JOINT INTERNATIONAL TROPICAL MEDICINE MEETING 2016 (JITMM 2016)

"Uncover Asian Tropical Medicine"

Amari Watergate, Bangkok, Thailand
The biggest Tropical Medicine conference in Southeast Asia
Hosted by the Faculty of Tropical Medicine, Mahidol University

Abstracts

ORAL PRESENTATIONS

7-9 December 2016

ORGANIZERS :

- Faculty of Tropical Medicine, Mahidol University
- SEAMEO TROPMED Network
- TROPMED Alumni Association
- The Parasitology and Tropical Medicine Association of Thailand

CO-ORGANIZERS :

- Department of Disease Control Ministry of Public Health (MOPH)
- Mahidol - Oxford Tropical Medicine Research Unit (MORU)

WEDNESDAY 7 DECEMBER 2016

09.00-10.30
Watergate Ballroom

OPENING SESSION

Opening Ceremony By Organizer and Co-organizers

- **Report**
  Professor Dr. Yaowalark Sukthana
  Chairman Organizing Committee

- **Welcome Address**
  Dr. Panumard Yarnwaidsakul
  Duputy Director General, Department of Disease Control

Professor Nicholas Day
Director, Mahidol-Oxford Tropical Medicine Research Unit
Mahidol - Oxford Tropical Medicine Research Unit (MORU)

- **Opening Address**
  Associate Professor Pratap Singhasivanon
  Dean, Faculty of Tropical Medicine

- **TROPMED Alumni Award Presentation**
  Presented by Associate Professor Chukiat Sirivichayakul

AWARD RECIPIENTS :

1. **Associate Professor Chomsri Kositchaiwat**
   Department of Medicine, Faculty of Medicine Ramathibodi Hospital

2. **Associate Professor Mathirut Mungthin**
   Department of Parasitology, Phramongkutklao College of Medicine, Bangkok, Thailand

3. **Dr. Ole Wichmann**
   Head, Immunization Unit, Robet Koch-Institute, Germany

WEDNESDAY 7 DECEMBER 2016

09.30 - 10.30
Watergate Ballroom

S1: THE 22ND CHAMLONG-TRANAKCHIT HARINASUTA LECTURE

Chairperson :

Associate Professor Pratap Singhasivanon
Dean, Faculty of Tropical Medicine

Keynote Speaker (Opening) :

Professor Pradipsinh K. Rathod
Director of the NIH International Center of Excellence for Malaria Research (ICEMR) for South Asia, Department of Chemistry, University of Washington

Professor Pradipsinh K. Rathod

Director of the NIH International Center of Excellence for Malaria Research (ICEMR) for South Asia, Department of Chemistry, University of Washington

Keynote Speaker (Opening) :

"CHASING THE UNKNOWNS: MALARIA IN ASIA"

Over centuries, public health research has helped determine causes of diseases and applied the findings to successful disease control. Today, expanding economies allow for vast investments in additional health research, but these are often accompanied by pressures to deliver profitable consumer products and deliver them fast. This can distract from work that breaks open previously insurmountable barriers and leads to vital new understandings. Using malaria research as an example, Professor Rathod illustrates the importance of venturing beyond common questions in public health. Investments in basic scientific training and in scientific tools and resources are important. However, the true determinants of public health advances may rest more on the freedom for inquiry, hunger for game-changing ideas, and institutional cultures that promote these ideals.

WEDNESDAY 7 DECEMBER 2016

11.00 - 12.30
Room A

S2: UPDATE AND CHALLENGES OF MALARIA TREATMENT

Chairperson :

Rick Fairhurst

Invited Speakers :

1. Olivo Miotto
"Novel genetic markers of piperaquine resistance"
Mahidol-Oxford Tropical Research Unit, Faculty of Tropical Medicine, Mahidol University
(Abstract not available)

2. Didier Leroy
"MMV's strategy to tackle ART resistance"
Medicines for Malaria Venture, Switzerland
(Abstract on pages 173)

3. Brice Campo
"MMV's strategy and recent advances for *P. vivax* radical cure"
Medicines for Malaria Venture (MMV)

4. Joel Tarning
"Pharmacometric modelling of antimalarial drugs"
Mahidol-Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University

MMV'S STRATEGY AND RECENT ADVANCES FOR *P. VIVAX* RADICAL CURE

Brice Campo

Medicines for Malaria Venture (MMV)

