disease and health hazards. To propel such strategy one crucial strategy was the operation of risk communication intended to raise health literacy and public awareness and its application to promote desirably health behaviors.

Methods: This study was the quantitative method by field survey. The sample consisting of 400 persons from Ubon Ratchathani and Mukdahan Province. Study about the perception of information, sources of Information, satisfaction in information, knowledge on diseases, health Literacy, preventive behaviors and the images of Department of Disease Control.

Results:
1.Perception of Information the average score was at a moderate level.
2.Source of Information the average score was at a high level. The top 5 sources of information with the highest accessibility were: 1)Village Health Volunteer, 2)Internet, Public Health Personnel, 3)Friends, relatives, 4)family members, 5)Television/Cable .
3.Satisfaction in information the average satisfaction score was at a "highly satisfied" level.
4.Knowledge on disease the average score was at a low level.
5.Health Literacy in Prevention, Control Disease: the average score was at a problematic level.
6.Preventive behaviors against diseases: the average score was at a moderate level.
7.Images of Department of Disease Control was at a high level.

Conclusion: The results of this study are applicable for planning of risk communication and systematic development of public health behavior as well as planning of public communion development to effectively promote information acknowledge, knowledge, health literacy, public health behavior and images of Department of Disease Control in upcoming future.

Keywords: Mosquito-Borne diseases, Health literacy

Abstract No.: ABS0002123

DEVELOPING VISUAL AND VERBAL INFORMED ASSENT FOR CHILDREN ENGAGEMENT IN RESEARCH IN THAI BORDER SCHOOLS

Worarat Khuenpetch

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Introduction: Assent vs consent, verbal or written are still challenging to comprehend even among researchers. While the ability or competence of children to give their own consent is still up for debate. This article introduced the child-centered approach to develop an infographic card and 3D coronavirus model to facilitate children's understanding of informed assent with visual, clear and simple language.

Methods: Children age between 7 to

Results: With a total of 1,077 students in 9 border schools in Chiang Rai province, Thailand. Among them 62.3% were Thai, 37.7% were Non-Thai, 40.7% were girls, 44.8% were boys and 14.5% were unidentified and unspecified. Approximately 25% (age between 8 to 15 years old) of students in primary school levels and 75% (age between 13 to 20 years old) of students in secondary school levels consented to opt in 99.6%, while the dropout rate was 0.4%.

Conclusion: The construction of a simple, clear and visual model of informed assent could be used in engaging all ethnic or linguistic minority group of children in research.

Keywords: Assent, Consent, Ethics, Children

Abstract No.: ABS0002024

GREEN-SYNTHESIZED COPPER NANOPARTICLES USING ANDROGRAPHIS PANICULATA: TOXICITY AGAINST THE DENGUE MOSQUITO VECTOR, AEDES AEGYPTI (DIPTERA: CULICIDAE)

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Introduction: Mosquitoes are an important vector that is capable of transmitting potential pathogens to human beings and responsible for several infectious diseases like dengue, zika, filariasis, malaria, yellow fever and chikungunya etc. The aim of the present study to green-synthesized copper nanoparticles (Cu NPs) using leaf extracts of Andrographis paniculata were tested larvae and adult against the dengue mosquito vector, Aedes aegypti.

Methods: To green-synthesized A. paniculata by various bio-physical characterizations were carried out with UV–vis spectrophotometry, FTIR, SEM, TEM, and EDAX analysis. The larval and adult mortality was recorded after 24h of exposure. The toxicity assays of dengue vector, Ae. aegypti larvae and adults using standard methods (WHO 2005; WHO 1981).

Results: For larvicidal assay, the methanolic leaf extract showed maximum effects, with the least LC50 and LC90 values (A. paniculata (50.96 and 77.49 μg/ml) and bio-synthesized A. paniculata Cu NPs (4.28 and 8.99 μg/ml), respectively. The adulticidal activity of both leaf extract and Ag NPs (0–60 min interval periods) recorded best results in methanolic extracts and the LC50 and LC90 values were recorded as A. paniculata (22.10 and 46.00 μg/ml) and P. nilgiriensis synthesized Cu NPs (05.01 and 9.85 μg/ml), respectively.

