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Abstract Book



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Department of Disease Control

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Invited Session Abstracts

Abstract No. : ABS0001643

Status : Approved

INCREASED HIV RISK AS AN OUTCOME OF (UN)MET SEXUAL GOAL SETTING OF MSM AROUND THAI SONGKRAN FESTIVITIES



Prof. Kai Jonas

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Human behavior in general, but also sexual activity is driven by goals. Hence, goal attainment processes need to be investigated to determine potential sexual health risks. Oftentimes, sexual activity goals are tied to specific events, such as the Songkran festivities in Thailand for men who have sex with men (MSM). We present first longitudinal data that investigates sexual activity goals and related HIV/STI prevention measures among MSM living in Thailand. We investigated sexual goal setting and sexual risk taking in a longitudinal study (three points of assessment, prior to, post and 6 months after Songkran festival) in 150 MSM. Results showed that MSM who plan sexual activity around Songkran have a higher likelihood of using substances, have more sexual partners and anal sex. Condom use did not differ between the groups, PrEP use was absent in the non-planning impulsive MSM. Both groups showed equally suboptimal levels of HIV/STI testing four weeks and 6 months post Songkran. Taken together, our findings point to the need of targeted HIV testing campaigns that take (un)planned sexual activities taking place around the Songkran festivities into account.

Keyword : HIV, men who have sex with men, Thailand

Abstract No. : ABS0001642

Status : Approved

EVALUATION OF AN INTEGRATED ONLINE HIV SELF-TESTING PROGRAM (JOMTEST) IN MALAYSIA



Dr.Sin How Lim

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High prevalence of HIV among MSM in Malaysia has been documented. However, due to prevalent stigma, uptake of facility-based HIV testing is low among this high-risk population. Our previous online survey shows high intention to conduct HIV self-testing (HIVST) among Malaysian MSM.

In early 2020, University of Malaya, Malaysian AIDS Council and Love Foundation from Thailand developed the online integrated HIV self-testing platform (JOMTEST) for MSM and other key populations in Malaysia. Participants chose either OraSure/oraquick (saliva based) or INSTI self-test kit (fingerprick) and followed instructions on the test kit pamphlet and JOMTEST to conduct HIVST. Subsequently, participants were required to share the results via JOMTEST. Those who tested reactive were linked to confirmatory testing and treatment and those who test negative were advised on preventive measures such as PrEP. Baseline and post-test online surveys were used to collect demographic information, HIV risk behaviors, perceived likelihood of HIV infection, and social harms related to self-testing. Data collection was from Nov 2020 to Oct 2021. A total of 3,005 individuals registered and provided mailing address but 2868 provided online informed consent. 2,526 test kits were delivered. Only 42.6% of participants who received the test kits returned the test results. 7.0% of participants tested positive. Almost all who tested positive were linked to HIV treatment by NGO peer navigators. An on-going qualitative study is conducted to explore the barriers to HIVST at each step of the study. Future study needs to examine implementation factors to reach, retain MSM and scale up self-testing.

Keyword : HIV, Malaysia, JOMTEST

Abstract No. : ABS0001641

Status : Approved

Applications and Methodologies of droplet digital PCR (ddPCR) for Development of Vaccine



Dr. Alfred Chan

Authors : Alfred Chan

Affiliation : Bio-Rad Laboratories Asia Pacific

Vaccines have been used to prevent disease for more than 70 years and are the best hope for COVID-19 management. Because of the pandemic's extraordinary health and economic consequences, scientists are racing to design, test, and produce a vaccine on a global scale. As a result of this difficulty, a large number of prospective vaccination platforms, including next-generation vaccine technologies, have emerged. While proven technologies using recombinant protein or live attenuated/inactivated viruses are also in development, nucleic acid (DNA or RNA) and viral vectors may offer unique scalability and efficacy. It is critical to select the appropriate tools and technology during the development process. Droplet digital PCR (ddPCR) provides great sensitivity, accuracy, and reproducibility without the need for a standard curve, allowing researchers to move forward with their research. ddPCR is used in conjunction with cell line engineering to detect positive clones and characterize the predicted frequency of homologous recombination. It also allows for the precise and repeatable determination of vector copy number and viral titer. Furthermore, because of its inhibitor tolerance, ddPCR is a highly sensitive approach for detecting Mycoplasma.

Keyword : Vaccines, COVID-19, Droplet digital PCR

Abstract No. : ABS0001644

Status : Approved

CHALLENGES AND LESSON LEARNT FROM CANADA TROPICAL MEDICINE CLINIC DURING COVID-19 PANDEMIC



Mr.Dylan Kain

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001640

Status : Approved

Multi-omics characterization of the molecular mechanisms underlying malaria protection: implication for vaccine discovery



Dr. Carla Proietti

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Malaria remains a significant public health burden worldwide, with an estimated 229M of cases in 2019 and 409K of related death. The complexity of the host-parasite interaction and the dynamic network of molecules involved in the disease outcome poses a great challenge for identifying relevant biomarkers for protection against the disease that can be targeted for therapeutic intervention or immunodiagnostics. To address these challenges, we have generated unique omics-scale datasets of IgG and T cell reactivity to *P. falciparum* using a variety of technology platforms, including protein microarrays and innovative proteome-wide T cell screening. These data have provided unique insights into host-parasite responses. Importantly, we have established that host immune responses target only 30% of the *Plasmodium* proteome and that antigens preferentially recognised by T-cells are distinct from antibody targets. A wide range of computational tools and machine learning algorithms were applied to analyse the synergistic interaction between immune responses to multiple targets and identify predictive signatures of immunity. We defined a set of 15 *P. falciparum* antigens that could accurately predict an individual's immune status for the following malaria season with high accuracy. We also integrated immunological reactivity with genomics determinates and identified a set of molecular and structural features that accurately predicted the preferential type of immune response associated with a given antigen on a genome-wide scale. Finally, we identified DNA methylation marks and novel cell population associated with the outcome of malaria protection observed in individuals the sickle cell phenotype HbAS, highlighting novel loci that provide insight

Keyword : malaria, vaccine

Abstract No. : ABS0001638

Status : Approved

Exciting job with MSF



Dr.Lenin Daniel Martinez Aguilar

Authors : Lenin Martinez

Affiliation : Médecins Sans Frontières

No abstract available

Keyword : No abstract available

Abstract No. : ABS0001637

Status : Approved

From Rickettsia to COVID-19 expert



Dr.Muhamad Yazli Bin Yuhana

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No abstract available

Keyword : No keywords available

Abstract No. : ABS0001636

Status : Approved

Alveolar echinococcosis in Swiss Tropical Institute



Dr. Andreas Neumayr

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No abstract available

Keyword : No keywords available

Abstract No. : ABS0001635

Status : Approved

Dengue and Covid-19 co-infection cases in NOW normal



Prof.Somsak Lolekha

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No abstract available

Keyword : No keywords available

Abstract No. : ABS0001634

Status : Approved

WILDFIRE SMOKE EPIDEMIOLOGY: EVIDENCE, GAPS AND CHALLENGES FOR HEALTH PROTECTION



Prof.Yuming Guo

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Several large wildfires that have occurred recently, for example, wildfires in Australia in 2019 to 2020, the Amazon rainforest in Brazil in 2019 and 2020, the western United States in 2018 and 2020, and British Columbia, Canada, in 2017 and 2018. Robust projections indicate that the risk of wildfires will continue to increase in most areas of the world as climate change worsens. Understanding health impacts of wildfire smoke and intervention strategies is essential to develop health protection policies. However, there are still many knowledge gaps and challenges in bushfire smoke epidemiological studies. This presentation will discuss the evidence, gaps and challenges of wildfire smoke epidemiology.

Keyword : Wildfire, smoke, health protection

Abstract No. : ABS0001633

Status : Approved

Endocytic transport in COVID-19 and other infectious diseases



Assoc. Prof. Amandio Vieira

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Endocytosis of microbial pathogens is a typical pathological process involved in most infectious diseases. Viruses, bacteria, and parasites are internalized by the host cell as part of the initiation and progression of infectious diseases. There is evidence that disruption of such microbe entry can interfere with the normal infection cycle. Pharmacological agents that disrupt endocytosis of the pathogen may, thus, be therapeutically useful in some infectious diseases. Current research on the screening and identification of endocytic transport disruptors and their possible application to COVID-19 and other viral diseases will be presented. Possible therapeutic compounds that have been identified to date as disruptors of cell entry and endocytic transport for Sars-CoV-2 and other human viral pathogens include some natural products (e.g., flavonoids, dietary and medicinal plant extracts) as well as several previously approved drugs (i.e., drug repurposing; e.g., suramin, sunitinib).

Keyword : endocytic, Endocytosis, COVID-19, nutrition

Abstract No. : ABS0001632

Status : Approved

Role of nutrition and supplements in COVID-19



Assist. Prof. Daruneewan Warodomwicht

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001631

Status : Approved

Behavioral Studying and Community Capacity Building for Helminth Disease Solution at Ban Morkrota Hilltribe Community in Omkoi District, Chiang Mai Province



Mrs.Thongroo Kophachon

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001630

Status : Approved

OVCCA Web Application as Supplementary Material to Facilitate Health Literacy Regarding Carcinogenic Human Liver Fluke: a Randomized Controlled Trial in Thailand



Mrs.Oranard Wattanawong

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Assoc. Prof. Schawanya K. Rattanapitoon
Asst. Prof. Dr. Nathkapach K. Rattanapitoon
Asst. Prof. Dr. Apiporn T. Suwannatrai
Thirayu Meererksom

Affiliation : Department of Disease Control, Ministry of Public Health Thailand

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001629

Status : Approved

Current status of Helminthiases in Thailand: A cross – sectional, nationwide survey; 2019



Dr. Thitima Wongsaroj

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001628

Status : Approved

Zika serology testing in the context of co-circulating arboviruses - lessons from Latin America



Prof. Thomas Jaenisch

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001627

Status : Approved

Seroprevalence of zika virus in pregnant women from central Thailand



Assoc. Prof.Chayawat Phatihattakorn

Authors : Chayawat Phatihattakorn

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001626

Status : Approved

Zika surveillance and investigation in Thailand



Dr.Darin Areechokchai

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001625

Status : Approved

Feasibility and effectiveness of reactive focal mass drug administration targeting malaria in high-risk populations in Thailand: Preliminary findings



Dr.Adam Bennett

Authors : Adam Bennett

Affiliation : University of California, San Francisco & PATH

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001624

Status : Approved

NDV-HXP-S Covid-19 Vaccines



Prof.Punnee Pitisuttithum

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001623

Status : Approved

mRNA Covid-19 Vaccines



Prof.Kiat Ruxrungtham

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001622

Status : Approved

Challenges and Opportunities: COVID R&D of Thailand during the Pandemic



Prof.Sirirug Songsivilai

Authors : Professor Sirirug Songsivilai

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001621

Status : Approved

WEB RECRUITMENT AND SUPPORT SYSTEMS FOR DELIVERY OF HIV SELF-TEST KITS FROM LOCAL PHARMACIES



Ms.Chomnad Manopaiboon

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In August 2020, the Thai Ministry of Public Health implemented a study to deliver self-test kits through pharmacies and to assess the type of support HIV self-testers will need in Bangkok.

The study recruited Men who have sex with men (MSM) and transgender women (TGW) who were Thai, >18 years old, lived or worked in Bangkok, were never diagnosed with HIV, and had a smart phone with internet connection.

Through a study webpage, participants reviewed study information, provided online consent, completed eligibility-screening and baseline questionnaires, and registered for test kit pick up at participating pharmacies. Short Message Service (SMS) was used throughout the study to remind participants of procedures and to provide links for completing questionnaires, uploading image results, and sending electronic coupons for compensation. Hotline were available for information about the test kit, pre- or post-test counseling, and referrals for follow-up services.

From August 2020-October 2021, over 5,000 people expressed interest in joining the study and 4,587 completed the eligibility questionnaire. Of 2,022 (44%) persons eligible for the study, 1,969 (97%) registered to pick up test kits at pharmacies. Of those registered, 765 (39%) picked up test kits, of whom 486 (64%) reported using the self-test and 24 (5%) reported having a reactive result

Our findings suggest that online recruitment to obtain and use HIV self-test kits from pharmacies is feasible. To increase use of self-test kits from pharmacies and address COVID-19 social restrictions, the study has recently provided a postage delivery as an additional option for participants.

Keyword : web recruitment, HIV, self-test kits

Abstract No. : ABS0001620

Status : Approved

Online platform and social media influence to recruit transgender populations



Ms.Rena Janamnuaysook

Authors : Rena Janamnuaysook

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001619

Status : Approved

A sentinel system for active detection of mosquito-borne arbovirus presence in South Africa



Prof. Marietjie Venter

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001618

Status : Approved

VISPA- a global access framework to coordinate PvSeroTaT efforts



Dr. Leanne Robinson

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001617

Status : Approved

Mathematical modelling to predict PvseroTaT impact



Dr. Michael White

Authors : Dr. Michael White

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001616

Status : Approved

PROJECTION OF EXCESS MORTALITY DUE TO ENTERIC INFECTIONS



Prof.Masahiro Hashizume

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Enteric infections are one of the leading causes of mortality and morbidity globally, predominantly affecting children in developing countries. The incidence of many enteric infections shows clear seasonality suggesting that weather factors could play a role. Some studies have projected diarrheal outcomes due to climate change. In 2015, World Health Organization reported the projection of the global diarrheal excess deaths using temperature-morbidity risk relation from the literature. We updated the systematic review and meta-analyses for temperature-enteric infections associations and projected the excess deaths due to pathogen-specific enteric infections based on various scenarios.

Keyword : Enteric infections

Abstract No. : ABS0001615

Status : Approved

Eliminate of Viral Hepatitis



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Authors : Anchalee Avihingsanon

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001614

Status : Approved

VIRAL HEPATITIS ELIMINATION



Dr.Kittiyod Poovorawan

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Viral hepatitis is a global burden. This infection is endemic globally and the leading cause of death by its complications. Chronic viral hepatitis B and C are the majority causes of death. The road to elimination for hepatitis B is universal vaccination, effective vertical transmission prevention, and the successful development of radical cure anti-viral treatment. In hepatitis C infection, the rate of the new transmission is low and the current treatment of chronic hepatitis C is simple and highly effective. The limitation of hepatitis C elimination is the lack of awareness of infection in the population, re-infection in some clusters, and inaccessibility to treatment

Keyword : viral hepatitis, elimination

Abstract No. : ABS0001613

Status : Approved

Covid-19 Vaccine production from plant



Prof. Dr. Waranyoo Phoolcharoen

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Affiliation : Faculty of Pharmaceutical Sciences, Chulalongkorn University

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001612

Status : Approved

Household Air Pollution and SDGs: the plight of rural India



Dr.Gopika I

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Household Air Pollution (HAP) from solid fuels is one of the largest health risk factors in India that caused an estimated 1.04 million deaths per year in 2010 and 0.61 million deaths per year in 2019, according to the Global Burden of Disease studies. Women who are traditionally responsible for cooking, as well as their young children, are especially exposed to the resulting air pollution in developing nations like India, where these solid fuels are commonly used. Solid fuels are still widely used, and intervention attempts in developing countries like India appear to be lacking due to its population growth. Actions to reduce household air pollution in developing countries should also help to achieve important SDG targets. The issue of household air pollution in rural India comes under multiple SDG goals, such as SDG3: Good health and wellbeing, SDG7: Affordable and clean energy, SDG13: Climate action, and so on. In this regard, India requires a number of action plans, including the implementation of WHO indoor air quality guidelines on household fuel combustion, effective promotion and dissemination of improved cookstoves through the formation of country alliances for clean cookstoves, expansion of liquefied petroleum gas production facilities and distribution networks, harnessing renewable energy potential, promotion of biogas production at both the household and community level, ensuring improved ventilation of homes through education and enforcement of building standards, and exploiting opportunities in the health and other sectors for changing health-damaging cooking behaviour, and ensuring the availability of clean cooking fuels.

Keyword : Household Air Pollution and SDGs

Abstract No. : ABS0001611

Status : Approved

Clean Environment and Planetary Health Approach (CEPHA) Network initiatives for sustainable development in Asia



Prof. Shiva Nagendra SM

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Planetary health is the fundamental principle cardinal to the workings of the CEPHA network. The network on Clean Environment and Planetary Health in Asia (CEPHA) is essential to understand and reduce the burdens of public health, environment quality, and to achieve sustainable development. This network builds relationships across sectors (research, business, government, public health), citizens and communities (including vulnerable groups), and disciplines (health & social sciences, engineering, planning, economics, education). CEPHA is a truly interdisciplinary/inter-sectoral network comprising of partners from academia, public health, industry, government, local authorities, NGOs and local communities. CEPHA aims to work towards creating a harmony between planetary health and traditional environmental health. CEPHA actively expand its efforts to enhance interdisciplinary aspects (particularly social science) and provide a platform for deeper engagement with industry, regulators, practitioners and local communities, including disadvantaged groups, especially in Asia. The CEPHA Network cohesively assimilates, innovates and develops new ideas and products and work towards achieving the primary goal of creating a sustainable environment. After all, it's imperative for us to understand that the ecological footprint which ballooned over the decades without any leaps and bounds are now making us vulnerable. There is a pressing need to retrospect, plan and carefully investigate. CEPHA intends to expand, extensively network and take larger steps to reach our goal of improving environmental quality and achieving sustainable development.

Keyword : Planetary Health Approach

Abstract No. : ABS0001610

Status : Approved

Travel medicine practices during COVID-19 era in Thailand



Dr. Wasin Matsee

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001608

Status : Approved

ECONSENT FOR CLINICAL TRIALS DURING COVID



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eConsent has proven to be a valuable way to conduct informed consent for subjects safely during COVID. Although eConsent has many advantages, these must be weighed against any potential pitfalls with any new technology. Using the concepts of Pain, Claim, and Gain, the presentation focuses on identifying the root problems or pain points that eConsent attempts to solve. It is also essential to consider all stakeholders, including the sponsor, IRBs, sites, monitors, and subjects. Gathering their input ensures that solving the problems of one group does not create an undue burden for others. By identifying the pain points of all stakeholders, adequate solutions can be developed and successes measured. A well-thought-out alignment of Pain, Claim, and Gain is the key to the successful implementation of eConsent in clinical trial research.

Keyword : eConsent remote informed consent

Abstract No. : ABS0001607

Status : Approved

USING MOBILE APPS TO INCREASE SUBJECT ENGAGEMENT



Ms.Lisa Ondrejcek

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Affiliation : DF/Net Research, Inc.

The COVID-19 pandemic accelerated the use of new technologies, including ePRO (Electronic Patient Reported Outcomes). This presentation describes lessons learned in a COVID-19 treatment study where participants completed questionnaires and recorded symptoms using a mobile app.

Keyword : ePRO (Electronic Patient Reported Outcomes)

Abstract No. : ABS0001606

Status : Approved

CAPACITY-BUILDING FOR ARBOVIRUS SURVEILLANCE AND CONTROL



Dr.Raman Velayudhan

Authors : VELAYUDHAN. R

Affiliation : WORLD HEALTH ORGANIZATION

Effective and sustainable vector control is achievable only with sufficient human resources, an enabling infrastructure and a functional health system. A vector control needs-assessment will help to appraise current capacity, define the requisite capacity to conduct proposed activities, identify opportunities for improved vector control and guide resource mobilization to implement the national strategic plan. These should take into account ongoing, routine vector control as well as activities defined for specific circumstances, such as response to outbreaks, epidemics or humanitarian crises. Many countries continue to experience an ongoing high burden or risk of vector-borne diseases because of inadequate delivery of vector control interventions, resulting from limited investments. The lack of sustainable and targeted financing has been underpinned by many factors, such as poor coordination within and between sectors, weak or non-existent monitoring and evaluation systems, and limited sustainable and proven interventions for certain vectors and situations. In addition, most countries suffer from a dire lack of public health entomology capacity. Given the recent alarming increase in numerous vector-borne diseases and the serious threat posed to economic development, there is a need to reposition vector control as a key approach to prevent and eliminate vector-borne diseases. It builds on the basic concept of integrated vector management with renewed focus on improved human capacity at national and subnational levels. The presentation highlights the few capacity building initiatives at the global level.

Keyword : Capacity building, Vector borne diseases

Abstract No. : ABS0001605

Status : Approved

NETWORKS FOR RESEARCH AND COMMUNICATION TO SUPPORT IDENTIFICATION OF PRIORITY GLOBAL ISSUES ON ARBOVIRAL DISEASES



Dr. Florence Fouque

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The vector-borne diseases are accounting for about 17% of the communicable diseases worldwide and are claiming more than 700,000 lives every year. Although malaria is still the more deadly vector-borne disease, the distribution of arboviral diseases is continuously spreading, becoming global and putting three quarters of the world population at risks of emergence of epidemics. The challenges encountered to face these diseases cannot be solved in isolation and are thus requiring the establishment of networks. The objectives, structure and activities of such networks can vary based on their expected achievements. A few examples of communication and research Networks initiated through TDR activities are presented and will help to identify global issues on Arboviral diseases.

Some networks have a more regional focus on arboviral diseases such as the CariVecNet, lead by CARPHA (the Caribbean Public Health Agency), other networks have a focus on a specific challenge such as the WIN (Worldwide Insecticide resistance Network) network and other are delivering required resources such as the Directory of Courses in Medical Entomology hosted by the GVH (Global Vector Hub). Although, the challenges for emerging and re-emerging arboviral diseases are global, the solutions are also contextual and require the networking at different levels from local to global. Further and because of the magnitude of the changes (demographics, climate, urbanization and others) and the interdependency between situations and transmission patterns, the needs of exchange, collaboration and coordination between region, countries, disciplines and sectors has never been so huge.

Keyword : arboviral diseases, networks, TDR/WHO activities

Abstract No. : ABS0001604

Status : Approved

Going Digital with Pathogen Detection



Mr. Luke Tan

Authors : Tan L¹

Affiliation : ¹QIAGEN Singapore Pte Ltd

Digital PCR is an emerging molecular tool, which has gained much interest since its commercial debut in 2011, for its ability to offer unparalleled sensitivity and precision, without the need for standards. The technique was first described as "limiting dilution PCR" in the 1990s as a method to detect rare targets from a high wildtype background. It has since seen a rapid growth in new applications, such as the early detection of infectious agents during the latent and incubation phases, where pathogens are present at levels too low for reliable detection by traditional means.

However, despite the popularity of digital PCR, it has been plagued in the past with tedious workflows, high costs, and complex multiplexing strategies that has deterred its mainstream adoption. With advances in the technology, QIAGEN hopes to address these issues with the launch of the QIAcuity digital PCR system, which aims to deliver a scalable and automated solution, that is both simple and affordable. In this presentation we hope to provide insights into digital PCR, the QIAcuity and discuss its utility in applications such as pathogen detection and gene therapy.

Keyword : QIAGEN, Digital PCR, Pathogen, Detection

Abstract No. : ABS0001603

Status : Approved

Doctor who got COVID-19



Dr.Nestor, Jr Arce

Authors : Nestor Arce Jr.

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001602

Status : Approved

Biocompatibility and Toxicity testing of Products



Dr.Sareeya Reungpatthanaphong

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001601

Status : Approved

Cytotoxicity of herbal extracts with OECD GLP compliance



Assist. Prof.Sarawut Jindarat

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001600

Status : Approved

Immunity to SARS-CoV-2 in the Vietnamese population conferred by natural infection and vaccination



Assoc. Prof.Le Van Tan

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Affiliation : Oxford University Clinical Research Unit

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001599

Status : Approved

Immune responses to SARS-CoV-2 in Kenya



Dr.Francis Ndungu

Authors : Francis Ndungu

Affiliation : KEMRI-Wellcome Trust Research Programme

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001598

Status : Approved

Antibody and T cell responses to SARS-CoV-2 following COVID-19 in Dhaka, Bangladesh: the impact of diabetes mellitus



Dr.Mohammad Ali

Authors : Mohammad Ali

Affiliation : Directorate General of Health Services, Bangladesh and University of Oxford

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001597

Status : Approved

Systems-based approaches to antigen discovery: implication for rational malaria vaccine design



Prof. Denise Doolan

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001596

Status : Approved

Bangladesh- COVID-19: Context, Engagement and Modelling, Milestones



Assoc. Prof.mofakhar hussain

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001595

Status : Approved

An overview of pathophysiology of malaria The effects of temperature on Plasmodium falciparum development



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Affiliation : Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001594

Status : Approved

Increase efficiency of data management process through automated reports



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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001593

Status : Approved

Inhibitory effects of KAE609 and KAF156 on cytoadherence of *Plasmodium falciparum*



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No abstract available

Keyword : No keywords available

Abstract No. : ABS0001592

Status : Approved

Monitoring of Covid-19 vaccination coverage



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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001591

Status : Approved

Implementation of Covid-19 vaccination



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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001590

Status : Approved

Overview of Thailand Covid-19 vaccination roll-out



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Authors : Chaninan Sonthichai

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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001589

Status : Approved

Safety and Long-Term Immunogenicity of a Chikungunya Virus-Like Particle (CHIKV VLP) Vaccine



Ms.Sarah Royalty Tredo

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Affiliation : Emergent Biosolutions, Inc

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001588

Status : Approved

EVIDENCE OF POSSIBLE LONG-TERM ENDEMICITY OF CHIKUNGUNYA TRANSMISSION IN SOUTHERN THAILAND



Dr.KATHRYN ANDERSON

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Chikungunya virus (CHIKV) infections are distributed broadly across the globe, causing significant and, often, lasting morbidity. CHIKV vaccines and antivirals are in development, but their evaluation is limited by the unpredictability of CHIKV transmission, which classically manifests as explosive epidemics separated by long interepidemic periods. A passive surveillance study for undifferentiated febrile illness was established in southern Thailand in 2012 and is ongoing. Among 1473 individuals with paired acute and convalescent specimens, 391 (26.5%) had molecular or serological evidence of acute CHIKV infection. Seroconversion rates differed by age and by year, being highest among those aged 20-39 and during epidemic periods (39.2% in 2018-2019, corresponding to a large regional CHIKV outbreak, compared to 18.9% in 2012-2017). These data indicate possible stable endemicity of CHIKV in the study area, though additional studies are needed to discern whether this persistence reflects widespread, low-level transmission or migrating bursts of focal epidemic activity.

Keyword : Chikungunya, transmission, Southern Thailand

Abstract No. : ABS0001587

Status : Approved

Optimized clinical management to reduce COVID-19 outbreak



Dr.weerawat manosuthi

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No abstract available

Keyword : No Keyword available

Abstract No. : ABS0001586

Status : Approved

Natural history of SARS-CoV-2 variants



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No Abstract available

Keyword : No Keyword available

Abstract No. : ABS0001585

Status : Approved

Pre-departure COVID-19 screening: Is it worth it?



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No abstract available

Keyword : No keywords available

Abstract No. : ABS0001584

Status : Approved

Travel medicine practices during COVID-19 era in Thailand



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The coronavirus disease 2019 (COVID-19) pandemic has disrupted air travel because of the need for public health measures to contain the spread of the virus. Most countries have sealed their international borders, resulting in a substantial decline in international travel by > 70% in 2020 especially in Thailand. Travel medicine practices during COVID-19 pandemic in Thailand has been a challenge.

During the pandemic, travel medicine practitioners provide comprehensive approach on pre-departure screening for COVID-19. Although there was a rare post-travel visit due to travel restriction, we have also played an important role on COVID-19 patient care including acute respiratory illness (ARI) clinic and ward round. We have also contributed to COVID-19 vaccination rollout in our hospital.

In this session, we discuss the experiences and lessons that we have learnt during the pandemic in our travel clinic.

Keyword : COVID-19, Travel medicine, Thailand

Abstract No. : ABS0001583

Status : Approved

Defining severe malaria



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No abstract available

Keyword : No keywords available

Abstract No. : ABS0001582

Status : Approved

INTRODUCTION: PATHOPHYSIOLOGY OF SEVERE MALARIA



Prof. Arjen Dondorp

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Affiliation : ¹ Mahidol Oxford Tropical Medicine Research Unit

In the pre-treatment era an estimated one in five children in sub-Saharan Africa lost their life to severe falciparum malaria. In the present day still more than 1000 children die from malaria every day. Although severe malaria can be defined as a sepsis syndrome, its pathophysiology is essentially different from bacterial sepsis. The microcirculation of vital organs is compromised by sequestration of red cells containing the more mature forms of asexual stage P. faciparum. Intravascular haemolysis of both parasitised and unparasitised erythrocytes cause high plasma concentrations of haemoglobin, which is a nitric oxide scavenger, and toxic for the kidney and other organs. These pathophysiological pathways and possible interventions for mitigation will be discussed during this session.

Keyword : Pathophysiology, severe malaria

Abstract No. : ABS0001581

Status : Approved

HUMAN LEUKOCYTE ANTIGEN (HLA) AND SUSCEPTIBILITY TO VIRAL AND BACTERIAL INFECTIONS



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Keyword : HLA, Bacterial, Viral, Association, Susceptibility

Abstract No. : ABS0001580

Status : Approved

EVALUATION OF POINT-OF-CARE TEST AND PCR FOR MELIOIDOSIS IN THAILAND



Ms.Chawitar Noparatvarakorn

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Melioidosis is a tropical infection caused by *Burkholderia pseudomallei*. Melioidosis is associated with diverse clinical manifestations and high mortality. Early diagnosis is needed for appropriate treatment, but bacteria culture gives delayed results. We previously developed a rapid immunochromatography test (ICT) based on hemolysin co-regulated protein 1 (Hcp1) and two ELISAs based on Hcp1 (Hcp1-ELISA) and O-polysaccharide (OPS-ELISA) for serodiagnosis of melioidosis. This study prospectively validated the diagnostic accuracy of the Hcp1-ICT of suspected cases and determined its potential use in identifying occult-melioidosis cases. Patients were enrolled and grouped by culture results. The patients included 62 melioidosis cases, 61 other infection patients and 50 patients with no growth in bacterial culture. The results of Hcp1-ICT were compared with culture, a quantitative PCR based on a type-3 secretion system1 (TTS1-qPCR), Hcp1-ELISA, and OPS-ELISA. The patients with no growth results were followed up for subsequent culture results. Using bacterial culture as a gold standard, the sensitivity and specificity of Hcp1-ICT were 75% and 91.8%, respectively, comparable to Hcp1-ELISA and OPS-ELISA. The sensitivity and specificity of TTS1-qPCR were 71.1% and 100%, respectively. The diagnostic accuracy was markedly improved if Hcp1-ICT was combined with TTS1-qPCR (sensitivity and specificity were 96.7% and 91.8%, respectively). In the no-growth group, Hcp1-ICT identified 5 (7.1%) occult melioidosis cases, all of whom were subsequently confirmed as melioidosis by repeated bacterial culture. The combined Hcp1-ICT and TTS1-qPCR test are useful for early diagnosis, and Hcp1-ICT is a promising Point-of-care test for rapid identification of melioidosis in culture-negative individuals.

Keyword : *Burkholderia pseudomallei*, melioidosis, rapid immunochromatography test, serodiagnosis, PCR, TTS1

Status : Approved

UP COLLEGE OF PUBLIC HEALTH/TROPMED PHILIPPINES' COLLABORATION WITH THE COMMISSION ON HIGHER EDUCATION IN RESPONDING TO THE COVID-19 PANDEMIC



Dr. Paul Michael Hernandez

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The COVID-19 pandemic disrupted provision of services, particular those in healthcare. Although the Commission on Higher Education is only mandated to lead higher education programs in the Philippines, it realized that it can maximize its main resource in contributing to the pandemic response – the State Universities and Colleges (SUCs). In response to the lack of Community Isolation Units (CIUs) in the country, CHED established the CHED-Public Health Experts Group last March 2020. CHED-PHEG is an interdisciplinary group of experts, with majority serving as faculty members coming from SEAMEO TROPMED Philippines, initially created to develop guidelines for the establishment of SUCs as CIUs. Throughout the pandemic, the CHED-PHEG continued to provide technical assistance in the establishment of vaccination centers and recently, in offering limited face-to-face classes among Higher Education Institutions (HEIs). The group also served as resource persons in COVID-19 webinars offered by CHED. These tasks required an expansion of the membership with the group now composed of 10 experts. As of August 2021, 28 SUCs served as CIUs, 63 HEIs served as vaccination centers, and 130 HEIs offered limited face-to-face classes. Hundreds of CHED and HEI employees benefitted from the COVID-19 webinars. The CHED-PHEG experience exemplified the Seven C's of Strategic Collaboration developed by Austin in 2000. It also demonstrated the effectiveness of the Whole-of-Government Approach in addressing societal challenges. Maximizing resources, regularly consulting stakeholders, and closely monitoring initiatives, enabled the expert group to provide immediate but evidence-based solutions in addressing public health challenges brought about by the COVID-19

Keyword : COVID-19, patient isolation, mass vaccination, return to school, capacity building, public health practice

Abstract No. : ABS0001578

Status : Approved

Evidence on SARS-CoV-2 transmission and physical distancing



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Non-pharmaceutical interventions (NPIs) have been used to contain respiratory epidemics; not only for influenza, RSV, SARS or MERS, but also for recently emerged COVID-19. It has been justified that SARS-CoV-2, the virus that causes COVID-19, mainly transmit through droplets and contact, while aerosol transmission is possible in some circumstances. The systematic review on COVID-19, SARS, and MERS revealed 1 m or more of physical distance, face masks, and eye protection were associated with reduction of infection. Current evidences also support the increased risk of SARS-CoV-2 aerosol transmission under the predisposing conditions (not only considering the particle's size) including; poorly ventilated or indoor settings, increased exhalation (e.g., exercising, shouting, singing) or aerosol generating activities, and prolong exposure (more than 15 minutes) to those predisposing conditions. Then, concern has been raised regarding possibility of inhalation of virus at any distance, though higher aerosol concentration should be presented near the source cases. Evidences also revealed viability of SARS-CoV-2 in aerosols for hours , which its role in disease transmission need to be further explored. Then, in this COVID-19 era and beyond, to yield the most effective prevention, optimum physical distance (as part of NPIs) should always be considered in the contexts of individual compliance of mask wearing and hand hygiene, magnitude of exhaled activities, exposure times and environmental influences.

Keyword : SARS-CoV-2 transmission, physical distancing, COVID-19, airborne transmission

Abstract No. : ABS0001577

Status : Approved

Tropical and travel medicine education in the tropics



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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001576

Status : Approved

Online Tropical medicine education: Challenges and opportunities



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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001575

Status : Approved

COVID and marginalized urban communities



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No abstract available

Keyword : No keyword available

Abstract No. : ABS0001574

Status : Approved

Diversity in COVID response, BKK experience



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No abstract available

Keyword :

Abstract No. : ABS0001571

Status : Approved

THE USE OF BIO-PLEX SARS-COV-2 NEUTRALIZATION ANTIBODY ASSAYS TO STUDY VACCINE EFFICACY AND ANTIBODY RESPONSES TO ARISING VARIANTS OF CONCERN.



Ms.Angele Koh

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Affiliation : Bio-Rad Laboratories (S) Pte Ltd

There is a need to understand the longevity of the humoral immune response and how effective neutralizing antibodies are against arising variants of interest or concern, in order for public health researchers and therapeutic developers to attribute appropriate levels of concern to arising variants for the protection of individuals and communities.

We present a highly efficient, multiplex Bio-Plex Pro SARS-CoV-2 neutralization assays against the two wild-type and 11 variants of RBD and S1 subunits which would allow researchers to assess the efficacy of COVID-19 vaccines and compare effectiveness of naturally acquired or vaccine-induced antibody response, from as little as 15 μ l of human serum or plasma samples.

Briefly, antigens are coated on magnetic beads that bind neutralizing antibodies in competition with a biotinylated detection ACE-2 receptor. For quantitative assays, a standard and a positive control are included in the kit. A lower median fluorescence intensity (MFI) corresponds to samples with higher levels of neutralizing antibodies against the various SARS-CoV-2 Receptor Binding Domain (RBD) and Spike 1 (S1) antigens. Clinical specificity ranged from 95-100% from 118 human samples and clinical sensitivity ranged from 89-100% from 84 samples. In particular, clinical specificity for the Delta RBD and Spike Trimer was 95-97% from 114 samples and clinical sensitivity was 98.7-100% from 76 samples. Cross-reactivity to other samples positive for non-SARS-CoV-2 pathogens had less than 5% CV.

Individual assay components are also available, offering the flexibility to assay only the IgG, IgA, IgM or neutralization antibodies of interest. Moreover, the Custom Assay Developer kit could be used to develop assays with future variants of interests.

Keyword : neutralization antibodies, serology, COVID, public health, vaccine

Abstract No. : ABS0001570

Status : Approved

FUTURE PREPAREDNESS AND RESPONSE TO COVID-19 OUTBREAK IN PRISONS



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In order to prepare and deal with future COVID-19 outbreaks in prisons, efforts should be made in the following aspects: 1. Learning to live with COVID-19 2. Developing a resilient prison health system 3. Preparing a guideline for dealing with emerging infectious diseases 4. Preparing the incident action plans and conducting the drill regularly 5. Applying the DMHTT measure appropriately, in accordance with the disease situation 6. Building standardized quarantine rooms and isolation rooms 7. Increasing the coverage of COVID-19 vaccination, as per the guideline of the Ministry of Public Health 8. Putting in place a post-release monitoring system and 9. Improving staff's abilities by integrating the training course on COVID-19 prevention and control as part of the Department of Disease Control's

training course on Correctional medicine and training course on disease prevention and control for the prison volunteers.

Keyword : preparedness and response, COVID-19, prison

Abstract No. : ABS0001569

Status : Approved

RESURGENCE OF CHIKUNGUNYA IN THE KINGDOM OF CAMBODIA: FEBRILE AND ENTOMOLOGICAL SURVEILLANCE



Ms. Daliya Nop

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Chikungunya virus (CHIKV) poses a major public health threat in Cambodia. Since the last major outbreak in 2012, CHIKV has maintained a relatively low detection rate, up until July 2020, when a cluster of suspected Chikungunya cases was reported in Banteay Meanchey province. These cases turned into a resurgence that by October 2020 had quickly spread across 20 Provinces.

During the 2020 outbreak, the U.S. Naval Medical Research Unit TWO (NAMRU-2) conducted both febrile illnesses and outbreak response surveillance, with 1,152 blood samples collected from 5 provinces, and 689 households inspected for vectoring mosquitoes. Adult and immature mosquitoes were collected and identified to species. *Aedes* mosquitoes were pooled and screened for CHIKV using real time RT-PCR, with the immatures reared and screened for insecticide resistance.

The majority of CHIKV cases were detected from July to December 2020: 6.9% (n=1,152) were positive for PCR, 19.7% (n=691) by IgM, and 24.4% (n=718) by IgG (paired acute-convalescence). Immature *Aedes* were collected from 860 out of 3,505 containers inspected, with the majority collected from cement jars. *Aedes aegypti* and *Ae. albopictus* accounted for 10.6% and 1.4% of the total 4,611 adult mosquitoes collected. Chikungunya virus was detected in 4.8% (n=247) of *Ae. aegypti* pools. At WHO diagnostic concentrations, the mosquitoes had less than 90% mortality for both permethrin and deltamethrin.