Malaria remains a disease of devastating global impact, killing more than 600,000 people every year—the vast majority being children under the age of 5. *P. vivax* puts as many people at risk as *P. falciparum* and is more prevalent outside of sub-Saharan Africa. In 2007, the call for malaria eradication was made to researchers in the malaria community. The eradication of malaria will, however, only be possible if effective, well-tolerated medicines that kill hypnozoites in vivax malaria, and thus prevent relapses are available to patients. Over the last decade there has been an increased investment in antimalarial research and development through the work of organizations such as Medicines for Malaria Venture (MMV), their partners, and others; new molecules with new modes of action are entering into preclinical development and beyond. Despite progress in the 8-aminoquinoline series, with tafenoquine in Phase III showing clear benefits over primaquine, the drug discovery challenge to identify new hypnozoiticidal or hypnozoite-activating compounds has been hampered by the dearth of biological tools and affordable in vitro assays fit for screening large libraries of chemical compounds. This is due mainly to the immense scientific and logistical challenges associated with accessing relevant human tissue and sporozoites. There are now emerging good quality and exciting tools that have recently demonstrated the proof of concept that such robust assays could be developed. This presentation will the MMV strategy to increase the number of new hypnozoiticidal drug candidates. As part of this, the recent progresses on the delivery of accessible in vitro decision making assays for *P. vivax* liver stages and our efforts to team up together with academic researchers, industrial partners, non-governmental agencies, foundations and funding agencies for the extra "push" that will allow the scale up and industrialization of these assays necessary for the screening of large small molecule libraries and subsequent drug discovery and development will be presented.

Keywords: *P. vivax*, Hypnozoites, Drug Discovery

PHARMACOMETRIC MODELLING OF ANTIMALARIAL DRUGS

Joel Tarning

Mahidol-Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahdiol University, Thailand; Centre for Tropical Medicine, Nuffield Department of Medicine, University of Oxford, Oxford, UK

Malaria is still the most important parasitic disease of humans with an estimated 214 million new cases per year. Approximately 1,200 people die every day from malaria, mainly young children under the age of five. We rely on effective antimalarial drug therapy to control and treat malaria. Artemisinin-based combination therapy is the recommended first-line therapy worldwide. These therapies comprise a short acting but potent artemisinin derivative, and a partner drug with a longer elimination half-life (e.g. piperaquine or lumefantrine). The artemisinins reduce the majority of the parasite biomass during the first three days of treatment and the slower acting partner drug eliminates residual parasites in order to prevent recrudescent malaria. However, many of the antimalarial drugs used today were introduced at the wrong doses, especially in young children, and it is therefore crucial to optimise dosing regimens to reduce treatment failures and the risk of resistance development. Well controlled antimalarial drug trials in patients with malaria, including special risk groups, can provide the data needed to optimise treatments through pharmacometric modelling. Here we present different granularity trial data used in pharmacokinetic-pharmacodynamic modelling of antimalarial drugs, e.g. time-to-recrudescence, time-to-reinfection, microscopy-based parasite counts, and/or PCR-based parasite counts. These developed pharmacometric models have been used to optimise antimalarial treatments in young children and can provide a rational framework for dose-finding in antimalarial drug development.

Keywords: Malaria; Pharmacokinetics; pharmacodynamics; modelling

WEDNESDAY 7 DECEMBER 2016

11.00 - 12.30
Room B

S3: ERADICATION AND DETECTION OF BLOOD AND INTESTINAL HELMINTHS

Chairpersons :

1. Akira Ito

2. Peter Odermatt

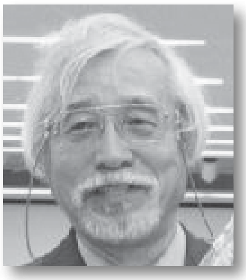
Invited Speakers :

1. Akira Ito
"Towards the control of neurocysticercosis: challenges in rural and remote endemic regions"
Asahikawa Medical University

2. Peter Odermatt
"Strongyloides stercoralis epidemiology and control: Cambodia experience"
Swiss Tropical and Public Health Institute
(Abstract not available)

3. Poom Adisakwattana
"Transcriptomics analysis of sex-biased genes in *Schistosoma mekongi*"
Department of Helminthology, Faculty of Tropical Medicine, Mahidol University