Conclusion: Among the both leaf extract and Ag NPs have good larvicidal and adulticidal against Ae. aegypti. Moreover, this leaf extracts of A. paniculata and Cu NPs had significant mosquitocidal properties against Ae. aegypti vector mosquitoes. The scientific report on the A. paniculata cn Cu NPs play a role for prevention of the vector control programme.

Keywords: Andrographis paniculata, Cu NPs, Aedes aegypti, mosquitocidal activity

Abstract No.: ABS0002039

FACTORS AFFECTING ACCEPTANCE AND PREFERENCE OF THE JAPANESE ENCEPHALITIS VACCINE AMONG THAIS AND WESTERN TRAVELERS

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Introduction: There is a scarcity of the acceptance and preference data of the Japanese encephalitis vaccines (JEV) among Western international and Thai travelers. This study aims to investigate the factors determinants in acceptance and preference proportion between two groups.

Methods: This cross-sectional study was conducted using a questionnaire among Thais and Western international travelers visiting Thai travel clinics at Hospital for Tropical Diseases, Bangkok, Thailand between July 2023 and December 2023. Our interested outcomes were the acceptance and preference rates, represented as percentages. The appropriate statistical method per data distribution was applied to demonstrate the factors differences among those travelers.

Results: Of 200 participants were recruited, in which 150 (75%) were Thais and the remain were Western travelers. A majority of Thais were female (66%). Most of Western travelers are European (72%) and the main purpose was tourism (78%). Overall, the acceptance proportion of the JEV among targeted populations were similar, with the proportion in Thais and Western travelers of 80.7% and 84%, respectively (P-value = 0.59). Thai travelers had a preference toward vaccine types (69.3%) and manufacturing countries (67%), whereas only half of Western travelers did. Of 20% Western travelers accepted to JEV regardless of efficacy data. Both demonstrated the minimal side effects of JEV such as localized reactions were concerned. The preferred JEV price was less than 57 USD per shot for all.

Conclusions: There was no significant difference in acceptance and preference proportion between Thais and Western travelers. The affordable price of JEV for all was less than 57 USD per shot.

Keywords: Japanese encephalitis, Japanese encephalitis vaccine, acceptance, preferences, and travelers

Abstract No.: ABS0002108

OPTIMIZING ENDECTOCIDE EXPERIMENTS IN ANOPHELES VECTORS

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Introduction: The most well-known endectocide is ivermectin, which is a possible malaria control tool as treated humans or livestock are lethal to blood-feeding Anopheles. Laboratory experiments show variability in the killing effect of ivermectin across experiments and laboratories. Thus, it is crucial to optimize methods for preparing mosquitoes and blood meals to achieve consistent and transferable experimental results. Multivitamin syrup is frequently provided to improve mosquito survival and fecundity. However, it is an artificial diet, thus it may not be appropriate in experiments when assessing mortality effects of insecticides.The most well-known endectocide is ivermectin, which is a possible malaria control tool as treated humans or livestock are lethal to blood-feeding *Anopheles*. Laboratory experiments show variability in the killing effect of ivermectin across experiments and laboratories. Thus, it is crucial to optimize methods for preparing mosquitoes and blood meals to achieve consistent and transferable experimental results. Multivitamin syrup is frequently provided to improve mosquito survival and fecundity. However, it is an artificial diet, thus it may not be appropriate in experiments when assessing mortality effects of insecticides.*Anopheles*

Methods: The impact on survival of *Anopheles dirus* and *Anopheles minimus* raised on various sugar and multivitamin diets prior to a blood meal containing a range of ivermectin concentrations was assessed. The lethal concentration that kills 50% (LC50) of mosquitoes was calculated for each diet. In a second set of experiments, the mosquito-lethal outcome of fresh whole blood and fresh plasma spiked with concentrations of ivermectin at the predicted concentrations that kill 25%, 50%, and 75% of the mosquitoes was assessed.