This study highlights the need for robust and synergistic CHIKV monitoring systems for early detection, and to guide communities and decision-makers for appropriate vector control efforts and precautionary measures to prevent future outbreaks.

Keyword : *Aedes aegypti*, *Aedes albopictus*, Entomological Surveillance, Chikungunya, Cambodia

Abstract No. : ABS0001568

Status : Approved

Droplet digital polymerase chain reaction (ddPCR) for the detection of *Plasmodium knowlesi* and *Plasmodium vivax*



Prof. Yee Ling Lau

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Background: *Plasmodium knowlesi* and *Plasmodium vivax* are the predominant Plasmodium species that cause malaria in Malaysia and play a role in asymptomatic malaria disease transmission in Malaysia. The diagnostic tools available to diagnose malaria, such as microscopy and rapid diagnostic test (RDT), are less sensitive at detecting lower parasite density. Droplet digital polymerase chain reaction (ddPCR), which has been shown to have higher sensitivity at diagnosing malaria, allows direct quantification without the need for a standard curve. The aim of this study is to develop and use a duplex ddPCR assay for the detection of *P. knowlesi* and *P. vivax*, and compare this method to nested PCR and qPCR.

Methods: The concordance rate, sensitivity and specificity of the duplex ddPCR assay were determined and compared to nested PCR and duplex qPCR.

Results: The duplex ddPCR assay had higher analytical sensitivity (*P. vivax* = 10 copies/ μ L and *P. knowlesi* = 0.01 copies/ μ L) compared to qPCR (*P. vivax* = 100 copies/ μ L and *P. knowlesi* = 10 copies/ μ L). Moreover, the ddPCR assay had acceptable clinical sensitivity (*P. vivax* = 80% and *P. knowlesi* = 90%) and clinical specificity (*P. vivax* = 87.84% and *P. knowlesi* = 81.08%) when compared to nested PCR. Both ddPCR and qPCR detected more double infections in the samples.

Conclusions: Overall, the ddPCR assay demonstrated acceptable efficiency in detection of *P. knowlesi* and *P. vivax*, and was more sensitive than nested PCR in detecting mixed infections. However, the duplex ddPCR assay still needs optimization to improve the assay's clinical sensitivity and specificity.

Keyword : Droplet digital polymerase chain reaction; Malaria; Plasmodium knowlesi; Plasmodium vivax.

Abstract No. : ABS0001567

Status : Approved

COVID-19 OUTBREAK CONTROL AND THE NOW NORMAL IN PRISON SETTINGS.



Prof. WISIT WISITSORA-AT

Authors : Prof. Wisit Wisitsora-at

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The Department of Corrections, Thailand has encountered the first confirmed Covid-19 case in 2020. The Number of cases started to grow rapidly since April 2021 affecting 75 prisons across the country with more than 110,000 total cases. Due to prison overcrowding, the virus is widespread across the entire prison soon after the first confirmed case is detected in a prison which becomes extremely challenging for prison authorities and medical teams to treat hundreds of patients simultaneously.

The Ministry of Justice, directed by the permanent secretary, established an Emergency Operation Centre (EOC) in response to the crisis within detention facilities, specifically in prisons and juvenile detention centres. The EOC and the Department of Corrections, in collaboration with the Ministry of Public Health, has developed strategies to combat the outbreak. Several measurements including proactive screening, quarantine, infection control, spontaneous and optimal treatment and vaccination have been implemented in 143 prisons across Thailand to ensure that every patient gets access to effective treatment and minimise the mortality.

The department of corrections is successfully managing the situation by increasing treatment accessibility and reduce case fatality ratio to approximately 0.12%.

Keyword :

Covid-19 Prison Pandemic Management

Abstract No. : ABS0001566

Status : Approved

Optimal compliance with appropriate use of PPE to reduce HAI



Mr.Visal Moolasart

Authors : Dr Visal moolasart

Affiliation : Department of Disease Control

Combining optimized using personal protective equipment (PPE) and hand hygiene is the principal policy to reduce healthcare-associated infections (HAI) and the importance preventing COVID-19 in hospital. Hundreds of millions of people are afflicted every year by preventable HAIs in the world. Globally, the infections acquired in hospitals has brought suffering to more than 1.4 million people. HAIs not only threaten the patients' health and life but also bring additional economic burden to the patients and healthcare provider including direct economic disadvantage and prolongation of hospital stay.

As the COVID-19 pandemic swept through Thailand, the pandemic response located burden on acute care facilities, which may have altered staffing management, increased critical care capacity, and modified use of PPE.

COVID-19 is generated by the severe acute respiratory syndrome coronavirus 2. This disease is highly contagious, spread through droplet transmission, life threatening, and the public health emergency of international concern. The WHO recommendations for PPE for HCWs working in patient rooms or wards in the absence of aerosol-generating procedures are according to the setting, personnel, and type of activity. They comprise medical masks, gown, glove, and eye protection accompanied by hand hygiene. Coveralls, double gloves, or head covers (hoods) that cover the head and neck used in the context of filovirus disease outbreaks are not required when handling COVID-19 patients.

Keyword : optimized using personal protective equipment (PPE)

Abstract No. : ABS0001565

Status : Approved

Fish-borne Parasite: Situation and Integration



Dr.Choosak Nithikethkul

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Fish-borne parasitic zoonoses have been important public health problems in many parts of the world, particularly in countries of lower Mekong regions ie; Thailand, Lao People's Democratic Republic (Lao PDR), Vietnam, Cambodia and Myanmar. Presently, several reports indicate that metacercariae of pathogenic trematodes are found in freshwater fish commonly small liver fluke, *Opisthorchis viverrini*; minute intestinal flukes (MIF); family of Heterophyidae. Opisthorchiasis is also the highest public health problem which had been recognized as the main parasitic zoonoses which stated as the national control programs in Thailand. The strategy of prevention and control programs dealing with parasitic progress, many crucial factors influence the transmission rates of infection. In the case of opisthorchiasis, the raw consumption habit or undercooked fish is the primary source of transmission for infection. The spatial analysis would be the trends and analyze the risk factors that correlate with infections among rural Thai people. The national campaign program recommendation that already showed the impact of National program useful for every country especially in Mekong basin for elimination and control for opisthorchiasis. The trends of the overall prevalence of opisthorchiasis decline were showed the crucial support from strategy and policy maker from 10 years' strategic plan for the elimination of the liver fluke and CCA. Through theoretical addition, this health informatics model can be subsequently utilized to develop tools and programs for the prediction, prevention and control of fish-borne parasitic zoonoses and thus could lead to a decline in the prevalence of infection, especially in the remote areas.

Keyword : Situation, Fish-borne parasite, Opisthorchiasis, *O. viverrini*

Abstract No. : ABS0001564

Status : Approved

CHALLENGES AND LESSONS LEARNT FROM NEPAL DURING COVID-19 PANDEMIC: EXPERIENCES OF CIWEC HOSPITAL AND TRAVEL MEDICINE CENTER



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CIWEC Hospital and Travel medicine center is a 25 bed hospital, catering mainly to tourists and expatriates. With the beginning of pandemic and the unpredictable circumstances, there were almost no tourists and most expatriate families returned home.

Redesigning our infrastructure to take care of Covid-19 patients and boosting the morale of our staff and patients that they are working in a safe environment were our initial major challenges. Training of staff in covid-19 care, organizing necessary materials and equipment to maintain international level of care were quite demanding in the time of scarcity and lockdown and constrained financial resources. Investment skyrocketed with almost no income.

Optimizing patient care with minimal nurse visits was overcome by putting glass windows in the wooden doors and putting monitors in private rooms. Need of additional space compelled us to shut down our dental service.

We learnt to prepare for the worst while being optimistic. Use of technology to communicate with the patients and their families helped us to stay connected which we have continued to practice. We learnt to optimize our resources.

COVID 19 pandemic further strengthened the core value of team work by making us resilient and supportive and prepared us for future disasters/pandemics. It taught us to accept our new normal: "use masks and consider your safety first".

Overall, the lessons we learnt will help to build a robust system for better patient care.

Keyword : COVID 19, Pandemic, Travel Medicine, Nepal

Abstract No. : ABS0001563

Status : Approved

Healthy Environments And Lives (HEAL) – a new Australian initiative in human health and environmental change



Prof. Sotiris Vardoulakis

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The HEAL (Healthy Environments And Lives) Network aims to strengthen the Australian community and health system resilience to climate change, extreme weather events, and other environmental change. This will be achieved by building capacity and stimulating collaborative research that will improve our understanding of the interactions between climate, the natural and built environment, public health, and their inequitable impacts across communities.

The HEAL is distributed and includes multiple Communities of Practice, comprising researchers, practitioners, communities and decision-makers from all jurisdictions. Based on initial gap analyses and stakeholder consultations, we have established 10 interdisciplinary research themes (Indigenous Knowledge Systems; Data and Decision Support Systems; Science Communication; Health System Resilience; Bushfires and Extreme Events; Food, Soil and Water Security; Biosecurity and Emerging Infectious Diseases; Urban Health; Rural and Remote Health; At-risk Populations and Lifecourse Solutions) and a range of capacity building activities.

HEAL will address capacity and gaps in health and environmental change, and credibility gaps in interactions between policy-makers, practitioners, industry and communities. One crucial outcome is developing the meta-capacity needed to formulate priorities, and conduct and translate research into policy and practice. HEAL is grounded in existing and new interdisciplinary collaborations with communities, health departments, government agencies, professional organisations, charities and industry.

HEAL will prioritise evidence and capacity needs, and local action with community-led co-design of Community Resilience Plans embedded in a monitoring and evaluation framework. This will lead to more effective national, regional and local policies to protect and improve public health and reduce inequalities within and across communities.

Keyword : human health, environmental change, HEAL

Abstract No. : ABS0001561

Status : Approved

DISEASES PREVENTION AND CONTROL REGARDING

“THE ROYAL GOOD HEALTH GOOD HEART PROJECT” AND PRISON MANAGEMENT AMIDST THE COVID-19 CRISIS IN THAILAND.



Dr. Subin Chewprecha

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Prison healthcare including diseases prevention and control for people in prisons and jails are the medical specialty both in normal situation and diseases pandemic. Enclosed prison populations are particularly vulnerable to infectious diseases as well as hepatitis, tuberculosis, AIDS, and HIV, including COVID-19. In Thailand prison health is under the Royal “Good Health, Good Heart” project, which was initiated under the royal patronage of His Majesty the King, had enhanced the quality of health care inside prisons. Fortunately, all these efforts had been timely, as the country was confronting the COVID-19 pandemic, and as of result, only out of 73,800 prisoners had been infected with the COVID-19 virus and mortality rate 0.23 percentage lower than in communities 1.01. Actually, the COVID-19 crisis is not only effects to prisoners’ health but also prison healthcare and other diseases prevention and control measurement. Meanwhile, the main infectious diseases need to be screening, initial curing and well-organized since the first month of prisoner arrives the prison. Therefore, diseases prevention and control procedure amidst the COVID-19 pandemic is challenge for public health issue, need to re-organized, flexible, and suitable to COVID-19 situation. Moreover, concerning of prisons are a complicated, stigmatized environment to practice medicine, as well as the standard of health care service in prisons must be equivalent to the services available outside prisons is the most concern too.

Keyword : COVID-19 Crisis, prison healthcare, diseases : prevention and control, The Royal Good Health Good Heart Project

Abstract No. : ABS0001560

Status : Approved

INCREASED KNOWLEDGE AND AWARENESS OF MELIOIDOSIS IN THAILAND: A COMMUNITY-BASED PARTICIPATORY ACTION ANALYSIS



Ms. Rungnapa Phunpang

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INTRODUCTION: Melioidosis is caused by infection with an environmental bacterium, *Burkholderia pseudomallei*. It is a public health threat in tropical regions and is associated with high mortality. Improvement in knowledge and awareness of melioidosis among community members is crucial to ensure prevention and reduce mortality.

METHODS: A study was conducted in the Thawat Buri district of Roi Et Province, Northeast Thailand to assess the knowledge and awareness of melioidosis among community residents with the aim of generating and implementing an appropriate educational campaign from focus group discussions (FGDs).

RESULT: Thirty-six percent of 372 residents had heard of melioidosis. Sources of information about melioidosis were mainly from healthcare providers (35.1%). Of those participants who were unaware of melioidosis, 61.8% had attained elementary education and 73.9% had an agriculture occupation. To address this knowledge deficit, five FGDs with 39 different study participants were conducted to develop a strategy to increase knowledge and awareness about melioidosis for their community. A Mor-Lam, a local song, was created as the best strategy to raise awareness. A song describing the symptoms, transmission, and prevention of melioidosis is broadcast every day as a tool for the educational campaign. Residents' knowledge about melioidosis significantly improved from 14% to 80% after the educational campaign.

CONCLUSION: The study revealed that baseline knowledge and awareness of melioidosis were poor in this community. These could be improved after educating the public through mass media. Delivering disease information and strengthening the engagement of stakeholders at different levels in the health system is recommended.

Keyword : Northeast Thailand, Melioidosis, Knowledge, Awareness, Participatory action research

Abstract No. : ABS0001559

Status : Approved

“PUBLIC HEALTH IN THE TIME OF COVID-19 AND THE NEW NORMAL”: A WEBINAR SERIES FOR PUBLIC HEALTH WORKERS



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The COVID-19 pandemic has brought innumerable challenges to public health service delivery in the country, thereby impeding the achievement of the UN Sustainable Development Goals. There is a need to ensure that policy makers, professionals, providers and the general public are informed on changes that COVID-19 has brought to various public health programs and are able to sustain implementation of public health programs. The 12-part webinar series, co-organized with the British Embassy Manila, aimed to provide updates on COVID-19 and their impact on public health program implementation, present challenges in service delivery, offer solutions and good practices, and discuss next steps on how major public health programs could adapt to the New Normal.

Twelve webinars were organized with the following topics: 1) COVID-19 in the Asia Pacific Region, 2) vaccine preventable diseases, 3) tuberculosis, 4) non-communicable diseases, 5) mental health, 6) HIV/AIDS and hepatitis, 7) parasitic neglected tropical diseases, 8) water, sanitation and hygiene, 9) occupational health, 10) maternal and reproductive health, 11) stunting prevention and 12) health communication. Each webinar had three speakers and

two reactors representing the following sectors: national government, academe, civil society and international agencies.

The webinar attracted a cumulative total of 9,910 attendees, mostly from the Philippines but also from other Southeast Asian countries, and also including overseas Filipino workers in the Middle East, Europe, and the United States. Generally, the webinar series underlined the multidisciplinary nature of public health and the importance of building credibility and trust using appropriate channels, while emphasizing solutions that

Keyword : webinar series, public health, New Normal

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MANAGEMENT OF COVID-19 IN THE COMMUNITY SETTING: COMMUNITY ISOLATION (CI) AND HOME ISOLATION (HI)



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In June 2021, the number of new COVID-19 cases had begun to surge in Bangkok, Thailand. Hospital beds had been occupied, too many patients waiting for hospitalization, and some died because of delayed treatment.

The Public Health Ministry Policy was to place asymptomatic and symptomatic COVID-19 patients with no risk factors in home isolation to free up beds for those in more need. Patients should be confined to their home for observation so beds in medical facilities can go to those with worse symptoms. Home isolation was implemented in the Hospital for Tropical Diseases using technology, so doctors can monitor patients' symptoms remotely. A thermometer and an oximeter was provided to each patient for measuring and reporting his/her body temperature and blood oxygen level when the sick stayed at home. Three meals were also delivered to the patients every day.

In the meantime, COVID-19 patients who were unable to isolate themselves from other family members due to limited area at home could be admitted to the community isolation (CI) facility provided by local authorities with a designated hospital in Bangkok. Our hospital had set our community isolation under the collaboration with Phayathai District Office and local public health service center to provide 44 beds capacity for mild to moderate COVID-19 patients. We designed the monitoring and logistic system for patient care in the CI.

In this session, we will share the experience on the management of Home Isolation and Community Isolation under the Hospital for Tropical Diseases.

Keyword : Community Isolation, Home Isolation, COVID-19

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Food and Nutrition related to COVID-19



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Proper nutrition and hydration are vital. People who eat a well-balanced diet tend to be healthier with strong immune systems and lower risk of chronic illnesses and infectious diseases, including COVID-19. So you should eat a variety of fresh and unprocessed foods every day to get the vitamins, minerals, dietary fibre, protein and antioxidants your body needs, including vitamin D. Drink enough water. Avoid sugar, fat and salt to significantly lower your risk of overweight, obesity, heart disease, stroke, diabetes and certain types of cancer.

Keyword : COVID-19, Food, Nutrition

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Status : Approved

CLASSES AND SUBCLASSES OF ANTIBODY RESPONSES TO SAR-COV-2 VARIANTS THROUGH NATURAL INFECTION AND IN RESPONSE TO VACCINES IN THAILAND



Dr. Prapassorn Poolchanuan

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Antibody response is a central part of the immune system to develop after COVID-19 and vaccination to provide protection to SAR-CoV-2 infections. Although COVID-19 pandemic has been ongoing with higher mortality rate and series of new variants are emerging, little is known about the classes and subclasses of antibody responses to different SAR-CoV-2 variants through natural infections and in response to vaccines. We tested the hypothesis that there is a different in kinetics of IgM, IgA, IgG and IgG subclasses developments in infected individuals and their profiles are different from those of vaccinated individuals. We prospectively enrolled and collected blood samples from 30 COVID-19 patients and 30 CoronaVac vaccinated healthcare workers at day 0, day 14 and day 28. IgM, IgA, IgG and IgG subclasses of antibody specific to recombinant receptor binding protein (RBD) of SAR-CoV-2 was determined by ELISAs. RBD-specific IgM, IgA, IgG and IgG subclasses antibodies were observed in COVID-19 patients and vaccination. Among IgG subclasses, IgG1 and IgG3 were the major IgG subclasses detected in both natural infections and vaccinations. IgG2 subclass was significantly increased in natural infections. Furthermore, we observed significant higher IgM, IgA, IgG, IgG1 and IgG3 antibody responses in natural infections compared with vaccination. Our results suggest that different kinetic levels of IgM, IgA, IgG and IgG subclasses antibodies against RBD proteins of different SAR-CoV-2 wild type and variants occurs during natural infections and vaccinations. These antibody profile may link to different clinical manifestations and protection in COVID-19.

Keyword : Covid-19, SAR-CoV-2, Antibody responses, Natural infections, Vaccination

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Status : Approved

CAPACITY BUILDING FOR ENVIRONMENTAL RISK MANAGEMENT AMONG VILLAGE HEALTH VOLUNTEERS IN SURIN PROVINCE, THAILAND: STEP TOWARDS ACHIEVING THE SUSTAINABLE DEVELOPMENT GOALS



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Non-communicable diseases (NCDs) are currently the major cause of death worldwide. NCD and their major risk factors pose a huge economic burden on individuals, families, communities and countries. However, despite being most common and costly of all health problems, NCDs are preventable. Environmental factors are one of the main causes of NCDs. Reducing the risks of environmental health would greatly reduce the burden of NCDs, and it would be a crucial step towards achieving the Sustainable Development Goals.

To foster capacity building program on environmental risk management for community people the National Research Council of Thailand provided financial support to the Faculty of Public Health, Mahidol University to undertake this collaborative project with the Surin Provincial Administrative Organization (PAO).

Participatory methods were designed to include participants in the group and build self esteem and sense of responsibility. A two day workshop was held to train 80 community leaders and village health volunteers from five villages in Surin province to become environmental health risk reduction change agents. Training included module on the following: overview of environment and its effect on NCDs; process of environmental pollution management; project planning and evaluation.

Five new community projects were initiated as a result of the training program. Although this was not a specific outcome that was intended to be measured these projects support the assertion that this training program was educational, motivational, and applicable at the community level. This will contribute to control of NCDs prevalence and incidence in Thailand.

Keyword : NCD, environment, risk management, capacity building, village health volunteer

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Status : Approved

Climate Change and National Adaptation Plan: Thailand perspectives



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Introduction

Climate change has significant impacts on human health, particularly for Asia Pacific region (APR) including Thailand. If both average temperatures and extreme heat events increase as prediction. Many countries in APR will be at high risk of increased heat strain during summer..

Methods

This research is the integration of literature review, modeling approach and policy analysis. The overall purposes of this project are to generate essential scientific evidence needed by policy-makers and stakeholders for the development, prioritization and implementation of health protection strategies and policies regarding climate change.

Results

This project has been started in 2021 and the initial results of reviewing indicated that Thailand has been facing the climate change in various situation. Therefore, public health is essential as one key factor mentioned in Thailand Climate Change Master Plan (CCMP), public health aspect was identified as the outcomes of climate change. In order to take care people health and well-being as mentioned in target 3 of SDGs, adaptation plan was created and needed to be implemented in health sectors particularly in risky community. Thailand National Adaptation Plan (TNAP) was launched for implementation under the supporting from related organizations. However, it still needs more scientific information to drive the policy implementation in both central and the whole countries.

Conclusion

NAP is required to be strengthen for the country and supports from all stakeholders. Scientific information of relationships between climate change factors and health impact are needed for supporting policy maker.

Keyword : Adaptation, Climate Change, Health Impacts, Thailand

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Status : Approved

Strengthening Community Capacities for Environmental Health Management in Thailand



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Nowadays many countries especially the newly industrialized countries are faced with problems in handling air pollution especially indoor air pollution that affecting health of people in community. Some indoor air pollutions such as Volatile Organic Compounds (VOCs) and Phthalate pose various health effects ranging from acute to chronic health conditions in particular increase risk of developing chronic non-communicable diseases.

It has been significant that in light of promoting and protecting health of people in community, the training for the community health staff is one of the key success factors. This project aims to develop the knowledge and capacities of community health staffs about environmental health risk assessment and management of indoor air pollution, Phthalate, particularly with regards to establishing sustainable work practices and knowledge transfer to protecting health of people in community.

The capacity building program begins with an online five-day training course and follows by a pilot project on the community level under the supervision of experts. The five-day training course combines theory (lectures, training documents, and manuals), practical field and group work. Its training curriculum covers all essential topics in environmental health risk assessment and management of Phthalate. At the end of the course, all trainees will be evaluated by measuring of the extent to which learning objectives are met.

The study is financially supported by the National Research Council of Thailand.

Keyword : Community/ Environmental health/ Capacity building/ Phthalate/ Indoor air pollution

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MANAGEMENT OF COVID-19 IN HOSPITAL SETTING



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Treatment of COVID-19 inpatients is a stage of art that requires both scientific knowledge and a preventive mind. COVID-19 has a wide range of clinical manifestations ranging from asymptomatic infection to critical illness. To date, various antiviral agents have promising outcomes in mild to moderate COVID-19 patients, especially when given during an early phase of the disease. Unfortunately, none of the available antivirals have shown benefits in reducing mortality rates. Moreover, the head-to-head comparison study of antiviral agents is lacking. Immunomodulators are the only effective treatment in the inflammatory phase of the disease. Corticosteroid and JAK-2 inhibitors can decrease mortality in severe cases, while tocilizumab has controversial results. However, the usage of immunosuppressive agents should be strict with clinical indication, besides a high awareness of superimposed infections. Although the monoclonal antibodies revealed promising results in mortality rate reduction in mild to moderate cases, their clinical benefit in treating severe COVID-19 which requires hospitalization is unclear. Many drugs are studying in-line. The contact tracing and quarantine might not be practical in the pandemic setting; however, they are still essential, especially in household contacts of the venerable population who are at high risk for progression to severe COVID-19 disease. The hospital policies regarding patient triage and infection control are fundamental issues, especially during the epidemic of the high transmissible variants of concern, that require tailoring to the hospital context. The data and knowledge regarding COVID-19 have accumulated along with the persisting pandemic. A continuous update in the management of COVID-19 is necessary.

Keyword : COVID-19, HOSPITAL

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DISEASES PREVENTION AND CONTROL REGARDING THE GOOD HEALTH GOOD HEART PROJECT AND PRISON MANAGEMENT AMIDST THE COVID-19 CRISIS IN THAILAND.



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Prison healthcare including diseases prevention and control for people in prisons and jails are the medical specialty both in normal situation and diseases pandemic. Enclosed prison populations are particularly vulnerable to infectious diseases as well as hepatitis, tuberculosis, AIDS, and HIV, including COVID-19. In Thailand prison health is under the Royal "Good Health, Good Heart" project, which was initiated under the royal patronage of His Majesty the King, had enhanced the quality of health care inside prisons. Fortunately, all these efforts had been timely, as the country was confronting the COVID-19 pandemic, and as a result, only out of 73,800 prisoners had been infected with the COVID-19 virus and mortality rate 0.23 percentage lower than in communities 1.01. Actually, the COVID-19 crisis is not only effects to prisoners' health but also prison healthcare and other diseases prevention and control measurement. Meanwhile, the main infectious diseases need to be screening, initial curing and well-organized since the first month of prisoner arrives the prison. Therefore, diseases prevention and control procedure amidst the COVID-19 pandemic is challenge for public health issue, need to re-organized, flexible, and suitable to COVID-19 situation. Moreover, concerning of prisons are a complicated, stigmatized environment to practice medicine, as well as the standard of health care service in prisons must be equivalent to the services available outside prisons is the most concern too.

Keyword : COVID-19 Crisis, prison healthcare, diseases prevention and control, The Royal Good Health Good Heart Project

Abstract No. : ABS0001549

Status : Approved

ANTIBODY IMMUNOTHERAPY FOR VIRUS-RELATED LYMPHOMA



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Monoclonal antibody (mAb) immunotherapy is a promising treatment for B cell non-Hodgkin lymphoma (NHL). Anti-CD20 Ab has become a therapeutic mAb for B-cell lymphoma. Primary effusion lymphoma (PEL) is an aggressive B cell NHL and AIDS-related lymphoma, mainly occurs in HIV patients. Most PEL cases have no CD20 expression. Thus, new target antibody immunotherapy is mandatory to explore. Daratumumab and Elotuzumab are mAbs targeting CD38 and SLAMF7 respectively, and approved for MM treatment. Herein, the effect of Daratumumab and Elotuzumab were tested against PEL. Methods: We analyzed the expression of CD38 and SLAMF7 on PEL cells. We found that PEL cells express SLAMF7 and CD38, representing CD38 and SLAMF7 are promising targets for mAb immunotherapy. We performed antibody dependent cell cytotoxicity (ADCC) by co-culturing NK cells and PEL, determined % dead target cells. NK activity was assessed by the expression of CD107a. We conducted complement dependent cytotoxicity (CDC) assay. The % CDC was indicated by propidium iodide staining. Results: CD38 and SLAMF7 were highly expressed on PEL. The % NK mediated cytotoxicity was increased in an Effector:Target (E:T) dependent manner. In the presence of Daratumumab or Elotuzumab, the ADCC assay demonstrated an increase of NK mediated cytotoxicity against PEL. Daratumumab showed potent CDC activity whereas Elotuzumab had no CDC. CD107a expression were higher in the presence of Daratumumab and Elotuzumab. Conclusions: Daratumumab and Elotuzumab exert ADCC activities against PEL. CD38 or SLAMF7 targeting Abs could be an effective therapeutic strategy for PEL.

Keyword : Primary effusion lymphoma, Daratumumab, Elotuzumab, CD38, SLAMF7

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Status : Approved

EPIGENETIC CONTROL OF PRIMARY EFFUSION LYMPHOMA



Prof. Seiji Okada

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[Introduction] Primary effusion lymphoma (PEL) is an aggressive B-cell lymphoma arising from Kaposi sarcoma-associated herpesvirus (KSHV)/human herpesvirus-8 (HHV-8) infection. PEL shows invasive behavior through making body cavity effusions without apparent solid tumors. Typical clinical course and prognosis of patients with PEL are potentially lethal and poor. Therefore, the pathogenic mechanisms of PEL are needed to be clarified to propose novel therapy and we are focusing on epigenetic control of PEL with PU.1 and PAX5 transcription factors.

[Results] PU.1 and PAX5 were silenced in PEL cells via the methylation of the promoter regions. PU.1 and PAX5 expression were restored in PEL cells by the treatment of DNA methyltransferase inhibitors (DNMTi), which induced apoptosis for PEL cells. Upregulation of PU.1 and PAX5 by Tet-on system also induced apoptosis for PEL cell lines in vitro. Guadecitabine (SGI-110) induced apoptotic cell death against PEL cells and inhibited tumor formation in PEL-xenografted BALB/c Rag-2/Jak3 double deficient mice.

[Conclusion] PU.1 and PAX5 were silenced by methylation of these promoters in PEL cells. DNMTi could restore the expression of PU.1 and PAX5 and induced apoptosis in PEL cells. A novel DNMTi, Guadecitabine could be a potential candidate for the treatment of PEL.

Keyword : Primary effusion lymphoma, Kaposi sarcoma-associated herpesvirus (KSHV)/human herpesvirus-8 (HHV-8), DNA methyltransferase (DNMT), PU.1, PAX5

Abstract No. : ABS0001547

Status : Approved

ALTERED T CELL IMMUNOMETABOLISM IN DIABETES-IMPACT ON SUSCEPTIBILITY AND IMMUNE RESPONSE TO MELIOIDOSIS



Dr. Barbara Kronsteiner-Dobramysl

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Background

Diabetes mellitus (DM) is currently affecting over 460 million people worldwide and substantially increases the risk of infection. Melioidosis, caused by *Burkholderia pseudomallei* (BP), shows the biggest known impact of DM on acquiring infection. We have previously shown that melioidosis patients with DM use different immune response patterns for survival compared to those without DM.

Methods

We used extracellular flux analysis and flow cytometry to metabolically, functionally and phenotypically characterize peripheral blood mononuclear cells (PBMC) and activated T cells from people with DM and without (non-DM) using a Thai cohort of melioidosis patients alongside endemic controls.

Results

Polyclonally stimulated T cells from endemic controls with DM showed reduced basal glycolysis and glycolytic capacity compared to those without. In line with this, we found a reduced frequency of activated CD4⁺ and CD8⁺ T cells and impaired cytokine production (IFN- γ +TNF⁺) in the DM compared to the non-DM group. The ability of PBMC to engage in oxidative phosphorylation was reduced in recovered melioidosis patients with DM compared to those without suggesting metabolic dysfunction. Furthermore, we demonstrate a protective effect of metformin in melioidosis cases with DM with a significantly lower case-fatality rate in the group on metformin compared to the group without. Ongoing work is looking at the effect of metformin on T cell metabolism.

Conclusions

Our findings on metabolic and functional alterations of T cells in DM and melioidosis open up new avenues for therapeutic intervention for people with DM in the context of infection and vaccination.

Keyword : Melioidosis, Diabetes, T-cells, Metabolism

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Status : Approved

PERCOLATION ACROSS HOUSEHOLDS IN MECHANISTIC MODELS OF NON-PHARMACEUTICAL INTERVENTIONS IN SARS-COV-2 DISEASE DYNAMICS



Ms. Caroline Franco

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Introduction: Since the emergence of COVID-19, mathematical modelling has become an important tool for planning strategies to control the pandemic by supporting decision-making, as well as allowing an assessment of the effect of different non-pharmaceutical intervention (NPI) scenarios. A proliferation of compartmental models was observed in the modelling community, aiming to understand and make predictions regarding the spread of COVID-19. Such an approach has its own advantages and challenges: while compartmental models are suitable to simulate large

populations, the underlying well-mixed population assumption might be problematic when considering NPIs which strongly affect the connectivity between individuals in the population.

Methods: Here we propose a correction to an extended age-structured SEIR framework with dynamic transmission modelled using contact matrices for different settings in Brazil. By assuming that the mitigation strategies for COVID-19 affect the connections between different households, network percolation theory predicts that the connectivity across all households decreases drastically above a certain threshold of removed connections. We incorporated this emergent effect at population level by modulating the home contact matrices through a correction function, with the few remaining parameters fitted to hospitalisation and mortality data from the city of Sao Paulo.

Results: We have shown how different model implementations can affect the system's basic reproduction number and found significant support for the model with implemented percolation effects using the Akaike Information Criteria (AIC).

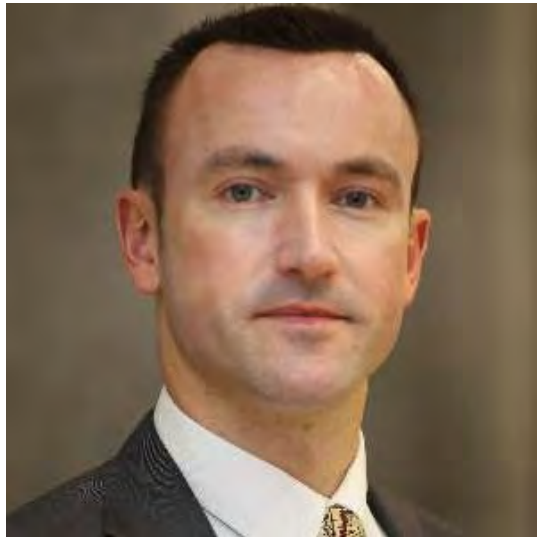
Conclusion: Beyond better agreement to our SARS-CoV-2 data, this improvement also allows for a more reliable assessment of NPI impact on other disease's epidemiological dynamics.

Keyword : compartmental model, SEIR, COVID-19, percolation

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HOW CAN AN INTERNATIONAL SOCIETY FACILITATE PROFESSIONAL EDUCATION AND TRAINING: PERSPECTIVES FROM THE INTERNATIONAL SOCIETY OF TRAVEL MEDICINE (ISTM)



Prof. Gerard Flaherty

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The International Society of Travel Medicine (ISTM) is the largest professional society devoted to education and scholarship in travel medicine. Now in its 30th year, the ISTM continues to set high standards in travel medicine clinical education with an online discussion forum, circulation of a periodic newsletter, regular webinars, an emerging podcast series, an annual review and update course, and a biennial conference, which typically attracts up to 1500 delegates from around the world. The launch of a modern learning management system and the pivot since 2020

towards virtual and hybrid delivery of educational events as well as the flagship Certificate in Travel Health examination have greatly facilitated the participation of ISTM members in its vibrant educational program. This symposium presentation will be delivered by an experienced travel medicine practitioner and educator who serves on the ISTM Executive Board as the current President-elect of the ISTM. It will describe the educational advantages of ISTM membership to delegates of JITMM 2021 and explore how ISTM can better meet its regional members' learning needs.

Keyword : Travel medicine education

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UNDERSTANDING TREATMENT-SEEKING BEHAVIOUR FOR ACUTE FEVERS THROUGH AN ABUI CULTURAL LENS: AN ETHNOGRAPHIC STUDY IN EASTERN INDONESIA



Ms.Lenny Ekawati

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Introduction. Acute fever associated with infectious disease only sometimes leads to seeking out medical attention amongst Abui-speakers on remote Alor island in southeastern Indonesia. The ways Abui people recognize fevers and apply their understanding of them are core aspects of culture, which carry important implications to community health.

Methods. Community observation and interviews are ongoing on Alor, covering demographic, socio-economic, fever social constructs, treatment-seeking behaviours and associated recent mortality. Deductive and inductive approaches are used to analyse the data.

Results. The word *tootatuk* is used locally for fever. Most frequently mentioned are *keel pasing* (seasonal influenza), *taraai tootatuk* (fever due to spleen enlargement), and *tooming kamural* (liver related fever). The latter two are commonly translated as malaria. Differentiating causation is challenging because described symptoms are non-specific. *Taraai tootatuk* is understood to be caused by consuming fatty foods, while *tooming kamural* links to mosquitoes (*kuumal*). Particular folk illnesses, *takaaya* and *loku*, involve fevers but are perceived as supernatural events. The community reports *teelmunuk* (traditional massage), *teelmaal* (body steaming), and *teelhadaq* (hot water compress) for treating fever. Self-medication with over-the-counter products is rarely expressed. Faith healers and health facilities are considered the last options only for when illnesses have become severe.

Conclusion. Traditional understanding of fevers, associated beliefs, and treatment-seeking, are thus still dominant ways of perceiving and responding to acute fevers. Health promotion, community engagement, and health workers

understanding local perception of fever illness may be key to engaging with traditional ethnic people with modern means of improving their health.

Keyword : Indonesia, acute fever illness, indigenous community, ethnography

Abstract No. : ABS0001542

Status : Approved

THE EXPERIENCE IN THE CONDUCT OF AN ONLINE LEARNING COURSE IN MANAGING MULTIDRUG-RESISTANT TB (MDRTB) OF CLINICIANS IN THE PHILIPPINES



Dr. Maria Margarita Lota

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Background: The Philippines is among the 30 countries classified as high-burden not only for tuberculosis, but also for multidrug-resistant tuberculosis (MDRTB). As a response, the Department of Medical Microbiology, College of Public Health, University of the Philippines Manila in collaboration with the UNION and Johnson & Johnson, Philippines launched TB Academy. This is a 4-week online course with asynchronous lectures and weekly live sessions which aims to strengthen the knowledge of physicians on MDRTB management. This paper describes the experiences of course participants based on the scores in the evaluation and final assessment.

Methodology: A descriptive, cross-sectional study design was employed. Pre- and post- tests were administered. Course evaluation forms were given upon completion of the course.

Results: One hundred thirty-nine physicians from 16 Philippine regions participated in seven runs of the course. Most participants are female (75%, n=104), affiliated with public institutions (84%, n=117) and managing at least 50 TB patients annually (31%, n=43). The course content was rated very satisfactory to outstanding in terms of timeliness and relevance, organization, clarity and opportunity for interaction. Majority of the participants (>90%) were satisfied

with the speakers and organizers. The average increase in the pre- and post- test scores was 36%. A total of 113 participants (81%) have graduated and successfully accomplished all the course requirements. Twenty-six participants (19%) were not able to complete the course due to the lack of time to comply with the course requirements, as a result of their workload or their poor internet connection.

Keyword : MDRTB, Philippines, online learning

Abstract No. : ABS0001541

Status : Approved

Rodent-Borne Parasites and Pathogens at Wildlife-Human Interface in Bangkok Metropolitan and Urban Public Parks



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Extensive field studies were conducted in the area of Bangkok Metropolitan to investigate parasites/pathogens carried by small mammals. The green areas such as urban public parks could exist an animal-human interface and potential risk of zoonotic disease transmission particularly in the big city. In total, 197 small mammals (5 species), i.e. synanthropic rodents: *Rattus exulans*, *Rattus norvegicus* and *Rattus rattus-complex*; Scadentia: *Tupaia belangeri*; and Insectivore: *Suncus murinus* were captured and examined for infections of macroparasites and microbial pathogens. In terms of macroparasites, high prevalence and diversity of helminths (74.6%, 25 species) and ectoparasites (70.1%, at least 5 species of chiggers, mites, fleas and lice) were found, including several potential zoonotic helminth species and important arthropod disease vectors. Parasite diversity was influenced by either host intrinsic (i.e. gender, maturity and body mass) or extrinsic factors (habitat and land use type). In terms of microbial pathogens, pathogenic *Leptospira interrogans* was detected (3.5% mean prevalence of infection). Rickettsiae (i.e. *Rickettsia typhi* and *Rickettsia felis*) were detected in four spleen samples of the rodent hosts, yielding about 2% prevalence of infection. We also screened for rabies virus and *Orientia tsutsugamushi* infection using serological and molecular diagnostic approaches, but the two pathogens were not presented in the animal tissues. These results provide essential information not only to assess the existence of potential zoonotic health threats for humans in Bangkok, but also provide cautious information to the Bangkok Public Park Office, Bangkok Metropolitan Administration for further implementation of disease prevention in the parks and nearby communities.