4. Arporn Wangwiwatsin
"Schistosoma life in the blood (and in the lab) illuminated by RNA-sequencing"
Wellcome Trust Sanger Institute, University of Cambridge



TOWARDS THE CONTROL OF NEUROCYSTICERCOSIS: CHALLENGES IN RURAL AND REMOTE ENDEMIC REGIONS

Akira Ito

Asahikawa Medical University

Humans, pigs, and even dogs can develop cysticercosis or neurocysticercosis (NCC) through accidental ingestion of Taenia solium eggs released from tapeworm carriers. Humans become tapeworm carriers through eating under-cooked pork contaminated with cysticerci. The *T. solium* life cycle is commonly found in areas where pigs are raised using traditional methods, parasite transmission education is lacking, and sanitation is poor. Individuals with an adult tapeworm infection (taeniasis) may also develop cysticercosis/NCC via autoinfection. Since pigs are often allowed to roam freely in endemic areas, they frequently have access to the feces of a variety of species, including humans. Due to their scavenging behavior, pigs are often at risk of developing infections with numerous parasites, including several Taenia species (e.g., *T. solium, Taenia asiatica, Taenia hydatigena*). Serological methods have been developed to detect human NCC cases. These tests typically detect specific antibody responses using *T. solium* antigens or antigens from other parasite species which may be cross-reactive in NCC patients. An alternative is to detect circulating antigens using monoclonal antibodies to components of *T. saginata*, with the belief that *T. solium* shares certain epitopes with *T. saginata*. Unfortunately, these methods are not specific for the detection of *T. solium* infection in pigs in endemic areas. Therefore, serological screening of pigs should be followed by necropsy to confirm the infecting species. In this presentation, data from pigs in Indonesia, Thailand, and China through international joint projects will be presented and possible ways to overcome the problem of cross-reactivity in pigs will be discussed.

Keywords: Taeniasis, Neurocysticercosis, Cestode zoonosis, Asia

TRANSCRIPTOMICS ANALYSIS OF SEX-BIASED GENES IN *SCHISTOSOMA MEKONGI*

Poom Adisakwattana [1]

[1] *Department of Helminthology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand*

Schistosoma mekongi is a causative agent of human schistosomiasis in Southeast Asia, which is concerned as re-emerging parasitic disease. In this study, high throughput RNA-Seq analysis was utilized to differentially identify sex-biased genes from male and female *S. mekongi.* The result showed that the adult female abundantly transcribed genes playing roles in egg production and cellular metabolism such as peptidase and fatty acid binding protein. While adult male up-regulated structural components and adhesion molecules. Moreover, antioxidant proteins were predominantly detected in both adult male and female. Neuroglobin (SmeNgb) is a novel antioxidant protein up-regulated in female *S. mekongi*, which may exhibit role in protection of oxidative stress. Homology prediction and phylogenetic analysis showed that SmeNgb has low identity with other orthologs, especially human Ngb. A multiple alignment revealed that SmeNgb has a structural conservation within Ngb family and consist of conserved distal and proximal His residues. Immunolocalization of SmeNgb suggested that the native protein was expressed in gastrodermis of adult female, which may play role in neutralizing oxidative by-products during blood degradation. Further investigations on functions and molecular mechanisms of SmeNgb *in vitro* and *in vivo* will advance our knowledge about the specific roles of SmeNgb that possibly leads to a development of new approach for control schistosomiasis.

Keywords: *Schistosoma mekongi*, high throughput RNA-Seq analysis, antioxidant, neuroglobin

SCHISTOSOMA LIFE IN THE BLOOD (AND IN THE LAB) ILLUMINATED BY RNA-SEQUENCING

Arporn Wangwiwatsin [1], Anna Protasio [2], Gabriel Rinaldi [1], Christian Owusu [1], Magda Lotkowska [1], Michael Doenhoff [3], Matthew Berriman [1]

Wellcome Trust Sanger Institute, University of Cambridge, 2 University of Cambridge, 3 University of Nottingham