Results: There were substantial survival differences between *An. dirus* and *An. minimus* when raised on different sugar/multivitamin diets prior to ingestion of ivermectin. There were also survival differences between the two species after ingesting fresh whole blood and plasma containing the same concentrations of ivermectin.

Conclusion: These outcomes demonstrate substantial differences in mosquito mortality associated with identical ivermectin concentrations at different experimental designs, and will be highly useful to optimize experimental designs to produce consistent results for the evaluation of mosquito-lethal effect of endectocides.

Keywords: Anopheles dirus, Anopheles minimus, ivermectin, sugar, multivitamin, blood, plasma

Abstract No.: ABS0002065

ASSOCIATED FACTORS OF FATAL OUTCOME IN SEVERE PLASMODIUM VIVAX MALARIA: A META-ANALYSIS

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Background: Plasmodium vivax, a widely geographical distributed malaria species, is a second largest contributor to symptomatic malaria worldwide. Although vivax malaria patients rarely turn to severe condition and relate with a low mortality, recent reports convinced that severe vivax malaria might be raised concerns. We conducted a meta-analysis to determine associated factors for predicting poor prognostic outcome in severe vivax malaria patients.

Method: Severe vivax malaria was defined according to WHO criteria, 2015. The selection process for potentially relevant articles was based on 2 electronical databases (Medline and Scopus) and 2 independent reviewers. MeSH and keywords were applied for searching strategy, according to PICO concept. Quality assessment and risk of bias for the included studies were evaluated, following the criteria of the 2011 Quality Assessment of Diagnostic Accuracy Studies. Pooled estimates of odds ratios were calculated for predicting poor prognostic outcome in severe vivax malaria.

Results: 512 relevant articles were examined. Only 42 published articles met the inclusion criteria and included for statistical analysis. Regarding the meta-analysis, only 6 associated factors-respiratory distress, cerebral malaria, jaundice, severe anemia, renal impairment, and shock-were significant predictors for poor prognosis in severe vivax malaria patients with pORs (95% CI) of 4.15 (2.66-5.74), 3.82 (2.21-4.72), 3.25 (2.32-5.45), 3.23 (1.15-7.12), 2.81 (2.23-3.55), and 2.23 (1.54-3.15), respectively.

Conclusion: Severe vivax malaria patients who presented with comorbid respiratory distress, cerebral malaria, jaundice, severe anemia, renal impairment, or shock should be closed-monitoring to reduce fatal outcome. Further studies in severe mixed malaria infection or co-infection with other infectious diseases may be warranted

Keywords: Plasmodium vivax, severe malaria, fatal outcome, prognostic factors

Abstract No.: ABS0002075

FIELD BASED APPLICATION AND DEEP LEARNING TECHNOLOGY FOR MOSQUITO OF VECTOR SURVEILLANCE MONITORING

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Surveillance of vector-borne disease necessitates mosquito monitoring. Incorporating deep learning enhances the morphological identification process. However, there has been unclear investigation on the model\'s accuracy for species complexity.This study aims to enhance mosquito identification using multi-stage deep learning on the CIRA CORE platform. An image collection of 177,600 samples from 7 mosquito species is utilized (Ae. aegypti, Ae. albopictus, An. minimus, An. harrisoni, An. dirus, An. maculatus, Cx. quinquefasciatus). The identification model employs three AI models integrated entomological methods. Datasets consist of 100 adult mosquito vectors from laboratory and field strains. Model evaluation, based on 173 observations. The model showed 90±5% accuracy distinguishing among genus level (Aedes, Anopheles, and Culex groups). Optimization processes demonstrated the model accuracy in Ae. aegypti 99%, Ae. albopictus 99%, An. minimus 94%, An. harrisoni 86%, An. dirus 98%, An. maculatus 98%, and Cx. quinquefasciatus 98%. We further evaluated the mosquito identification efficacy of AI and public health officers by 30 unknown images among 7 total mosquito species. Results showed no significant difference in species classification between AI system and public health officers (P value > 0.05). Surprisingly in the species complex identification level, AI system demonstrated a significant 90% accuracy advantage over public health officers (P value < 0.05). This AI system will be the optional challenge to support vector surveillance tool in the local public-health officers to faster measure mosquito monitoring.