Keyword : Small mammals, Rodents, Parasites, Pathogens, Parasite ecology, Public parks, Bangkok

Abstract No. : ABS0001540

Status : Approved

Immunity to SARS-CoV-2 from Past Infection and Vaccines in UK Healthcare workers



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Effective vaccines for SARS-CoV-2 are now available, but there are huge global inequalities for access. It is therefore crucial to understand the immunity induced by different vaccine regimens, and the real-world vaccine effectiveness. The UK represents a high vaccination, high prevalence setting for comparison to other countries.

Extension of the interval between vaccine doses for the Pfizer BNT162b2 mRNA vaccine was introduced in the UK to accelerate population coverage with a single dose, we evaluated this in a study of UK healthcare workers. The first vaccine dose induced protection from infection from the circulating alpha (B.1.1.7) variant over several weeks. In a sub-study of 589 individuals, we showed that this single dose induces SARS-CoV-2 neutralizing antibody (NAb) responses and a sustained B and T cell response to spike protein. NAb levels were higher after the extended dosing interval (6-14 weeks) compared to the conventional 3-4 week regimen, accompanied by enrichment of CD4+ T cells expressing IL2. Prior SARS-CoV-2 infection amplified and accelerated the response. These data on dynamic cellular and humoral responses indicate that extension of the dosing interval is an effective, immunogenic protocol. Real-world vaccine effectiveness data in support of the extended dosing interval is now emerging from UK and Canada.

Ongoing work includes evaluation of the durability of vaccine-induced immunity in comparison immunity from infection, measuring the impact of third “booster” doses, and working with international collaborators to determine immunity from global vaccines. These studies will help inform international policy on vaccine deployment.

Keyword : COVID-19, SARS-CoV-2, Vaccine, Immunology

Abstract No. : ABS0001539

Status : Approved

USING OF POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT LENGTH POLYMORPHISM FOR DETECTING SOIL-TRANSMITTED HELMINTH (GENUS TRICHOSTRONGYLUS) IN LIVESTOCK, FARMERS, AND ENVIRONMENT



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Introduction: Zoonotic soil-transmitted helminths, caused by *Trichostrongylus* spp., affect livestock and humans worldwide. The aim of this study was to address this by characterizing the infection caused by *Trichostrongylus* spp. in livestock, farmers, and the environment using a combination of microscopic and molecular detection techniques.

Methods: Stool samples were collected from livestock farmers, their families, and herbivores in the provinces Nongkhai, Ratchaburi and Satun within Thailand. Vegetable samples were also collected from the farmers' households and local markets. The human and livestock fecal samples were then examined using the modified Kato-Katz technique and the Mini Parasep solvent-free fecal parasite concentrator, respectively. Subsequently, fecal and vegetable-sediment DNA extractions were performed and a fragment of the ribosomal internal transcribed spacer 2 (*ITS2*) gene (211 base pairs) was amplified using a polymerase chain reaction (PCR). The PCR products were cut using a *Hinf*I restriction enzyme; they were then sequenced and a phylogenetic tree was constructed.

Results: Single *Trichostrongylus colubriformis* infections were found in 5.29% (12 out of 227) individuals, and co-infections of *T. axei* were found in 1.32% (3 out of 227) farmers residing in Satun province. The herbivorous feces and vegetable sediments from this area also provided positive *Trichostrongylus* results, while no human *Trichostrongylosis* cases were detected in the Nongkhai and Ratchaburi provinces.

Conclusion: *T. colubriformis* and *T. axei* are zoonotic soil-transmitted helminths that have caused Satun province's residents to be a mainly asymptomatic population. Health strategies should be implemented control this issue and should focus on the human–livestock–environment interface.

Keyword : herbivorous, livestock farmer, PCR-RFLP, *Trichostrongylus*

Abstract No. : ABS0001538

Status : Approved

SEMI-DOMESTICATED DOGS AS A POTENTIAL SOURCE FOR ZONOTIC SOIL TRANSMITTED HELMINTHS IN BANGKOK, THAILAND



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Soil-transmitted helminthiasis (STH) remain a significant cause of morbidity and mortality and they are highly prevalent in the Asia-Pacific region. STH infections are common clinical disorders in humans particularly in children. Therefore, the study of potentially zoonotic helminths in animal reservoir hosts will be beneficial to the improvement of the quality of life in the region. This study was performed to determine the prevalence and genetic characterization of STH among semi-domesticated dogs in Bangkok temples. In total, 500 dog faecal samples were collected from 91 temples in 48 districts of Bangkok, Thailand. DNA was extracted and screened for STH (hookworm, roundworm and whipworm) using polymerase chain reaction (PCR). In addition, all PCR positive samples were characterized to a species level by sequence analysis. The overall prevalence of STH in dogs was 14.6% while, hookworm (6.2%) was the most common parasite followed by roundworm (5.4%) and whipworm (5%) respectively. Molecular characterization of positive hookworm samples identified 67.7% of them as the *A. ceylanicum* species and 32.3% as *A. caninum* species. Furthermore, all the roundworm present in the samples were identified as *Toxocara canis* and all whipworm in the respective positive samples as *Trichuris trichiura*. The incidence of *A. ceylanicum*, *T. canis* and *T. trichiura* in dog samples highlights the risk of environmental contamination and zoonotic transmission to the human population. Attention therefore must be directed to the further study of zoonotic helminths and to the implementation of a one health policy towards the contamination control and prevention of zoonotic helminth infections.

Keyword : Soil-transmitted helminthiasis; Zoonotic, Dogs; Temples; Bangkok

Abstract No. : ABS0001537

Status : Approved

WHAT DO WE KNOW ABOUT MOSQUITO-BORNE ARBOVIRUS PREVALENCE IN AFRICA, AND HOW CAN WE IMPROVE OUR UNDERSTANDING?



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Mosquito-borne viruses such as dengue, chikungunya, Zika and Yellow fever (YF) viruses are originating from Africa. However, diseases caused by these viruses were formerly considered as scarce in the continent except for YFV for which outbreaks are frequently reported despite of the availability of an efficient vaccine. The scarcity of cases of dengue, Zika and chikungunya was probably due to the under-diagnosis/misdiagnosis and/or similar symptoms with malaria and other infectious diseases like typhoid prevalent in Africa. During the last two decades several Aedes-borne viral diseases outbreaks have been reported in several African countries. Nowadays, it possible the prevalence of these diseases in Africa could be higher than expected. Indeed, certain studies revealed that several acute febrile patients consulting hospitals for malaria suspicion were due to dengue. It was previously considered that domestic *Aedes aegypti* in Africa was not a good vector for dengue but recent studies demonstrated that this mosquito species is rather very efficient to transmit many arboviruses including dengue and Zika in some countries. Additionally, the invasive *Aedes albopictus* mosquito is now the most prevalent *Aedes* species in certain African countries. All this could contribute to increase the prevalence of Aedes-borne viral diseases in the continent. To improve our understanding, it would be good to encourage research on arboviruses in Africa and each African country to put in place a programme to fight against arbovirus diseases with mission to ensure virological and entomological monitoring.

Keyword : Arbovirus, dengue, Aedes, prevalence, Africa

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Status : Approved

SARS-CoV-2: Genomic Surveillance for Variants of the Virus



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Genomic surveillance for SARS-CoV-2 is very important to monitor circulation of variants and lineages of SARS-CoV-2. It allows scientists to identify and monitor how the virus changes over time into new variants or lineages. This enables better understanding on how these changes in the virus affects transmissibility, severity of the disease and efficacy of the existing vaccines or therapeutics, which then assist in important public health measures.

Malaysia started genome surveillance in February 2021, through the Institute for Medical Research, Ministry of Health. During the initial stage, there were only limited capacity for genome surveillance. Most of the lineages detected were related to the Wuhan Ancestral lineage. As the prevalence of COVID-19 increased in Malaysia, there was also an increase in the diversity of the COVID-19 virus where lineages with mutations on the spike protein including D614G and A701V were detected. With the report on the global circulation of variants of concern and variants of interest, the capacity for genome surveillance was increased with other agencies. The criteria for sample selection were adapted from WHO and PAHO guidelines.

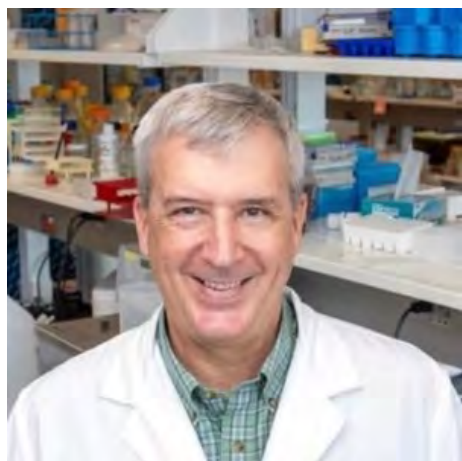
Based on the genome surveillance, Malaysia detected its first cases of alpha in January 2021, beta in March 2021 and delta in May 2021. Initially these VOCs were detected among travelers from outside Malaysia but after some time, the VOCs have been detected among local citizens without any history of travel to outside of Malaysia, suggesting local transmission. Surveillance also indicates that currently, Delta VOC is the major circulating variant in Malaysia.

Keyword : Genomic Surveillance, SARS-CoV-2 Variants of Concern

Abstract No. : ABS0001534

Status : Approved

Artemisinin resistance hijacks the *Plasmodium falciparum* heat shock response



Prof. John Adams

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Introduction: *Plasmodium falciparum* parasites resistant to artemisinin therapies represent a primal threat that may undermine our ability to control malaria. The pleomorphic nature of emerging resistance is an obstacle to counter its spread and a better understanding of resistance mechanisms is needed.

Methods: Large-scale forward genetic phenotype screens are used to decipher the complex biology involved in artemisinin resistance. The screens use libraries of random single insertion *piggyBac* transposon mutants of *P. falciparum*. Fold-change differences in growth of mutants exposed to drugs and other conditions are used to elucidate genotype-phenotype associations. In this study parasites were exposed to artemisinin, febrile temperatures, and oxidative stress.

Results: *P. falciparum* mutants sensitive to febrile temperatures were more likely to be sensitive to artemisinin derivatives as well as to heightened oxidative stress. Major processes critical for *P. falciparum* tolerance to febrile temperatures and artemisinin included highly essential, conserved pathways associated with protein-folding, heat shock and proteasome-mediated degradation, and unexpectedly, isoprenoid biosynthesis, which originated from the ancestral genome of the parasite's algal endosymbiont-derived plastid, the apicoplast. Apicoplast-targeted genes in general were up-regulated in response to heat shock, as were other *Plasmodium* genes with orthologs in plant and algal genomes.

Conclusions: *P. falciparum* exploits their innate febrile-response mechanisms to mediate resistance to artemisinin. Both responses depend on endosymbiont-derived genes in the parasite's genome, suggesting a link to the evolutionary origins of *Plasmodium* parasites in free-living ancestors.

Keyword : malaria, artemisinin, genetic screens

Abstract No. : ABS0001530

Status : Approved

CHALLENGES OF COVID-19 VACCINE DEVELOPMENT IN MALAYSIA



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COVID -19 pandemic has taught us many lessons including the need for the country to be self-reliance in vaccine production as COVID-19 vaccine is seen as one of crucial measures in combating the spread of SAR-CoV-2 in the community and in the hope to get a better life. Despite a well-established vaccine production platform, SAR-CoV-2 vaccines have been successfully developed and produced by using a newer platform, mRNA. Currently, there are 126 vaccines in clinical phase while 194 vaccines in the pre-clinical phase globally. In addition, many companies in various countries are still racing to produce quality, safe and efficacious COVID-19 vaccines despite at least 9 vaccines have been commercialized and used in human worldwide. Malaysia also realizes that the development of local vaccine production is paramount in battling the current pandemic as well as to prepare the country for any future pandemics. It is known that vaccine production is a highly complex field which requires huge financial support, various expertise in the area and suitable facilities that well equipped with certifications. Thus, each phase of the vaccine development need to be explored and highlighted as many challenges in each phase need to be overcome in making the country prepared for the local vaccine production.

Keyword : Vaccine development, challenges, Malaysia

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Status : Approved

THE ROLE OF FLAGELLIN IN *BURKHOLDERIA PSEUDOMALLEI* INFECTION OF PRIMARY HUMAN LUNG AND BLOOD CELLS



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Introduction:

Burkholderia pseudomallei (*Bps*) is a flagellated bacterium that causes the infection melioidosis. Pneumonia and bloodstream infection are common clinical presentations. The objective of this study was to evaluate the role of flagellin in the interaction of *Bps* with primary human lung and blood cells.

Methods:

Alveolar macrophages (AMs) were isolated from bronchoalveolar lavage fluid and monocytes were isolated from peripheral blood drawn from healthy volunteers. Cells were infected with wildtype (WT) or flagellin-deficient deltafliC *Bps* 1026b using a kanamycin protection assay. Bacterial uptake and intracellular CFUs were determined at serial time points following infection. Cytokines were quantified in cell supernatants using an electrochemiluminescence assay.

Results:

Primary AMs and blood monocytes were infected with WT or deltafliC *Bps* in a paired fashion. No flagellin-dependent differences in uptake or in the subsequent trajectory of intracellular bacterial concentrations were observed in either AMs or monocytes. In AMs, IL-18, IL-1alpha, IL-1beta, and IL-6 induced by *Bps* in the absence of flagellin were significantly reduced four hours after infection; both IL-18 and IL-1alpha in the absence of flagellin remained lower at 20 hours. In monocytes, G-CSF, IL-18, IL-1alpha, IL-1beta and IFN-gamma induced by *Bps* in the absence of flagellin were lower at 4 hours; IL-18 and IL-1beta remained lower at 20 hours.

Conclusions:

Uptake and subsequent intracellular concentrations of *Bps* in primary human AMs and blood monocytes are independent of flagellin. In contrast, *Bps*-induced release of multiple cytokines, especially IL-1 and IL-18, by both cell types is impaired in the absence of flagellin.

Keyword :

Melioidosis, *Burkholderia pseudomallei*, flagellin

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Status : Approved

Modelling of Health IT involved strategies in cross border controlling of COVID-19.



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Since the outbreak began, non-pharmaceutical interventions such as case-finding, high-risk screening, isolation of case, quarantine of inbound visitors, or border closure, has been rolled out to halt importing of the case and to contain domestic spreading. Such strategies subsequently, led to Thailand's economic recession. To recover the economy, allowing quarantine-free cross border travel with effective control measures must be soonest resumed.

Health IT has been proven useful while fighting against the pandemic i.e., contact tracing application, exposure notification, monitoring of cases, certifying of test results and vaccines, or algorithm-led disease screening application. Integration of such strategies and tools to inform policy on cross border movement of the population includes inbound visitors and returnees is hoped to facilitate and monitor the re-opening of Thailand. We reviewed emerging and existing mobile applications developed to proceed with international border control, then develop a

conceptual framework of Health IT -involved strategies. The framework was reviewed by a panel of stakeholders using group discussion to redefine the framework for modelling the impacts of the strategies.

Mathematical modelling is a decision-making tool, increasingly used to speculate the effectiveness of strategies against pandemics. In this study, a COVID-19 transmission dynamic model will be used to assess the impacts of mobile health technology to facilitate and monitor international border control, with or without other public health interventions. The result is expected to highlight its ability in controlling the pandemics in Thailand when its international borders are reopened.

Keyword : MATHEMATICAL MODELLING / COVID-19 / HEALTH IT / MOBILE HEALTH / CROSS BORDER TRAVEL / INTERVENTIONS / CONCEPTUAL FRAMEWORK

Abstract No. : ABS0001527

Status : Approved

UPDATE ON IMMUNITY TOWARDS SARS-CoV-2



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Less than a year into the COVID-19 pandemic, our understanding of immunity to SARS-CoV-2 is developing rapidly. A substantial portion of our current knowledge is derived from serosurveillance studies conducted in the very early stages of the pandemic and subsequently from evaluations of T-cell responses among convalescent patients with varying degrees of disease severity. Hospitalized patients who eventually died of COVID-19 have also been analyzed to help correlate the immune response with disease trajectory. Although it is becoming clear that most infected individuals achieve some form of immunity against COVID-19, with extremely few reported reinfections, the extent and durability of this immunity, including breadth of coverage of SARS-CoV-2 variants, are among the key research questions. Addressing these queries will guide research into potential vaccines and immunotherapeutic and inform vaccination recommendations from national vaccine technical committees. Therefore, the aim of this update on immunity towards SARS-CoV-2 is to summarize the latest understanding of immunity to SARS-CoV-2 infection.

Keyword : IMMUNITY; SARS-CoV-2; ANTIBODY; CELLULAR IMMUNITY

Abstract No. : ABS0001524

Status : Approved

DEFINING THE HIDDEN BURDEN OF DISEASE IN RURAL COMMUNITIES IN SOUTH AND SOUTHEAST ASIA: A HOUSEHOLD HEALTH SURVEY



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Introduction

Most people in low-and-middle-income-countries in South and Southeast Asia live in rural areas where the burden of diseases is poorly defined. This knowledge gap limits the ability of health services to identify healthcare priorities, set targets, and monitor progress. Where data are available, they show there is an ongoing epidemiological transition with communicable and, increasingly, non-communicable diseases both major causes of morbidity. Within the newly-formed South and Southeast Asia Community-based Trial Network (SEACTN), we plan a household health survey to define the prevalence of disease, disability, and pathogens.

Methods

In 2022, a cross-sectional survey will be conducted in villages in Bangladesh, Cambodia, Myanmar, and Thailand. Using two-stage cluster-sampling (village and household) it will survey approximately 1500 individuals per site. Questionnaires using electronic case record forms will record self-reported health and health history, household wealth and demographics, health-seeking behavior, and disease risk factors. Physical examinations and point-of-care tests will be performed. Venous blood will be sent to a central laboratory for assay of chronic and acute infectious diseases, and biomarkers of cardiovascular disease and diabetes.

Results

Descriptive analyses will determine the prevalence of multiple diseases and conditions, and other factors affecting health, with stratification by site, sex, risk factors, and by age-group. Primary analyses will report chronic and acute infections, non-communicable conditions diseases, disability, febrile illnesses, and self-perceived health status.

Conclusion

This survey will provide a comprehensive overview of the disease burden in rural areas of Southeast Asia to identify appropriate interventions for future research and disease control priorities.

Keyword : household survey, South and Southeast Asia, rural population, prevalence, infectious disease, non-communicable disease, risk factor, self-perceived health status

Abstract No. : ABS0001522

Status : Approved

Brain matters: improving diagnosis and outcomes in children with tuberculous meningitis



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Background

Tuberculous meningitis (TBM), a brain infection caused by *Mycobacterium tuberculosis* and the most devastating form of tuberculosis is notoriously challenging to diagnose and treat. At least 100,000 people worldwide develop TBM, many of whom are young children. Undiagnosed and untreated, all children with TBM die. Of those diagnosed and treated 20% will still die whilst 60% of those who survive will suffer long-term disability.

Aim To evaluate the role of a new rapid diagnostic test, the lipoarabinomannin (LAM)-FujiLAM, in TB meningitis in children.

Study design

Setting: Pham Ngoc Thach Hospital, Children's Hospital 2 in Ho Chi Minh City and National Lung Hospital, Ha Noi, Vietnam

Population: 200 HIV-infected and uninfected infants and children aged > 28 days to 15 years of age with TBM, and 100 with non-TBM brain infection.

Methods: All enrolled patients will have cerebrospinal fluid collected and tested for LAM using the second generation LAM(FujiLAM) and current standard tests: Xpert MTB/Rif, Acid Fast Bacilli smear and mycobacterial culture. Test performance (sensitivity, specificity, positive predictive and negative predictive values) of FujiLAM will be compared against a microbiological and clinical reference standards.

Outcomes: This study will evaluate diagnostic accuracy of a new rapid diagnostic test, yet to be evaluated in this population. It may have value either as an initial test or an add-on test with current diagnostic approaches. Results are awaited.

Conclusion: Early diagnosis and treatment of TBM are the most crucial predictors of favourable outcome. Simple, inexpensive, and rapid diagnostic testing with adequate sensitivity to 'rule-out' the disease are an urgent priority.

Keyword : Tuberculous meningitis, TBM, paediatric, Lipoarabinomannin, diagnosis

Abstract No. : ABS0001517

Status : Approved

Molecular detection of *Bartonella henselae*, *B. claridigiae*, *B. koehlerae* infected in semi-domesticated cats roaming in monasteries of Bangkok, Thailand



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Introduction: Bartonellosis is caused by pleomorphic gram-negative bacteria *Bartonella*. The most virulence and well-known *Bartonella* species is *B. henselae*. As zoonotic potential, surveillance of *Bartonella* is important and needed for public health monitor. Cats become human friends as pet however, they are carrying pathogens including *Bartonella* to their owner and surrounding people. There were large amount of abandoned cats especially in Thai monastery which has indicated as semi-domesticated cats.

Methods: We aimed to detect *Bartonella* spp. infection using molecular techniques in semi-domesticated cats roaming in the monastery collected in Bangkok. Total of 1,329 cats blood DNA were first screened for *Bartonella* spp. *gltA* gene. Thereafter, 16s rRNA was used to confirm the species specific in the *gltA* positive samples. Sequencing and phylogenetic analysis were also conducted.

Results: The results revealed the overall *Bartonella* spp. prevalence as 27.09% (360/1,329). *Bartonella henselae*, *B. claridigiae*, *B. koehlerae* and mixed infection were 11.45% (152), 5.42% (72), 0.08% (1) and 1.88% (25), respectively. High prevalence of *B. henselae* was detected in Huai Kwang (56.52%), Yan Nawa (47.83%) and Wattana (45.83%) district, respectively. Molecular detection and sequencing analysis of partial sequences were successfully showed 92-100% similarity to those published in GenBank.

Conclusion: This study revealed the zoonotic situation associated with *Bartonella* infection in semi-domesticated cat roaming in monasteries where people might get infection through cat scratch or biting. Semi-domesticated cats were crucial reservoirs and can be transmitted the pathogens to housed cats and humans who lived in the same environment.

Keyword : *Bartonella*, feline, prevalence

Abstract No. : ABS0001513

Status : Approved

DOG POPULATION SURVEY AMONG HIGH SCHOOL DOG OWNERS - A COMMUNITY-BASED PARTICIPATORY RESEARCH USING MIXED METHODS



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Rabies is a neglected disease primarily caused by dog mediated transmission. Dog information are necessary for effectively planning and evaluating population managements throughout interventions against rabies. In Thailand, longitudinal survey data on dog population is scarce. This study aimed to describe the dog demographics and dog owner perceptions. Mixed method study was conducted to define dog characteristics, gain a better understanding of contextual perception and awareness among dog owners, and describe the knowledge, disease awareness, and social responsibility regarding rabies prevention and control. We proposed a new way of performing the dog survey using owner self-report with a mobile application based on community-based participatory research (CBPR), targeting on school-age children among 4 provinces in Thailand. The dog survey data will be presented together with the rabies awareness and perception about disease prevention and control of the study participants from the interview.

This information is useful for further development of mathematical modelling to study optimal control strategies for prevention and control of rabies in Thailand.

Keyword : Dog population, Dog owner, Rabies awareness, Community-based participatory research, Mixed method

Abstract No. : ABS0001511

Status : Approved

BACTERIAL CYTOLOGICAL PROFILING (BCP): A FLUORESCENCE MICROSCOPY-BASED PLATFORM FOR ANTIBIOTIC DISCOVERY



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After the golden era of antibiotic discovery, we have been falling behind in stocking up our arsenal in fight against bacterial pathogens. The rise of multidrug resistant bacteria together with depleted reservoir of novel antibiotics have alarmed scientists around the world to step up their game in the war against antibiotic resistance. To regain control over the pathogens, one of the direct approaches is to find novel antibiotics and understand their mechanism of actions (MOAs). Finding compounds that can inhibit the growth of the bacteria is relatively easy, however elucidating their MOAs is notoriously challenging, thereby diminishing overall success rate of antibacterial discovery programs. Here we presented a high-resolution phenotypic analysis method, bacterial cytological profiling (BCP), that can identify bacterial cellular pathways inhibited by antibacterial molecules based on morphological changes upon antibiotic treatment. In addition, by comparing with known morphological profiles, BCP can also predict MOA of unknown compounds without prior knowledge of their activities nor structures. BCP offers a simple, one-step assay that could help solve a longstanding bottleneck of the antibiotic discovery pipeline in identifying MOA of candidate antibacterial molecules.

Keyword : Phenotypic screening, mechanism of action, antibiotic discovery

Abstract No. : ABS0001509

Status : Approved

Rejuvenation of aging rats by molecular scissors producing DNA gaps



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Introduction

DNA damage accumulation drives the aging process so that DNA damage prevention may result in rejuvenation. The eukaryotic genome contains naturally occurring DNA gaps in both replicating and non-replicating cells. The gap improves DNA durability. Aging cells reduce the number of DNA gaps, and DNA gap reduction accumulates DNA damage and diminishes cell viability. We named the gaps because of their role as youth-associated genome-stabilizing DNA gaps or Youth-DNA-GAPs. Our current research identified an exon of a gene that acts as molecular scissors producing the gaps.

Methods

Two aging models, D-galactose induced and aging naturally of Wistar rats, were prepared. To deliver the molecular scissors, control, and functional mutant plasmids, each type of plasmids was coated with Ca-P nanoparticle solution before the animal intraperitoneal administration. We monitored DNA gap quantity, serum hepatic biochemical parameters, SA- β -Gal staining, immunohistochemical staining, histopathological analysis, Morris water maze performance, NOL, visceral fat, liver and brain DNA damage response, and senescence-associated proteins.

Results

The molecular scissors ultimately reversed all aging features in the two aging rat models to be similar to those of young organisms. The plasmid increased DNA gaps, improved liver and brain function, reduced liver fibrosis, visceral fat, and aging and DNA damage associated proteins.

Conclusion

Youth-DNA-GAP formation protects DNA. Consequently, the molecular scissors rejuvenated aging rats. Youth-DNA-GAP formation is a potential strategy to treat aging- and DNA damage-associated diseases.

Keyword : Aging, DNA damage, DNA protection, DNA gap, Youth-DNA-GAP, Epigenetic, Rejuvenation

Abstract No. : ABS0001508

Status : Approved

THE DISCOVERY AND IMPLICATIONS OF DNA PROTECTION AND REJUVENATION EFFECTS OF DNA GAPS



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Epigenetic loss causing DNA damage accumulation in the elderly is a master key initiating and driving the aging process. Since 2008, my research team has discovered and studied the DNA protection role of a poorly recognized epigenetic mark, which are naturally occurring DNA gaps. Our current research identified an exon of a gene that acts as molecular scissors producing the gaps. Transfection of the molecular scissors produced new DNA gaps. These gaps protected DNA from being damaged and ultimately rejuvenated senescent cells and aging rats. First, we found significant levels of naturally occurring DNA gaps in all kinds of eukaryotic cells in both replicating and non-replicating cells. The DNA gaps were found retained in the hypermethylated genome and nonacetylated heterochromatin. The DNA gap levels were decreased in the mutants that lacked chromatin-condensing proteins, such as high-mobility group box proteins and Sir2. Chronological aging in yeast reduced the number of DNA gaps, and the DNA gap reduction diminished cell viability. Therefore, the naturally occurring DNA gaps are more common in youth and play epigenetic roles in preventing DNA damage. We named the gaps because of their role as youth-associated genome-

stabilizing DNA gaps or Youth-DNA-GAPs. This discovery has immense implications in medicine to cure age and DNA damage-associated diseases. For example, the molecular scissors may improve the immune function of the elderly exposed to tropical pathogens.

Keyword : Aging, DNA damage, DNA protection, DNA gap, Youth-DNA-GAP, epigenetic, Rejuvenation

Abstract No. : ABS0001505

Status : Approved

EVALUATING THE SUITABILITY OF GENETIC MARKERS FOR HELMINTH MOLECULAR STUDIES USING BIOINFORMATIC TOOLS



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With an estimated 100,000 helminth species, majority remain undiscovered. Species identification using genetic markers is vastly utilized in helminth research, not only for biodiversity, but also for disease diagnosis. The accuracy of species identification using genetic markers depends on their suitability for the specified organism. For helminths, genetic markers from the nuclear and mitochondrial DNA have been utilized. However, there is no general consensus on which is most appropriate and general assumptions of genetic distance are usually used for species delimitation. We aim to assess and select suitable genetic markers for helminth molecular studies, and provide estimated cut-off genetic distances as a yardstick for future users, useful for helminth species delimitation. Ten genetic markers from four classes were assessed for nematodes, trematodes, and cestodes. Phylogenetic analysis and genetic distance calculations were conducted to assess their suitability for species-level resolution. Statistical and an unsupervised machine learning analysis using the 'K-means' clustering algorithm were performed to estimate cut-off genetic distances. Sequence variation was dependent on the helminth group and genetic marker, substantiating that a general assumption of genetic distances is not appropriate for species delimitation. High sequence variation was present among nematodes albeit being at same taxonomic level. Additionally, the mitochondrial rRNA genes were deemed most suitable for helminth molecular studies. Using bioinformatics, popular genetic markers were assessed for their suitability for helminths. We provided a novel way of analyzing genetic distance using the 'K-means' clustering algorithm. These findings can assist in helminth species identification and to define species boundaries for delimitation.

Keyword : Genetic marker, Molecular identification, Species delimitation, Helminth, K-means

Abstract No. : ABS0001501

Status : Approved

INFECTION AND INVASION: ON PARASITES OF INVASIVE ANIMALS



Assist. Prof. Hsuan-Wien Chen

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Being one of the most active trading and transportation hubs around the world, the Southeast Asia represents a unique model for studying biological invasions. The region is not only the hot spots of biodiversity but also focal areas of highly threatened by species invasions. Nevertheless, the invasive alien animals were often introduced along with their co-invaders, such as symbiotic/pathogenic microbes or parasitic worms. Herein, I provided a case of the invasive green iguana (*Iguana iguana*) which originated in Latin America and invaded to Taiwan via pet trade couple decades ago. The parasitic infections of the invasive iguanas in Taiwan were investigated and the result has shown that >90% of wild populations of green iguana, with one exception, in Taiwan were heavily loaded with parasitic infections. The infection intensity ranged from hundreds to hundred thousand. When comparing parasitic fauna of iguanas from introduced areas with those in their native ranges, we found all parasites from invasive iguanas in Taiwan were new to local fauna. They were obviously co-introduced with their iguana hosts from various sources in America. We then used these comparisons to examine the hypothesized emery released, spill-over, spill-back as well as the dilution effect resulted from species invasions and their impacts on infection dynamics can be illustrated.

Keyword : species invasion, co-introduction, parasite spill-over, parasite spill-back

Abstract No. : ABS0001500

Status : Approved

COMMENSAL RODENT HABITAT EXPANSION ENHANCES ARTHROPOD DISEASE VECTOR ON A TROPICAL VOLCANIC ISLAND



Assoc. Prof. Chi-Chien Kuo

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Release from competitors on islands can lead to increased body size and population density, as well as expanded habitat usage of introduced animals. Such alterations might help the spread of diseases when exotic animals carry pathogenic agents. The commensal *Rattus tanezumi* is confined to residential surroundings in Taiwan mainland but can occur in the forests of a nearby volcanic Orchid Island. Orchid Island is also a hotspot of scrub typhus, a disease transmitted by trombiculid mites (chiggers) infected primarily with *Orientia tsutsugamushi* (OT). A rodent survey in three habitats (human resident, grassland, and forest) found more *R. tanezumi* and chiggers in forest than in residential sites. There was a positive association between abundance of rodents and chiggers, and between rodent body weight and load of chiggers. Lastly, >95% of chiggers were *Leptotrombidium deliense* and their OT infection rates were similar among habitats. Our study demonstrated potentially elevated risks of scrub typhus when commensal rats invaded natural habitats on islands. Additionally, while the success of invasive species can be ascribed to parasites being left behind, island invaders might instead attain more parasites when the parasite requires only a single host, is a host generalist, and is transferred from unsuitable to suitable habitats.

Keyword : rodent, invasive species, volcanic island, scrub typhus, *Orientia tsutsugamushi*, vector-borne diseases, island syndrome, *Rattus tanezumi*

Abstract No. : ABS0001497

Status : Approved

DEFINING CORRELATES OF VACCINE-INDUCED IMMUNITY AGAINST INHALATIONAL MELIOIDOSIS



Dr. PAUL BRETT

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Introduction: *Burkholderia pseudomallei* (*Bp*), the etiologic agent of melioidosis, causes severe disease in humans and animals. Diagnosis and treatment of melioidosis can be challenging and no licensed vaccines currently exist. This pathogen expresses a variety of structurally conserved protective antigens that are important components of the subunit vaccines that we are currently developing. **Methods:** In the present study, the 6-deoxyheptan capsular polysaccharide (CPS) from *Burkholderia thailandensis* E555 was purified using a phenol-less extraction procedure, chemically activated and covalently linked to recombinant CRM197 to produce CPS-CRM197. Additionally, immobilized metal affinity chromatography was used to prepare highly purified, recombinant, tag-less *Bp* hemolysin co-regulated protein 1 (Hcp1). **Results:** Immunization of C57BL/6 mice with nanogram (low dose) or microgram (high dose) amounts of CPS-CRM197 plus Hcp1 resulted high-titer IgG and opsonizing antibody responses against the CPS component of the glycoconjugates as well as high-titer IgG and robust IFN- γ secreting T cell responses against Hcp1. Following an inhalational challenge with a high dose (~ 40 LD₅₀) of *Bp* K96243, 75% of the mice immunized with the low dose formulation and 67% of the mice immunized with the high dose formulation were still alive upon termination of the study at day 60. Importantly, the majority of the tissues (lungs, livers and spleens) from the survivors in both groups were found to be sterile when assessed for bacterial loads. **Conclusion:** Collectively, these studies help to better establish correlates of antigen-induced immunity against *Bp* and provide valuable insights towards the development of a safe, affordable and effective melioidosis vaccine.

Keyword : *Burkholderia pseudomallei*, melioidosis, vaccine, capsular polysaccharide, hemolysin co-regulated protein

1

Abstract No. : ABS0001496

Status : Approved

EVALUATION OF *BURKHOLDERIA PSEUDOMALLEI* AHPC AS A NOVEL MELIOIDOSIS VACCINE CANDIDATE



Dr.Mary Burtnick

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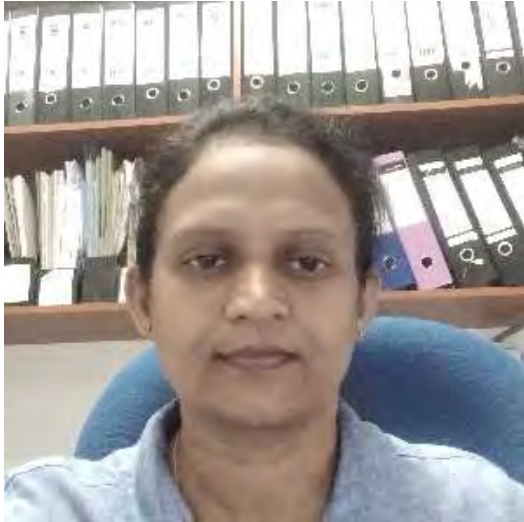
Introduction: *Burkholderia pseudomallei*, the causative agent of melioidosis, is a facultative intracellular, Gram-negative pathogen that is highly infectious via the respiratory route, and can cause severe, debilitating and often fatal diseases in humans and animals. At present, no licensed vaccines for immunization against this CDC Tier 1 select agent exist. Studies in our lab have previously demonstrated that subunit vaccine formulations consisting of a *B. pseudomallei* capsular polysaccharide (CPS)-based glycoconjugate (CPS-CRM197) combined with hemolysin co-regulated protein (Hcp1) provided C57BL/6 mice with high-level protection against an acute inhalational challenge of *B. pseudomallei*. **Methods:** In this study, we evaluated the immunogenicity and protective capacity of *B. pseudomallei* alkyl hydroperoxide reductase subunit C (AhpC) in combination with CPS-CRM197. AhpC is a peroxiredoxin involved in oxidative stress reduction and has been shown to be a potential protective antigen. To facilitate our studies, recombinant *B. pseudomallei* AhpC harboring an active site mutation (AhpC^{C57G}) was expressed in *Escherichia coli* and purified using tandem nickel-cobalt affinity chromatography. **Results:** Immunization of C57BL/6 mice with CPS-CRM197 combined with AhpC^{C57G} stimulated high-titer IgG responses against the CPS component of the glycoconjugate as well as stimulated high-titer IgG and robust IFN- γ , IL-5, and IL-17 secreting T cell responses against AhpC^{C57G}. When challenged via an inhalational route with a high-dose (~27 LD₅₀) of *B. pseudomallei*, 70% of the immunized mice survived 35 days post-challenge. **Conclusion:** Collectively, our findings demonstrate that AhpC^{C57G} is a potent activator of cellular and humoral immune responses and a promising melioidosis vaccine candidate.

Keyword :

Burkholderia pseudomallei, melioidosis, vaccine candidate, capsular polysaccharide, alkyl hydroperoxide reductase

Abstract No. : ABS0001495
Status : Approved

***Anopheles stephensi*, THE NEW INVASIVE MALARIA VECTOR; LESSONS FROM SRI LANKA**



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Introduction: *Anopheles stephensi* Liston, an efficient vector of urban malaria was first detected in Sri Lanka in December 2016 in Mannar district. Since then, its spread into four other districts is considered a major threat to prevention of malaria re-establishment in Sri Lanka.

Methods: Upon first detection, studies on *An. stephensi* were conducted to characterize breeding habitats, adult abundance, biological form, resistance to insecticides and seasonal variations as part of the entomological surveillance programme of Anti Malaria Campaign. Intense control interventions directed against larvae of *An. stephensi* were mounted with the aim of eliminating this species from the areas invaded. In addition, active entomological surveillance for *An. stephensi* in other districts were conducted to assess the possible expansion.