The life cycle of the parasitic blood fluke Schistosoma mansoni is split between aquatic snail and mammalian hosts. Many studies on interactions between the parasites and their mammalian hosts have previously used mature ex vivo adult worms or early schistosomules cultured in vitro. In this study, we have investigated gene expression changes during a poorly characterised period of infection, from early developmental stages when the parasites morphologically transform, migrate within the mammalian host and develop into adults. After leaving the lung, schistosomes accumulate in the liver, where males and females pair up before – in the case of S. mansoni - migrating into mesenteric circulation. To find potential molecular processes involved in this journey, we collected the parasites over an in vivo time course and investigated changes to the transcriptome by RNA-sequencing. We next examined host-parasite interactions aiming to identify specific processes and cross-talks that could influence the tropism or enhance parasite and host survival. For this, we co-cultured mechanically transformed schistosomules with host cell lines over time and analysed the transcriptomes of the parasites and the host. Upon deciphering this information and together with the *in vivo* data, we are approaching a better understanding on the life of S. mansoni in the blood - how they survive and navigate within the mammalian hosts - as well as limitations and relevance of using an in vitro system for studying intra-mammalian parasites.

Keywords: Schistosome, RNA-sequencing, bioinformatic, host-parasite interactions

WEDNESDAY 7 DECEMBER 2016

11.00 - 12.30
Room C

S4: NON-COMMUNICABLE DISEASES IN THE TROPICS

Chairpersons :

1. Weerapong Phumratanaprapin

2. Theerarat Kochakarn

Invited Speakers :

1. Chayasin Mansanguan
"Paradigm Shift in Management of Hypertension"
Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol University
(Abstract not available)

2. Duangrurdee Wattanasirichaigoon
"Genetics / Inborn Erros of Metabolism"
Department of Pediatrics, Faculty of Medicine Ramathibodi Hospital, Mahidol University
(Abstract not available)

3. Wasun Chantratita
"Pharmacogenomics and Non-Communicable diseases"
Department of Pathology, Faculty of Medicine Ramathibodi Hospital, Mahidol University
(Abstract not available)

NON-COMMUNICABLE DISEASES IN THE TROPICS

Research interests in non-communicable diseases in tropical countries have been renewed in recent years due to the rise of genome research and precision medicine. Counties in the tropics can no longer rely on the data from western countries to develop treatment guidelines without determining their own molecular and physiological factors unique to defined populations and genetic admixtures. This session aims to bring Thai leading medical researchers on Cardiovascular Diseases, Metabolic Diseases and Precision Medicine to present latest trends and research opportunities specific to the tropical countries.

WEDNESDAY 7 DECEMBER 2016

11.00 - 12.30
Room D

S5: QIAGEN'S WORKFLOW SOLUTION TO IMPROVE IN LIFE POSSIBLE (ORGANIZED BY QIAGEN)

Chairperson :

Dr. Wang Nguitragool

Speakers :

1. Arun Buaklin
"QIAGEN's Sample to Insight for detection of infectious diseases"
QIAGEN Thailand (Senior Sales Application Specialist)
(Abstract on pages 170)

2. Andrea Wijeweera
"An introduction to QIAGEN's Sample to Insight solutions for NGS"
QIAGEN Singapore (Sales Application Specialist, BRC – SEA)
(Abstract on pages 174)

WEDNESDAY 7 DECEMBER 2016

11.00 - 12.30
Room E

S6: MEETING THE CHALLENGE OF OUTDOOR TRANSMISSION OF MALARIA

Chairperson :

Jeffrey Hii

Invited Speakers :

1. Michael Macdonald
" New paradigms for outdoor malaria transmission control – moving from concept to program implementation"
Consultant, WHO Emergency Response to Artemisinin Resistance Hub

2. Marc Coosemans
" Is there room for topical repellents in a malaria elimination strategy?"
Institute of Tropical Medecine Antwerp Belgium

3. Bruce Wilcox
" A systems approach to integrated malaria control"
Global Health Asia Office, Faculty of Public Health, Mahidol University

4. Fredros Okumu
" Options for surveillance and control of residual malaria vector populations in Africa"
Ifakara Health Institute, Tanzania