Keywords: ARTIFICIAL INTELLIGENCE, MOSQUITOES IDENTIFICATION, DEEP LEARNING, VECTOR SURVEILLANCE

Abstract No.: ABS0002095

The comparison study of the clinical characteristics of chikungunya and dengue fever in children at Bamrasnaradura Infectious Diseases Institute

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Introduction: Chikungunya fever (CHIKF) and dengue fever (DF) are a mosquito-borne diseases. During 2017-2021, the incidence rates of CHIKF and DF in Thailand were 0.02-19.73 and 16.04-131.59 per 1000,000 population, respectively. The clinical presentations of CHIKF and DF in pediatric patients are similar, these make the diagnosis delayed which precipitate the poor outcomes of treatment and disease control. Currently, the studies about the differences of CHIKF and DF in children are limited.

Objective: To find the differences of CHIKF and DF in children aged less than 15 years in aspect of symptoms, signs, complications and prognosis.

Methods: The retrospective analytic observational study by chart review among the children age less than 15 years who were diagnosed as CHIKF and DF at Bamrasnaradura Infectious Diseases Institute from January 1st, 2018 to October 31st, 2022

Results: This study found 250 eligible cases- 38 CHIKF and 212 DF cases. The mean age was 8.3 + 4.0 years, the male: female ratio was 1.2:1. The clinical characteristics which were prominent in CHIKF than DF cases were arthralgia (adjusted odds ratio [AOR] =26.00, 95%CI: 6.22-109.01) and rash (AOR=3.58, 95%CI: 1.53-8.41) significantly. No difference in complication and prognosis.

Conclusion: The different clinical characteristics of children with CHIKF compare to DF were arthralgia and rash. These characteristics are the supportive evidences for sending of confirmed diagnosis of CHIKF for the proper outcomes of treatment and diseases control.

Keywords: Chikungunya fever, Dengue fever, Pediatric patients, Differences

Abstract No.: ABS0002112

INSECTICIDE SUSCEPTIBILITY STATUS OF DENGUE MOSQUITO VECTOR, AEDES AEGYPTI, IN BAN PONG DISTRICT, RATCHABURI PROVINCE, THAILAND

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Aedes aegypti is the primary vector for many arboviral diseases affecting human especially dengue virus infection, which have high transmission in Thailand and currently no specific treatment. Control of Aedes mosquitoes is the important role for prevention of disease transmission. The various mosquito control usually involves the use of chemical insecticides such as pyrethroid, organophosphate, and carbamate. The adverse effect of the heavy and long-term use of insecticide is the susceptibility reduction of Ae. aegypti mosquitoes then cause of insecticide resistance. One of the resistance mechanisms leading to pyrethroid resistance, known as metabolic resistance which involves with detoxification enzymes. The phenotypical determination of insecticide resistance by WHO susceptibility bioassay is essential for the implementation of vector management. In this study, the Aedes mosquitoes in generation F1-F2 of Tha Pha and Sammaram village were determined the phenotypic resistance by WHO susceptibility bioassay (1x insecticide concentration), intensity of resistance by WHO intensity bioassays (5x and 10x insecticide concentration) and metabolic resistance by WHO synergist-insecticide bioassays with piperonyl butoxide (PBO). Ae. aegypti from two villages mostly confirmed phenotypic resistance in pyrethroid, organophosphate, and carbamate. For pyrethroid, they had the high-intensity resistance with mortality of the highest (10x) concentration at Tha Pha and Sammaram as 9-89%, and 8-81%, respectively. Moreover, the synergist bioassay showed a metabolic mechanism for detoxifying pyrethroid toxicity partially involved with mortality 87% at Tha Pha and 80% at Sammaram. It seems that insecticide resistance poses a growing threat and resistance management must be integrated into mosquito control programs.