Results: The major breeding site of *An. stephensi* was found to be built wells. Adults were found in cattle baited traps and indoor and outdoor resting collections during the peak breeding season. The biological form was Type form based on the counts of ridges in the egg float. Adults showed resistance to tested insecticides of four main classes while larvae were susceptible to temephose. When Larvivorous fish (*Poecilia reticulata*) present in wells adequately, breeding of *An. stephensi* was absent or very low.

Conclusion: Due to enhanced entomological surveillance and vector control, currently the spread of *An. stephensi* has been curtailed limiting to three districts from the five invaded initially. Even though chemical larviciding with temephose and larvivorous fish have shown promising results in control, *An. stephensi* increases the receptivity for malaria during peak breeding season.

Keyword : *An. stephensi*, Malaria, insecticide resistance, Larvivorous fish

Abstract No. : ABS0001493

Status : Approved

INVESTIGATING THE SPATIOTEMPORAL DYNAMICS OF *P. FALCIPARUM* MALARIA TO GUIDE TARGETED INTERVENTION DELIVERY IN EASTERN MYANMAR: A 5-YEAR OBSERVATIONAL STUDY.



Ms.Jade Rae

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Malaria risk is non-randomly distributed across space, with regions of high and low risk determined by population characteristics, geography, proximity to vector breeding sites, intervention exposure, population movement and the impact of surrounding areas.

It is because of this spatial heterogeneity in malaria risk that untargeted interventions often lead to ineffective outcomes for malaria control. The strategic targeting of interventions is particularly important when resources are limited and at the elimination phase when factors associated with increased malaria risk may also play a role in the risk of malaria resurgence.

Using model-based geostatistics we explore the spatiotemporal distribution of *P. falciparum* in the Kayin State of Myanmar, accounting for intervention delivery, altitude and the spatial correlation between malaria posts to ultimately identify locations with increases in *P. falciparum* incidence over space and time. This analysis will not only inform programme operations in the Kayin State but will provide valuable insight into how longitudinal data can be effectively used by malaria elimination programmes to both understand the progression towards elimination and how past incidence can inform the delivery targeted interventions.

Keyword : *P. falciparum*; malaria elimination; spatiotemporal trends

Abstract No. : ABS0001492

Status : Approved

USING SEROLOGY TO DIAGNOSE RECENT *P. VIVAX* INFECTION



Dr. Rhea Longley

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A key challenge for elimination of *Plasmodium vivax* malaria, the dominant *Plasmodium* species in the Asia-Pacific, is the lack of surveillance tools appropriate for use in low transmission settings where total case numbers are low. Traditional monitoring tools rely on detecting parasites in a blood sample; a novel strategy is to measure antibodies induced in response to infection. Our aim was to characterise antibody responses following *P. vivax* infection and to identify specific *P. vivax* proteins as serological markers of recent exposure. Using a panel of 60 *P. vivax* proteins, we identified a bi-phasic pattern of IgG antibody decay following a peak 1-2 weeks after symptomatic *P. vivax* infection in Thai patients (n=34). IgG1 was the dominant IgG antibody subclass and followed similar kinetics to total IgG. For some proteins IgM responses were acquired and maintained independently to that of IgG. We tested the use of both IgG and IgM antibody responses to all 60 proteins for classifying individuals as recently exposed to *P. vivax* infections using large year-long observational cohort studies. We could accurately classify recent *P. vivax* infection with more than 80% sensitivity and specificity in the Thai (n=829), Brazil (n=928) and Solomon Islands (n=754) cohorts using a panel of 8 proteins. These novel serological markers have the potential to be used as a monitoring tool in global efforts to control and eliminate *P. vivax* in resource-constrained settings.

Keyword : *Plasmodium vivax*; serology; antibodies; recurrent infection; sero-surveillance; hypnozoites

Abstract No. : ABS0001489

Status : Approved

RECRUITMENT AND RETENTION OF YOUNG MSM USING SOCIAL MEDIA AND ONLINE PLATFORMS FOR THE COPE STUDY



Dr. Andrew Hickey

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Introduction: The COPE study targeted combination HIV prevention services, including the option for HIV Pre-exposure prophylaxis (PrEP), for young men who have sex with men (MSM) and transgender women (TGW). Although status and in-person recruitment were important, recruitment of the young study participants substantially improved upon implementing an internet-based recruitment campaign using targeted electronic materials.

Methods: A Thailand-based LGBTI advocacy organization (APCOM) developed marketing materials and an internet-based campaign to recruit young MSM and TGW who exchange sex for the COPE study. The campaign featured tailored electronic materials disseminated using popular web-based, application-based and social media platforms. The campaign, which first launched in September 2018, targeted supplementing peer referrals, venue/location recruitment, and engagement through health services.

Results: Meme, video, and electronic engagement materials were disseminated on popular dating websites, networking apps, and social media platforms, targeted by location and age, where available. After launch of the first social media campaign, study enrolments increased dramatically (2.1-fold increase in weekly enrolment; 95% CI, 1.6-6.3; $p=0.001$). A second social media boost did not significantly impact weekly recruitment, though the timing of the second boost may have been too near the close of participant enrolment to observe the potential benefits.

Conclusions: The COPE targeted electronic recruitment campaign successfully augmented more common static and in-person recruitment methods, for engagement of young MSM and TGW in Thailand. This study demonstrates social media is an important engagement tool, particularly for young populations where HIV incidence may be highest and who may benefit most from HIV prevention research/services.

Keyword : Young MSM, HIV PrEP, Social Media, Online

Abstract No. : ABS0001484

Status : Approved

MALARIA MASS DRUG ADMINISTRATION



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Malaria mass drug administration (MMDA) is the strategy of administering antimalarials to all age group of a defined population at the same time regardless of malaria infection status to accelerate malaria elimination via rapid and sustained reduction of transmission, mainly in areas approaching interruption of *Plasmodium falciparum*. Since World Health Organization (WHO)'s recommendation in 2015, novel investigations have been conducted in areas of low to moderate malaria transmission in Greater Mekong subregion (GMS) and Africa to generate additional data involving rapidly reducing transmission and accelerating malaria elimination.

Nevertheless, the lack of empirical evidence that MMDA can achieve sustained interruption of malaria transmission has contributed to reluctance in the malaria communities to support the use of MMDA. Newer evidence is discussed for effectively implemented MMDA to be kept in the *Plasmodium falciparum* elimination toolbox for use in a variety of settings. Several lines of evidence revealed that the use of an artemisinin-based combination treatment (ACT), such as the long-acting anti-malarial dihydroartemisinin-piperaquine (DHAP) for MMDA for *Plasmodium falciparum* has been demonstrated to be safe, poorly implemented MMDA by using a monotherapy may lead to anti-malarial drug resistance, whereas there is no evidence that effectively implemented MMDA with an ACT has contributed to drug resistance.

In conclusion, MMDA with an ACT, such as DHAP in combination with high coverage of vector control, strong surveillance, and good access to case management has been demonstrated

Keyword : Malaria, mass-drug-administration, drug-resistance, transmission

Abstract No. : ABS0001483

Status : Approved

MALARIA VACCINE ANTIGEN DISCOVERY AND INITIAL CHARACTERIZATION LEVERAGING THE WHEAT GERM CELL FREE SYSTEM



Assist. Prof. Bernard Kanoi

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Introduction: Broadly reactive antibodies against antigens expressed on merozoite surface or invasion organelles, and infected erythrocytes surface play an important role in protective immunity against *Plasmodium falciparum* malaria, and are candidates for anti-malaria therapeutics and vaccines.

Methods and Results: Here, we report wheat germ cell-free system-based production and serological profiling of a comprehensive library of VSAs (PfEMP1s, RIFINs, STEVORs and SURFINs) and merozoite-stage proteins derived from *P. falciparum* 3D7 parasite strain. We observed > 95% protein immunoreactivity in malaria-exposed individuals in Uganda. The overall breadth of immune responses significantly correlated with age but not with clinical malaria outcome among the study volunteers. We identified several proteins whose antibody profiles associate with prospectively reduced risk to symptomatic malaria suggesting that only a restricted set of specific domains or proteins are essential for eliciting naturally acquired protective immunity in malaria. Functionally, we demonstrate that rabbit antibodies against PfMSP10, one of the identified proteins, have growth inhibitory activity against cultured parasites, with the N-terminal region (PfMSP10-N), critical for its interaction with PfGAMA, being the key target. We also observe that PfMSP10-N is highly conserved among African field isolates. Individuals in a malaria endemic region with high antibody levels against PfMSP10-N have a reduced risk of having a symptomatic malaria.

Conclusion: Put together, these findings provide a rational approach that can be exploited to expand the immunoscreening and functional characterization of proteins with important role in erythrocyte invasion, in the induction of sequestration or cytoadherence towards unveiling novel asexual blood-stage malaria vaccine targets.

Keyword : Malaria, PfMSP10, antibodies, protein-protein interaction

Abstract No. : ABS0001478

Status : Approved

MOSQUITO REPELLENCE INDUCED BY TARSAL CONTACT WITH HYDROPHOBIC LIQUIDS



Mr. Hiroyuki Takizawa

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The legs of mosquitoes are distinctly long and slender among insects. This unique leg shape plays a crucial role in the mosquito's escape response after sucking blood from vertebrate hosts, reducing the load applied from the tarsus to the host's skin thus reducing the chances of detection during landing. Here, we show that the restriction of delicate tarsus manoeuvring can induce a novel contact-based repellent system facilitated by dynamic wetting. We tested mosquito (*Aedes albopictus*) substrate preference by topically applying oils of high wettability with mosquito tarsi. The mosquitoes initiated an escape response immediately after contacting the surfaces coated in oil and avoided landing on these substrates. We suggest that contact-based dynamic wetting generates an attractive force acting on the mosquito's tarsi triggering an escape response due to the threat of the restriction of delicate tarsus movement and thus, avoidance behaviours. Our results demonstrate that a liquid's high wettability with mosquito tarsi is associated with a low surface tension and low viscosity. This novel wetting-based method of repellence opens up opportunities in the design of safer, more effective products.

Keyword : Mosquito, Hydrophobic Liquids, Wettability, Repellent Effect

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ANTIBIOTIC SUSCEPTIBILITY OF CLINICAL *BURKHOLDERIA PSEUDOMALLEI* ISOLATES IN NORTHEAST THAILAND DURING 2015-2018 AND THE GENOMIC CHARACTERIZATION OF β -LACTAM-RESISTANT ISOLATES



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Introduction: Melioidosis is an often fatal infection in tropical regions caused by an environmental bacterium, *Burkholderia pseudomallei*. Current recommended melioidosis treatment requires intravenous β -lactam antibiotics such as ceftazidime (CAZ), meropenem (MEM) or amoxicillin-clavulanic acid (AMC) and oral trimethoprim-sulfamethoxazole. Emerging antibiotic resistance could lead to therapy failure and high mortality.

Methods: We performed a prospective multicentre study in northeast Thailand during 2015-2018 to evaluate antibiotic susceptibility and characterize β -lactam resistance in clinical *B. pseudomallei* isolates. Collection of 1,317 *B. pseudomallei* isolates from patients with primary and relapse infections were evaluated for susceptibility to CAZ, imipenem (IPM), MEM and AMC. β -lactam resistant isolates were confirmed by broth microdilution method and characterized by whole genome sequence analysis, penA expression and β -lactamase activity. The resistant phenotype was verified via penA mutagenesis.

Results: All primary isolates were IPM-susceptible but we observed two CAZ-resistant and one CAZ-intermediate resistant isolates, two MEM-less susceptible isolates, one AMC-resistant and two AMC-intermediate resistant isolates. One of 13 relapse isolates was resistant to both CAZ and AMC. Two isolates were MEM-less susceptible. Strains DR10212A (primary) and DR50054E (relapse) were multi-drug resistant. Genomic and mutagenesis analyses supplemented with gene expression and β -lactamase analyses demonstrated that CAZ-resistant phenotype was caused by PenA variants: P167S (N=2) and penA amplification (N=1).

Conclusion: Despite the high mortality rate in melioidosis, our study revealed that *B. pseudomallei* isolates had a low frequency of β -lactam resistance caused by penA alterations. Clinical data suggest that resistant variants may emerge in patients during antibiotic therapy and be associated with poor response to treatment.

Keyword : β -lactam resistance, penA, Melioidosis, Genome, *Burkholderia pseudomallei*, Ceftazidime, Thailand

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AN EMERGING LINK BETWEEN PHTHALATES EXPOSURE AND CYTOKINE ALTERATION TO DEVELOP TYPE 2 DIABETES



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Type 2 diabetes mellitus (T2DM) is a serious cause of morbidity and mortality. There are many risk factors that can contribute the disease, such as inappropriate dietary intake. The elevation of inflammatory markers including C-reactive protein (CRP), tumor necrosis factor alpha (TNF- α), and interleukin 6 (IL6) were suggested to associate with an increased risk of T2DM. Phthalate is a substance that inhibits the activity of endocrine glands. Exposure to phthalates can cause damage to organs and health systems. Products used in daily life such as electrical appliances, PVC-floor tiles, Cosmetics and perfumes contain phthalates. Phthalates are chemical compounds that are often used as plastics in a wide range of industrial applications including cosmetics, household products food packaging materials and medical equipment. Phthalates are easily contaminated into the environment, so it can enter the human body through food intake, inhalation or skin absorption. Elderly people are at high risk for phthalate exposure because they spend most of their time indoors and they are vulnerable. Therefore, it is more prone to get sick than the population at other ages. Moreover, in Thailand, diabetes is the 4th leading cause of death among the elderly. Most of them are type 2 diabetes. People with diabetes are more likely to have other health-threatening complications, such as coronary artery disease, cerebrovascular disease, chronic renal failure, high blood pressure,

macular degeneration and wound infection, resulting in violence and death. Such complications are often a chronic problem and lose a lot of medical expense.

Keyword : T2DM, Cytokine, CRP, TNF- α , IL6, Phthalate

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Status : Approved

Emergency Preparedness under the Thai Communicable Diseases Act 2015/2021 ; Insect Control Unit



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Under the Communicable Diseases Act B.E.2558, 6 vector-borne Diseases (DVBDs) are listed as “Disease under surveillance”; dengue fever, chikungunya, malaria, zika, leishmaniasis and scrub typhus. These diseases require 4 groups of stakeholders; hospital, laboratory, factory owners and house owners to report to Disease Control Officer. Meanwhile, disease investigation and control are not regulated under this act and are carried out by local health staffs.

However, VBDs are at risk of becoming “Dangerous contagious disease” for which the investigation and control activities are done by either Disease Control Officer or Communicable Disease Control Unit (CDCU).

To strengthen CDCU’s capacity, Division of Vector Borne Disease (DVBD) proposes “CDCU plus” or “Insect Control Unit”. This unit will enable at least one public health entomologist and one VBD laboratory staff to join the investigation and control of VBDs, if they become dangerous contagious diseases.

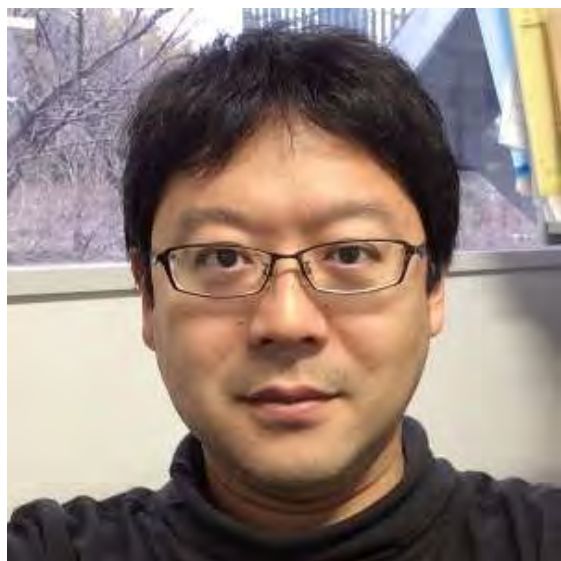
DVBD plans to recruit public health entomologist and VBD laboratory staff from regional offices; Office of Disease Prevention and Control (ODPC) 1-12 and other medical institutes. Concurrently, training is needed for both these 2 specialists and CDCUs so as to perform VBD investigation and control effectively. In addition, this expanded unit definitely needs support, in terms of policy and resources, from the Provincial and Bangkok Disease Control Committees.

Keyword : Insect Control Unit, Vector Borne Disease, Investigation

Abstract No. : ABS0001467

Status : Approved

REGULATION OF GLYCAN STRUCTURES IN HOST CELLS FOR PRODUCTION OF HIGH-QUALITY ANTIBODIES



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Chinese hamster ovary (CHO) cell is widely used for production of recombinant biopharmaceutical proteins as a main platform. Most of these proteins including antibodies are glycoproteins. The glycosylation, particularly *N*-glycosylation has been known to be a key factor in maintaining protein quality such as biological activity, solubility, half-life, immunogenicity, and so on. However, some glycan residues show antigenicity to humans because CHO cells have a glycosylation pathway partially different from humans. Moreover, α 1,6-fucosylation is known to suppress the antibody dependent cell cytotoxicity (ADCC). Therefore, it is desirable to improve the CHO's glycosylation pattern so that the functionality of biopharmaceuticals is enhanced. Here, we focus on glycan-modification of CHO host cells and introduce our works, glycoengineering for production of high-value-added antibodies.

We knocked out α 1,6-fucosylation-related enzyme genes in CHO cells using genome editing technologies for production of IgGs that induce high-ADCC. Although we firstly established the knockout CHO cells, Δ GMD Δ GFT, this mutant cell line produced fucosylated glycans a little. To solve this problem, we adapted the Δ GMD Δ GFT to serum-free medium as suspension cells and succeeded in no detection of the fucosylation on a mass spectrometry. Then, production of human IgGs in the Δ GMD Δ GFT resulted in higher interaction with Fc receptor compared to those produced in the wild-type cells. We also succeeded in large increase of sialic acid and production of high-sialylated IgGs in CHO cells. This enrichment of sialylation is expected to elongate half-life of produced proteins. Our works will provide extremely beneficial functions to production of antibodies as next-generation biopharmaceuticals.

Keyword : CHO cells; Antibody; Glycoengineering; Fucosylation, Sialylation

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Status : Approved

SURVEY OF KNOWLEDGE, ATTITUDES, AND PRACTICES REGARDING MALARIA IN AN INFORMAL GOLD-MINING SETTLEMENT IN THE MALARIA-ENDEMIC GAMBELLA REGION OF ETHIOPIA



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Background: In Ethiopia there have been large migrations from malaria-free highland areas of the country to lowland areas where malaria is endemic. Some of this movement is related to official government initiatives while other movements are informal. The goal of this pilot study was to analyse migrants' knowledge, attitudes, and practices (KAP) towards malaria in an informal gold mining settlement, that has only recently been settled, in Gambella Region of Western Ethiopia. Gambella has one of the heaviest burdens of malaria in Ethiopia and movement to-and-from this region can influence malaria control and elimination efforts throughout the region.

Methods: We conducted a household survey (n=51) and interviewed heads of households. Participant's places of origin were also geocoded and mapped. We used simple descriptive statistical analyses to assess the general KAP of the setting with regard to malaria.

Results: While most people surveyed at the study site had moved there from nearby areas, there was a group of migrants who had moved to the study site from much further away (from high-elevation areas). Overall understanding of malaria symptoms and protective measures against malaria was low. Only 17.65% of respondents believed that pregnant women were at risk of severe malaria and 88.24% stated they did not use mosquito nets in their household (largely because they had no bed nets).

Conclusion: The results from our pilot study suggest that public health outreach and material investment is needed in this area.

Keyword : Malaria

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ACUTE KIDNEY INJURY IN MALARIA



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Acute kidney injury (AKI) is a serious and well recognized complication of severe malaria in both adults and children as it is associated with significant morbidity and mortality. AKI in children has been associated with post-discharge mortality, and increased risk of neurocognitive impairment and behavioral problems. Pathophysiological pathways include impaired microcirculation, due to sequestration of parasitized erythrocytes, systemic inflammatory responses, endothelial activation. Recent literature supports that cell-free hemoglobin oxidative stress is involved in the pathophysiology of AKI in both adults and children. Paracetamol has been shown to be renoprotective in adults with severe malaria likely by inhibiting cell-free-mediated oxidative stress. The direct causes of kidney dysfunction remain incompletely understood. Optimal treatment involves prompt diagnosis and effective antimalarial treatment with artesunate. Renal replacement therapy reduces mortality in AKI but delayed diagnosis and limited access remain challenges. Further research focused on adjunctive therapy with paracetamol in children with severe malaria is currently underway as the potential application of this safe and extensively used drug would be of great benefit.

Keyword : acute kidney injury, malaria, pathophysiology, management

Abstract No. : ABS0001460

Status : Approved

SCREEN AND TREAT STRATEGIES BY FOREST MALARIA WORKERS: RESULTS FROM A LARGE FIELD TRIAL



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Introduction: Malaria elimination in the GMS is a priority because of the frequent emergence of antimalarial drug resistance. In Cambodia, malaria transmission is mostly inside forests (the vectors' habitat). Strategies based inside forests should be assessed as a potential key to malaria elimination. **Methods:** For 16 months, two large Cambodian malaria-endemic forests, 700 km² in Stung Treng and 300km² in Kratie, underwent continuous Mass Screening and Treatment (MSAT) using conventional (P falciparum + P vivax) RDTs to detect and treat all malaria infections among forest goers (FGs). Forests were divided into 66 sectors, each with an FG trained on study procedures. A mobile computerized system was developed to support them offline: GPS tracking, real-time monitoring of field activities and malaria indicators. Malaria incidence estimates from Health Centers (HCs) neighboring intervention forests were compared with 41 remote control HCs to assess intervention effectiveness. **Results:** 6380 FGs were enrolled between August 2019 and December 2020: 3,824 in Stung Treng and 2,650 in Kratie; 84% males, mostly adults. No strong risk factor was associated with malaria infection and approximately half of the infections were outside malaria hotspots. Using PCR as the reference standard, RDT sensitivity was 6.2% [2-15] for P. falciparum and 3.5% [2-5] for P. vivax. Comparisons between intervention and control HCs did not suggest an effectiveness of MSAT. **Conclusion:** The very low RDT sensitivity among asymptomatic FGs left more than 90% of malaria infections untreated.

Intermittent Preventive Treatment of FGs (IPTfg) may be promising to stop malaria transmission and clear reservoirs in Cambodia.

Keyword : Malaria, Plasmodium falciparum, Plasmodium vivax, Cambodia, Greater Mekong subregion, Forest, Forest-goers, Rapid diagnostic test, Mass screening and treatment, Elimination

Abstract No. : ABS0001459

Status : Approved

COMMUNITY ACCEPTABILITY OF MASS DRUG ADMINISTRATION WITH PRIMAQUINE FOR PLASMODIUM VIVAX ELIMINATION IN SOUTHERN THAILAND: A MIXED METHODS APPROACH



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Introduction: Plasmodium vivax (P. vivax) remains a problem in the South of Thailand. Targeted mass drug administration (MDA) with primaquine is being considered in the active foci of P. vivax transmission. This study aimed to explore knowledge, perception regarding malaria, and acceptability of MDA with primaquine for vivax malaria elimination.

Methods: A cross-sectional study was conducted in five endemic villages of Narathiwat and Yala Province in 2019. Demographics, knowledge, perceptions regarding malaria, and acceptability of MDA with primaquine were collected using questionnaires among heads of households. Qualitative data were also collected using in-depth interviews and focus group discussions.

Results: A total of 469 participants, 71.43% had experienced malaria infection. Approximately 58% of participants could accurately explain how people acquire malaria infection, 75% could accurately describe malaria symptoms and reinfection and more than 80% agreed malaria infections can be prevented, but only 5.15% was correct knowledge in all items. Most of the participants had high perceptions regarding malaria (75.32% across all participants). The participants recognized malaria as a community problem. Still, some misunderstandings remain especially about the cause of malaria and treatment behaviors. Total 341 participants (72.71%) agreed to participate. Acceptability of MDA with primaquine was highest among participants who knew malaria is preventable (AOR: 2.39 [95% CI: 1.33-4.49]), that malaria can be cured (1.71 [1.04-2.83]) and with higher scores of perceptions regarding malaria (1.13 [1.01-1.26]).

Conclusion: Knowledge and perception was associated with MDA with primaquine acceptance. Health education and accurate information should be promoted to raise community understanding and participation.

Keyword : Acceptability, mass drug administration, primaquine, Plasmodium vivax elimination

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Status : Approved

Interactions between *Burkholderia pseudomallei* genetic variations and host diabetic status modulate infection outcomes in melioidosis



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Individuals with diabetes mellitus are at higher risk of developing melioidosis but intriguingly less likely die from the disease. However, the effects of host diabetes on bacterial virulence have received little attention. To explore this, we

generated whole-genome sequence data from a collection of 1,912 bacterial isolates recovered from melioidosis patients in northeast Thailand, 64.3% of which had diabetes. We showed that genomic variation in the bacteria could explain approximately 10% of mortality outcomes in non-diabetic patients, but not in patients with diabetes mellitus; indicating that diabetic condition or their clinical interventions could modulate the result of infection. We performed genome-wide association studies (GWAS) for two separate phenotypes: 28-day mortality and host diabetic status. Preliminary analyses found 680, 295 and 81 genetic variations in bacteria being associated with patient 28-day mortality alone, patient diabetes alone, and both host mortality and patient diabetes (FDR < 0.01), respectively. Bacterial variants positively associated with patient mortality alone were enriched in cell defense mechanism ($p = 0.019$), many of which match known virulent determinants. By comparing the goodness of fit of the mortality-outcome models with and without interactions with diabetes, our results further revealed that host diabetes could act as both magnifiers which enhance the effect of 15 bacterial variants on mortality outcome; and dampeners which decrease the effect of 52 bacterial variants, many of which are bacterial surface proteins, on host mortality. A better understanding on bacterial factors influencing disease outcome and their interaction with host conditions could improve our ability to

Keyword : Melioidosis, GWAS

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MALARIA MDA IN LOW AND VERY LOW TRANSMISSION SETTINGS IN SOUTHERN AFRICA



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To reduce malaria transmission in low and very low-endemic settings, screening and treatment near index cases (reactive case detection (RACD)), is widely practiced, but the rapid diagnostic tests (RDTs) used miss low-density infections. Reactive focal mass drug administration (rfMDA) with or without reactive vector control (RAVC) may be safe and more effective. We conducted two cluster randomized controlled trials. The first trial used a 2x2 factorial design and was in the low transmission setting of Namibia. 56 clusters were randomized to RACD only, rfMDA only, RAVC plus RACD, or rfMDA plus RAVC. RACD involved RDTs and AL with single low-dose primaquine; rfMDA involved AL; and RAVC involved indoor residual spraying with pirimiphos-methyl. The second trial was in the very low endemic setting of Eswatini, where 77 clusters were randomised to rfMDA using dihydroartemisinin–piperaquine (DP) or RACD involving RDTs and artemether–lumefantrine (AL). In both sites, interventions were administered to household members and neighbors of index cases identified in passive case detection. An intention-to-treat analysis was used to compare cluster-level cumulative confirmed malaria incidence among clusters with cases. In Namibia, rfMDA and RAVC, implemented alone and in combination, reduced malaria transmission and we conclude it should be considered as alternatives to RACD for elimination of malaria in low transmission settings. In Eswatini rfMDA was safe, but did not lower incidence compared with RACD, potentially due to insufficient coverage and/or power. To better assess impact in such very low-endemic settings, trials may require improved coverage, complementary interventions and adaptive ring trial designs.

Keyword : malaria, mass drug administration, Plasmodium falciparum

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CHALLENGING TIME FOR *Aedes*-BORNE DISEASES LEARNING TECHNOLOGIES: THE RISING OPPORTUNITY AMIDST THE COVID-19 CRISIS



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Dengue is the major seasonal and endemic vector-borne health problem in Thailand. Moreover, Chikungunya and Zika viruses are epidemic in Thailand in recent years. *Aedes* mosquito is the principal vector for the transmission of these viruses. The national *Aedes*-borne diseases prevention and control strategies were formulated under the Department of Disease Control, which supported the prevention and control measures in the community before, during and after an epidemic. Human, chemical, and other resources, including knowledge and technology, will be allocated as needed during an emergency for the regional level requirements.

Even during the COVID-19 crisis, the training activities on mosquito larvae survey for public health volunteers need to be conducted to prevent the increasing number of breeding sites in public places. Educational tools and e-learning platforms are created for village health volunteers to understand about *Aedes*-borne diseases. These methods can turn crisis into opportunities for distance learning, by increasing knowledge and self-assessment of mosquito-borne diseases.

Additionally, two technologies have been developed as mobile applications, known as TanRabad and Or-Sormor Online, for mosquito larval survey for health staffs and public health volunteers. These applications are useful for calculating the container and house index to predict the risk of community transmission. These will be the opportunities to utilize the tools in combination with the learning technology during the COVID-19 epidemic in Thailand.

Keyword : Dengue, learning technology, COVID-19 pandemic, *Aedes*-borne diseases

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Status : Approved

SEROLOGICAL PROFILING OF PLASMODIUM VIVAX EXPOSURE



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Introduction: The increased proportion of asymptomatic *Plasmodium vivax* infections, compared to *P. falciparum*, is impeding malaria elimination in low-transmission settings. Serological profiling, as a surveillance approach to identify recent *P. vivax* exposure, will enable residual transmission foci to be specifically targeted and thus assist acceleration towards malaria elimination.

Methods: We applied a panel of validated *P. vivax* proteins, that can inform on recent exposure to *P. vivax* infections, to multiple cohorts from several *P. vivax*-endemic areas in Thailand to measure antibody responses. We analysed the association and correlation of those antibody responses with several epidemiological factors and *Plasmodium* infections detected by qPCR.

Results: IgG levels to a panel of *P. vivax* proteins library proteins were significantly higher in the presence of a *P. vivax* infection (t test, p18 years, p

Conclusion: Serological markers of surveillance can be used as an important and reliable tool for assessing malaria endemicity and exposure history. These data can be used to better identify geographical areas with asymptomatic infection burdens that harbor at-risk populations who should be targeted in elimination campaigns.

Keyword : *Plasmodium vivax*, serology, surveillance, serological exposure marker, antibodies,

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Status : Approved

NEXT NORMAL MALARIA SERVICE TO ACHIEVE MALARIA ELIMINATION IN THAILAND



Dr. Aungkana Saejeng

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An integrated drug efficacy surveillance (iDES) is a case-based surveillance system, which is an alternative option to TES in areas of elimination, where inadequate number of malaria cases enroll. A pilot iDES commenced in May 2017 in three provinces of northern Thailand, and scaled it up in 2018. The objective of this presentation is to review and discuss results of the recent implementation iDES and G6PD testing. Data was taken from malaria online and iDES samples that sent to DVBD laboratory during 2018 -2019. The accuracy of malaria microscope was compared to expert microscopist was 98.4% with parasite detection 98.8% and parasite identification 98.1%. The correlation of identifying malaria parasite species between the microscope and PCR was 96.4% including *P.knowlesi*. The prevalence of K13 mutations were also detected in Mae-Hong-Son, Tak and Sisaket, but not in Surat-Thani and Songkhla. The result of G6PD test was 7% (38/573) G6PD deficiency, while 71% (408/573) of malaria cases tested G6PD were in Mae-Hong- Son. In this province two type of G6PD tests used, FST-G6PD and SD Biosensor G6PD, which comparison result revealed 100% compatible. In conclusion, it is strongly suggested that the improve performance and competency of microscopist in 1) the accuracy microscope diagnosis 2) safety treatment with G6PD testing before antimalarial 3) supervise treatment and 4) follow up to ensure patients were cure. These all activities are mandatory activities iDES, for the country ready to move to elimination malaria and should be a next normal malaria service in all health facilities.

Keyword : Key word: Integrated drug efficacy surveillance, *P.knowlesi*, G6PD Deficiency, FST-G6PD, SD Biosensor G6PD

Abstract No. : ABS0001434

Status : Approved

NEUTRALIZING HUMAN MONOCLONAL ANTIBODIES AGAINST DENGUE VIRUS NONSTRUCTURAL PROTEIN 1



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Introduction Dengue virus (Denv) nonstructural protein 1 (NS1) has been considered as both pathogenic agent and candidate antigen for vaccine development. During DENV infection, antibody-dependent enhancement (ADE) is one of the major causes of severe disease progression that enhances the heterotypic DENV infection of macrophages through Fc-gamma receptor. Anti-NS1 antibodies have been showed the cross-reactivity with host proteins leading to host tissue damage and dengue pathogenesis. However, these antibodies do not support ADE and provide the protective effects against Denv infection. These studies, human antibodies-specific Denv NS1 generated from hybridomas derived from dengue-infected patients, were collected for studying the potential therapeutic mechanisms in endothelial cell. **Methods** HMEC-1 cells were infected with DENV, then treated with either medium containing anti-NS1 HuMAbs or antibodies-containing complement. At interval times, culture supernatants were collected for investigating neutralization and dengue replication via complement, respectively. **Results** The results demonstrated a great of both neutralization and reduction in viral replication in the presence of anti-NS1 HuMAbs, as compared to control IgG plus complement or complement alone at various times. **Conclusion** Our findings suggested that anti-Denv NS1 HuMAbs provided the potential neutralizing DENV and caused a complement-dependent reduction in virus output indicating a pivotal role in viral control.

Keyword : Dengue virus, Dengue nonstructural protein 1, monoclonal antibody

Abstract No. : ABS0001433

Status : Approved

TRANSCRIPTIONAL REGULATION OF THE *PLASMODIUM FALCIPARUM* PROTECTIVE HEAT-SHOCK RESPONSE



Prof. Alfred Cortes

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The *P. falciparum* transcription factor PfAP2-HS drives an extremely compact protective heat-shock response. At febrile temperatures, this transcription factor activates the expression of the *hsp70-1* and *hsp90* genes, which encode conserved cytoplasmic chaperones. Parasites in which *pfap2-hs* has been knocked out cannot survive heat shock. Additionally, knockout parasite lines have severe growth defects at 37°C, the physiological temperature for *P. falciparum* blood stages, but not at 35°C. The defects observed in the knockout line at 37°C are consistent with an imbalance in protein homeostasis (proteostasis). These results indicate that PfAP2-HS plays a role in the regulation of the expression of genes important for proteostasis maintenance under basal conditions, in addition to activating the heat-shock response at febrile temperatures. Furthermore, *pfap2-hs* knockout parasites lines of several different genetic backgrounds show increased sensitivity to artemisinin. Previous investigations demonstrated a link between the endoplasmic reticulum-based unfolded protein response (UPR) and artemisinin resistance. Our results reveal that PfAP2-HS, the master regulator of the other main cell stress-response pathway, the heat-shock response, also plays a role in artemisinin resistance.

Keyword :

Malaria; *Plasmodium falciparum*; transcription; heat-shock response; PfAP2-HS; transcription factor; fever; artemisinin

Abstract No. : ABS0001432

Status : Approved

MELIOIDOSIS - THE BEGINNINGS



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Introduction

Many people know of melioidosis as 'Whitmore's disease', but how did Whitmore come to be associated with the disease and what were the circumstances surrounding his discovery?

Methods

Information has been gathered from the published literature, from archival material in the UK, Myanmar and India, and from the families of Alfred Whitmore and CS Krishnaswamy.

Results

Whitmore studied medicine in Cambridge and London and then joined the Indian Medical Service. Posted to Burma, he was appointed as Pathologist and Police Surgeon at Rangoon General Hospital in 1909 despite having no specialist qualifications, having shown an aptitude for bacteriology. Krishnaswami, who had obtained the LMS from Madras Medical College, was appointed as one of his assistants. The disease was found in some 5% of autopsies at RGH up to 1917 but then disappeared from the Burmese medical literature. Whitmore was obliged to revert to military service during WWI and returned to a different role after the war ended, eventually ending up as Superintendent of the Burma Government Medical School. Although Krishnaswami assumed responsibility for the mortuary during Whitmore's absence, the rest of his career was spent working in 'lunatic asylums'.

Conclusion

The unhygienic circumstances surrounding morphine injection in in early 20th century Burma are likely to have favoured contamination of injections with environmental organisms like *Burkholderia pseudomallei*. When these two pioneers moved to other roles, the colonial authorities are unlikely to have had any interest in a disease that had little or no economic or public health implications for the British empire.

Keyword : Melioidosis; Whitmore

Abstract No. : ABS0001428

Status : Approved

AN OPEN-LABEL INDIVIDUALLY RANDOMISED CONTROLLED TRIAL OF ARTEMETHER-LUMEFANTRINE ANTIMALARIAL PROPHYLAXIS VERSUS MULTIVITAMINS AMONG FOREST GOERS IN SOUTHEAST ASIA



Dr. Rupam Tripura

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Introduction

Malaria in the Greater Mekong Subregion (GMS) has declined to historic lows and infections are increasingly concentrated in remote, forested foci. Several interventions are under investigation but none has demonstrated satisfactory efficacy against forest-acquired malaria. Hence antimalarial prophylaxis for people working and sleeping in forested areas may hold some promise.

Methods

An open-label, individually randomised trial in Cambodia recruited participants aged 18-65 years visiting forests and staying overnight. Participants were randomly allocated to antimalarial prophylaxis, a 3-day course of artemether-lumefantrine (AL) followed by weekly AL, or multivitamins (MV) with no antimalarial activity. Primary outcome was a composite endpoint of either an episode of clinical malaria with any Plasmodium species within 4 weeks or subclinical infection detected by PCR detected on day 28. Participants could continue taking prophylaxis for up to 3 consecutive months if they continue visiting and sleeping in forested areas.

Results

In total, 1,613 participants were assessed for eligibility and 1,480 (91.8%) were enrolled to receive either AL (738, 49.9%) or MV (742, 50.1%) and 133 (8.2%) participants were excluded. Among enrolled participants, 1,242/1,480 (83.9%) received prophylaxis and completed the trial (AL: 607/738, 82.2% and MV: 635/742, 85.6%). Over a three months follow-up period 19/713 (3%) participants in the AL arm versus 121/714 (17%) participants in the control arm were found to have Plasmodium infections (risk difference 14.6; 95%CI 11.6 to 17.6; p

Conclusion

Prophylaxis with AL was acceptable and well tolerated. Forest prophylaxis made a significant impact on reducing the proportions of participants

Keyword : Keywords: Chemoprophylaxis, Clinical trial, Community engagement, Malaria, Southeast Asia

Abstract No. : ABS0001424

Status : Approved

Importance of adaptive and responsive approach to deliver quality malaria services to dynamic at-risk population in Cambodia



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Affiliation : Malaria Consortium

Forest goers, mobile and migrant populations in Cambodia are most at-risk of malaria due to their highly mobile nature in forested areas and across international borders, the limited access to any malaria services and their exposure to the vectors in the forest.