NEW PARADIGMS FOR OUTDOOR MALARIA TRANSMISSION CONTROL – MOVING FROM CONCEPT TO PROGRAM IMPLEMENTATION

Michael Macdonald

Consultant, WHO Emergency Response to Artemisinin Resistance Hub

Outdoor malaria transmission, beyond the reach of our traditional use of Long Lasting Insecticidal Nets and Indoor Residual Spraying, is a critical challenge to malaria elimination throughout the world, but particularly in the Greater Mekong Sub-region. "Outdoor Transmission" is considered in three general contexts. First, transmission outside the house but still within the compound; second, where the person is sleeping outside the house in a temporary shelter, such as a farm field hut, a campsite in the forest on a construction worksite or displaced person's camp; and third, where the person is active and moving at night, such as on military patrol, forest work or rubber tapping. Many "brilliant ideas" are conceived but eventually fail for lack of a clear pathway to move from proof of concept to policy adoption and implementation. WHO and partners have developed a framework to guide the process, addressing critical steps, not just for entomological and epidemiological impact, but also for the "Target Product Profile", technical feasibility, intellectual property rights, manufacturability, user acceptance, regulatory, safety and environmental impact issues and of course costs. With this framework as a guide, potential new paradigms for outdoor transmission are considered, from treated materials, topical and spatial repellents, attractant traps and toxic baits, animal treatments, novel larvicide application methods both equipment and auto-dissemination and strategies against the male mosquito. Options and opportunities are considered in the contexts of the Greater Mekong Sub-region.

Keywords: Entomology Malaria Vector Controol

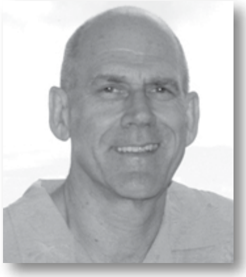
IS THERE ROOM FOR TOPICAL REPELLENTS IN A MALARIA ELIMINATION STRATEGY?

Marc Coosemans

Institute of Tropical Medecine Antwerp
Belgium

Highly effective vector control measures such as impregnated bed nets and indoor residual spraying have significantly contributed to a worldwide decline in malaria morbidity and mortality. Persisting transmission due to early and outdoor mosquito biting behavior hampers further reduction in malaria infections, particularly in the Mekong Region aiming to eliminate malaria. Additional control measures have been proposed to address such residual transmission. One of the most promising tools being topical repellents. Prior to our study, several small-scale studies had demonstrated inconclusive results. A first large-scale cluster randomised trial was launched to assess the effectiveness of mass-use of a topical repellent in addition to insecticide impregnated bed nets at the community level. The design of the study was scaled-up by a factor six compared to earlier community-based trials on repellents. The study was conducted in a low-endemic setting in Ratanakiri province, Cambodia and included a total of 98 clusters, covering 113 of the most endemic villages and a population of nearly 50,000 inhabitants. Building upon the existing public health system, repellent distribution and consumption were maximized. We demonstrated that after a two year consecutive mass-distribution, topical repellents have no additional public health value in preventing malaria at the community level. However topical repellents are still relevant for personal protection against malaria.

Keywords: malaria, repellents, elimination strategy



Bruce A. Wilcox

Director and Professor Global Health
Asia Integrative Education & Research
Programme Faculty of Public Health
Mahidol University

A SYSTEMS APPROACH TO INTEGRATED MALARIA CONTROL

Despite substantial advances in malaria control, elimination and eradication worldwide major challenges remain. Residual transmission in the Mekong region and similarly the hyperendemic zones elsewhere in the world, for example, where transmission cycles are deeply embedded ecologically, to simply achieve control seems elusive with current intervention methods. The need for new, more integrated approaches based on systems thinking that take into account human and natural ecology in greater depth have been suggested. This presentation provides a brief overview of the efforts to apply a well-substantiated and applicable systems framework, social-ecological systems and resilience (SESR), to this challenge. Applied to malaria and other vector borne diseases SESR employs the perspective of people, parasites and mosquitoes as co-inhabitants of the same ecosystems, and whose dynamics are interconnected and interdependent. Its three methodological pillars, transdisciplinarity, participation and equity are described. Finally, the specific knowledge, skills and procedural guidelines recently adopted, along with the advantages and disadvantages over conventional methods are discussed.