Keywords: Mosquito, Aedes, Insecticide resistance, WHO bioassay, Synergist

Abstract No.: ABS0002120

GENETIC VARIATION IN THE FIELD-COLLECTED MALARIA VECTOR, *ANOPHELES MINIMUS*, ASSOCIATED WITH HOST-SEEKING BEHAVIOR AT THE THAI-MYANMAR BORDER

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For host detection, mosquitoes utilize CO2, host odor, and body heat as main cues. Compared to other species members of the Maculatus Group along the Thai-Myanmar border, Anopheles minimus shows a stronger anthropophilic behavior (prefer human blood). To investigate the genetic basis of host preference in wild An. minimus, we perform whole-genome sequencing analysis on cow blood feeding and human blood feeding (indoor and outdoor) mosquitoes. Adult An. minimus mosquitoes were collected in Tha Song Yang district, Tak province, Thailand, from July 2019 to November 2020. Collection methods consisted of cow-baited catch, human landing catch, CDC light traps. Female An. minimus accounts for 25% of total samples (504/1997). The number of haplotypes is 143 out of 287 samples based on cox-1 sequencing. There are 12,659,785 variants extracted using CLC Genomics Workbench software (QIAGEN, Aarhus, Denmark). After filtering, we identify 68,975 non-synonymous single-nucleotide polymorphisms (nsSNPs). Across three pooled groups (FDR-adjusted p-value

Keywords: Whole-genome sequencing, single-nucleotide polymorphisms, olfaction

Abstract No.: ABS0002163

The infectivity of *Plasmodium cynomolgi* gametocytes to *Anopheles dirus* after blood collection and storage

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One of the biggest challenges of malaria control and elimination is effectively interrupting the efficient process of parasite transmission to their hosts or vectors. To develop effective counter measures targeting transmission reduction or control, assays are needed to investigate the infectivity of the parasites to their mosquito vectors. At this moment, the method commonly used to infect the Plasmodium spp. to their vectors for the control counter measures evaluation is the direct membrane feeding assay (DMFA). To prevent the deterioration of the blood component and the infectious gametocytes, the venous blood drawn should be provided to the mosquitoes as soon as the parasitemic blood sample has been collected. Also, a drop in the temperature after blood drawing affects gametocyte fertilization. These are logistical challenges when the subject recruitment and blood drawing procedures are conducted far from the mosquito-membrane feeding facilities. In this study, we investigated the infectivity of P. cynomolgi-infected blood samples collected from monkey donors (Macaca mulatta) using the DMFA method to infect Anopheles dirus mosquitoes after maintaining at 37+10C in the thermo-cell transporter for different durations i.e., 0, 1, 2, 4, and 6 hrs. The parasitemia and morphology of the malaria parasites were counted and observed after Giemsa's staining using microscopic examination. The infectivity rates and oocyst rates among the groups of blood fed mosquitoes were compared with that of direct skin feeding and statistically analyzed. The optimal condition(s) for blood transportation described in this study may be an applicable method for malaria research in remote areas.

Keywords: Plasmodium cynomolgi, Anopheles dirus, gametocyte, and membrane feeding assay

Abstract No.: ABS0002026

Incidence and risk characteristics of SARS-CoV-2 infection among migrant and Thai children attending care at a hospital in Samut Sakhon, Thailand: A retrospective cohort study

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Background: The risk of COVID-19 was assumed to be heightened among children accompanied by their foreign migrant worker parents. This study aimed to assess the risk of SARS-CoV-2 infection and related characteristics among these foreign migrant children compared to Thai children.