Cambodia has made huge progress in reducing malaria incidence and mortality, aiming to eliminate *Plasmodium falciparum* by 2023, and being malaria free by 2025. Under the guidance of and in close collaboration with the National Center for Parasitology, Entomology and Malaria Control and funded by The Global Fund (RAI3E), Malaria Consortium delivers adaptive and responsive malaria testing, treatment and preventative services to hard-to-reach communities by supporting 85 Mobile Malaria Workers (MMW`s) in 6 Northern provinces of Cambodia along the international borders of Thailand, Laos and Vietnam.

The MMWs are recruited from the local communities and entrusted by their peers to provide malaria services, tailored to local and seasonal movement patterns, activities of the population and malaria epidemiology. Malaria posts are

strategically placed at entry points of inaccessible forests, while MMW's also perform outreach activities in the deep forest and remote areas, often with overnight stay, bringing the quality care closer to the at-risk populations. By continually reviewing quantitative evidence, operational experience and local knowledge, Malaria Consortium responds swiftly and delivers the most targeted interventions possible. This model has demonstrated that flexible, well targeted, and tailored interventions are more promising to achieve malaria elimination in the forested and border areas with intense migration.

Keyword : Forest goers - community - adaptive approach

Abstract No. : ABS0001421

Status : Approved

THE EFFECTIVENESS OF MASS DRUG ADMINISTRATIONS IN THE GREATER MEKONG SUBREGION: FINDINGS FROM A CLUSTER RANDOMIZED TRIAL



Dr. Thomas Peto

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Background

Mass drug administration (MDA) is a strategy to accelerate malaria elimination. We report a cluster randomised trial to assess the effectiveness of dihydroartemisinin-piperaquine (DP) MDA in reducing falciparum malaria incidence and prevalence in 16 villages in Myanmar, Vietnam, Cambodia, and Lao PDR.

Methods

We randomised village pairs to select 8 villages to receive early DP MDA and 8 villages as controls for 12 months, after which the control villages received deferred DP MDA. The MDA comprised 3 monthly rounds of 3 daily doses of DP. Cross-sectional surveys of the entire population of each village at quarterly intervals used quantitative PCR to detect Plasmodium infections.

Findings

86% participated in at least 1 MDA round. The primary outcome, *P. falciparum* prevalence by month 3 (M3), fell by 92% (from 5.1% [171/3,340] to 0.4% [12/2,828]) in early MDA villages and by 29% (from 7.2% [246/3,405] to 5.1% [155/3,057]) in control villages. Over the following 9 months, the *P. falciparum* prevalence increased to 3.3% in early MDA villages and to 6.1% in control villages (adjusted incidence rate ratio 0.41 [95% CI 0.20 to 0.84]; $p = 0.015$).

Conclusions

Added to community-based basic malaria control measures, 3 monthly rounds of DP MDA reduced the incidence and prevalence of falciparum malaria over a 1-year period in areas affected by artemisinin resistance. These results suggest that, if used as part of a comprehensive, well-organised, and well-resourced elimination programme, DP MDA can be a useful additional tool to accelerate malaria elimination.

Keyword : Elimination, Malaria, Mass Drug Administration, Southeast Asia

Abstract No. : ABS0001419

Status : Approved

ZIKA VIRUS POTENTIAL VECTORS AMONG AEDES MOSQUITOES FROM NORTHERN JAPAN



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[Introduction]

Recently Zika virus (ZIKV), a mosquito-borne virus which induces febrile illness in human has spread worldwide. *Aedes albopictus* and *Ae. aegypti* are considered to have been the main ZIKV vectors during the epidemic. Most experiments have focused on these two major species, which have well established laboratory colonies. However, the vector competence of other mosquito species distributed within northern Japan is not yet known. In this study, three species of *Aedes* mosquitoes from northern Japan were evaluated for their susceptibility against ZIKV.

[Methods]

Field-captured *Ae. galloisi*, *Ae. punctor*, and *Ae. japonicus* were fed *ad libitum* infectious blood meal containing 6.00 (log₁₀) FFU/ml of ZIKV PRVABC59 and/or MR766 strains. Virus titers were determined by focus formation assay in three body parts; abdomen, thorax and head, and legs and wings of both naturally dead and killed mosquitoes. In another experiment excretion of ZIKV in saliva was evaluated using *Ae. japonicus*.

[Results]

ZIKV PRVABC59 was detected in abdomens of *Ae. galloisi* and *Ae. japonicus* at 2 to 10 days post infection (dpi), and in thorax and head in *Ae. galloisi* at 10 dpi, but not in *Ae. punctor* at any time point. ZIKV MR766 was detected at 3 to 19 dpi in the above three parts of *Ae. japonicus* at higher titers than that used for inoculation. The virus was also detected in saliva from 20% of ZIKV-challenged *Ae. japonicus*.

[Conclusion]

This study confirmed ZIKV susceptibility of *Ae. galloisi* and *Ae. japonicus*, although their susceptibility seems lower than that of the major vectors, *Ae. albopictus* and *Ae. aegypti*.

Keyword : Zika virus; susceptibility; *Aedes japonicus*; *Aedes galloisi*; Japan

Abstract No. : ABS0001417

Status : Approved

THE ACCEPTABILITY OF TARGETED MASS TREATMENT WITH PRIMAQUINE FOR LOCAL ELIMINATION OF VIVAX MALARIA IN BANMAUK TOWNSHIP OF SAGAING REGION, MYANMAR: A MIXED-METHODS STUDY



Dr. Pyae Linn Aung

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Introduction: Targeted mass treatment with primaquine may be an effective mechanism for reducing reservoirs of vivax malaria. Since community engagement and high coverage are essential for the mass treatment programs, this study aimed to determine the acceptability of mass primaquine treatment among the targeted community in Banmauk township.

Methods: A cross-sectional mixed-methods study was deployed among household leaders in July 2019. Face-to-face interviews using structured questionnaires and standardized qualitative guidelines were conducted to gather information. Descriptive and inferential statistics, including logistic regression models, were applied.

Results: Among 609 study respondents, more than 90% agreed to participate in an upcoming targeted mass primaquine treatment (TPT) program. Factors contributing to higher odds of acceptability of the program were older age, secondary education level, possessing good knowledge of malaria, individuals experiencing malaria within the family, and those believing malaria elimination from the village is possible. Further, 50 community respondents, 6 midwives, and 4 public health staff (grade II) joined for the qualitative component of the study. Many thought that TPT seemed feasible and stressed that high coverage of underserved groups and health education are needed before commencing the activity.

Conclusion: Most respondents agreed to participate in the proposed mass treatment campaign. Older people with secondary education level, and those who experienced malaria within their families, were most likely to report willingness to participate. These same individuals may be important in the community engagement process for increasing community acceptance of the program.

Keyword : Acceptability, Targeted mass treatment, Primaquine, Mixed-methods, Myanmar

Free Papers Abstracts

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Status : Approved

Infection impact of COVID-19 epidemic in healthcare workers: seroprevalence report from El Salvador, Central America



Dr. Katherine Candray

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Introduction

The explosive spread of the coronavirus disease 2019 (COVID-19) owes to undetected transmissions caused by asymptomatic or mildly infected, though equally contagious, individuals. Serological tests are capable of exhaustively detecting past infections from SARS-CoV-2, including those never targeted for acute phase testing. We here tested the hypothesis that COVID-19 diagnoses made by PCR-based nucleic acid amplification tests reflect only a tip of an iceberg, and what underlies beneath is a significant burden of overlooked diagnoses and transmissions.

Methods

A cross-sectional sero-epidemiological survey was performed, targeting healthcare professionals from a National Hospital in El Salvador. Serological diagnosis was made orthogonally from the results of two reference chemiluminescent immunoassays. The PCR-confirmed population, together with the overall serological status, were further analyzed to elucidate any factors associated with receiving a COVID-19 diagnosis.

Results

Among the total 973 participants, seroprevalence rate among the healthcare professionals exceeded 50%. Nearly half of true COVID-19 cases had been overlooked. Overlooked diagnoses occurred most frequently during the early phase of the pandemic, up until July 2020. With the support of an alternative diagnostic modality, namely a point-of-care diagnostic, up to 70% of the missed acute diagnoses could have appropriately been picked up.

Conclusion

In a diagnostic fog, the frontline, high-exposure healthcare settings can unnoticeably carry high infectious loads, and serve as potential epicenters. A multi-tiered case detection approach may clear the fog, aid in tackling the unprecedentedly heterogeneous COVID-19 spectrum, and minimize the risks of healthcare setting outbreaks.

Keyword : SARS-CoV-2, COVID-19, Healthcare, Seroepidemiology

Abstract No. : ABS0001562

Status : Approved

IMPORTANCE OF MEASURING ENTOMOLOGICAL ENDPOINTS BEYOND HUMAN LANDING RATES WHEN EVALUATING PYRETHROID BASED MOSQUITO BITE PREVENTION INTERVENTIONS



Mrs.Élodie Vajda

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Introduction: Volatile pyrethroids provide a promising additional product class for vector control in areas where vectors bite outdoors or during waking hours as well as settings where standard indoor intervention are not adequate. New classes of vector control interventions are typically evaluated for protective efficacy based on epidemiological endpoints (i.e. public health value). However, it is necessary to understand the link between disease impacts and effects on mosquitoes to ensure that additional products within a class function in the same way, and will confer disease protection, without the need to conduct an epidemiological trial each time and in every setting.

Methods: Several studies were undertaken in semi-field systems with malaria vector mosquitoes to understand the impact of mosquito repellency measured by human landing as well as 'secondary endpoints', including disarming, blood feeding inhibition, mortality, and reduced fecundity, on epidemiological endpoints predicted by mathematical modelling.

Results: The evidence indicates that the standardized measure of human landing rates does not capture the overall intervention impact on mosquitoes and likely underestimates protective efficacies and impact on disease. These interventions cause a range of 'secondary effects' that directly affect vectorial capacity. Mathematical models of volatile pyrethroids including additional endpoints show enhanced reduction of vectoral capacity. Describing the cumulative impacts of these 'secondary effects' in intervention evaluations may help relate entomological measurements and endpoints to epidemiological outcomes.

Conclusion: Evaluation of these additional endpoints through studies in semi-field systems is critical for fully understanding how volatile pyrethroids function (i.e., modes of action) and the potential for public health impact.

Keyword : volatile pyrethroid, spatial repellent, personal protection, anopheles, entomological endpoints, pyrethroids, semi-field system

Abstract No. : ABS0001521

Status : Approved

HETEROGENEITY OF MULTIPLEX ANTIMALARIAL ANTIBODY RESPONSES CONFIRM STATUS OF HISTORICAL AND RECENT MALARIA TRANSMISSION IN ENDEMIC AREAS IN THE PHILIPPINES



Ms. Maria Lourdes Macalinao

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Assessing the status of malaria transmission in endemic areas becomes increasingly challenging as countries approach elimination. In this study, we evaluated the use of malaria-specific serological markers in classifying current or recent infections and historically exposed populations in the Philippines. We utilized dried blood spot samples (n=9132) from a health-facility based cross-sectional survey in 3 provinces – Palawan (with ongoing malaria transmission), Occidental Mindoro (with reduced transmission), and Bataan (pre-elimination area) – and quantified antibody responses against 8 *Plasmodium falciparum* (Pf)-specific and 6 *P. vivax* (Pv)-specific antigens using a multiplex bead-based assay. Consistent with each province's endemicity status, antimalarial antibody levels were highest in Palawan, followed by Occidental Mindoro, and lowest in Bataan. We then assessed different classification approaches to determine the utility of serological markers in predicting recent or historical exposure. A machine learning approach using 4 Pf markers accurately predicted current Pf incidence based on known diagnosis, and predictions also confirmed the absence of recent Pf and Pv exposure in Occidental Mindoro and Bataan, demonstrating the utility of this method in low and high transmission settings. Moreover, further analysis of antibody data from malaria-free Bataan suggested the long-term maintenance of antimalarial antibody responses in the absence of transmission. Our study emphasizes the utility of serological markers in predicting recent and historical exposure in a subnational elimination setting, establishes baseline antibody data for monitoring risk in malaria-endemic areas in the Philippines, and provides a backdrop to understanding the longevity of immune responses to malaria in a country aiming for elimination.

Keyword : antimalarial antibody responses, malaria serology, multiplex serological assays, transmission heterogeneity

Abstract No. : ABS0001518

Status : Approved

“FIND A CURE FOR THIS VIRUS”: VIEWS OF THE COVID-19 PANDEMIC IN MALAYSIA



Assoc. Prof. Phaik Kin Cheah

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1. Introduction

As Covid-19 vaccinations have reached 90% of the eligible population in Malaysia, the government announced the lifting of the Movement Control Order on 11th October 2021, allowing unrestricted travel within the country and outbound travels. This paper reports the views among the people in Malaysia pertaining to the Covid-19 pandemic. Other aspects of the results have been reported elsewhere.

2. Methods

This study, conducted between 2 May and 4 July 2020, involved 18 adult participants, aged between 29 and 84 years old. In-depth phenomenological interviews with participants were limited to phone and online due to Covid-19 restrictions. Participants were recruited online through the quantitative survey of this same study, “Social, ethical and behavioural aspects of COVID-19”, and social networking sites. Data was collected until saturation was reached. Data was analysed using thematic analysis.

3. Results

Participants were hopeful that that a “cure” and long-term solution can be found to treat the coronavirus disease, and that the solutions found can then contain the spread of coronavirus and treat people who are infected. Consequently, life can resume to pre-pandemic normalcy such as travel and business activities. Participants also implicitly expressed their confidence and trust in the scientific communities such as researchers and healthcare workers to “find a cure”.

4. Conclusion

This study provides insights into the views of the people in Malaysia about the Covid-19 pandemic. Results from this study could be used to inform future studies and government policies and plans for future health disasters.

Keyword : Malaysia, lockdown, pandemic, vaccine, Coronavirus

Abstract No. : ABS0001515

Status : Approved

PHENOTYPIC AND GENOTYPIC ANALYSIS OF DIHYDROARTEMISININ-RESISTANT MALARIA PARASITE *PLASMODIUM FALCIPARUM*



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Artemisinin-based combination therapies (ACTs) are the first-line drugs for treatment of malaria parasites, *Plasmodium falciparum*. Unfortunately, clinical resistance to artemisinin and its derivatives has emerged in Southeast Asia. The clinical manifestation of artemisinin resistance as delayed parasite clearance is mediated by mutations in the kelch-domain protein PfK13. To identify whether additional resistance mechanisms are involved, we selected dihydroartemisinin (DHA) resistance in the *P. falciparum* Dd2 strain using a step-wise procedure with continuous DHA exposure. The resistant clones showed significant increases in IC₅₀ to most of commonly used antimalarial drugs in an in vitro assay. In addition, ring-stage survival assay and mature-stage survival assay revealed DHA resistance occurred at both of ring and trophozoites stage. Further, the resistant parasites showed prolonged ring stage. Using whole-genome sequencing, more than 10 genes with SNP were found and may be associated with the acquisition of DHA resistance. This study identified phenotypic and genotypic changes in vitro selected DHA-resistant *P. falciparum* and provides important information for monitoring artemisinin resistance under field settings.

Keyword : Artemisinin, Resistance, DHA, Mechanism

Abstract No. : ABS0001490

Status : Approved

An efficient and rapid microinjection method to generate *Orientia tsutsugamushi* infected *Leptotrombidium* mites.



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Introduction: Scrub typhus is a life-threatening disease caused by chigger-borne *Orientia tsutsugamushi* infection, which is estimated to affect at least one million people per year. Our understanding of this disease's fundamental biology, such as vector-pathogen-host interaction, lags behind that of other vector-borne diseases of equivalent prevalence and severity. In addition, the development of the natural disease model to support vaccine study or novel therapies requires infected chiggers with well-characterized *O.tsutsugamushi*. This study reports an alternative method to efficiently transfect the selected strain of *O.tsutsugamushi* to chiggers under laboratory conditions.

Methods: *Leptotrombidium chiangraiensis* adults and tritonymphs were infected by direct injection of a suspension of *O.tsutsugamushi* (Gilliam) through dorsal surface of the opisthosomal haemocoel or ventral side in adults or at dorsal or genital region in tritonymphs. The transmission efficiency from infected parents to offspring or from chiggers to immunocompetent hosts was followed for two generations.

Results: Microinjection did not cause a deleterious effect on survivability and development of the experimental mites. Microinjected mites successfully transmitted *O.tsutsugamushi* through transovarial transmission to chigger offspring. Although all experimental mice challenged with these chiggers developed mild and self-limited infections, the pathological hallmarks of scrub typhus disease including splenomegaly and hepatomegaly were observed. Serological analysis of mice at 30 dpi showed the development of specific immunoglobulin M and G antibodies. Evidence of persistent infection, but not multiplication, in the microinjected mite was observed.

Conclusion: The microinjection method is an effective option to establish the infected chiggers for developing of natural scrub typhus animal model.

Keyword : Scrub typhus, chigger, microinjection, artificial infection

Abstract No. : ABS0001486

Status : Approved

PEOPLE'S PERCEPTIONS TOWARDS SCABIES BASED ON THEIR AGE, GENDER, AND EDUCATIONAL BACKGROUND



Dr. Yulia Dwi Setia

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Introduction.

Scabies is a skin disease that is endemic in tropical and subtropical climates. For example, in Malang, Indonesia, the prevalence of scabies in Islamic boarding schools reaches 37.30%. The strategy for breaking the scabies transmission cycle is associated to a person's level of scabies knowledge. As a necessary consequence, the objective of this study is to assess the correlation between scabies and respondents' age, gender, and educational background in Malang, Indonesia.

Method.

This study is a cross-sectional observational analytic study with an online questionnaire distributed through an accidental sampling method. The sample includes 223 adults over the age of 18 who live in Malang, Indonesia. A Chi Square test was utilized to see a correlation between age, gender, education, and scabies knowledge.

Results.

56,1 percent of the 223 respondents were adults (26–45 years old), 61 percent were female, and 58,3 percent had a high level of education (Diploma – Doctorate Degree). As it related to Scabies knowledge, age and educational groups exhibited significant results ($p < 0,05$), while gender groups did not. The odd ratios for age and educational groups were 1.4 and 2.1, respectively.

Conclusion.

The perceptions of scabies are associated with age and educational background, with the greater the age and education, the better the perception of scabies.

Keyword : age, educational background, scabies perception

Abstract No. : ABS0001480

Status : Approved

KNOWLEDGE ATTITUDE AND PRACTICE AMONG BORDER FRONTLINE STAFFS TOWARD COVID-19 (DELTA AND NEW VARIANTS)



Dr.SIRIRAK THANASAKULPRASERT

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Introduction: COVID-19 variants, especially Delta variant, challenged humankind in term of prevention and protection. Since the protection of what being use vaccine is vary. Good Knowledge Attitude and Practice could strengthen the prevention the surge of Delta variant and other variants, especially for people at border's frontline who at risk of exposure to inbound threat.

Materials and Methods: Cross-sectional study conducted among 767 border frontline staffs at Suvarnabhumi Airport, Thailand using structured questionnaires. The statistical analysis of the data was done with descriptive statistics. For descriptive analysis, the total values and percentages were utilized for categorical variables and the mean or median value with standard error of the mean or interquartile range of median were utilized for the numerical values.

Results: Knowledge directly affected both attitude (e.g., perceived risk and efficacy belief) and practice (e.g., personal hygiene practices and social distancing) (p value < 0.05). Majority of participants more than 70% of participants believed that to prevent the spread of COVID-19 were the responsibility of everyone, every community, and every government. Almost 90% of participants got high score in practices to the prevention of COVID-19.

Conclusion: The spreading of COVID-19 and their variants is still ongoing. Border frontline staffs are the people who firstly expose to those variants. Prevention measures which are now normal, should be emphasized for protection of one own health and others in addition to COVID-19 vaccine promotion.

Keyword : KAP, knowledge, attitude, practice, COVID-19, Delta, variant

Abstract No. : ABS0001474

Status : Approved

IMPACT OF EARLY DETECTION MULTI-DRUG RESISTANT TUBERCULOSIS ON TIME TO SPUTUM CONVERSION



Mrs.Samorn Numpong

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Introduction: Globally, the treatment success rate of multi-drug resistant tuberculosis (MDR-TB) was only 56%. Different diagnostic methods have different result turn-around times, which may impact the treatment outcomes. The objectives of the study were to compare median time to sputum conversion.

Methods: A retrospective cohort study was conducted at Makarak hospital, Kanchanaburi province, Thailand. A total of 163 persons with MDR-TB diagnosis were reviewed medical records from 2010 to 2015. They were divided into three groups including conventional drug susceptibility testing (conventional DST), real-time polymerase chain reaction (RT-PCR), and clinical diagnosis. Survival analysis was performed to compare median time to sputum conversion among the three groups.

Results: About half of the study population were male (51.53%). The mean age was 46.90± 16.59 years, 35.59% employment, 51.53% underweight. Median time to sputum culture conversion from initiated MDR-TB treatment was 63 (95% CI: 56, 81), 77 (95% CI: 63, 91), and 46 (95% CI: 25, 66) days among conventional DST, RT-PCR, and clinical diagnosis groups, respectively. This difference was statistically significant (p-value = 0.003).

Conclusions: Early detection MDR-TB using RT-PCR helps the physicians make a decision to initiate the MDR-TB treatment early. Logically, early detection and prompt treatment will reduce the transmission of bacilli in households and communities within days after receiving proper treatment. Detected MDR-TB by using RT-PCR increased the chance of sputum conversion 2 times at 6 months when compared to conventional DST.

Keyword : Multi-Drug resistant tuberculosis, Early detection, Real-Time Polymerase Chain Reaction

Abstract No. : ABS0001473

Status : Approved

PHARMACOKINETIC AND PHARMACODYNAMIC INTERACTIONS OF THE TRIPLE COMBINATION OF DIHYDROARTEMISININ-PIPERAQUINE AND MEFLOQUINE IN HEALTHY THAI VOLUNTEERS



Dr. Kanoktip Puttaraksa

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Introduction: Artemisinin and partner drug resistance have been reported throughout Southeast Asia, resulting in substantially reduced efficacy of artemisinin-based combination therapy (ACT) in certain regions. Co-administration of a third antimalarial drug, with a different mechanism of action, to an existing ACT is a promising treatment alternative of multi-drug resistant infections. One of the proposed triple combinations are DHA-piperaquine co-administered with mefloquine. This study aimed to evaluate potential drug-drug interactions between mefloquine and DHA-piperaquine as well as evaluating the effect on the QT-interval.

Methods: Population pharmacokinetic and pharmacodynamic properties of DHA, piperaquine, and mefloquine were assessed in 15 healthy Thai adults (29 – 56 years old) using an open-label, randomized, crossover study design. Drug concentration-time profiles and electrocardiographic measurements were evaluated using nonlinear mixed-effects modeling in NONMEM.

Results: Pharmacokinetic properties of the three drugs could be described adequately with compartmental models, characterizing the absorption, distribution, and elimination of the drugs. Concomitant treatment with mefloquine had no significant effect on the cardiovascular outcome of DHA or piperaquine. Therefore, mefloquine can be added safely to DHA-piperaquine treatment in the treatment of multi-drug resistant malaria infections.

Conclusion: The present study successfully described the pharmacokinetic and pharmacodynamic properties of the triple combination of DHA-piperaquine and mefloquine in healthy Thai adults, and the relationship between drug concentrations and QT-prolongation. The findings from this study can help with the further development and implementation of this triple combination therapy.

Keyword : Dihydroartemisinin, Piperaquine, Mefloquine, Artemisinin-based combination therapy, Triple combination therapy, Population pharmacokinetic-pharmacodynamic model, QT prolongation

Abstract No. : ABS0001471

Status : Approved

LESSONS LEARNED FROM THE HISTORY OF THE MALARIA ELIMINATION IN YAEYAMA, OKINAWA, JAPAN-IN ORDER TO OVERCOME THE ERA OF INFECTIOUS DISEASES



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Introduction: The 21st century has become the era of infectious diseases. Globalization, land use change, and global warming, are promoting the emergence, reemergence, and spread of infectious diseases. The Yaeyama Islands, a part of Okinawa, Japan, have suffered from endemic malaria for more than 400 years. During WWII, the islands experienced a tragedy in which one tenth of the residents died of malaria. Later, under the U.S. military occupation, despite social and economic disadvantages, Yaeyama achieved malaria elimination in 1962 through strong scientific leadership, diligent health administration work, and active community involvement. This study reviews the history of malaria elimination in Yaeyama, and discusses lessons that can be applied to the present day.

Methods: A reevaluation of the history of malaria control in Yaeyama was conducted by reviewing publications, public documents, newspapers, and grey literature. Interviews were conducted with key people in the malaria control activities.

Results and Conclusion: After the war, once the disease was nearly eliminated by scientific leadership, policy turned to the economy and the area actively accepted immigrants. This caused a malaria epidemic in the immigrant population. During this period, a trial and error process leads to building trusting relationships. The subsequent U.S. military-led evidence-based malaria elimination program was successful. This goal-oriented intervention by the U.S. was preceded by a phase in which the health center staff entered the community to approach and work with the immigrants. In addition to the scientific phase, this adaptive phase may have been the key to achieving this goal.

Keyword : History, Science, Adaptive, Leadership, Malaria, Lesson

Abstract No. : ABS0001465

Status : Approved

RISK STATUS FOR SPREAD OF EXTENDED SPECTRUM β -LACTAMASE PRODUCING ENTEROBACTERIACEAE THROUGH MARKETPLACES AROUND HOSPITAL AREAS OF KATHMANDU



Ms. Jenny Shah

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Introduction: Fruits and Vegetables comprise an essential part of the human diet as they are the major source of dietary nutrients of great importance. A diet rich in fruit and vegetables has been shown to protect against various types of ailments. However, on the other hand, the consumption of fruits and vegetables has an increase in the number of human infections and outbreaks as these can also serve as reservoirs for opportunistic bacterial pathogens. These opportunistic pathogens could lead to life-threatening infections mainly in immunocompromised patients.

Methods: A total of 16 samples was collected from randomly selected vendors near the 10 major hospitals of Kathmandu. The samples were collected and washed separately with the Maximum Recovery Diluent (MRD). Bacteria were then isolated from the samples using MacConkey agar (MCA) and Violet Red Bile Glucose Agar (VRBGA), both before and after the initial incubation of MRD at 37 °C for 3 hours. Following the isolated, the bacteria were identified based on staining and biochemical characterization. Antibiotic susceptibility for the bacteria was carried using 20 different antibiotics. Polymerase Chain Reaction was carried for detecting the presence of blaTEM gene on ESBL producing bacteria.

Result: From the different samples collected, altogether 59 bacteria were isolated. Among them, 22(37 %) were found to be ESBL producers and 4 (7%) were even carbapenem-resistant. Among the ESBL producers, the blaTEM gene was detected in 10 bacteria.

Conclusion: The presence of ESBL producers as well as carbapenem-resistant bacteria indicates the rising risk of acquiring resistant bacteria not just from the hospital, but

Keyword : blaTEM, Kathmandu, Enterobacteriaceae, ESBLs

Abstract No. : ABS0001463

Status : Approved

A SHINY WEB-APPLICATION FOR POPULATION PHARMACOMETRIC SIMULATIONS



Mr. Prasert Yodsawat

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Introduction: Population pharmacometric approaches are used to describe the pharmacokinetic, pharmacodynamic, and biomarker-outcome behaviours, using a complex mathematical and statistical framework. Visualisation of pharmacometric models facilitates effective communication, enhances quantitative decision making, and increases the impact of pharmacometrics in drug development. This project aimed to develop an interactive web-application for simulation and visualisation of population pharmacometric models.

Methods: Pharmacokinetic and pharmacodynamic systems are usually described by nonlinear mixed-effects models. In this project, different pharmacokinetic and pharmacodynamic models were implemented in R using a RxODE package. Interactive model visualisation was implemented as a web-application using the Shiny framework.

Results: A wide range of population pharmacokinetic and pharmacodynamic models was successfully implemented in this interactive web-application, e.g. several different absorption and distribution models. External data can be imported and overlaid with the simulated pharmacometric profiles, which help the user visualize the appropriateness of the chosen model with respect to their data. This web-application can generate a comprehensive report, including all simulated plots, summary tables, and simulated data. The developed web-application offers a simple way to simulate and visualise a population pharmacometric model without any coding or web development skills.

Conclusion: R and Shiny are free software, supporting a wide range of applications, including nonlinear mixed-effects modelling. The developed interactive web-applications will be a useful tool for scientific communication and it would assist researchers to investigate and assess population pharmacometric models. It can be developed further as a platform for designing prospective pharmacometric studies and for dose optimization applications.

Keyword : Pharmacometric; Simulation; Web Application; R programming; Shiny

Abstract No. : ABS0001461

Status : Approved

PHARMACOKINETIC AND ELECTROCARDIOGRAPHIC EVALUATION OF CHLOROQUINE AND AZITHROMYCIN IN HEALTHY VOLUNTEERS



Mr. Palang Chotsiri

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Objective: Since the COVID-19 pandemic began, chloroquine and azithromycin have been speculated as possible COVID-19 preventive and treatment options. Despite the fact that billion doses of chloroquine have been administered worldwide over the past 70 years, concerns regarding cardiotoxicity, notably the risk of *Tosade de Points*, remain. This study aimed to characterize the pharmacokinetics and electrocardiographic effects of chloroquine and azithromycin.

Methods: Healthy volunteers (n = 119) were randomized into five study arms: placebo, chloroquine alone (600 mg base), or chloroquine with either 500 mg, 1000 mg, or 1500 mg of azithromycin. Plasma drug concentrations and electrocardiographic intervals were extensively measured before and after drug administration. Electrocardiographic intervals were rate-corrected individually. Time-match changes in the PR, QRSc, JTc, and QTc intervals were calculated and the relationship with plasma drug concentrations were evaluated using non-linear mixed-effects modelling.

Results: The pharmacokinetics of chloroquine and azithromycin were characterized using a two- and three-compartment model, respectively. There was no evidence of a drug-drug interaction. Chloroquine caused a concentration-dependent prolongation of the PR, QRSc, and JTc intervals with minimal effect of azithromycin. Chloroquine prolonged the QTc interval by approximately 101 ms per 1000 ng/mL, of which 35.7% was contributed by the QRSc widening and 64.3% was contributed by the JTc prolongation.

Conclusion: Chloroquine caused concentration-dependent delays in atrioventricular (PR interval) and intraventricular depolarization (QRSc interval) and repolarization (JTc). Co-administration of azithromycin did not significantly increase these effects. The arrhythmogenic risk associated with chloroquine may have been substantially overestimated in studies which did not separate

Keyword : **Keywords:** Chloroquine; Azithromycin; Pharmacokinetics; Electrocardiographic effects; Pharmacometric; non-linear mixed-effect modelling; QT prolongation

Abstract No. : ABS0001457

Status : Approved

Pathogenic free-living amoeba from various water sources in Southern Thailand.



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Introduction: Several free-living amoeba found in various environmental sources such as lakes, ponds, drinking water etc. may cause some serious illness.

Naegleria spp. is associated with primary amebic meningoencephalitis *Acanthamoeba* spp. Infect CNS, causing granulomatous amebic encephalitis, etc. This study aims to screen for free-living amoebas from water sources around areas associated with human activities in Southern Thailand using culture techniques.

Methods: The samples were filtered through 0.45 µm membrane filter, the sediment were culture in non-nutrient agar spread with inactivated *Escherichia coli*. The presence of the amoebas was observed using an inverted microscope or with a conventional microscope.

Result: A total 25 water samples were collected from 3 provinces in Southern Thailand including Songkhla, Phatthalung and Nakhon Si Thammarat, Free-living amoebas were found 8 samples. 3 sample are estimated to be of *Acanthamoeba* spp. and 1 samples are estimated to be of *Naegleria*.

Conclusion: Free-living amoeba that cause disease in humans are two genera, including *Acanthamoeba* spp. and *Naegleria fowleri*. For *Acanthamoeba* spp. has only two stages, cysts and trophozoites. The trophozoite has an irregular shape with pseudopodia and a single nucleus. The cyst contains double cyst walls and a single nucleus. For *Naegleria fowleri* has 3 stages, cyst trophozoite and flagellate stage. Trophozoites shows moving, feeding and proliferation activity. Cysts are round shape formed. This study indicated the present of free living amoeba that may risk for consumption or contacting with contaminated water.

Keyword : Amoebas, *Naegleria*, *Acanthamoeba*, free-living amoeba, environmental source

Abstract No. : ABS0001455

Status : Approved

A MULTI-COUNTRY EVALUATION OF A POINT-OF-CARE DIAGNOSTIC TO IDENTIFY GLUCOSE-6-PHOSPHATE DEHYDROGENASE DEFICIENCY.



Ms. Pooja Bansil

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Introduction: This study evaluated the performance of the point-of-care STANDARD™ G6PD Test (PocG6PD) and explored whether a common set of thresholds to classify glucose-6-phosphate dehydrogenase (G6PD) deficient or intermediate individuals can be applied across populations.

Methods: Quantitative data were obtained from 4,136 participants from studies in Brazil, Ethiopia, India, and the US. G6PD activity was normalized and pooled using the adjusted male median (AMM), representing 100% G6PD activity. Receiver operating characteristics (ROC) curves and diagnostic performance against a quantitative laboratory G6PD reference assay were used to categorize G6PD deficient, intermediate, and normal individuals at 30% and 70% thresholds for G6PD activity, on both capillary and venous specimens.

Results: The AMM of the reference assay varied from 7.9 to 12.9 U/g Hb, whereas ranged from 6.6 to 8.1 U/g Hb for the PocG6PD. The area under the ROC curve for capillary specimens was 1.00 at 30% activity, and 0.91 at 70% activity. The PocG6PD showed a sensitivity of 100% for G6PD deficient males and females in both venous and capillary specimens. For females with intermediate G6PD activity (30% to 70%), the PocG6PD had a sensitivity of 75.0% for capillary samples and 78.2% for venous samples. The majority of false negative intermediate females

resulted from females with > 60% activity and the negative predictive value for any females with activity < 65% was 99.3% for both venous and capillary specimens.

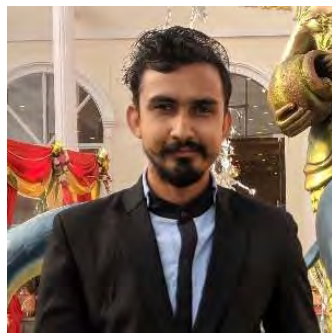
Conclusion: A single set of thresholds on the STANDARD G6PD Test can reliably inform *Plasmodium vivax* case management across multiple populations.

Keyword : G6PD enzyme activity, malaria, *Plasmodium vivax*, diagnostic performance

Abstract No. : ABS0001453

Status : Approved

IMMINENT DANGERS OF COMMUNITY-LEVEL SPREAD OF EXTENDED SPECTRUM β -LACTAMASE PRODUCERS THROUGH FRESH PRODUCE SOLD IN MAJOR MARKETS OF KATHMANDU



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Introduction: The role of fresh fruits and vegetables (fresh produce) in nutrition and healthy diets is well recognized and in recent years many countries have undertaken various initiatives to encourage consumers to eat more of these products. However, this fresh produce continues to be the main source of foodborne illness outbreaks. Initially, the extended-spectrum β -lactamase producing bacteria were confined to nosocomial infections but recently this has shifted to community-acquired infections as well.

Methods: Nineteen fruits and vegetables were collected from 8 different market places viz. of Kathmandu i.e Balkhu, Kalimati, Gwarko, Kalanki, Koteshwor, Lagankhal, Chaysal, and Nakhhu. The samples were collected and washed separately with the Maximum Recovery Diluent (MRD). Bacteria were isolated on MacConkey Agar and Violet Red Bile Glucose Agar (VRBGA) both before and after 3 hours of incubation at 37 °C. Isolated bacteria were identified based on their biochemical properties, an antibiogram was performed, and PCR was done to detect the blaTEM gene responsible for causing the resistance to β -lactam antibiotics.

Results: A total of 107 bacteria were isolated, of which 42(39 %) were found to be ESBL producers while 7 (6.5%) were found to be carbapenem-resistant (CR). Among the ESBL producers, nine were positive for the blaTEM gene.

Conclusion: Although routine surveillance takes place for hospital-based resistance, our study shows that community-level spread of multi-drug resistant bacteria could occur through seemingly harmless or even beneficial foods like fruits and vegetables.

Keyword : blaTEM, Community-Acquired Infections, Enterobacteriaceae, Extended Spectrum β -lactamase, Nepal

Abstract No. : ABS0001452

Status : Approved

EFFECT OF ARTEMISININ RESISTANCE ON THE TRANSMISSION BLOCKING ACTIVITY OF PRIMAQUINE



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Malaria transmission is only sustained when mature viable female and male gametocytes are ingested during a single bloodmeal by the female Anopheline mosquito. Preventing gametocytes from onward development will block malaria transmission. The 8-aminoquinoline primaquine, that acts by rapidly sterilising the male gametocyte, is the only transmission blocking drug being used clinically. Its mode of action remains ill-defined but CYP2D6 dependent bioactivation of the parent drug creating highly active redox metabolites leading to detrimental intracellular stress, has been suggested. Artemisinin and partner drug resistance is a global health emergency. Resistant *P. falciparum* parasites often display upregulation of intracellular stress response pathways along with reduced cellular uptake of haemoglobin, possibly causing a reduced ferrous-iron mediated activation of artemisinin. We have previously shown, that artemisinin and derivatives sterilise mature male gametocytes and reduce mosquito infectivity *in vitro*. Male gametocytes carrying artemisinin resistant PfK13C580Y SNPs are more competent in mosquito infectivity compared to non-resistant male gametocytes upon dihydroartemisinin drug treatment. This raises the question whether *P. falciparum* gametocytes carrying artemisinin resistance are still sensitive to the transmission blocking effects of primaquine. We have developed an *in vitro* CYP2D6 primaquine metabolism approach to assess its effectivity in the *P. falciparum* dual gamete formation assay on culture adapted artemisinin sensitive and resistant clinical isolates. Successfully metabolised primaquine irreversibly sterilises male *P. falciparum* gametocytes of the NF54 strain, *in vitro*, at clinically relevant concentrations. First results of ongoing work suggest no difference in bioactivated primaquine IC₅₀s between the control and culture adapted artemisinin resistant parasites.

Keyword : Malaria, *Plasmodium falciparum*, transmission, gametocyte, primaquine, artemisinin resistance

Abstract No. : ABS0001448

Status : Approved

EPIDEMIOLOGY OF INTESTINAL PROTOZOAN INFECTION IN DOCTORS ATTENDING RESIDENCY TRAINING IN SAIFUL ANWAR GENERAL HOSPITAL IN MALANG, INDONESIA



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Introduction: Intestinal protozoan infection is a neglected global health issue. Due to the innocuous symptoms, they are often neglected. Prevalence studies often targeted children, population in rural areas or symptomatic patients. Nevertheless, as with most infectious agents, health-care workers are verily at risk for contracting protozoan infection. Thus, in this preliminary study, we aim to evaluate the prevalence of intestinal protozoan infection in doctors attending residency training in Saiful Anwar General Hospital, Malang, Indonesia.