OPTIONS FOR SURVEILLANCE AND CONTROL OF RESIDUAL MALARIA VECTOR POPULATIONS IN AFRICA

Fredros Okumu

Ifakara Health Institute

The Global Technical Strategy for Malaria recognizes that elimination will require new complementary control methods but also improved surveillance-response strategies to optimize resource allocation and implementation. More attention is needed to develop targeted approaches, particularly in countries where epidemiological malaria profiles increasingly depict high geographical stratification of risk. Despite the successes accrued from past malaria control efforts, the progress seems to be leveling off, leaving obvious spatial fragmentation of the risk in countries. In many settings, low-level residual transmission now persists even where LLIN and IRS coverage already exceed 80%. Specific challenges now include inability to effectively identify and target residual sources of malaria infections, and the lack of low-cost and scalable strategies for targeted control. Unfortunately, despite the widely accepted benefits of vector control, the unclear correlations between field-measured entomological parameters and incidence of infections in humans, particularly in hypoendemic settings, remains a major concern for malaria control officers. They cannot rely on entomological correlates to map population level incidence, nor predict thresholds for elimination. My talk addresses these key concerns. Drawing from the African experience, we I first examine what the minimal essential entomological data and sampling framework is necessary to monitor incidence of infections in both humans and mosquitoes, residual transmission settings, and also have effectively characterized these settings. A discussion on specific approaches to surveillance and control of residual malaria transmission in Africa is then included. By integrating entomological measurements with parasite surveys, this talk considers various new options for rapid assessment of residual transmission.

Keywords: Residual Malaria; Outdoor Transmission; Vectors

WEDNESDAY 7 DECEMBER 2016

12.30 - 14.00
Room C

LUNCH SEMINAR BY MÉDECINS SANS FRONTIÈRES (MSF), DOCTORS WITHOUT BORDERS "HUMANITARIANISM IN TROPICAL MEDICINE – ACCESS TO HEALTH CARE AND BEYOND"

Chairpersons :

1. Direk Limmathurotsakul

2. Ivo Mueller

Proposed Speakers:

Direk Limmathurotsakul
"Introduction of symposium by chairperson"
(Abstract not available)

1. Anne Loarec
"Update o DAAs for Hepatitis C and implementation challenges in Asia"
Epicentre, Geneva
(Abstract not available)

2. Leena Menghaney
"Improving access to DAAs for those most in need - an MSF strategy"
ACCESS, India
(Abstract not available)

4. Sakib Burza
"Elimination of Visceral Leishmaniasis in South Asia – challenges and opportunities"
MSF, India
(Abstract not available)

4. Gabriele Rossi
"Contribution to elimination of *Plasmodium falciparum* marlaria in an area of artemisinin resistance"
MSF, Cambodia
(Abstract not available)

5. Eric Pujo
"Using drones to ensure access to TB i papau New Guinea - an MSF pilot project"
MSF, Tokyo
(Abstract not available)

WEDNESDAY 7 DECEMBER 2016

14.00 - 15.30
Room A

S7: BIOLOGY OF MALARIA TRANSMISSION STAGE

Chairpersons :

1. Ivo Mueller

2. Wanlapa Roobsoong

Invited Speakers :

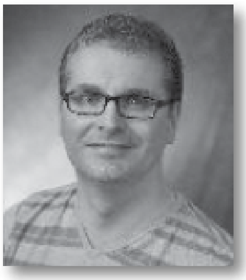
1. Ivo Muller
"Molecular Epidemiology of *P. vivax*"
CRESIB and the Walter & Eliza Hall Institute, Australia
(Abstract not available)

2. Wanlapa Roobsoong
"*P. vivax* Gametocyte"
Mahidol Vivax Research Unit (MVRU), Faculty of Tropical Medicine, Mahidol University
(Abstract not available)

3. Aaron Jex
"Transcriptome / Proteome of Sporozoite"
Faculty of Veterinary Science, The University of Melbourne, Australia
(Abstract not available)

4. Sebastian Mikolajczak
" Proteomic profiling of *P. vivax* salivary gland sporozoites"
Center for Infectious Disease Research, USA

5. Justin Boddey
"*Plasmodium falciparum* POFUT facilitates malaria transmission and liver infection"
Walter & Eliza Hall Institute, Australia



PROTEOMIC PROFILING OF *P. VIVAX* SALIVARY GLAND SPOROZOITES

Sebastian Mikolajczak

Center of Infectious Disease Research

Plasmodium falciparum and *Plasmodium vivax* cause the majority of human malaria cases. Infection by *Plasmodium* is initiated by the mosquito-transmitted sporozoite stage, a highly motile invasive cell that targets hepatocytes in the liver for infection. Blocking this initial stage of infection is a promising malaria vaccine strategy. A subunit vaccine based on *P. falciparum* CSP, the sporozoite's major surface protein, showed 50% efficacy for up to 1 year. It is thought that a multivalent vaccine comprised of multiple sporozoite surface antigens will provide better protection. We used mass spectrometry-based proteomics to identify over 1700 proteins expressed in *P. vivax* salivary gland sporozoites. We then used chemical labeling of live sporozoites to isolate and identify dozens of putatively surface-exposed proteins. Importantly, among these candidate surface antigens were proteins with no homolog in *P. falciparum*. We also confirmed that, as we have reported for *P. falciparum*, the sporozoite surface proteins CSP and TRAP are glycosylated in *P. vivax*, information that may affect the design of subunit vaccines incorporating these antigens.