Methods: This retrospective cohort study included all under-15, both migrant and Thai children who were at risk of COVID-19 since the start of its outbreak in Samut Sakhon and later had PCR testing to determine infection outcomes at a public hospital from December 3, 2020, to October 31, 2021. Exposure variables included sex, age, nationality, province of house registration, type of health insurance, and medical conditions. Univariable and multivariable Poisson regression with robust standard errors were used to estimate crude and adjusted risk ratio (RR) which indicated factors associated with SARS-CoV-2 infection.

Result: Among 9,097 children, 52% were males and 13.45% were migrant children. The overall infection rate was 37.52%. Infection rates in Thai and migrant children were 39.08% and 27.45% (p

Conclusions: The risk of SAR-CoV-2 infection among foreign migrant children was significantly lower than that of their Thai counterparts. Children aged ≥ 2 years were at higher risk of the infection compared to those under 2.

Keywords: COVID-19, SAR-CoV-2, Migrants, Migrant children, Epidemiology

Abstract No.: ABS0002027

REINFECTION WITH SARS-CoV-2 WITH RECURRENCE OF MULTISYSTEM INFLAMMATORY SYNDROME IN CHILDREN

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Background: Children with COVID-19 are unique to multisystem inflammatory syndrome in children. Multisystem inflammatory syndrome in children (MIS-C) is a rare, potentially life-threatening post-infectious complication in children after severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection. It is currently well unknown if multisystem inflammatory syndrome in children (MIS-C) can recur with reinfection with SARS-CoV-2. Here, we report on a former MIS-C patient that a recurrence of MIS-C with reinfection SARS-CoV-2.

Methods: Case study report

Results: A-4 years old boy was admitted on April 2022 with presenting complain of fever and cough for a week, dyspnea 3 days before admission. Laboratory performed polymerase chain reaction SARS-Cov-2 on nasopharyngeal swab was positive, evaluation 10 days later was negative. Two weeks after infection, laboratory performed high D-Dimer 5075 ng/mL, LDH 455 U/L, Interleukine-6 167 pg/mL, ferritin 509 ng/mL, CRP >150 mg/L, procalcitonin 1.88 ng/mL, hs troponin T 21.8 ng/L, NT pro BNP >35.000 pg/mL. The patient has clinical improvement after intravenous immune globulin (IVIG) and high-dose corticosteroids therapy. The patient's medical history was infected by SARS-COV-2 in December 2020 with serology results that IgM SARS-Cov-2 was positive and was hospitalized in Pediatric Intensive Care Unit on February 2021 with PCR SARS-Cov-2 on nasopharyngeal swab was negative, a hypercoagulable state with D-dimer 14.000 ng/mL. The patient than was diagnosed with MIS-C and was treated with Intravenous immune globulin (IVIG) and high-dose corticosteroids.

Conclusion: The recurrence of MIS-C still needs to consider in a patient with severe manifestation of SARS-CoV-2 reinfection

Keywords: MIS-C, pediatric COVID-19, SARS-CoV-2, reinfection, recurrence

Abstract No.: ABS0002037

INCIDENCE AND RISK FACTORS OF FATTY LIVER IN HUMAN IMMUNODEFICIENCY VIRUS PATIENTS ON ANTIRETROVIRAL TREATMENT

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Introduction: Fatty liver disease has been reported to increase in HIV patients on long-term ARV. The objective of this study is to obtain data on the prevalency and risk factors of fatty liver in HIV patients on ARV.

Methods: A cross-sectional study was done on HIV patients aged 18 to 50 years old, whom had been on ARV for more than three years, with undetectable viral load, and had a body mass index of 18.5 to 22.9 were conducted at Manado General Hospital. Hepatitis B, Hepatitis C, chronic liver disease before HIV, illicit drug users, and alcoholics were excluded. Examinations of fatty liver was done using liver ultrasonography. Variables examined are the duration of ARV, CD4 level, LDL level, transaminase level, age, gender, triglyceride level, and abdominal circumference.