Methods: We collected stool samples from first year residents of the Department of Internal Medicine Saiful Anwar General Hospital. All subjects were healthy and asymptomatic. The fresh samples were subjected to direct smear examination and two floatation techniques using zinc sulphate and sheather sucrose floatation.

Results: Twenty-eight residents were enrolled in this study, consisting of 72.4% males and 27.6% females, with the age range of 24–34 years. Surprisingly, direct smear examination revealed that 24.1% of samples were positive for at least one intestinal protozoa. The zinc sulphate and sheather sucrose floatation methods performed on the same sample population showed positive results in 17.2% and 6.9% of samples, respectively.

Conclusion: The high prevalence of intestinal protozoa found in this study highlighted the importance of a routine parasitology screening in health-care workers, including residents. Although several protozoa were thought to be non-pathogenic, further molecular examination of the samples is underway to confirm the presence and species of these intestinal protozoa.

Keyword : intestinal protozoan infection; health-care providers; asymptomatic prevalence; parasitology screening

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Status : Approved

Incidence and influencing factors of psychological problems among international arrivals during quarantine in Thailand – Preliminary data.



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Introduction

The coronavirus disease 2019 (COVID-19) pandemic has disrupted air travel globally. Thailand uses a strict policy of mandatory quarantine for all international arrivals to mitigate COVID-19 transmission. The sudden social isolation and lack of autonomy puts travellers at risk for psychological distress. This study determines the incidence and influencing factors of mental health problems among international arrivals during quarantine in Thailand.

Methods

This is a cross-sectional study using an online questionnaire completed by eligible participants within 7 days of leaving quarantine, accessed via QR or web link, distributed online and by hotels. Psychological symptoms were assessed using standardised questionnaires (PHQ-9 for depression, GAD-7 for anxiety, PCL for Post-Traumatic Stress Symptoms). Additional information was surveyed on demographics and the quarantine environment.

Results

The preliminary data consists of the first 100 eligible participants from July-September 2021. Mean age was 43, 60% male, 49% were in Thailand for work, 88% had undergraduate degree or higher. 30% showed symptoms of moderate to severe depression, 10% moderate to severe anxiety, 22% moderate to high PTSS, and 12% had thoughts of suicide/deliberate self-harm. The most common symptom was sleep disturbance in 78%. Day 8 was the most difficult across all mental health symptoms. Risk factors for higher score on PHQ9, GAD7 and PCL were low income, poor internet connection, and previous COVID-19 bereavement.

Conclusion

Our preliminary data shows that quarantine may cause high levels of psychological distress in travellers. If quarantine persists, urgent changes are needed to reduce the mental health burden.

Keyword : COVID-19 pandemic, Travel Medicine, Quarantine, Mental Health

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DISTRIBUTION OF *LEPTOSPIRA* SPP. IN THE LOW INCIDENCE CASE AREAS: MILITARY HUMANITARIAN MISSIONS



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Leptospirosis, a neglected zoonotic disease, has been regarded as an environment-borne infection and most human cases usually occur through exposure to soil or water contaminated with the urine of chronically infected animals. Rodents have become a major reservoir animal in the transmission cycle of this disease.

In this study, we conducted pre-exercise surveillance to evaluate risk of leptospirosis by surveying rodent populations and environmental areas around the sites where military humanitarian missions were conducted in Thailand from 2017 through 2020. Carriage prevalence in rodents was assessed by targeting *lipL32* and the presence of *Leptospira* DNA in environmental samples was determined by 16S rRNA gene (*rrs*). Species identification of *Leptospira* was analyzed using *rrs*/PCR.

Rodents (n= 861) and environmental samples (water n=363 and soil n = 41) were collected in the same areas. *Leptospira* prevalence in rodents was 1.1% (9/861) with infected pathogenic *Leptospira interrogans* (n=7) or *L. borgpetersenii* (n=2). *Leptospira* DNA was detected in 11.0% (40/363) of water and 9.8% (4/41) of soil samples. Based on dark field microscopy, 0.2% (2/861) rodents, 6.3% (23/363) water, and 58.5% (24/41) soil cultures were positive for *Leptospira* spp. The circulating *Leptospira* spp. from the environment belong to three primary clusters: pathogenic, saprophytic, and intermediate.

Our surveillance results suggest a high level of environmental contamination with *Leptospira* and should inform public health medical surveillance efforts. These results also clarify the risk factors for *Leptospira* infection as well as the civilian and military populations that are most vulnerable to this disease in Thailand.

Keyword : *Leptospira*, Leptospirosis, Surveillance

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Status : Approved

DETERMINATION OF THE DIAGNOSTIC POTENTIAL OF AN ELISA ZIKA/DENGUE SEROLOGICAL PARAMETER IN DISTINGUISHING ZIKA VERSUS DENGUE INFECTION



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INTRODUCTION: Serological diagnosis of Zika infection remains a challenge due to the high cross-reactivity of Dengue antibodies which most serological diagnostic tests can confound as false positive Zika infection. Thus, serological diagnostics in Zika often involve further confirmation relative to Dengue serological results. Three test parameters using a Zika/Dengue ratio (P/N Ratio, OD ratio and relative OD) are compared in this study in terms of their diagnostic potential in discerning between Zika and Dengue infections.

METHODOLOGY: A panel of 30 samples (10 Zika-positive, 20 Dengue-positive) were tested against a developed Zika and Dengue ELISA protocol. Three ELISA test parameters (P/N Ratio, OD Ratio, Relative OD) were calculated and compared in terms of Receiver Operating Characteristic (ROC) curve and sensitivity and specificity to determine the best serological test parameter. A commercially-available anti-Zika IgG ELISA kit is also tested for comparison of the performance of the Zika/Dengue ELISA parameter.

RESULTS: ROC curve analysis showed that across all test parameters, the Zika/Dengue parameters have very good diagnostic potential (AUC= 0.8200 to 0.8450) than using standalone Zika parameters having lower diagnostic potential (AUC= 0.700 to 0.7200). The ELISA Z/D ratio also performed better than a commercial ELISA test kit which yielded an AUROC of only 0.6050 and 60% sensitivity and 68.18%% specificity.

CONCLUSION: Using the Zika/Dengue ELISA diagnosis drastically improves measures of diagnostic performance instead of just using Zika ELISA reading. Using this measurement may be a promising tool for distinguishing Zika from Dengue infection which may be applicable to use instead of performing

Keyword : Zika, Dengue, ELISA, Serological diagnosis

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Identification of genetic regions affecting proliferation and infectivity of dengue virus type 2



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Introduction

Genome sequencing of dengue virus 2 (DENV2) isolates in Thailand in 2016 and 2017 showed that the Cosmopolitan type coexisted with the Asian-I type. Focus Forming Assay (FFA) of these clinical isolates showed differences in the focus size and proliferative capacity. In the present study, we attempted to identify the genetic regions that affect the proliferative and infectious potential of two phenotypically different DENV2 strains.

Method

We generated the parental DENV2 and chimeric viruses using CPER, and compared their focus sizes and infectivity titers by FFA. We then compared the functions of structural and non-structural proteins using SRIP and replicons. We also analyzed pathogenicity of the virus using IFNR KO mice.

Results

Chimeric viruses carrying either the structural proteins or NS1-NS2B regions of Cosmopolitan virus showed large foci. All of them showed higher infectious titer than the Asian-I type parent strain, and equal to or higher titer than the Cosmopolitan parent strain. Capsid region of Cosmopolitan virus was not needed for the large focus phenotype. The chimeric viruses with Cosmopolitan structural proteins showed significantly higher infectivity in SRIP assay. In contrast, the non-structural proteins of Cosmopolitan virus also showed higher reporter gene expression levels in the replicon assay. Furthermore, higher viral RNA levels in the blood and more lethality was observed in mice infected with chimeric viruses containing the NS1-NS2B regions of Cosmopolitan virus.

Discussion

Differences in sequences within both the structural protein (prM/E) and non-structural proteins (NS1-NS2B) affected the differences in proliferation and infectivity between Asian-I and Cosmopolitan.

Keyword : DENV2, Asian-I, Cosmopolitan, Focus size, SRIP, Replicon.

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LIVER INVOLVEMENT IN ADULT PATIENTS WITH CHIKUNGUNYA AT THE HOSPITAL FOR TROPICAL DISEASES AND BAMRASNARADURA INFECTIOUS DISEASES INSTITUTE, THAILAND



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Introduction – Chikungunya, a mosquito-borne disease, is endemic in Thailand. It commonly presents as fever with polyarthralgia. In severe cases, patients may experience life-threatening conditions, including liver failure. Our objectives were to assess the prevalence, severity, risk factors of liver involvement, and association between severity and disease prognosis.

Methods – A retrospective cohort study enrolled 400 confirmed patients recorded at the Hospital for Tropical Diseases and Bamrasnaradura Infectious Diseases Institute, Thailand from January 2016 to April 2021. The study data were collected from medical records and analyzed.

Results – Among the enrolled 400 confirmed cases presenting with febrile illness, the mean age was 41.5 + 14.1 years; the female: male ratio was 1.7:1. Gastrointestinal presentations were nausea or vomiting (62; 15.5%), abdominal pain (4; 1%), and diarrhea (33; 8.3%). Abdominal examination found abdominal tenderness (8; 2%) and hepatomegaly (3; 0.8%). Eighty-eight (22%) cases had liver-function test results; in this group, the cases with abnormal ALT levels numbered 35 (39.8%); 30 (34.1%) cases had mild hepatitis, which presented during weeks 1-2 of illness and resolved later. None of the cases had severe hepatitis. After treatment, all enrolled cases survived (400; 100%).

Conclusion – The prevalence of liver involvement was low. Severity of hepatitis was mild/moderate with good prognosis and outcome. In studying chikungunya cases with severe liver injury, co-existing causes should be considered.

Keyword : Chikungunya, Liver involvement

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USING *ANOPHELES* SALIVARY ANTIBODY BIOMARKERS TO ASSESS THE EFFECTIVENESS OF PERSONAL INSECT REPELLENT IN SOUTHEAST MYANMAR



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Innovative approaches that enhance vector surveillance capacity are urgently needed to advance the malaria elimination agenda, as current tools are inefficient and insensitive. Human antibodies to *Anopheles* salivary proteins could serve as proxy biomarkers of vector exposure and malaria transmission, providing a surrogate outcome measure in vector-control intervention effectiveness trials but evidence for the appropriateness of this approach is limited.

This study uses data from a stepped-wedge cluster randomised control trial that demonstrated repellent distribution was protective of *Plasmodium* infection. As this is likely due to reduced *Anopheles* biting, we sought to quantify the association between repellent distribution and antibodies to *Anopheles* salivary proteins by ELISA in 14,128 samples, measured monthly over 15-months. Furthermore, as personal repellent may be more effective for at-risk populations (i.e. migrants and forest-goers), we estimated the extent to which the effect of repellent was moderated by risk-group. We observed no instantaneous effect of repellent on antibody levels to *Anopheles* salivary proteins ($b=0.01$; 95%CI=-0.03,0.05), however estimation of a series of lagged effects of repellent distribution (modelling gradual antibody decay from prolonged use) showed reduced antibody levels after transition to repellent (i.e. repellent distribution 6-months prior saw a 0.03-unit (95%CI=-0.08,0.03) decrease in antibody levels). More specifically, we observed reductions in antibody levels for migrants (6-month lag: $b=-0.10$; 95%CI=-0.21,-0.01) and forest-dwellers ($b=-0.05$; 95%CI=-0.10,0.00), but not village-residents ($b=0.02$; 95%CI=-0.04,0.08).

These findings suggest antibodies to *Anopheles* salivary proteins could be an informative trial outcome measure and provide important parameters on antibody decay dynamics to inform the design of future vector-control interventions effectiveness studies.

Keyword : Anopheles salivary biomarkers; Vector surveillance

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The role of anti-malarial immunity in the spontaneous clearance of molecular-detectable Plasmodium spp. infection



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The Greater Mekong Sub-Region is approaching malaria elimination. However, in areas of very low transmission there are high proportions of sub-clinical Plasmodium spp. infections, that can act as reservoirs of transmission and are a barrier to elimination efforts. There is emerging evidence that molecular-detectable sub-clinical infections can spontaneously clear in the absence of antimalarial treatment. Naturally acquired immunity may play a role in determining the natural course of (untreated) sub-clinical infections.

A nested cohort study was undertaken in Cambodia recruiting 150 asymptomatic individuals with uPCR-detectable Plasmodium spp. infections at baseline. Individuals were sampled monthly for 12 months to evaluate the duration of infections. Antimalarial blood-stage antibodies specific for merozoite antigens PfAMA1 and PfMSP2 were quantified by ELISA. Accelerated time failure models were used to estimate the relative reduction of infection duration associated with immunity.

Spontaneous clearance was observed in 96% of baseline infections, with median infection duration of 63 days (range 17-301). Seroprevalence at baseline was 42.7% and 38% for anti-PfAMA1 and PfMSP2 IgG, respectively. Doubling of antibody levels at the preceding timepoint (time varying) were associated with a reduced median duration of all P.

spp. infections by 18% (~11 days) (aTR0.82 95% CI:0.71-0.94) for PfAMA1 and by 13% (~8 days) (aTR0.87 95% CI:0.79-0.96) for PfMSP2.

Naturally acquired antibodies are associated with a reduction in the duration of molecular-detectable malaria infections. This has important implications for our understanding of the drivers of the epidemiology of the malaria infectious reservoir in the Greater Mekong Sub-region.

Keyword : malaria, plasmodium, spontaneous clearance, immunity, IgG, antibodies, epidemiology, GMS, Cambodia, Laos, duration of infection,

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PREVALENCE OF TOXOPLASMOSIS AND ITS ASSOCIATED FACTORS AMONG SLAUGHTERHOUSE WORKERS IN YANGON REGION, MYANMAR



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Introduction

Toxoplasmosis, a worldwide endemic zoonosis infection, is one of the occupational diseases with or without symptoms concerning activities executed by humans in their working environment. Currently, major gaps in surveillance are existing in Myanmar. The aim of the study was to find out the prevalence of toxoplasmosis and its associated factors among slaughterhouse workers in Yangon Region, Myanmar.

Methods

A cross-sectional study was conducted among 139 slaughterhouse workers at five slaughterhouses and sub-slaughterhouses in Yangon Region, Myanmar from June to November 2020. Whole blood was collected to detect IgM

and IgG anti-*Toxoplasma gondii* antibodies using *OnSite Toxo IgG/IgM Combo Rapid Test*. In addition, face-to-face interview was done using pretested structural questionnaires to assess the sociodemographic characteristics, level of knowledge, occupational and environmental factors related to *Toxoplasma gondii* infection. Data were analyzed by Chi square and Fisher's Exact tests using SPSS (version 25.0) software.

Results

Of all participants, 43.9% were current infection with *Toxoplasma gondii*. The factors associated with seropositivity of *Toxoplasma gondii* antibodies were blood transfusion history ($p=0.022$), level of knowledge ($p=0.002$), working in contact with animal organs, tissue or blood ($p=0.001$), hand washing behavior when smoking in working condition ($p=0.021$), and most frequently slaughtering cattle, sheep, and goat ($p=0.049$).

Conclusion

There was high seroprevalence of toxoplasmosis among slaughterhouse workers in Yangon Region. Providing health education regarding toxoplasmosis, enforcement of personal hygiene practices in workplaces and establishment of trainings for occupational hygiene and awareness for toxoplasmosis could reduce the risk of *Toxoplasma gondii* infection among slaughterhouse workers.

Keyword : Knowledge, Prevalence, Slaughterhouse workers, Toxoplasmosis, Myanmar

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SEROLOGICAL DETECTION OF TOXOPLASMA GONDII AMONG FREE-GRAZING DUCKS FROM CENTRAL THAILAND



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Toxoplasmosis, which is caused by the obligate intracellular protozoan *Toxoplasma gondii*, is an important worldwide zoonosis in warm-blooded animals, including poultry. Free-grazing ducks with their feeding styles are considered as one of the vital intermediate hosts and an indicator for soil contamination with *T. gondii* oocysts. Central Thailand is the major duck breeding and meat producer for the domestic and export markets. However, the significance of infection and the seroprevalence in ducks are still largely unknown. In total, 217 duck serum samples were collected in 2021 from 6 provinces (Kanchanaburi, Nakhon Pathom, Phetchaburi, Prachuap Khiri Khan, Ratchaburi, Saraburi)

in the central area and examined for the evidence of *T. gondii* infection using indirect fluorescent antibody test (IFAT). The antibodies against *T. gondii* were detected in 68 (31.3%) out of 217 free-grazing ducks. The seroprevalence in fattening ducks and spent layers were similar at 29.1% and 32.3%, respectively. The most common titer was 1:100 (75%), followed by 1:200 (23.5%) and 1:400 (1.5%). To the best of our knowledge, this is the first report of the antibody detection of *T. gondii* in ducks from Thailand. Additionally, seropositive samples were widely distributed in all investigated provinces, revealing a considerable risk of infection for humans, and indicating the contaminated environment in the central country. Therefore, consuming undercooked duck meat should be restricted to avoid the possibility of zoonosis.

Keyword : Toxoplasmosis, IFAT, free-grazing ducks, Thailand

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Morphological characterization and genetic identification of cercariae from infected snails intermediate host, genus *Stenomelania* in Satun province, Thailand



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Trematode infection is still a major public health problem, there are many species of food-borne such as intestinal flukes and etc. *Stenomelania* sp. belongs to family Thiaridae, it has been known that the snails in this family played an important role as intermediate host of human and animal trematodes. In this study, we investigated cercarial infection in snail genus *Stenomelania* from 10 localities of Satun province, Thailand in February 2019. Collected snails were investigated trematode infections by shedding and crushing methods. The cercariae would identified by morphology and molecular study by ITS2 gene. Then, it was analyzed with Neighbor joining method. The collected snails were categorized to *Stenomelania* cf. *torulosa*. A total of 70 snails were collected and examined for trematode infections. The infection rate was 4.29%. The obtained cercariae were classified morphology to *Haplorchis taichui*. It could be used ITS2 gene amplification. The sequence had a length approximately 310 bp. All isolate of *Haplorchis taichui* were included in a single clade and was grouped together with relatively high support. In additional, we studied on cercaria behavior. After emerge from host, the cercaria were moved towards to the upper water about 5 seconds and swim fast forward for 3-5 seconds by the tail bending toward and spinning their body together while

resting for 4-6 seconds. This work will help in basic knowledge about the larval trematode fauna and aim to provide the groundwork for future studies and more details of the parasite and snail.

Keyword :

Trematode infections, genus *Stenomelania*, ITS2 gene

Abstract No. : ABS0001407

Status : Approved

COVID-19: FEVER, RASH AND ORGAN FAILURE



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Introduction: The severe acute respiratory syndrome virus (SARS-CoV-2) is a highly transmissible respiratory virus, SARS-CoV-2, that has caused more than 200 million confirmed cases of COVID-19 and over 4 million fatalities since its first official report in late 2019. Although most infections are asymptomatic or accompanied by sub-clinical symptoms, many infected individuals develop a fever with extra-pulmonary manifestations such as ageusia, anosmia, and rash, thus adding SARS-CoV-2 to the plethora of etiological agents that cause a febrile illness with rash.

Methods: De-identified clinical and laboratory data were retrospectively reviewed to detail the clinical course. The patient provided informed consent to use photographs, and the guidelines of the Declaration of Helsinki were adhered to for the case report, including obtaining approval by the Institutional Review Board of Indira Gandhi Memorial Hospital, Malé, Republic of Maldives. **Results:** SARS-CoV-2 infection was confirmed by RT-PCR in an adult male Maldivian patient. The patient presented to the hospital within one week after the onset of symptoms with shock. The hematological profile revealed marked leukocytosis with an elevation of inflammatory markers. Cutaneous manifestations included a maculopapular rash and an erythema multiform-like rash, which appeared before heart failure. The patient was managed in the intensive care unit requiring multiple interventions to achieve hemodynamic stability to recovery. The rash ultimately resolved two weeks later with residual post-inflammatory hyper-pigmented patches and scaly plaques. **Conclusion:** Infection from SARS-CoV-2 can manifest as a febrile exanthema that, in some cases, precedes severe organ dysfunction requiring hospitalization.

Keyword : Betacoronavirus, SARS-CoV-2, COVID-19

Abstract No. : ABS0001405

Status : Approved

LABORATORY STUDIES OF OVIPOSITION SITE CHOICE OF *TOXORHYNCHITES SPLENDENS*: ROLE OF CONSPECIFIC LARVAE AND PREDATOR-PREY INTERACTIONS



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Oviposition preference by *Toxorhynchites* mosquito species is an important aspect of their biological control potential. When ovipositing, the females deposit individual eggs by hovering above the water indicating that they may be capable of detecting chemical cues from above the water surface. These chemical cues may help the females to determine whether the water is suitable for their larvae. We tested the hypothesis that a female *Tx.splendens* has the ability to discriminate against oviposition sites in habitats containing conspecific larvae and live or dead larvae of *Aedes aegypti*. In this experiment, oviposition preference was determined by comparing number of eggs in test and control cups as well as in cups containing live or dead *Ae.aegypti* larvae together with *Tx.splendens* larvae. The results in first trial showed that females preferred ovipositing in cups with live and dead prey when compared with clean water. Results from the second trial showed that cups with live and dead *Ae.aegypti* larvae proved strongly attractive to *Tx.splendens* females, while those from conspecific *Toxorhynchites* larvae caused oviposition deterrence. *Tx.splendens* preferentially oviposited in cups with live and dead prey compared with cups containing only conspecific larvae (at 100% effective attractiveness; EA), with cups containing 50 live *Ae.aegypti* larvae alone (61.6%EA), and with predator feeding on prey (56.9%EA). Fewer numbers of eggs were oviposited in cups containing conspecific *Toxorhynchites* larvae when compared with other treatments. Our results indicated that water containing a mixture of 25 dead and 25 live *Ae.aegypti* larvae was more preferred for oviposition by female *Tx.splendens*.

Keyword : *Toxorhynchites splendens*, oviposition, preference, larvae, mosquito, *Aedes aegypti*

Abstract No. : ABS0001403

Status : Approved

GENETIC DIVERSITY OF DENGUE VIRUS IN CLINICAL SPECIMENS FROM BANGKOK, THAILAND, DURING 2018–2020: CO-CIRCULATION OF ALL FOUR SEROTYPES WITH MULTIPLE GENOTYPES AND/OR CLADES



Ms.KANAPORN POLTEP

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Dengue is an arboviral disease highly endemic in Bangkok, Thailand. To characterize the current genetic diversity of dengue virus (DENV), we recruited patients with suspected DENV infection at the Hospital for Tropical Diseases, Bangkok, during 2018–2020. We determined complete nucleotide sequences of the DENV envelope region for 111 of 276 participant serum samples. All four DENV serotypes were detected, with the highest proportion being DENV-1. Although all DENV-1 sequences were genotype I, our DENV-1 sequences were divided into four distinct clades with different distributions in Asian countries. Two genotypes of DENV-2 were identified, Asian I and Cosmopolitan, which were further divided into two and three distinct clades, respectively. In DENV-3, in addition to the previously dominant genotype III, a cluster of 6 genotype I viruses only rarely reported in Thailand was also observed. All of the DENV-4 viruses belonged to genotype I, but they were separated into three distinct clades. These results indicated that all four serotypes of DENV with multiple genotypes and/or clades co-circulate in Bangkok. Continuous investigation of DENV is warranted to further determine the relationship between DENV within Thailand and neighboring countries in Southeast Asia and Asia.

Keyword : Bangkok; clades; co-circulation; DENVs; genetic diversity; genotypes

Abstract No. : ABS0001402

Status : Approved

OPENING THE POLICY BLACKBOX: UNRAVELLING THE PROCESS FOR CHANGING NATIONAL DIAGNOSTIC AND TREATMENT GUIDELINES FOR VIVAX MALARIA IN SEVEN COUNTRIES



Ms. Varunika Ruwanpura

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Introduction:

After more than 60 years of limited development, novel tools for vivax malaria are now available, but need integration into national policies. This paper maps malaria policymaking processes in seven countries to identify areas where it can be improved for optimal efficiency.

Methods:

Data were collected during a workshop convened by the Asia Pacific Malaria Elimination Network's Vivax Working Group in 2019, and subsequent interviews with select national stakeholders. Policy processes documentation provided by respondents was reviewed. An analytic framework focused on three a priori defined domains namely, "context", "actors" and "processes" guided the data analysis.

Results:

Policymaking context varied with available funding for malaria, population size, socio-economic status, and governance systems. There was limited documentation of the process itself or terms of reference for involved actors. In all countries, the National Malaria Programme plays a critical role in initiating and informing policy change, but involvement of other actors varies considerably. Available evidence is a key factor in policy change however the importance of local evidence, and global endorsement of new treatments and diagnostics varies. The policy process itself and its complexity varied and was mostly semi-siloed from other disease specific policy processes or the wider Ministry of Health. Time required to change and introduce a new policy guideline previously varied from three months to three years.

Conclusion:

In the medium to long term, better alignment of antimalarial policy making processes with overall national health policy making would strengthen health governance. In the immediate term, shortening timelines for policymaking is key to meet elimination milestones.

Keyword : *P. vivax* malaria, national malaria policy processes

Abstract No. : ABS0001401

Status : Approved

Estimates of people infected with soil-transmitted-helminthiasis and drug requirements for preventive chemotherapy in Ogun, Nigeria



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Background

Soil transmitted helminthiasis (STH) are among the most common human infections worldwide with over 1 billion people affected. This study produced predictive risk maps of STH and estimated the number of people infected, and the amount of drug required for preventive chemotherapy in Ogun state, Nigeria.

Methods

Georeferenced STH infection data obtained from community cross-sectional survey, at 33 locations between July 2016-November 2018, together with remotely sensed environmental and socio-economic data were analyzed using Bayesian geostatistical models.

Result

An overall prevalence of 17.2% (95 % CI: 14.9, 19.5) was recorded for STH infection. *Ascaris lumbricoides* infections was the most predominant, 13.6% (95% CI: 11.5, 15.7), while Hookworm and *Trichuris trichiura* had 4.6 % (95% CI: 3.3, 5.9) and 1.7% (95 % CI: 0.9, 2.4), respectively. The predictive maps reveal a spatial pattern of high risk in the central, western and on the border connecting Republic of Benin. The model identified soil pH, soil moisture and elevation as important predictors of the STH infection. Approximately 1.1 million persons (preschoolers, school-aged children (SAC) and adults) are infected and requires 7.8 million doses. Also, 375,374 SAC were estimated to be infected, requiring 2.7 million doses for annual PC.

Conclusion

Our predictive risk maps and estimated PC needs provide useful information for the elimination of STH, by identifying priority areas for delivery of interventions in Ogun State, Nigeria.

Keyword : Bayesian modelling, Nigeria, Ogun State, School-aged children, Adults, Preschoolers, Soil-transmitted helminthiasis

Abstract No. : ABS0001396

Status : Approved

PRODUCTION AND EVALUATION OF *RICKETTSIA TYPHI* RECOMBINANT 17-KDA PROTEIN FOR SERODIAGNOSIS OF MURINE TYPHUS



Mrs.SABREEN AHAD

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Introduction: Murine typhus or endemic typhus is a rickettsiosis caused by *Rickettsia typhi* and transmitted to human via fleas from rodents, cats and dogs. Common clinical manifestations are fever, malaise, myalgia, nausea, and vomiting, with presence or absence of rash and eschar, and lymphadenopathy, which also present in other febrile illnesses such as scrub typhus, leptospirosis and melioidosis. Murine typhus can be found worldwide and its re-emergence has been reported in Southeast Asia. Serodiagnosis of murine typhus currently relies on an immunofluorescence assay (IFA). Despite precision and accuracy, IFA uses antigens prepared from intracellular culture of *R. typhi* which requires biosafety level 3 facility. The use of whole cell lysate antigens also leads to the difficulty in protocol standardization. Thus, a development of sensitive, specific, standardizable, rapid and affordable murine typhus serodiagnostic method is needed.

Methods: Laboratory scale-production of recombinant 17-kDa antigen of *R. typhi* (rRty17-kDa) was successfully done using bacterial cloning system, confirming by Western blot and mass spectrometry. Purified rRty17-kDa was evaluated for its reactivity with patient sera positive for antibodies to murine typhus, scrub typhus, leptospirosis and melioidosis by indirect ELISA.

Results: Results showed cross-reactivity of rRty17-kDa with sera from healthy donors, leptospirosis and melioidosis patients. Sensitivity of 15.0% and 65.0%, and specificity of 87.5% and 42.5% for IgG and IgM ELISA were observed, which overall do not meet the requirement for an ideal diagnostic test.

Conclusion: The results suggested an inadequacy of rRty17-kDa for a potent murine typhus serodiagnosis in its present form.

Keyword :

Murine typhus, *Rickettsia typhi*, recombinant protein, 17-kDa outer membrane protein, ELISA

E-posters Abstracts

Abstract No. : ABS0001533

Status : Approved

ANALYSIS OF THE MICROBIOME OF THE HAMSTERS GASTROINTESTINAL TRACT DURING INFECTION WITH THE LIVER FLUKES *OPISTHORCHIS FELINEUS*, *OPISTHORCHIS VIVERRINI* AND *CLONORCHIS SINENSIS*



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The liver flukes *Opisthorchis felineus*, *Opisthorchis viverrini* and *Clonorchis sinensis* are parasites of the mammalian hepatobiliary system. Their geographic areas practically do not overlap: *O. felineus* is endemic to Russia, *C. sinensis* – China and South Korea, *O. viverrini* is endemic to Thailand, Lao PDR and Vietnam.

The species have different carcinogenic potential: *O. viverrini* and *C. sinensis* are recognized to be 1A group of biological carcinogens, whereas *O. felineus* belongs to 3A group. Microbiota of the flukes might contribute to the difference in the carcinogenicity of the species.

For the study, golden hamsters from the Specific Pathogen Free Animal Facility were infected with metacercariae collected from endemic regions. DNA libraries were constructed using the V3-V4 region of the 16S rRNA gene from hamster feces, bile and from adult worms and sequenced on the MiSeq Illumina (2 × 300 bp).

As a result, 18,830,015 reads were assigned to 17,625 operational taxonomic units (OTUs) and, in turn, to 261 bacterial genera.

In the infected animals bile, there is a significant increase in phylogenetic diversity ($p < 0.05$) compared to uninfected animals. Taxonomic comparison of bile samples significantly changes 53 OTUs. The microbiome of intestinal feces of infected animals significantly differs from uninfected animals in beta-diversity terms (Bray-Curtis dissimilarity). The largest number of OTUs were found in worms (1200-1600). Adult trematodes microbiomes differ significantly in alpha and beta diversity terms.

The *C. sinensis* microbiome differs significantly from the microbiomes of *O. felineus* and *O. viverrini*. Found unique for worms 140 genera of bacteria (Salmonella, Ochrobactrum, etc.).

Keyword : carcinogenicity, liver flukes, microbiome, bacterial taxonomy

Abstract No. : ABS0001532

Status : Approved

MAMMALIAN WOUND HEALING BY THE TREATMENT WITH EXCRETORY-SECRETORY PRODUCT AND LYSATE OF THE TREMATODE OPISTHORCHIS FELINEUS



Ms. Alena Tarasenko

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The opisthorchiasis after the infection by the liver fluke *Opisthorchis felineus* in mammals is characterized by huge proliferation processes of the bile duct epithelial cells. The idea was to investigate the opportunities of liver fluke proteins to stimulate the skin wound healing.

Objective: To study the stimulation of wound healing in C57BL /6J mice by the treatment with the *O. felineus* excretory-secretory product and lysate with the assessment of wound area, histology and Real-time PCR. Full-thickness wounds (1 cm) in mice were treated with ESP (excretory-secretory product) and *O. felineus* lysate proteins for 7-10 days. ESP and *O. felineus* lysate proteins significantly reduced wound area in mice ($P < 0.05$). The inflammatory infiltration area in the wounds treated with lysate and ESP was significantly smaller compared to the control ($P < 0.05$), with the increased number of eosinophils, macrophages, fibroblasts, but not that of neutrophils. The mRNA expression of inflammatory marker genes (*Arg1*, *Ltb4r1*, *Nos2*), epithelization processes (*Krt19*), angiogenesis (*Vegfa*), organization of the extracellular matrix (*Mmp2*, *Mmp9*) in experimental groups were similar to those in healthy mouse skin at 10 days after the treatment. In contrast to this, in untreated group (control) inflammation was significantly higher, whereas epithelization processes and angiogenesis were comparatively lower. Thus, the treatment with the *O. felineus* promotes accelerated healing of full-thickness wounds. Presumably, the liver fluke produces factors that can be used to stimulate the mammalian tissue regeneration. The activity of the individual components of the secretory product must be further investigated in more detail.

Keyword : opisthorchiasis, regeneration, wound healing, excretory-secretory product, growth factors

Abstract No. : ABS0001531

Status : Approved

REDUCED RISK OF PLACENTAL PARASITAEMIA ASSOCIATED WITH COMPLEMENT FIXATION ON *PLASMODIUM FALCIPARUM* BY ANTIBODIES AMONG PREGNANT WOMEN



Dr. Herbert Opi

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INTRODUCTION: The pathogenesis of malaria in pregnancy (MiP) involves accumulation of *P. falciparum*-infected red blood cells (pRBCs) in the placenta, contributing to poor pregnancy outcomes. Parasite accumulation is primarily mediated by *P. falciparum* erythrocyte membrane protein 1 (PfEMP1). IgG magnitude to pRBCs has been associated with reduced risk of MiP, but associations have been inconsistent. Further, antibody effector mechanisms are poorly understood, and the role of antibody complement interactions is unknown.

METHODS: Studying a longitudinal cohort of pregnant women (n=302) from a malaria-endemic province in Papua New Guinea, we measured the ability of antibodies to fix and activate complement using placental binding pRBCs and PfEMP1 recombinant domains. We determined antibody-mediated complement inhibition of pRBC binding to the placental receptor, chondroitin sulfate A (CSA) and associations with protection against placental parasitaemia.

RESULTS: Some women acquired antibodies that effectively promoted complement fixation on placental-binding pRBCs. Complement fixation correlated with IgG1 and IgG3 antibodies, which dominated the response. There was, however, limited evidence for membrane-attack complex activity, pRBC lysis or killing. Importantly, a higher magnitude of complement-fixing antibodies was prospectively associated with reduced odds of placental infection at delivery. Using genetically-modified *P. falciparum* and recombinant PfEMP1 domains, we found that complement-fixing antibodies primarily targeted a specific variant of PfEMP1 (VAR2CSA). Furthermore, complement enhanced the ability of antibodies to inhibit pRBC binding to CSA, primarily mediated by complement C1q protein.

CONCLUSIONS: These findings provide new insights into mechanisms mediating immunity to MiP and reveal new strategies for developing malaria vaccines that harness antibody-complement

Keyword : Complement, Malaria in pregnancy, *Plasmodium falciparum*, VAR2CSA, Antibodies

Abstract No. : ABS0001526

Status : Approved

THE PROTEOMIC ANALYSIS OF EXTRACELLULAR VESICLES DERIVED FROM PLASMODIUM FALCIPARUM-INFECTED RED BLOOD CELLS DURING GROWTH DEVELOPMENT



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Introduction

Plasmodium falciparum is the leading cause of severe malaria. During its intra-erythrocytic maturation, *P. falciparum*-infected red blood cells (iRBC) release nano-sized extracellular vesicles (EVs) into the extracellular milieu. These EVs cargo both host and parasite biomolecules from iRBC and are important mediators in pathogenesis and host-parasite communication. Proteomic profiling of *P. falciparum*-derived EVs (Pf-EVs) during growth development is significant in understanding their biological function in the course of infection.

Methods

Four *P. falciparum* strains were maintained in human red blood cells. The cultured media during parasite growth of early-stage (ring-to-trophozoite) and late-stage (trophozoite-to-ring) was daily collected to isolate EVs by multi-step centrifugation. Two types of EVs, microvesicles (MVs) and exosomes, were collected. Their proteomes were characterized by Liquid Chromatography-Tandem Mass Spectrometry (LC/MS-MS) and comparisons were made using bioinformatics analysis.

Results

The proteomic analysis revealed the 161 and 155 parasite proteins were found in MVs and exosomes, respectively. EVs derived from all *P. falciparum* strains contained the major virulence-associated parasite proteins such as merozoite surface protein 1 (MSP-1), elongation factor 1-alpha, knob-associated histidine-rich protein, apical membrane antigen 1 (AMA-1) and invasion ligands (EBA-175 and RESA). Bioinformatics analysis revealed that MVs and exosomes during the early stage were enriched in proteins that function in the ribosome pathway and DNA replication, respectively. In contrast, both MVs and exosomes released in the late stage were enriched in proteins associated with metabolic pathways.

Conclusions

This proteomic analysis provided an insight into the Pf-EVs protein profile that may correlate with physiological activity and virulence during the host-parasite interaction

Keyword : *Plasmodium falciparum*; extracellular vesicle; proteomics

Abstract No. : ABS0001519

Status : Approved

MOLECULAR SURVEILLANCE OF KELCH13 (*pfk13*) AND PLASMEPSIN-2 (*pfpm2*) GENES IN *PLASMODIUM FALCIPARUM* ISOLATES IN MALAKA DISTRICT, WEST TIMOR, INDONESIA



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Introduction: The global spread of artemisinin and piperaquine resistant parasites has stressed the importance of conducting molecular surveillance in the endemic countries. The data of resistant markers *kelch13* (*pfk13*) and *plasmepsin-2* (*pfpm2*) remains limited in Indonesia despite dihydroartemisinin-piperaquine being used as the first-line antimalarial drug since 2009. This study aims to assess the mutation status of both genes among *Plasmodium falciparum* isolates in endemic area.

Methods: Isolates were collected from 113 subjects infected with *Plasmodium falciparum* during Mass Blood Survey activities in the Malaka District, East Nusatenggara province, in 2013. The infection was detected by microscopy and/or Real-Time PCR. Nested polymerase chain reaction (PCR) was performed to amplify the propeller domain of the *pfk13* gene, followed by sequence analysis to evaluate single nucleotide polymorphisms (SNP). qPCR was utilized to measure copy number variation (CNV) of the *pfpm2* using the derived delta-delta CT value relative to 3D7 strain. Copy numbers >1.6 was determined as the cut-off value for gene amplification.

Results: 76 (67%) of the 113 isolates were successfully analysed for SNP. No polymorphisms were found in the *pfk13* gene. As for *pfpm2*, only 29 (25.6%) were successfully typed, and amplification were detected in 3.4% (1/29) isolates.

Conclusion: This study supports continued utilisation of dihydroartemisinin-piperaquine as the first-line antimalarial drug in Malaka District, Indonesia.

Keyword : *Plasmodium falciparum*, surveillance, *pfk13*, *pfpm2*, Malaka

Abstract No. : ABS0001516

Status : Approved

HOST BIOMARKERS FOR THE DIAGNOSIS OF SEVERE IMPORTED PLASMODIUM FALCIPARUM MALARIA



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INTRODUCTION:

Severe imported *Plasmodium falciparum* malaria is a source of mortality and morbidity in non-endemic regions. Hyperparasitaemia is a finding which doesn't accurately predict severity in these population. Therefore, there is a need to evaluate biomarkers as a tool to better discriminate patients with severe malaria.

METHODS:

Case-control study including patients with *P.falciparum* malaria attended at Hospital Clinic of Barcelona (Spain). Participants were classified as severe and non-severe malaria according to WHO criteria, except for parasitaemia. Angiotensin-1 (ANG-1), angiotensin-2 (ANG-2) and s-TREM-1 concentrations were determined. Biomarker concentrations were compared between groups and with different reference parasitaemia cut-off values (2% following European guidelines and 10% according to WHO).

RESULTS:

73 participants were included: 13 severe and 60 non-severe malaria cases. Median ANG-1 concentration was statistically lower in severe than in non-severe cases ($p=0.001$) whereas median ANG-2 and s-TREM-1 concentrations were higher in severe cases ($p=0.001$ and $p=0.010$, respectively). The ratio ANG-2/ANG-1 was higher in the severe group (5.51 vs 0.45, p

CONCLUSION:

ANG2/ANG-1 ratio showed better diagnostic performance than 2% parasitaemia, and better sensitivity compared with 10% parasitaemia. Therefore, ANG2/ANG1 could be a useful tool to predict severity in imported *P.falciparum* malaria

Keyword : Severe imported malaria, *Plasmodium falciparum*, biomarker, Angiotensin-2

Abstract No. : ABS0001514

Status : Approved

MOLECULAR EPIDEMIOLOGY OF *GIARDIA* IN BLACK GOATS, PIGS AND CATTLES IN HAINAN, CHINA



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Introduction: *Giardia* is a widespread intestinal protozoan that causes diarrhea in humans and animals. No systematic research was reported on *Giardia* in black goats, pigs and cattles in Hainan, China.

Methods: A total of 1,480 feces samples were collected in Hainan, including 710 black goats, 456 pigs and 314 cattles. *Giardia* was detected and genotyped by nested PCR targeting small subunit ribosomal RNA (SSU rRNA) gene and sequence analysis.

Results: The infection rates of black goats, pigs and cattle of were 6.2% (44/710), 2.6% (12/456) and 2.2% (7/314), respectively ($P < 0.05$). Higher infection rates of younger livestock were observed than older ones. *Giardia* assemblages A(n=17), B (n=8), and E (n=19) were identified black goats. Only assemblages E was identified in pigs (n=12) and cattle (n=7). Interestingly, among the 16 positive samples from 115 samples in black goats from Haikou, 15 were assemblage A. Eight positive samples were all assemblage B among 53 samples from Wuzhishan.

Conclusions: This study found that the wide distribution of *Giardia* in black goats, pigs and cattles in Hainan, China. Significant variation for genotypes distribution existed in different regions. Black goats, pigs and cattles might a potential source of human giardiasis.

Keyword : *Giardia*; Genotype; Black goats; Pigs; Cattles; Hainan

Abstract No. : ABS0001512

Status : Approved

MOLECULAR DETECTION AND GENOTYPING OF *ENTEROCYTOZOON BIENEUSI* IN HUMANS FROM HAINAN PROVINCE OF CHINA: HIGH DIVERSITY AND UNIQUE ENDEMIC GENETIC CHARACTERISTICS,



Mr. Guangxu Ren

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Introduction: *Enterocytozoon bieneusi* (*E. bieneusi*) is a zoonotic potential pathogen which was found in humans and animals worldwide. We investigated the prevalence and the genetic characteristics of *E. bieneusi* in humans from Hainan, China.

Methods: 1264 fecal samples were collected from 628 patients with diarrhea (325 adults and 303 children), and 636 asymptomatic population including 383 college students (340 Chinese and 43 foreigners) and 253 kindergarten children. *E. bieneusi* was identified by nested PCR amplification the internal transcribed spacer (ITS) region. Phylogenetic tree was established by a neighbor-joining method.

Results: The overall prevalence of *E. bieneusi* was 3.7% (47/1264), with 5.6% in the patients with diarrhea (5.8% for adults and 5.3% for children) and 1.9% in the asymptomatic population (2.9% for Chinese, 2.3% for foreigners and 0.4% for kindergarten children). The prevalence of *E. bieneusi* in humans with diarrhea was significantly higher than that in without diarrhea ($P < 0.05$). Twenty-eight genotypes were identified, including ten genotypes (CHG5, CHG3, SHR1, CHG2, Type IV, EbpC, EbpA, PigEBITS7, CHG19 and CM21) and 18 novel genotypes (HNN-1 to HNN-18). The genotypes above were clustered into group 1 ($n = 6$), group 2 ($n = 14$) and group 13 ($n = 8$).

Conclusions: This is the first report on the identification of *E. bieneusi* in humans from Hainan, China. The association between *E. bieneusi* infection and diarrhea was observed. High diversity and distinctive distribution of *E. bieneusi* genotypes found here reflect the unique epidemic genetic characteristics of *E. bieneusi* in humans living in Hainan.

Keyword : *Enterocytozoon bieneusi*; Genotype; Human; Hainan

Abstract No. : ABS0001510

Status : Approved

SEROLOGICAL INVESTIGATION OF *TOXOPLASMA GONDII* AND *ANGIOSTRONGYLUS CANTONENSIS* IN A LI VILLAGE IN HAINAN, CHINA



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Introduction: *Toxoplasma gondii* and *Angiostrongylus cantonensis* are important foodborne parasites can cause serious diseases of human. Li people is a unique nationality only live in mountainous area in Central Hainan, China. Li people have the custom of eating wild mice and snails. This seroepidemiological study was set in a small li village, where little is known about *T. gondii* and *A. cantonensis* prevalence in li people.

Methods: 83 serum samples of li people were collected from Wangzha village, Changjiang Li Autonomous County, Hainan Province. Commercial enzyme-linked immunosorbent assay (ELISA) Kits for IgG anti *T. gondii* and *A. cantonensis* were carried out according to the instructions of the kits.

Results : The infection rates of *T. gondii* and *A. cantonensis* of li people were 13.25% (11/83) and 22.89% (19/83), respectively, and were higher in male than in female patients (18.37% vs 6.25% and 26.53% vs 17.65%). In addition, the average ages of male patients were younger than female patients (40.00 vs 66.50 and 41.92 vs 52.83). Meanwhile, 3 of these patients showed double infection, and they were all male.

Conclusions: To our knowledge, this is the first reported serological investigation of *T. gondii* and *A. cantonensis* in the li people in Hainan. However, we need conduct further and intensive analysis by using molecular biology method to genotype identification of these pathogens. The results provides baseline data that will be useful for controlling and preventing these pathogens in li village.

Keyword : *Toxoplasma gondii*; *Angiostrongylus cantonensis*; Li people; Hainan; Serological investigation

Abstract No. : ABS0001507

Status : Approved

GENETIC CHARACTERIZATIONS OF *CRYPTOSPORIDIUM* SPP. IN WILD RATS, FARMED BAMBOO RATS AND ASIATIC BRUSH-TAILED PORCUPINE FROM HAINAN, CHINA.



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Introduction: *Cryptosporidium* spp. are an important cause of diarrhea in both humans and animals. This study was to evaluate the prevalence, genotypic diversity of *Cryptosporidium* in various rodents in Hainan, China.

Methods: *Cryptosporidium* was detected from 219 wild rats, 360 farmed bamboo rats (*Rhizomyidae*) and 257 farmed Asiatic brush-tailed porcupine (*Atherurus macrourus*) by nest-PCR amplification of the partial SSU rRNA gene.

Results: The total prevalence of *Cryptosporidium* was 12.2% (102/836). The prevalence of *Cryptosporidium* in wild rats (53/219; 24.2%) was higher than that in farmed bamboo rats (37/360; 10.3%) and Asiatic brush-tailed porcupine (12/257; 4.7%). Seven species-*C. ubiquitum* (n = 15), *C. occultus* (n = 14), *C. parvum* (n = 6), *C. muris* (n = 3), *C. viatorum* (n = 2), *C. bovis* (n = 1) and *C. xiaoi* (n = 1)-and eleven genotypes (*C. parvum*-like, Bamboo rat genotype I and II, Civet genotype I, Rat genotype I to IV, Rat genotype VI and VII, *C. environmental* sequence) of *Cryptosporidium* were identified. Meanwhile, a novel genotype *C. environmental* sequence -like (similarity 95.39% with the sequence FJ205699) was found in a wild rat.

Conclusions: All the seven species identified here were found in humans previously highlights the possible cross-species transmission of *Cryptosporidium* between those rats and humans as well as other animals.

Keyword : *Cryptosporidium* spp.; Rodents; Hainan; Genotype

Abstract No. : ABS0001506

Status : Approved

GENETIC CHARACTERISTICS AND PUBLIC HEALTH RISKS OF *CRYPTOSPORIDIUM* SPP. FROM PIGS AND BLACK GOATS IN HAINAN, CHINA



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Introduction: *Cryptosporidium* spp. is an important zoonotic opportunistic intestinal protozoa causing serious diseases in immunocompromised population. No investigation about *Cryptosporidium* spp. in black goats and pigs in Hainan was reported. This study aimed to investigate molecular characteristics and assess the public health risks of *Cryptosporidium* spp. from pigs and black goats in Hainan, China.

Methods: 1105 fecal samples were collected in Hainan, 456 from pigs and 837 from black goats, respectively. Feces were detected for *Cryptosporidium* spp. by nested PCR of the 18S ribosomal RNA fragment and the sequences analysis.

Results: The infection rates of *Cryptosporidium* spp. of pigs and black goats were 7.9% (36/456) and 9.0% (75/837), respectively. Higher infection rate were observed in younger pigs (10.4%, 34/326) and younger black goats (12.9%, 47/363) compared with adults pigs (1.5%, 2/130) and black goats (5.9%, 28/474) ($P < 0.001$). Four genotypes were identified from pigs, including *C. scrofarum* (n=24), *C. suis* (n=9), *C. xiaoi* (n=2), *C. occultus* (n=1). Four genotypes

were identified from black goats, including *C. xiaoi* (n=40), *C. ubiquitum* (n=26), *C. parvum* (n=7) and *C. occultus* (n=2).

Conclusions: The results showed that *Cryptosporidium* spp. was widespread in pigs and black goats in Hainan. *C.xiaoi* and *C. occultus* in pigs and *C. occultus* in black goats were first identified. *C. parvum* in black goat and *C. xiaoi* in both livestock implied that it has public health risk.

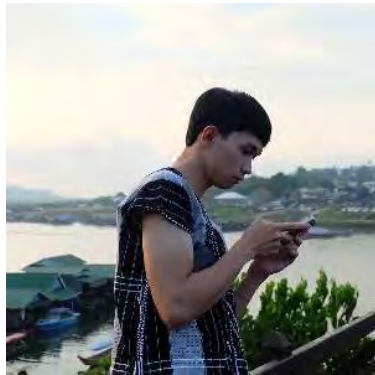
Keyword :

Cryptosporidium spp.; Genetic characteristic; Pig;Black goat; Hainan

Abstract No. : ABS0001503

Status : Approved

THE STUDY OF DEMOGRAPHIC CHARACTERISTICS IN TRAVELERS FROM ABROAD DURING CORONA VIRUS DISEASE 2019, THAILAND



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In situation COVID-19 Pandemic, Thailand has travelers from affected area. Health quarantine officer must be screening and surveillance for isolation, quarantine and declared Patients under investigation (PUI) are determined based on signs/symptoms, along with risk factors refer to medical services. The purpose of this study were to identify demographic characteristics in a travelers from abroad. The descriptive study based on the data form passenger health questionnaire (T8 form) between 1st April 2020 to 31th December 2020. There were 312,790 travelers from aboard. Gender ratio was 1.87 males per 1 female .The most travelers from aboard was the worker in high income countries. The most of age groups were males 30-39 year-old (30.90%). Thai nationality was 57.10%,Myanmar (5.09%).Most of country of origin were japan (7.77%), South Korea (6.82%).Most of them were workers (45.53%), container/cargo (9.01%).All travelers, there were 3,216 Cases definition for patients under investigation (2.67% of COVID-19 confirm cases.). Screening system is important to prevent and response pandemic, laboratory center in international health quarantine supported capacity for effective surveillance and disease control.

Keyword : COVID-19, Travelers

Abstract No. : ABS0001502

Status : Approved

QUALITY OF LIFE OF CHOLANGIOCARCINOMA PATIENTS AFTER BEING ADMINISTERED WITH THAI MEDICINAL CANNABIS



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Introduction: Cholangiocarcinoma (CCA) has a poor prognosis and is highly prevalent, especially in Northeastern (Isaan) region of Thailand (Sripa and Pairojkul, 2008), which is 100 times higher than the global rate (Alsaleh et al. 2018). Thailand was the first country in Southeast Asia to approve cannabis for medical treatment and there are two palliative care treatment protocols allowed for cancer patients; standard treatment (ST) and medical cannabis treatment (CT). So, aimed to compare the quality of life (HRQoL) outcomes between groups.

Methods: This prospective cohort study among 72 newly diagnosed CCA patients (42 CT : 30 ST) whom was carried out between 1st September 2019 to 31st October 2020. They were measured HRQOL at baseline, 2nd and 4th months after diagnosis by the EORTC QLQ-C30, HCC18, BIL21. Data was collected from 6 hospitals in four provinces of northeast Thailand. The Wilcoxon signed rank test was performed to compared within groups QoL scores.

Results: At pre-treatment, the mean score of Global health status and functional scales were similar (79.33 ± 5.83 : 80.23 ± 12.78). Later, at the 2nd and 4th month of follow-up, the CT group had consistent statistically significantly better PPS, and QoL scores, and many symptom scores than the ST group (P value

Conclusions: Medicinal cannabis may increase QoL for advanced CCA patients. Our findings support the importance of early access to palliative cannabis clinic before the terminal and acceleration phase close to death.

Keyword : Quality of life, CCA, medicinal cannabis, Northeastern Thailand

Abstract No. : ABS0001499

Status : Approved

SENSITIVITY AND SPECIFICITY OF LAMP TESTS FOR MALARIA DIAGNOSIS USING DRIED-BLOOD SAMPLES OF SUSPECTED MALARIA PATIENTS IN LAO PDR



Dr. Moritoshi Iwagami

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Introduction: Microscopy and RDT (rapid diagnostic test) are widely used for malaria diagnosis in the endemic areas. However, sub-microscopic and sub-RDT malaria infections have been reported from several endemic areas, and thus, highly sensitive and simple tests are expected to be adopted. We evaluated a performance of malaria-LAMP (loop-mediated isothermal amplification) tests using DBSs (dried-blood samples) collected in Laos.

Methods: DBSs were of suspected malaria patients (microscopy or RDT positive) in Savannakhet (n=473) and Sekong (n=430) provinces in Laos in 2015. The LAMP tests were performed using Loopamp™ Malaria Pan/Pf/Pv Detection Kit (Eiken Chemical Co., Ltd., Tokyo). Sensitivity and specificity of the LAMP tests were calculated based on the PCR test results.

Results: For the Sekong samples, the sensitivity and specificity of the LAMP tests for Pan were 100.0% and 90.0% respectively, for Pf were 91.4% and 97.8% respectively, and for Pv were 99.7% and 86.9% respectively. For the Savannakhet samples, those of the LAMP tests for Pan were 95.3% and 86.4% respectively, for Pf were 93.3% and 93.7% respectively, and for Pv were 89.9% and 92.9% respectively.

Conclusion: The sensitivity and specificity of the LAMP tests were slightly lower than those of the PCR tests. However, the procedure of the LAMP tests was found to be simpler and easier. The LAMP tests solely required a single 65°C incubator and the kit could be stored at room temperature. The LAMP tests can be reliably and usefully performed as a point-of-care testing at the endemic areas where the PCR testing is not available.

Keyword : malaria, LAMP, Laos

Abstract No. : ABS0001498

Status : Approved

FIRST CASE OF BALAMUTHIA MANDRILLARIS ENCEPHALITIS DIAGNOSED BY NEXT-GENERATION SEQUENCING AND PCR IN HAINAN, CHINA



Prof. Gang Lu

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Introduction: *Balamuthia mandrillaris* (*B. mandrillaris*) is a free-living amoeba that causes rare and fatal encephalitis in humans. More than 95% of confirmed patients were died due to the lack of effective diagnostic methods and therapy.

Methods: A 50 years old farmer had history of eating snails from Changjiang Li Autonomous County, Hainan, presented fatigue and numbness of left limb, irregular fever, dizziness, headache and walkless for more than 1 month. Four nodules about 0.5-0.8×0.3-0.5cm were found on both upper and left lower limbs. Multiple intracranial abnormal enhancement foci were found by MRI. He was suspected as having cerebral cysticercosis or Angiostrongyliasis cantonensis. Antiparasitic treatment was ineffective. Immunodiagnosis for parasitic diseases and next-generation sequencing (NGS) of the cerebrospinal fluid (CSF) were used. The nodule was biopsied.

Result: Cantonensis by ELISA method in CSF and sera was positive. 1019 reads of *B. mandrillaris* were found by NGS. PCR for *B. mandrillaris* of CSF and biopsy sample positive and sequencing analysis showed with 98% homolog with *B. mandrillaris* in GenBank. The patient was confirmed with *B. mandrillaris* encephalitis and past infection of *A. cantonensis*. The patient deteriorated rapidly and died 1 week after being.

Conclusion: This is the first case of *B. mandrillaris* encephalitis diagnosed by NGS and PCR in Hainan, China. The NGS method should be widely applied in clinical practice and help clinicians provide direction for the diagnosis of suspected infectious diseases, especially for unknown infectious cases.

Keyword : *Balamuthia mandrillaris*; encephalitis; Diagnosis; Next-generation sequencing (NGS); PCR; Hainan

Abstract No. : ABS0001491

Status : Approved

NOVEL MULTILOCUS SEQUENCE TYPES OF CARBAPENEM RESISTANT PSEUDOMONAS AERUGINOSA STRAINS FROM A MALAYSIAN TERTIARY HOSPITAL



Ms. Kalaivani Kalai Chelvam

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Introduction:

Pseudomonas aeruginosa is an important nosocomial pathogen that exhibits multiple drug resistance with increasing frequency, especially to carbapenems making patient treatment difficult. In this study, the incidence of genes responsible for carbapenemase production in carbapenem-resistant *Pseudomonas aeruginosa* (CRPA) and the genetic relatedness of the strains were assessed.

Methods:

Identification and antimicrobial susceptibility testing of multi-drug resistant (MDR) *P. aeruginosa* strains (n=250) was performed using the VITEK 2 system. Presence of metallo- β -lactamase genes (*bla*IMP-1, *bla*IMP-2, *bla*VIM-1 and *bla*VIM-2) in the CRPA were detected using polymerase chain reaction (PCR). Nine of the CRPA strains that were highly resistant to carbapenems were subjected to multi locus sequence typing (MLST) followed by sequence type (ST) alignment using the PubMLST database.

Results:

Overall, 165 strains were identified as CRPA with *bla*IMP-1 and *bla*VIM-1 genes present in 25 and four strains, respectively. MLST of the nine strains that were highly resistant to carbapenem indicated four different novel STs, ST3606, ST3607, ST3608 and ST3609. Four of the strains were identified as *bla*IMP-1 positive with an identical allelic profile of ST3606, among which two strains were isolated from the same patient in 2015 and 2018.

Conclusion:

Identification of novel ST may reveal genetic diversity which is important in shaping the evolution of *P. aeruginosa*. The isolation of CRPA strains is alarming as carbapenems with antipseudomonal activity are important to treat *P. aeruginosa* infections. This warrants strict infection control measures to reduce the spread of carbapenemase encoding genes among the *P. aeruginosa* strains.

Keyword : Carbapenem resistant *Pseudomonas aeruginosa* (CRPA), IMP-1 carbapenemase, multi-locus sequence typing (MLST)

Abstract No. : ABS0001487

Status : Approved

EVALUATION OF TRANSMISSION BLOCKING CAPABILITY OF ANTIMALARIAL DRUGS AFTER MULTI-STAGE INHIBITION OF PLASMODIUM GAMETOCYTE THROUGH STANDARD MEMBRANE FEEDING ASSAYS



Dr.AMIT KUMAR

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Introduction

Malaria elimination needs, drugs targeting sexual stages of *Plasmodium falciparum* need to be incorporated in treatment regimen along with schizonticidal drugs to interrupt transmission. Antimalarial drugs have been reported to affect gametocyte production in vivo, which leads to a potential increase in transmission of disease burden. Here, we used early and late stage *Plasmodium falciparum* gametocyte through SMFA assay to measure the effect of antimalarial drugs on gametocyte production in vitro.

Methods

Plasmodium falciparum strain were revived in vitro culture and induced to gametocyte production by hypoxanthine and culture was enriched for gametocyte stages using N-acetyl-glucosamine. Gametocytes were incubated with 10 antimalarial drugs for 24 and 48 h and stage specific gametocytocidal activity was evaluated by microscopic examination and further evaluated by standard membrane feeding assay.

Results

Plasmodium falciparum strain NF54 and MRC-2 were able to reproducibly produce gametocytes in high yield and were used to screen gametocytocidal drugs. Primaquine phosphate, quinine, mefloquine hydrochloride and artemisinin derivative was found to target gametocytes in a concentration dependent manner by either completely eliminating gametocytes or rendering them morphologically deformed with their different inhibitory concentration 106nM, 50nM, 30nM and 10nM.

Conclusion

Our results indicate that late-stage gametocytes are refractory to all of the classes of antimalarial agents that were tested in this study. Relatively little data are available on the effects of these drugs on gametocyte formation, as well as their ability to block transmission by killing the late-stage gametocyte.

Keyword : Plasmodium, Transmission Blocking, Antimalarial drug

Abstract No. : ABS0001481

Status : Approved

EPIDEMIOLOGICAL STUDY ON CORONAVIRUS DISEASE 2019 (COVID-19) CASES IN THE STATE QUARANTINE SITES



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Thailand reported its first confirmed cases of COVID-19 in early January 2020, the State Quarantine sites were established for Thais and foreigners with a total quarantine period of 14 days and samples testing for RT-PCR at least 2 times. The purposes of this study were to identify the characteristics of COVID-19 confirmed cases, study infection rates at quarantine sites. The descriptive study based on the data from passenger health questionnaire (T8 Form) between 1st April 2020 to 30th April 2021. There were 2,723 COVID-19 confirmed cases (0.84% of all travellers). Gender ratio was 1.16 males per 1 female, median 32 year-old (range 2 month – 83 year-old). Most of the age groups were 30-34 year-old (15.35%), 25-29 year-old (14.87%). Thai nationality was 67.68%, Indian (5.07%). Most of them were the students (17.77%), the workers (14.87%). There were 79.73% asymptomatic cases and 20.27% symptomatic cases. Most of them had a cough (42.83%), fever (33.10%). Infection rates were mostly observed among travellers from the USA (9.47%), India (7.64%). Confirmed cases occurred predominantly in December 2020 (16.42%). Earliest detection was found on the day 0, latest on the day 32 after entering Thailand. The highest detection was observed between day 3-4 (29.93%), day 5-6 (24.97%). Personal protection should be promoted among travellers, especially among 25-34 years old, those studying and working abroad. The health quarantine officer should verify signs other than measure temperature. The risk score for each country based on infection rates and detection date, may be used to reduce quarantine days.

Keyword : Quarantine, State Quarantine, COVID-19

Abstract No. : ABS0001477

Status : Approved

INVESTIGATING THE PREVALENCE OF TRYPANOSOME INFECTION IN CATTLE IN NORTHERN UGANDA



Mr. Ross Watson

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INTRODUCTION: The African Trypanosomes, protozoan parasites, are transmitted throughout Africa by the tsetse fly (*Glossina* spp.), infecting a range of mammals. Human African Trypanosomiasis is fatal unless treated and two sub-species of trypanosome cause geographically disparate acute (*Trypanosoma brucei rhodesiense* in Eastern and Southern Africa) and chronic (*Trypanosoma brucei gambiense* in Central Africa) forms of the disease. Animal African Trypanosomiasis is caused by a range of trypanosome species and can be asymptomatic or cause severe symptoms; this disease is responsible for food insecurity and economic hardship. Importantly, *T.b.rhodesiense* is a zoonotic parasite, and human cases are associated with spill-over from cattle populations and wild animals.

METHODS: A cross-sectional survey was undertaken in Northern Uganda to determine the prevalence of three trypanosome species in cattle in 2018: *Trypanosoma brucei* sensu lato, *Trypanosoma congolense* and *Trypanosoma vivax*. Blood samples were collected, stored and transported on Whatman FTA Cards, and analysed using the ITS and TBR Polymerase Chain Reactions.

RESULTS: The overall prevalence of trypanosomes in cattle was shown to be 15.17% (13.07% - 17.54%; 150/989). *T.brucei* sl was shown to be the most prevalent species, followed by *T.congolense* and *T.vivax*. Most infections were shown to be monolytic (90.00%; 135/150) whilst 15 infections were shown to be mixed (10.00%; 15/150).

CONCLUSION: This study demonstrates the presence of trypanosomes in livestock in this region, and ongoing works will detail the zoonotic risk to human populations.

Keyword : Animal African Trypanosomiasis (AAT); Human African Trypanosomiasis (HAT); One Health; Zoonosis

Abstract No. : ABS0001470

Status : Approved

TARGET-SITE MUTATION OF *Rdl* GENE AND INSECTICIDE SUSCEPTIBILITY IN FIPRONIL- AND PYRETHROID-RESISTANT *Aedes aegypti* MOSQUITOES FROM NAKHON PATHOM AND KANCHANABURI PROVINCES



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Introduction: Long-term and intensive applications of various insecticides in mosquito control have inevitably led to the development of resistance mechanisms. *Rdl* (Resistant to dieldrin) gene is the important target for dieldrin and fipronil. It is therefore important to investigate the presence of *Rdl* mutation and insecticide susceptibility in pyrethroid-resistant *Ae. aegypti* mosquitoes, the vector of dengue and Zika, from Nakhon Pathom and Kanchanaburi provinces. **Methods:** The pyrethroid-resistant female mosquitoes were exposed to 0.14% fipronil (phenylpyrazole), 1.00% fenitrothion (organophosphate) and 0.34% fenobucarb (carbamate) by WHO susceptibility test. Genomic DNA extracted from individual fipronil-resistant females was PCR amplified and then subjected to DNA sequencing. **Results:** 0.14% fipronil provided 94.00±5.20% and 96.00±3.30% mortality rates in the mosquitoes from Nakhon Pathom and Kanchanaburi provinces, respectively. A substitution of alanine at 302 with serine, A302S, was detected in the mosquitoes from Nakhon Pathom and Kanchanaburi provinces at mutation frequencies of 0.33 (2/6 sequences) and 0.25 (1/4 sequences), respectively. However, 1.00% fenitrothion and 0.34% fenobucarb gave a 100% mortality rate in the mosquitoes from all 2 provinces. The mean mortality rates of mosquitoes were significantly different among insecticides (*p*

Conclusion: The target-site mutation of *Rdl* gene, A302S, was present in the fipronil- and pyrethroid-resistant mosquitoes from all 2 provinces. However, the mosquitoes were completely susceptible to 1.00% fenitrothion and 0.34% fenobucarb. It suggests that those insecticides should be used sparingly and integrated with the safe mosquito control measures. The data on insecticide susceptibility test were reported to Tambon Health Promoting Hospitals in the study areas for effective mosquito control.

Keyword : *Rdl* gene, target-site mutation, insecticide susceptibility, *Aedes aegypti*

Abstract No. : ABS0001468

Status : Approved

NATURAL INFECTIONS WITH LARVAE OF *ONCHOCERCA* SPECIES TYPE IN THE HUMAN-BITING BLACK FLY, *SIMULIUM NIGROGILVUM* (Diptera: Simuliidae), IN CENTRAL THAILAND



Ms. Fan Huang

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Introduction

Zoonotic onchocerciasis is a human infection caused by *Onchocerca* species of animal origins and transmitted by black fly vectors. This study aims to clarify the vectorial roles of black fly species in zoonotic filarial transmission in central Thailand.

Methods

Natural filarial infections of adult black flies were investigated at Khlong Lan district, Kamphaeng Phet province (elevation 1,276 m), central Thailand, during cool and rainy seasons. An insect net was used to collect adult flies while they flew around human bait during 0700 to 0900 hours by sweeping. Herein, a combined approach of morphotaxonomic and molecular analyses (mitochondrial *cox1*, 12S rRNA, and nuclear 18S rRNA genes) was used to clarify the natural filarial infections in female black flies.

Results

A total of 911 wild-caught adult black flies were collected. *Simulium nigrogilvum* was the most abundant species (n = 708), followed by *S. doipuiense* complex (n = 179), *S. chamlongi* (n = 11), *S. umphangense* (n = 10), *S. chumpornense* (n = 1), *S. multistriatum* species-group (n = 1), and *S. maewongense* (n = 1). Two of 708 females dissected were naturally infected with one third-stage larva (infective larva) each in their thoraces. The NCBI BLAST results and phylogenetic analyses with those of previous reports strongly supported that both larvae were *Onchocerca* sp. type I.

Conclusion

Based on morphological and molecular analyses revealed that female *S. nigrogilvum* could be the natural vector of *Onchocerca* sp. type I in the central region of Thailand.

Keyword : Black fly; Zoonotic onchocerciasis; *Onchocerca*; Mermithid nematodes

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DENSITY DETECTION OF *PLASMODIUM FALCIPARUM* GAMETOCYTES IN SAMPLES FROM THAI MALARIA PATIENTS USING A QUANTITATIVE REAL TIME RT-PCR ASSAY



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Plasmodium falciparum gametocytes, the sexual-stage picked up from the peripheral blood by feeding mosquitoes, can be used as an estimator of potential infectiousness of individuals in molecular epidemiology studies.

We have developed a sensitive *P. falciparum* gametocyte detection technique using quantitative real time reverse transcriptase polymerase chain reaction (qRT-PCR) to quantify the *Pfs25* gene, which is expressed in mature female gametocytes. The quantity of inserted *Pfs25* plasmids was determined by droplet Digital PCR (ddPCR) and used as a standard control. *Pfs25* plasmids were ten-fold serially diluted ranging from 1,240,000 – 1.24 copies/μl. A standard curve was generated in triplicate to determine the limit of detection (LOD) of the assay, which was 1-2 copies/μl with a cycle threshold (CT) cut off of 35. This assay was then applied to quantify *Pfs25* mRNA transcripts from clinical malaria samples, collected in Paxgene tubes, from Ubon Ratchathani and Yala Provinces, Thailand. Detection and quantification of gametocytemia were successful in 8 out of 15 *P. falciparum* samples with concentrations ranging from 1 to 35 copies/μl. Comparison between qRT-PCR and nested RT-PCR showed concordance results in 8 samples, while only 3 blood smears were positive for gametocytes, with reads of 1-3 gametocytes per 200 white blood cells.

In this study, qRT-PCR was developed as a sensitive and quantifiable technique suitable for submicroscopic gametocyte detection. The technique can be applied in future studies evaluating drug efficacy for gametocyte clearance and as a tool to monitor potential transmission for malaria elimination.

Keyword : *Plasmodium falciparum* gametocytes, *Pfs25* gene, quantitative real time reverse transcriptase polymerase chain reaction (qRT-PCR)

Abstract No. : ABS0001456

Status : Approved

CURRENT INSECTICIDE SUSCEPTIBILITY STATUS ANOPHELES AND AEDES MOSQUITOES IN MALARIA AND DENGUE ENDEMIC AREAS, THAI-MYANMAR BORDER



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Introduction

In Thailand, the widespread of insecticide resistance has recently been reported as severe problem. Herein, we conducted the insecticide susceptibility tests in natural mosquitoes from Tha Song Yang District, a malaria hotspot area in Tak province.

Methods

Larvae and pupae of both Anopheline and culicine groups were collected from two villages [Saun Oi (SO) and Tala Oka (TO)] during December 2019 to April 2020. Insecticide susceptibility tests in adults were conducted with three classes of insecticide following WHO guidelines. The mortality and knockdown rates were calculated. V106G and F1534 mutations were detected by a multiplex PCR for *Aedes aegypti* adults. Their association with observed insecticide susceptibility status were determined.

Results

Emerging adult female mosquitoes of *Anopheles* spp. (n = 5339, 92.63%) and F1 *Ae. aegypti* (n = 425, 7.37%) adults were tested. *An. minimus* s.l. and *An. maculatus* s.l. were susceptible to pyrethroids, organophosphates, and carbamates. Low mortality rate when exposed with bendiocarb was shown. The observed mortality rate for *An. minimus* s.l. (SO and TO) and *An. maculatus* s.l. (SO) were 88.80%, 88.70%, and 89.92%, respectively. Interestingly, F1 *Ae. aegypti* adult were suspected resistance to deltamethrin and resistance to permethrin. V1016G and F1534C alleles were detected in three genotypes (VV/CC, VG/FC, GG/FF). The association between *kdr* alleles and resistance phenotype were found significantly only in deltamethrin.

Conclusion

Bendiocarb resistance was found in *An. minimus* s.l. and *An. maculatus* s.l.. No pyrethroid resistance was found in this study. In *Ae. aegypti* population, we found that they developed resistant to pyrethroids associated with *kdr* alleles.

Keyword : *Aedes aegypti*, *Anopheles* mosquitoes, Insecticide resistance, Pyrethroids

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COMPARISON OF MODIFIED JONES' CULTURE MEDIUM AND POLYMERASE CHAIN REACTION (PCR) FOR DIAGNOSIS OF *BLASTOCYSTIS HOMINIS* INFECTION



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Introduction:

Blastocystis hominis is an anaerobic intestinal protozoon that can infect human and other animals. *B. hominis* infection has a broad spectrum of symptoms from asymptomatic to intra-intestinal and extra-intestinal symptoms. *B. hominis* diagnostic tools vary from direct smear, staining, culture medium, immunoserology, and molecular examination. This study aimed to compare diagnostic accuracy of direct examination, Jones' culture medium, and PCR.

Methods:

A total of 36 HIV paediatrics patients were included in this study. Wet mount was placed in two separate slides and analysed by two trained microscopists. Another diagnostic test was conducted including modified Jones' culture medium and PCR. Jones' culture medium was modified from original medium by using fetal bovine serum as the basis of medium.

Results:

Out of 36 stool samples, 26 (72.2%) were found positive for *Blastocystis hominis* in wet mount examination, while 25 (69.44%) showed growth on culture media. Stool culture showed 84.6% sensitivity and 70% specificity. Positive predictive value (PPV) and negative predictive value (NPV) for stool culture were 88% and 70%, respectively. PCR only showed 11.5% sensitivity and 100% specificity, with 100% PPV and 30.3% NPV. When the result of wet mount and stool culture using modified Jones' medium were combined, greater sensitivity was obtained (84.6% vs 100%; P

Conclusion:

Modified Jones' culture medium showed high sensitivity and specificity compared to that of PCR alone. Improved diagnostic accuracy was observed when wet mount examination results were combined with stool culture results.

Keyword : *Blastocystis hominis*, diagnosis, accuracy, microscopy, culture, PCR, Indonesia

Abstract No. : ABS0001450

Status : Approved

ASEXUAL BLOOD STAGE PROFILES OF *PLASMODIUM FALCIPARUM* MALARIA AFTER TRIPLE ARTEMISININ-BASED COMBINATION THERAPY



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Artemisinin-based combination therapy (ACT) is the first-line drug of choice recommended by WHO for *P. falciparum* treatment. The artemisinin resistance was reported, particularly in Greater Mekong Subregions, including Thailand. We investigated the parasite density and stage distribution of *P. falciparum* in blood films of 40 uncomplicated *falciparum* malaria patients who were admitted at Phusing and Khunhan hospital, Srisaket as a part of the TRAC II clinical study in 2015-2018. Parasitemia and parasite stages were evaluated before and after treated with standard and triple-ACT using the microscopic examination. Out of 40 cases, 19 and 21 cases were treated with dihydroartemisinin/piperaquine (DHA/PPQ) and dihydroartemisinin/ piperaquine plus mefloquine (DHA/PPQ plus MQ), respectively. The parasitemia was ranged between 3,000-160,000/ μ L. They were no significant difference between the two groups for demographic and clinical features ($P \geq 0.05$). Parasitemia was decreased almost 94.6% and 53.8% after DHA/PPQ plus MQ and DHA/PPQ treatment, respectively ($P = 0.01$). The ring stage was cleared completely 100% at 120 hours after DHA/PPQ plus MQ treatment whereas 61.5% after being treated with DHA/PPQ ($P = 0.02$). Trophozoites were disappeared after 4 hours after treatment in both groups. Schizonts were not observed in all blood films. In the DHA/PPQ group, parasitemia showed recurrence in 15 cases, no recurrence in DHA/PPQ plus MQ group. These results demonstrated that the ring stage was less susceptible to artemisinin derivatives. The DHA/PPQ plus MQ is an alternative treatment for artemisinin-resistant *falciparum* malaria.

Keyword : Artemisinin-based combination therapy (ACT), *Plasmodium falciparum*, Parasitemia, Ring stage, Triple-ACT, Artemisinin-resistant

Abstract No. : ABS0001449

Status : Approved

HIGHLY PREVALENT ASYMPTOMATIC CRYPTOSPORIDIOSIS IN HIV-POSITIVE CHILDREN WITH MILD IMMUNODEFICIENCY: A HOSPITAL-BASED STUDY IN YOGYAKARTA, INDONESIA



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Introduction

Water-borne parasite *Cryptosporidium* spp. belongs to one of the major causes of diarrheal disease in children. In addition to inadequate hygiene and poor sanitation practices, individuals with HIV possess higher risk of contracting the disease. In major city of Yogyakarta, Indonesia, the disease burden of cryptosporidiosis in children with HIV is not well known. Current study aimed on estimating the disease burden and determinants of cryptosporidiosis this population.

Methods

A hospital-based cross-sectional study was conducted in HIV-positive children

Results

A total of 22 (42.3%) participants out of 52 enrolled subjects were found positive for cryptosporidiosis. Among these, 18 (81.8%; P 0.003) had well water for drinking water source. Approximately 63.6% subjects found positive for cryptosporidiosis showed no diarrhea (P 0.037), nor history of diarrhea in the past 3 months. Out of 22 positive subjects, 12 (54.4%) belonged to none to mild immunodeficiency and 15 (68.2%) had CD4 count of over 200 cells/ul. Multivariate logistic regression analysis showed that well water (AOR 6.75; 95%CI 1.87-24.9) and history of diarrhea (AOR 5.14; 95%CI 1.17-22.4) were identified as predictors of cryptosporidiosis in study population.