Results: A total of 31 subjects were included in the study, 24 males (77,4%), with an average age of 31.61 years. Fatty liver was found in 19 patients (61.3%). The results of hypertriglyceridemia (OR=6,875; 95% CI 1,171-40,378; p-value 0,032) and central obesity (OR=18,750; 95% CI 2,871-122,452; p-value 0,001) showed significant differences in HIV patients with or without fatty liver. The results of the duration of ARV, CD4, LDL, transaminase level, age, and gender did not show any significant differences in HIV patients with or without fatty liver.

Conclusion: 61.3% of HIV patients had fatty liver. Whereas hypertriglyceridemia and central obesity contributes as risk factors.

Keywords: Fatty liver, Human Immunodeficiency Virus, Antiretroviral, Hypertriglyceridemia, Obesity

Abstract No.: ABS0002064

PREVALENCE AND ANTIMICROBIAL SUSCEPTIBILITY OF *NEISSERIA GONORRHOEAE* AND *CHLAMYDIA TRACHOMATIS* AMONG HIGH-RISK PEOPLE IN PATTAYA, THAILAND

Dutsadee Peerapongpaisarn

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Introduction: Currently, there is no prevalence data on *Neisseria gonorrhoeae* (NG) and *Chlamydia trachomatis* (CT) among high-risk Thai population, especially for high risk females (HRF) and men who have sex with men (MSM). We conducted a cross-sectional study at the Pattayarak Health Unit and SWING, Thailand to enroll HRF and MSM, respectively.

Methods: Specimen collected from various anatomical sites were examined for the presence of NG and CT by Nucleic Acid Amplification Testing. Antimicrobial resistance of NG isolates were performed by E-Test.

Results: From June 2021 to July 2023, a total of 353 participants (188 HRF; 165 MSM) were enrolled. A prevalence rate of 9.3% for NG and 6.8% for CT were observed for HRF, and 8.8% for NG and 11.1% for CT were found in MSM. CT/NG co-infection prevalence rates were 4.3% and 8.5% in HRF and MSM, respectively. Fourteen NG isolates (3.2%) were detected in HRF, while 22 NG isolates (4.7%) were found in MSM. All 36 NG isolates were resistant to at least one of these antibiotics; azithromycin, cefixime, ceftriaxone, ciprofloxacin, gentamicin, penicillin, spectinomycin, and tetracycline. Of all 36 NG isolates, 28 (77.8%) were multi-drug resistant. High prevalence of resistant NG was shown against ciprofloxacin (83.3%), tetracycline (69.4%), and penicillin (55.6%). All NG isolates were susceptible to azithromycin, cefixime, ceftriaxone, gentamicin, and spectinomycin.

Conclusion: NG and CT remain significant health threats among high-risk populations in Thailand. Our findings highlight the importance of consistent surveillance of CT and NG along with monitoring antimicrobial resistant NG in this country.

Keywords: *Neisseria gonorrhoeae*, High risk females (HRF), Men who have sex with men (MSM)

Abstract No.: ABS0002308

Mitigating Malaria Resurgence: Enhancing Surveillance through Primary Health Care in Vulnerable Pha Phueng Sub-Village

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Background: Despite no prior malaria cases, Pha Phueng Sub-village in Wang Chao District remained vulnerable due to Anopheles mosquito presence and the temporary foreign workers. A 2023 malaria outbreak, caused by delayed detection, prompted an investigation to assess the outbreak’s distribution, address surveillance gaps, and establish a more contextualized system.

Methods: An active search conducted from May 1st to May 3rd, 2023, in Pha Phueng Sub-village involved testing all Thai residents and temporary foreign workers using Rapid Diagnostic Tests (RDTs) and microscopy. Additionally, a focus group discussion gathered information on the at-risk population, available resources, service accessibility, and workforce capacity. These findings informed the implementation of a new surveillance system, evaluated by comparing test volumes for effectiveness.