Conclusion

Cryptosporidium spp. infection was found to be more prevalent in mild immunodeficient children. Further study on drinking water quality inspection should be encouraged from the household to regional level.

Keyword : *Cryptosporidium*, children, HIV, diarrhea, Indonesia

Abstract No. : ABS0001447

Status : Approved

EPIDEMIOLOGY OF INTESTINAL PARASITE INFECTION AND ASSOCIATED RISK FACTORS AMONG THE SCHOOL CHILDREN IN THE PROVINCE OF MANZINI AND LUBOMBO, KINGDOM OF ESWATINI



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Background

Base on previous intestinal parasitic infections (IPs) survey of school-age children (SAC) in four provinces of the Kingdom of Eswatini from 2010~2011, the overall infection rate among SAC was high of 42.5%. Although long-term

deworming program has been conducted since 2009, the outcome remains unknown. In this study, investigation on SAC in Manzini and Lubombo was conducted to elucidate current IPIs status.

Methods

316 samples collected from SAC grade 1~3 in 4 schools in the two provinces (201 boys and 115 girls) were examined by Merthiolate-Iodine-Formaldehyde (MIF) method. Demographic characteristics and risk factors acquired by questionnaire surveys were statistically analyzed. The study was approved by the Eswatini Health and Human Research Review Board (EHHRRB; SHR172/2019).

Results

The overall prevalence was 40.5% (128/316), of which the infection rate in Manzini and Lubombo was 28.8% (19/66) and 58.3% (74/140), respectively. Infection rate of pathogenic protozoa was 20.6% (65/316), including *Entamoeba histolytica / dispar* 8.5% (27/316), *Giardia duodenalis* 14.6% (46/316) and *Blastocystis hominis* 9.8% (31/316). Almost one-third of SAC infected by more than one pathogenic parasite. However, only four cases of *Hymenolepis nana* and one case of *Enterobius vermicularis* infection were found. Washing hands before meal showed a protective role (OR=0.32, 95% CI=0.14-0.75, $p=0.009$). Rain and type of water supply showed a considerable risk factor (OR=2.44, 95% CI=1.25-4.79, $p=0.04$).

Conclusion

The infection rate of SAC remained very similar with that in past 10 years. It warrants to consider to reduce the intestinal protozoan infection by giving corresponding medication to infected children.

Keyword : Intestinal parasitic infections (IPIs), Kingdom of Eswatini, school-age children (SAC)

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Status : Approved

HEALTH WORKER SKILLS AND ATTITUDES ON POINT-OF-CARE TESTING FOR GLUCOSE-6-PHOSPHATE DEHYDROGENASE DEFICIENCY FOR MALARIA CASE MANAGEMENT IN LAOS AND VIETNAM



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Introduction: Recently commercialized diagnostics for glucose-6-phosphate dehydrogenase (G6PD) deficiency may improve health outcomes, align malaria care in remote settings with globally recommended clinical practices, and reduce transmission through the expanded use of radical cure treatments. Operational research on a point-of-care G6PD test was conducted in Laos and Vietnam to assess the feasibility of integrating the test into routine patient care.

Methods: Two prospective interventional studies were conducted in malaria endemic provinces in Vietnam and Laos. Health workers were trained on the use of the STANDARD™ G6PD Test. A mixed methods competency assessment, interviews, and focus group discussions were used to assess health worker skills and attitudes at multiple time points during the studies.

Results: Overall, 66 health workers were assessed. In Vietnam, 97% (30/31) of staff passed the initial training competency test and 74.1% (20/27) passed the competency test after three months. In Laos, 42% (14/33) passed initially and 89% (31/35) passed after six months. This variation is likely due to differences in the quality of training, the volume of patients, and the competency assessment method. Most of the health workers indicated that the test should and can be used at the lowest level of the health care system where most of malaria patients seek health care services.

Conclusion: Results from these studies suggest that health workers can use a G6PD test as part of malaria case management. These data provide insights into what changes to training, assessment, and supervision will be needed to adopt and scale G6PD testing in Mekong region.

Keyword : G6PD test, point-of-care G6PD test, skills, attitudes, malaria case management

Abstract No. : ABS0001444

Status : Approved

PFDHFR AND PFDHPS GENE MUTATIONS IN PLASMODIUM FALCIPARUM ISOLATES FROM RANONG, THAILAND



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Introduction: Malaria caused by the protozoan parasite, *Plasmodium falciparum*, infection is one of the most important diseases worldwide. *P. falciparum* resistant to antimalarial drugs, Sulfadoxine-pyrimethamine, is the main problem for control and elimination of the diseases. This study aimed to detect *Pfdhfr* and *Pfdhps* genes mutation associated with Sulfadoxine-pyrimethamine resistance in *P. falciparum* isolated from Ranong province, Thailand by nested PCR technique and sequencing.

Methods: Dried blood samples (40) were collected from malaria clinics in Ranong provinces. DNA were extracted and *Plasmodium* species were confirmed by nested-PCR. *Pfdhfr* and *Pfdhps* genes were amplified and sequenced.

Results: Forty blood samples of *P. falciparum* infection were studied. 25% (10/40) of *Pfdhfr* gene and 47.5% (19/40) of *Pfdhps* gene could be amplified. After sequencing, it was found that there were 40% (4/10) of triple mutations at N51I+C59R+S108N (IRN) and 60% (6/10) of quadruple point mutations at N51I+C59R+S108N+I164L (IRNL) of *Pfdhfr* gene. For *Pfdhps* gene, mutations at K540E/N (10/19, 52.6%) and A581G (4/19, 21.1%) were found. In addition, 26.31% (5/19) of them carried quintuple allele combinations (IRNLE and IRNLN) for both genes.

Conclusion: This study indicates that SP resistance was occurred in the study area. The surveillance guidelines and policy formulation of the most appropriate malaria treatment strategy in these areas must be implemented.

Keyword : Sulfadoxine-pyrimethamine-resistant, *Plasmodium falciparum*, *Pfdhfr* gene, *Pfdhps* gene

Abstract No. : ABS0001441

Status : Approved

NEXT GENERATION SEQUENCING BASED SCREENING OF DIFFERENTIAL GENES EXPRESSION RELATED TO HUMAN IMMUNE RESPONSES INDUCED BY THIRD-STAGE *GNATHOSTOMA SPINIGERUM* LARVAE



Ms.Pattarasuda Puasri

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Consuming raw food contaminated with *Gnathostoma spinigerum* third stage larvae (*G. spinigerum* L3) predominantly causes human gnathostomiasis in Thailand. Cutaneous gnathostomiasis characterized by intermittent migratory swelling usually occurs at trunk and upper limbs. Visceral larval migration is not frequently found but more serious and may be fatal due to migration through central nervous system. Presently, human immunity and pathogenesis of human gnathostomiasis is still uncertain. This study focused to explore human genes profiling related to the immune response to *G. spinigerum* L3. Peripheral blood mononuclear cells (PBMCs) obtained from healthy buffy coats were co-cultured with live *G. spinigerum* L3 for 3 days to mimic natural acute infection. On days 1 and 3 after cultivation, the cultured PBMCs were collected for RNA extraction and further performed transcriptomic analysis using next generation sequencing (NGS). The results show that approximately significant 3,000 differential expressed genes (DEGs) were observed during 3 days of cultivation. The extremely up-regulated DEGs involve activation of skin inflammatory, apoptosis, pathogen recognition, wound healing, IFN gamma, T-cells commitment toward Th17 and granulocytes receptors on day 1; anti-inflammatory, B,T cell development, cytotoxicity T cell, complements activation, and antibody production on day 3. While the predominant down-regulated DEGs play roles in lymphocyte development and recirculating, B, T , Fc and NK cells receptors, MHC class I & II on day 1; and genes regulate immunoproteasome, NF-kappa B and on day 3. This study can facilitate knowledge for further studies to clarify human immune response and pathogenesis of human gnathostomiasis.

Keyword : *G. spinigerum*, Gnathostomiasis, Next Generation Sequencing, PBMCs, Transcriptomics, Human immune response

Abstract No. : ABS0001440

Status : Approved

IMPLEMENTATION OF THAILAND'S SUBNATIONAL VERIFICATION PROGRAM



Ms. PRAPARAT PROMEIANG

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Thailand's National Malaria Elimination Strategy aims to reach zero indigenous malaria by 2024 and subsequently apply for the World Health Organization's (WHO's) Certification of Malaria Elimination. To track progress and to affirm ongoing transmission areas are shrinking, the country's Division of Vector Borne Diseases (DVBD) has launched a step-by-step subnational verification program. Methods Provinces that have interrupted local malaria transmission for three consecutive years apply by submitting standardized evidence across five technical modules: disease surveillance; diagnosis and treatment; disease prevention and control committee; planning, monitoring and evaluation; and resource mobilization. These modules coincide with the WHO's requirements, facilitating Thailand's preparations for national-level certification. A Regional Malaria Verification Committee reviews applications before the DVBD validates results. Results Since the program's launch in 2019, 40 provinces have qualified as malaria free. Most provinces showed strong surveillance to detect all malaria cases with support from 1-3-7 interventions; where routine data faltered, malaria officers reviewed source documents for evidence of sustained interruption of transmission and appropriate management of last-mile cases. These results coincide with the decline in active foci from 900 in 2019 to 448 in 2021. The DVBD is developing complementary prevention of reintroduction plans to ensure that gains are sustained and that new cases initiate swift response to prevent outbreaks. Conclusion The subnational verification program is supporting Thailand's elimination goals one province at a time. As the program strengthens, malaria officers from operational districts and provincial health offices are taking on enhanced leadership to support the path to malaria elimination.

Keyword : subnational verification, Certification of Malaria Elimination, malaria elimination

Abstract No. : ABS0001438

Status : Approved

THAILAND'S HOUSEHOLD MALARIA SURVEY 2020



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As Thailand aims for malaria elimination by 2024, the Division of Vector Borne Diseases (DVBD) commissioned a malaria household survey in 2020 to track progress on its key indicators and to measure knowledge, attitudes, and practices in target populations.

A complex survey design across 16 provincial strata and 40 clusters identified a random sample of “Thai” households and a purposive sample of “mobile” households proportional to malaria cases among Thailand’s mobile and migrant population (MMP). The final sample comprised respondents from 1,369 households (71.5% Thai and 28.5% mobile) who were interviewed from November 2020 to January 2021 with a purpose-built electronic survey tool.

Nearly all respondents (95.3%) had heard of malaria and identified fever and chills as key symptoms (83.7% and 80.2% respectively). Further, 82.2% of respondents knew that sleeping under a net can prevent malaria, and 68.5% of respondents slept under a net the previous night, with similar proportions among both Thai and MMP. However, only 36.78% of respondents slept under an insecticide-treated net. Risk awareness regarding night visits to forest, field, or plantation areas and to severity of illness was higher among MMP (p

As the DVBD strives for zero malaria, these results can be applied to refine behavior and communication strategies for both Thai and MMP in remaining transmission areas.

Keyword : Malaria, Malaria survey

Abstract No. : ABS0001436

Status : Approved

ESTABLISHMENT OF PSM ONLINE AMIDST THE NEW NORMAL OF COVID-19 PANDEMIC



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To ensure an uninterrupted supply of malaria commodities and help Thailand eliminate malaria by 2024, the Division of Vector-Borne Diseases (DVBD) initiated the development of PSM Online to replace paper-based reporting of malaria commodities in 2020 with the target of launching it by August 2021. This will improve stock visibility and logistics reporting along the supply chain, such as DVBD, provincial and district warehouses and malaria service delivery points.

PSM Online application was developed and tested starting in November 2020. Due to the COVID19 pandemic, virtual training for DVBD users and system administrators ran from June-August 2021. New features and enhancements, such as adding early warning for near expiring commodities. User manuals for system administrators and warehouses were completed, and the production environment was developed.

In September 2021, PSM Online was launched for the DVBD warehouse. DVBD can generate inventory reports, monitor expiry dates, track products received and distributed to 42 provincial, 12 regional warehouses and 5 non-government organizations (NGO) stores beginning October 2020. Phased rollout will follow among regional and provincial warehouses, districts and health facility levels in high-risk areas.

A reliable logistics data will improve forecasting, budgeting, procurement, supply, and management of malaria commodities. Monitoring shelf-life and locating products within the supply chain would allow redistribution when needed and reduce the risk of oversupply and expired products. The results will be improving availability and accessibility of malaria commodities to support malaria elimination. Amid COVID19 pandemic, electronic systems enable logistics data to flow smoothly without transporting paper-based reports.

Keyword :

malaria, commodity, supply chain management

Abstract No. : ABS0001430
Status : Approved

ENTOMOLOGICAL INOCULATION RATE (EIR) VALUE OF MALARIA TRANSMISSION IN MAMUJU DISTRICT (SULAWESI) AND SINTANG DISTRICT (KALIMANTAN), INDONESIA



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Background: Malaria is transmitted by the *Anopheles* mosquito vector of various species in Indonesia. Transmission of malaria in Indonesia occurs continuously. To determine the level of transmission intensity, the direct measurement of the calculation Entomological Inoculation Rate (EIR) is needed in terms of its vector. This study examined the intensity of malaria transmission using the EIR parameter and the characteristics of the malaria vector populations in endemic areas in Mamuju dan Sintang district.

Methods: Female *Anopheles* adults were caught, identified, and examined its characteristics in Mamuju and Sintang. Human-landing collection once a month is a sampling approach was used from three randomly selected houses.

Results: A total of 5616 mosquito vectors were caught in Mamuju dominated by *An. subpictus* 94.5% (4544/4805) with parity-rate 85%, meanwhile in Sintang dominated by *An. peditaeniatus* 32.3% (345/1068) with parity-rate 60%. *P. vivax* EIR *An. subpictus* in Mamuju was 36.14 infective bites/person/month and *P. falciparum* EIR was 0.43 infective bites/person/month, while *P. falciparum* EIR *An. barbirostris* in Sintang was 0.62 infective bites/person/month. Blood meal sources from a dried abdomen mosquito rested at the Mamuju were 46.1% positive of human blood, while in Sintang were 39.4% positive of human blood were examined.

Conclusions: Malaria transmission calculated by EIR in Mamuju was higher than EIR in Sintang. These endemic areas are predominantly with parous mosquitoes. The vectors had an exophagic dominant trait in finding a host with non-human blood meal sources. These areas are likely to be reduced in transmission if any interventions in vector control e.g. adding some livestock.

Keyword : Malaria transmission, Entomological Inoculation Rate (EIR), vector blood meal, *Anopheles*, endemic area.

Abstract No. : ABS0001426

Status : Approved

PREGNANCY OUTCOMES AND INFANTS BORN TO ZIKA INFECTED WOMEN, THAILAND, 2016–2020



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Introduction: In 2015, Brazil reported an association between Zika virus infection and microcephaly which WHO afterwards declared as a Public Health Emergency of International Concern. Thailand has reported zika outbreaks since 2016. The cases distributed throughout the country and affected pregnant women. We reviewed their pregnancy outcomes to determine maternal-child impacts of Zika infection.

Methods: Descriptive study was conducted to review data of Zika surveillance in Thailand during 2016–2020.

Women with laboratory evidence of Zika infection during pregnancy were recruited. Their pregnancy outcomes and infants were evaluated up to 2 years after birth. Birth defects and development were described.

Results: A total of 213 Zika infected pregnant women were reported to the surveillance system, 65% of them were symptomatic case. Most of them were infected in 2nd trimester (45%) and 3rd trimester (40%). One hundred and eighty-six women gave 191 live births. Abortion or stillbirth were reported in 12 women, four were confirmed Zika infection in their fetuses. Microcephaly at birth were reported in 11 infants. All infants have been followed up for 2 years after birth. Twelve of them had long-term developmental disabilities i.e. muscle weakness, hearing impairment, and mental defect. Two infants have chronic seizure.

Conclusion: Given this situation and considering the existing of Zika virus in Thailand. Pregnant women living in the affected area should be actively detected, give health education about mosquito prevention and signs and symptoms of Zika infection. Further guidelines on monitoring neurological syndromes and clinical management of Zika microcephaly and/or infants born to Zika infected

Keyword : Zika virus infection, Pregnancy, Pregnancy Outcomes

Abstract No. : ABS0001423

Status : Approved

A DEVELOPMENT HEALTH LITERACY OF ZIKA SCALE FOR THE REPRODUCTIVE AGE WOMEN IN UPPER CENTRAL REGION THAILAND



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Introduction: Health literacy is thought to impact women's Zika prevention behavior, yet no tool has been conducted on the topic. There were two objectives as follows 1) to develop the health literacy of Zika scales for the reproductive-age women. 2) to construct the norm of health literacy of Zika.

Methods: The sample was 778 reproductive-age women in the upper central region by multi-stage sampling. The data were analyzed by the second-order confirm factor.

Results: The finding follows as 1) The health literacy of Zika scales constructed four dimensions: the ability to access, understand, evaluate, and adapt the information for preventive behavior of Zika virus infections were factors loading score among 0.591-0.988. 2) The health literacy of Zika scales constructed 25 items were: IOC among 0.8 -1.0 and alpha coefficient = 0.956. 3) The health literacy of Zika scales for the reproductive-age women was the most efficient model consisted of four dimensions as well. This model was identified by $\chi^2 = 259.804$, $df = 161$, $\chi^2/df = 1.614$ $p = 0.00$, $GFI = 0.993$, $AGFI = 0.951$, $RMR = 0.017$ and $RMSEA = 0.028$ 4) The reproductive age women norm had the health literacy t-score in urban 73.26 and rural = 78.88

Conclusion: The result from this study, in order to solve the problem of prevention and improving health literacy among the reproductive-age women in upper central region Thailand.

Keyword :

Health Literacy, Zika, Scale

Abstract No. : ABS0001416

Status : Approved

DECLINING OF DENGUE CASES DURING COVID-19 EPIDEMICS IN THAILAND, 2021



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Introduction: Dengue incidence sharply declined in 2021 particularly during severe COVID-19 situation. This report examines changing of dengue trend including epidemiological factors and impacts of COVID-19 measures to the dengue prevention and control.

Methods: Descriptive study was conducted to review dengue cases, dengue serotypes and Aedes larva index during COVID-19 epidemics compared to previous years. The data of dengue cases were extracted from national surveillance. We reviewed distribution of Dengue serotypes from National laboratory centers. Larva index were captured from TanRabad® application.

Results: Dengue cumulative incidence in 2021 was 88% lower than the same period of previous 5-year median. During 2018–2019, there were large outbreaks of dengue throughout Thailand. After that the incidence continued to decline. This pattern may indicate the existing dengue immunity among population after a big epidemic wave. Moreover, 2018–2021, Thailand continued to have DENV-1 predominates every year except North region which reported DENV-2 replace DENV-1 in 2021. This change led to Dengue outbreaks in the North whereas other regions have low incidence. Larva survey showed the lower container indices compared to the previous years. It may reflect the behavior of people stay home during COVID-19 lockdown that spend more time to clean up environment around their houses.

Conclusion: Dengue incidence has declined in 2021 due to the nature of dengue epidemiology itself and also impact of COVID-19 lockdown. However, after relax of COVID-19 measures, movement of people will increase and may affect to the higher circulation of Dengue viruses. Larva index may also increase when people leave their houses. Dengue prevention and control should be strengthened afterward.

Keyword : Dengue, COVID-19, Thailand

Abstract No. : ABS0001415

Status : Approved

GAINS IN LIFE EXPECTANCY DUE TO ELIMINATING CAUSE OF DEATH; TUBERCULOSIS DISEASE IN THAI PEOPLE



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Tuberculosis, a bacterial infection that commonly affects the lungs, is one of the major causes of death in Thailand. This study estimated the gains of life expectancy from the elimination of major causes of death, in all age groups among Thai people by gender. Based on data on the cause of death during 2015 and 2019 from the Bureau of Policy and Strategy, Ministry of Public Health, Thailand, multiple decrements, and cause eliminated life tables were carried out for life expectancy estimates. By eliminating certain causes of death, a more accurate life expectancy, that can predict gender difference in life expectancy in all age groups, is obtained. This study revealed that mortality of age group 60 years and over has been extremely higher increased than other age groups in both sexes, however, males had a higher mortality rate than females. An overall net gain in life expectancy at birth would be 4.4,4.6,4.5, 4.5, and 4.6 years from Tuberculosis disease, respectively. Men are expected to gain an equal life expectancy to women after the elimination of Tuberculosis disease. There was a slight difference in life expectancy gained between men and women after eliminating the cause of death. This study outlined how Tuberculosis diseases could affect the life expectancy of Thai persons. Gains in life expectancy depend on particular causes of death and sex. Therefore, the findings provide potentially relevant evidence for the policymakers to provide improvement of public health policies for Thais to reduce their loss of life.

Keyword : LIFE EXPECTANCY , ELIMINATING CAUSE OF DEATH, TUBERCULOSIS DISEASE

Abstract No. : ABS0001413

Status : Approved

EFFECTS OF SALIVARY PROTEINS ON DUCK TEMBUSU VIRUS REPLICATION AND INFECTION IN *Aedes aegypti* SALIVARY GLAND



Dr. Chalida Sri-in

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Introduction: Duck Tembusu virus (DTMUV) infection is an arthropod-borne viral disease that affects poultry, including ducks, chickens, and geese. Although *Aedes aegypti* is the secondary vector of DTMUV, it is still a high infection and dissemination rate in this mosquito. Reducing the virus in mosquitoes is an alternative way to control DTMUV in nature without insecticide resistance and pollution problem.

Methods: We sought to determine whether any individual salivary protein modulated DTMUV replication in *Ae. aegypti* salivary gland. Five salivary proteins were examined the tissue specific expression after DTMUV infection. There is only AaSG34 salivary protein was upregulated following DTMUV infection. Thus, AaSG34 was silenced in mosquitoes by RNA interference using double strand RNA, and the mosquitoes were then infected with DTMUV to elucidate their effects on DTMUV replication and transmission by qPCR and plaque assay analysis, respectively.

Results: We found that the transcript of the duck Tembusu viral genome in the salivary glands were significantly diminished after an infectious blood meal when AaSG34 was silenced. The plaques were detected in the cell infected by saliva from DTMUV-infected control mosquitoes but not from the DTMUV-infected AaSG34-silenced mosquitoes.

Conclusion: This is the first study to emphasize the effect of *Ae. aegypti* salivary proteins on DTMUV replication and transmission. We showed that AaSG34 salivary protein not only facilitates the replication of DTMUV in the salivary glands but is also critical for the virus releasing from the salivary glands into the saliva, potentiated the exacerbation of virus transmission to the mammalian host cell.

Keyword : *Aedes aegypti*, AaSG34 salivary protein, duck Tembusu virus, salivary gland, RNA interference, transmission

Abstract No. : ABS0001412

Status : Approved

KNOCKDOWN RESISTANCE MUTATIONS OF THE VOLTAGE-GATED SODIUM CHANNEL IN MYANMAR *Aedes aegypti* MOSQUITOES



Mr. Tuan Cuong Vo

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Introduction: *Aedes aegypti* is one of the most important vectors that transmit diverse infectious pathogens. Pyrethroid insecticides have been widely applied in Myanmar as the primary control measure for *Ae. aegypti*, but the prolonged and repeated deployment of the insecticide has increased concern of insecticide resistance. Knockdown resistance (*kdr*) mutations in the voltage-gated sodium channel (*vgsc*) are known to confer pyrethroid resistance to *Ae. aegypti*.

Methods: *Ae. aegypti* mosquitoes were collected in five different areas in central Myanmar and analyzed. Segment 6 of the *vgsc*, flanking domains II and III, were amplified by two pairs of primer sets from individual *Ae. aegypti* genomic DNA. The amplified gene fragments were cloned and sequenced, respectively.

Results: High proportions of three major *kdr* mutations including S989P (49.75%), V1016G (73.6%), and F1534C (69.54%) were detected in the *vgsc* of *Ae. aegypti* collected from all study areas. Other mutations in *kdr* positions, T1520I and F1534L, were also found, but their frequencies were relatively low. Combinational analysis of all *kdr* mutations in the *vgsc* generated 11 distinct haplotypes. The triple mutation, S989P/V1016G/F1534C, was found in

the *Ae. aegypti* with frequencies ranging 17.3–56.3% by collection area. The S989P/V1016G/T1520I/F1534C quadruple mutation was also observed with a low frequency.

Conclusion: High frequencies of *kdr* mutations were observed in Myanmar *Ae. aegypti*, implying a high level of pyrethroid resistance in the Myanmar *Ae. aegypti* population. These findings warrant that the current vector control program in Myanmar should be carefully reconsidered for effective *Ae. aegypti* control.

Keyword : *Aedes aegypti*, voltage-gated sodium channel, knockdown resistance, genetic polymorphism, Myanmar

Abstract No. : ABS0001411

Status : Approved

MOLECULAR PROFILES OF MULTIPLE ANTIMALARIAL DRUG RESISTANCE GENES IN *PLASMODIUM FALCIPARUM* IN THE MANDALAY REGION, MYANMAR



Ms. Huong Giang Le

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Introduction: Emergence and spreading of antimalarial drug-resistant malaria parasites are a great hurdle to combat malaria. Few approaches to investigate antimalarial drug resistance in Myanmar malaria parasites have been done, but more expanded study is necessary to understand the nationwide aspect of antimalarial drug resistance. Molecular epidemiological study for antimalarial drug resistances in *Plasmodium falciparum* collected in Mandalay region of Myanmar was performed.

Methods: Blood samples were collected from malaria patients infected with *P. falciparum* in four areas of Mandalay region, Myanmar between 2013 and 2018. Partial genes flanking major mutations in antimalarial drug resistance genes of *P. falciparum* including *pf_{dhfr}*, *pf_{dhps}*, *pf_{mdr-1}*, *pf_{crt}*, *pk13*, *pf_{ubp-1}*, and *pf_{cytb}* were amplified by nested-PCR. Each PCR product was cloned and sequenced, respectively.

Results: Substantial levels of mutations in antimalarial drug resistance genes were detected in both Myanmar *P. falciparum* isolates. Extremely high levels of mutations related to sulfadoxin-pyrimethamine resistance were found in

pfdhfr and *pfdhps* of Myanmar *P. falciparum*. Meanwhile, moderate levels of mutations were detected in genes related to chloroquine resistance including *pfmdr-1* and *pfcr1* in Myanmar *P. falciparum*. Low frequency or none of mutations were found in *pfk13*, *pfubp-1* and *pfcytb*.

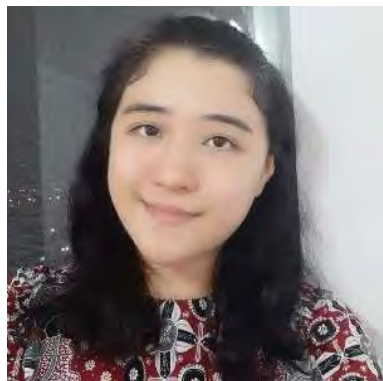
Conclusions: Overall patterns for antimalarial drug resistance genes in *P. falciparum* of Mandalay region suggest that the parasite population in the region showed lower levels of antimalarial drug resistances compared to those from border areas and Northern parts of Myanmar. Continuous monitoring of antimalarial drug resistance is necessary to plan a proper antimalarial drug regime to control and eliminate malaria in Myanmar

Keyword : *Plasmodium falciparum*; Drug resistance genes; Myanmar

Abstract No. : ABS0001409

Status : Approved

STEMONA COLLINSIAE AS BIOPESTICIDE FOR COCKROACH CONTROL



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Periplaneta americana is a synanthropic insect vector and reservoir of pathogenic and non-pathogenic microorganisms. Chemical insecticides are mostly used for cockroach control to decrease the spread of vector-borne diseases. *Stemona collinsiae*, an indigenous insecticidal plant, exhibits insecticidal activity against various pests and some insect vectors, but the activity has not yet been tested in *P. americana*. In this research, nymphicidal and adulticidal activities of *S. collinsiae* extracts against *P. americana* were tested.

Hexane, dichloromethane, ethanol and water crude extracts were produced from *S. collinsiae* roots. Bait containing the extracts and solution of the extracts were prepared. Oral toxic bait and topical application methods were tested in final instar nymphs and adult *P. americana*. Percentage of corrected mortality was calculated. Signs of toxicity and alteration of external appearance with internal organ were detected.

S. collinsiae hexane and dichloromethane extracts showed the highest potency for eliminating the both stages of *P. americana* through oral and contact administrations. The signs of toxicity included upward body bend, trembling hind

leg, body tremor, undirected rapid movement, motionlessness, swollen abdomen, and death. The abdomen and foregut were swollen. The water crude extract did not affect all *P. americana* ingesting the bait containing water crude extract or receiving the solution of water crude extract (0.0% corrected mortality).

Therefore, *S. collinsiae* hexane and dichloromethane extracts were plant-based insecticides able to terminate the life cycle of *P. americana*. These extracts can be developed as active ingredients in cockroach control products.

Keyword : *Stemona collinsiae*, Plant-based insecticides, Cockroach control, Biopesticides

Abstract No. : ABS0001406

Status : Approved

SURVEY OF ANTIBIOTIC RESISTANCE *ESCHERICHIA COLI* AND *KLEBSIELLA PNEUMONIAE* FROM CANALS IN LAK SI DISTRICT, BANGKOK



Dr.Woranich Hinthong

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Introduction

Laksi district is one of the major districts in Bangkok. The district has 6 major canals including Prem Prachakon, Bang Talat, Lat Tanot, Lat Yao, Wat Lak Si, and Ta Aut, which flow through many communities and hospital in the district which often release waste into the canals which lower the water quality and may lead to antibiotic resistant bacteria contamination, especially bacteria in Enterobacteriaceae family from fecal contamination.

Methods

Escherichia coli (*E. coli*), *Klebsiella pneumoniae* (*K. pneumoniae*), and other Enterobacteriaceae are isolate from water samples collecting from 6 canals using MacConkey agar. Biochemical tests are done using Citrate, Indole, Ornithine, Motility, and fermentation of glucose, lactose and sucrose using Triple Sugar Iron agar. Antibiotic resistant

characteristic of *E. coli* and *K. pneumoniae* against Ampicillin, Amoxicillin-clavulanate, Cefalexin, Norfloxacin, Tetracycline and Trimethoprim-sulfamethoxazole are tested using Kirby-Bauer method.

Results

Both *E. coli* and *K. pneumoniae* appear to resist mostly to Ampicillin and Amoxicillin-clavulanate antibiotics, especially the bacterial isolate from Prem Prachakon canal which flow through community and hospital, and Ta Aut canal which flow through big community. Interestingly, some *E. coli* found in Lat Tanot and Wat Lak Si canal, are found to resist to more than one antibiotic group.

Conclusion

The water in the main canals of Lak Si district is contaminated with antibiotic resistant *E. coli* and *K. pneumoniae* which pose as a threat to people living near these canals. The results call for more cautious approach to manage waste water from both community and hospital in the district.

Keyword : *Escherichia coli*, *Klebsiella pneumoniae*, Antibiotic resistance

Abstract No. : ABS0001404

Status : Approved

VECTOR COMPETENCE AND THE SUSCEPTIBILITY OF *ANOPHELES PULLUS*, *AN. BELENRAE*, AND *AN. DIRUS* TO *VIVAX* MALARIA-INFECTED BLOOD FROM THAI PATIENTS



Dr. Ratawan Ubalee

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A total of 1,000 each of *Anopheles pullus* (= *Anopheles yatsushiroensis*) and *An. belenrae* (Korea strains) and *Anopheles dirus* (Thai strain) were provided blood meals on *Plasmodium vivax* infected blood collected from Thai patients via artificial membrane feeding. The overall oocyst infection rates for *An. dirus*, *An. pullus*, and *An. belenrae* dissected on days 8-9 post-feed were 64.1%, 12.0%, and 11.6%, respectively. The mean numbers of oocysts were significantly higher for *An. dirus* (28.7) compared with *An. pullus* (2.0) and *An. belenrae* (2.8), whereas the mean numbers of oocysts for *An. pullus* (2.0) and *An. belenrae* (2.8) were similar. The overall sporozoite infection rates for *An. dirus*, *An. pullus*, and *An. belenrae* dissected on days 14-15 post-feed were significantly higher for *An. dirus* (84.5%) compared to *An. pullus* (3.4%) and *An. belenrae* (5.1%). The salivary gland sporozoite indices for positive females with +3 (100-1,000 sporozoites) (15.6%) and +4 (>1,000 sporozoites) (72.8%) were observed in *An. dirus*, but not observed for either *An. pullus* or *An. belenrae*. The salivary gland sporozoite indices observed for positive females of *An. pullus* and *An. belenrae* with +2 (10-100 sporozoites) were 16.7% and 28.6%, respectively, while most sporozoite-positive *An. pullus* (83.3%) and *An. belenrae* (71.4%) females were observed with only +1 (1-10 sporozoites) salivary glands. Based on these results, both *An. belenrae* and *An. pullus* are very poor vectors of *Plasmodium vivax*.

Keyword : *vivax* malaria, *Anopheles pullus*, *An. belenrae*, *An. dirus*, epidemiology

Abstract No. : ABS0001400

Status : Approved

IMPLICATIONS OF COVID-19 PANDEMIC ON LIFE SCIENTISTS IN THE PHILIPPINES



Dr. Pierangeli Vital

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Severe acute respiratory coronavirus 2 (SARS-CoV-2) has inflicted millions of people all over the globe for almost 2 years which have impeded all functions, including the science community. A comprehensive survey was conducted on life scientists in the Philippines, following a set of defined criteria. Out of the 103 survey respondents from the fields of applied science, engineering, natural science, physical science and social science, a heterogeneous impact was observed. Research manifested the greatest impact, reaching up to 40% decrease in time allotment. As for peer evaluation and editorial review, the time allotment has increased in all fields. Teaching, administrative, service and extension activities gave varying levels of impact depending on the field of study. Differences in demographics, such as gender and having dependents, also affected the work set-up of the Filipino scientists. As the majority of the researchers shift to a work-from-home set-up, initial analysis showed that female scientists and scientists with young dependents have a challenge balancing their research role at home while portraying other roles outside work. Results of the study can be used for policies that can be developed to help researchers and scientists during situations like the current global pandemic.

Keyword : COVID-19, scientists, survey, science-based policy

Abstract No. : ABS0001399

Status : Approved

SLEEPING SPACE AND SLEEPING PATTERN AS FACTORS ASSOCIATING BED NET UTILIZATION AMONG KAREN POPULATION ALONG THE THAI-MYANMAR BORDER: MIXED-METHODS APPROACH



Ms. Kasama Pooseesod

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Introduction: Malaria remained one of the public health concerns in Thailand. The use of long-lasting insecticidal nets is the key prevention and control strategy for reducing malaria transmission risk. This study aims to investigate bed net use in different sleeping spaces and sleeping pattern arrangements, misuse of bed net as well as bed net maintenance among population at risk of malaria among population living along Thai-Myanmar border in Tak province.

Methods: This study used a mixed-method approach with a cross-sectional study design, which included a survey using a questionnaire and a bed net inspection form; and semi-structured interviews. The study setting was in the ICEMR villages. Chi-square test was used to test the association of variables and thematic analysis was used to explain the utilization of bed nets.

Results: A total of 331 households participated in the study. Sharing a sleeping space with ≥ 2 persons was more likely to use bed net. Females were more likely to use bed net when compared with males. Most children (≤ 10 year) and pregnant woman used bed net every day. No report of misuse of the valid LLINs. If there were small holes, most people would repair by sewing or tying off with twine or rubber bands. Changing sleeping locations such as sleeping in the forest or during the mobility was less likely to use bed net.

Conclusion: Sleeping space and sleeping pattern were factors associated with bed net use among Karen population. Interventions need to be refocused on increasing utilization of bed net among non-user.

Keyword :

Malaria, Bed net, Sleeping space, Sleeping pattern, Thai-Myanmar border, Tak province, Thailand

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ESTABLISHMENT OF PCR ASSAY BASED ON 23S rRNA GENE FOR SPECIFIC DETECTION OF *MYCOPLASMA SUIS* INFECTION IN PIGS



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Introduction: *Mycoplasma (M.) suis* is one of hemoplasmas causing infectious anemia in pigs (IAP). It has been recognized as highly pathogenic hemoplasma and could be transmitted by mechanical vectors. This pathogen was also detected in farm workers suggesting its zoonotic potential. Due to high sequence similarities of popular 16S rRNA target within hemoplasma species, other markers such as 23S rRNA were suggested. This study aimed to establish a specific PCR assay based on the 23S rRNA gene for the detection of *M. suis* infection in pigs. **Methods:** PCR primers with 685 bp in product size were designed and explored with Primer-BLAST. Analytical sensitivity, specificity, and repeatability were applied for PCR validation. Then, this method was tested with 100 clinical samples. **Results:** PCR primers could amplify three possible target templates (CP002525, FQ790233, and MT530439) from Primer-BLAST. There was no cross-reaction with other hemoplasmas and pathogens in pigs with 10⁴ copies/μl of plasmid DNA as detection limit. In repeatability, all samples confirmed as *M. suis* were positive for this assay. The results of clinical samples showed that 11% were positive with PCR. Out of eleven samples, nine samples of PCR products were sequenced and analyzed with nucleotide BLAST. There were two types of *M. suis* 23S rRNA sequences: 100% similarity (n=6) to *M. suis* Illinois/KI3806 (CP002525 and FQ790233) and 99.83% similarity (n=3) to *Mycoplasma sp.* clone 43d0 (MT530439). **Conclusion:** This assay could be used for specific detection of *M. suis* by differentiating *M. suis* from *M. parvum* and other porcine hemoplasmas.

Keyword : *Mycoplasma suis*, hemoplasma, pig, PCR, 23S rRNA, Thailand

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IDENTIFICATION OF CIRCULATING miRNA AS A POTENTIAL BIOMARKER FOR LYMPHATIC FILARIASIS



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MicroRNAs are the important class of biomarker, that target and control the expression of mRNA, and can control highly complex signaling pathways like angiogenesis and inflammation. MicroRNAs profiling in serum or plasma hold great promise as minimally invasive diagnostic biomarkers for a wide range of diseases and biological processes. The major lymphatic endothelial markers- Podoplanin (PDPN), Prox-1, and VEGFR3 was analyzed by converting the RNA isolated from PBMCs to cDNA. Significant decrease in the expression levels of VEGFR3 in the filarial infected subjects compared to the uninfected, indicates that there is attenuation in lymphatic endothelial- cell development and function in secondary lymphedema subjects. While no significant difference was found in the expression of PDPN and Prox-1, suggesting the engagement and functionality of both genes remains unaltered. The RNA mimics for miR-363, miR-181 miR-331 were transfected in to cultured cells to check the expression level. The cells were harvested to measure VEGF3, Prox1- PDPN and mRNA levels. Results show that increasing the level of miR-363 and miR 331 resulted in the suppression of the mRNA as well as protein levels of infected samples. These findings show that miR 363a and miR331 to be serum biomarker of filarial samples.

Keyword : microRNA, filariasis, circular RNA