Results: The mass blood survey uncovered 22 confirmed Plasmodium vivax cases, predominantly among temporary foreign workers (4.3%) versus Thai residents (0.1%). Pha Phueng Primary Health Care (PHC) lacked on-site RDTs and antimalarial drugs, requiring residents to visit District Hospital. temporary foreign workers were rarely tested regarding discrepancies in work schedules and services. Hence, we implemented a new surveillance system at the PHC by ensuring adequate supplies, providing on-the-job training, and promoting the facilities' availability. Consequently, from May to October 2023, the system utilized 2600 RDTs and identified 315 cases at the Primary Health Care level.

Conclusions: Pha Phueng Sub-village faced substantial detection of temporary foreign workers, with surveillance challenges stemming from resource scarcity and limited healthcare access. Therefore, strengthening PHC was crucial to mitigate malaria reintroduction in this vulnerable area.

Keywords: malaria, primary health care, malaria reintroduction, surveillance system

Abstract No.: ABS0002309

Changing mosquito vector population structure during construction of Mae Sot Reservoir

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Longitudinal study of mosquito survey collecting during the construction of the reservoir project in Mae Sot District, Tak province since 2016 to 2023. Mosquitoes were captured by Human landing catch (HLC), DCD-light trap, and Larva survey into two 2 villages upper (Ban Khun Huai Mae Sod; BK) and lower (Ban Uaeng Doi; BU) site of the dam contraction. Total mosquito collection showed the increasing trends from the upper and lower reservoir sites among year (2016, 2018, 2023). Upper site (BU) presented higher density of all anopheline and culicine group than the lower BK village with majority of Anopheles minumus group, An. maculatus group, and An. barbirostris group corresponding to the malaria patients peak up in BK site in 2022. Culicine group showed the same increasing trends of mosquito capture density both areas. In 2023, Aedes aegypti were 1.9-time increasing capture numbers when compare upper and lower site while Ae. albopictus show 68% decreasing trend that might be more urbanization in the lower area. Culex species density presented the same increasing trend among year with the upper site higher density than lower one. This study image the reservoir construction impacts to the mosquito vector population structure that may concern for the vector borne risk transmission risk particularly in Malaria and Dengue.

Keywords: Mosquito vector, Anopheles, Aedes, Culex, Reservoir

Abstract No.: ABS0002310

Malaria Resurgence in Phop Phra Noi Village: Risk Factors and Strategies beyond 1-3-7

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Background: On 18 April 2022, Jadee Kho Malaria Clinic notified the ongoing malaria cluster despite conducting 1-3-7 strategy. Therefore, we conducted an outbreak investigation to determine the magnitude and distribution of malaria cases, identify outbreak sources, and implement effective control measures.

Methods: We performed an active surveillance and mass blood survey in Phop Phra Noi Village utilizing microscopic examination. Following this, we interviewed and observed confirmed cases, gathering demographic, movement, clinical, and risk factor data using standard questionnaires provided by the Department of Disease Control. Additionally, environmental and entomological studies were conducted. Existing gaps were also identified based on the national program.

Results: We identified 48 confirmed Plasmodium vivax cases in Phop Phra Noi Village, primarily male foreign migrant workers employed in adjacent regions. Many stayed overnight in their farm before illness onset while some returned to lodgings after 6:00 PM. The surrounding environment consisted of forests, farms, and streams running across the village. Mosquito sampling identified potential vectors—Anopheles maculatus and Anopheles barbirostris. Meanwhile, population movement, delayed mass blood surveys and incomplete case investigations contributed to reintroduction and ongoing malaria outbreaks. To counter this, we engaged the community, conducted intensive indoor and outdoor spraying, distributed impregnated and Long-Lasting Insecticide-treated Nets.

Conclusion: Confirmation of malaria resurgence in Phop Phra Noi Village involved 48 cases of Plasmodium vivax. Risk factors identified included overnight stays in farms and specific movement patterns, alongside the detection of potential mosquito vectors. Therefore, community involvement and intensified measures beyond the 1-3-7 strategy are imperative.

Keywords: malaria, Plasmodium vivax, malaria reintroduction, 1-3-7 strategy