Keywords: *P. vivax*, sporozoite, surface proteome

PLASMODIUM FALCIPARUM POFUT FACILITATES MALARIA TRANSMISSION AND LIVER INFECTION

Justin Boddey[1], Sash Lopaticki[2], Annie S.P. Yang[3], Alan John[4], Sara M. Erickson[2], Lachlan W. Whitehead[2], Nicholas E. Scott[5], Ethan D. Goddard-Borger[6]

[1] *1Infection and Immunity Division, The Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria 3052, Australia 2Department of Medical Biology, University of Melbourne, Parkville, Victoria 3010, Australia,*

[2] *1Infection and Immunity Division, The Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria 3052, Australia. 2Department of Medical Biology, University of Melbourne, Parkville, Victoria 3010, Australia,*

[3] *1Infection and Immunity Division, The Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria 3052, Australia. 2Department of Medical Biology, University of Melbourne, Parkville, Victoria 3010, Australia. ,*

[4] *2 Department of Medical Biology, University of Melbourne, Parkville, Victoria 3010, Australia. 3ACRF Chemical Biology Division, The Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria 3052, Australia.,*

[5] *4Department of Microbiology and Immunology, University of Melbourne at the Peter Doherty Institute for Infection and Immunity, Parkville, Victoria 3010, Australia,*

[6] *2Department of Medical Biology, University of Melbourne, Parkville, Victoria 3010, Australia. 3ACRF Chemical Biology Division, The Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria 3052, Australia*

Plasmodium *falciparum* has a complex lifecycle involving differentiation into invasive forms that infect the mosquito and human hosts. Recently, it was reported that malaria sporozoites O-glycosylate a subset of surface proteins containing thrombospondin repeat (TSR) domains. Here, we identify the endoplasmic reticulum-resident protein O-fucosyltransferase (POFUT) enzyme conserved in all Plasmodium spp. that fucosylates TSRs in secreted malaria proteins. Genetic inactivation of the POFUT locus in *P. falciparum* NF54 resulted in ookinetes that produced fewer oocysts as a result of impaired invasion of the mosquito midgut epithelium. POFUT-deficient ookinetes that successfully invaded the mosquito midgut differentiated into sporozoites that could invade salivary glands. However, POFUT-deficient sporozoites displayed reduced cell traversal activity and invaded human hepatocytes significantly less than NF54. This was attributed in part to destabilization of TRAP, a sporozoite surface adhesin. This study describes the first malarial POFUT enzyme and demonstrates that its function in O-glycosylation is important for the success of the most virulent malaria parasite during infection of the mosquito and human hosts.

WEDNESDAY 7 DECEMBER 2016

14.00 - 15.30
Room B

S8: FROM BASIC SCIENCE TO PUBLIC HEALTH: ACTIONS OF THE INSTITUT PASTEUR INTERNATIONAL NETWORK IN SOUTH EAST ASIA

Chairperson :

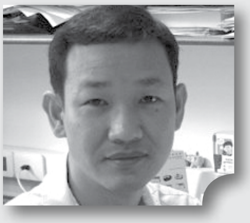
Jetsuon Prachumsri

Invited Speakers :

1. Anthony Cousien
"ECOMORE : Economic Development, Ecosystem Changes, and Emerging Infectious Diseases Risks Evaluation in Southeast Asia"
Epidemiology & Public Health Unit, Institut Pasteur du Cambodge, Cambodia

2. Chris Gorman
"Southeast Asia Encephalitis Project (SEAe)"
Institut Pasteur du Cambodge, Cambodia

3. Didier Ménard
"Artemisinin and drug partner resistance: from phenotype to genotype"
Malaria Molecular Epidemiology Unit, Institut Pasteur in Cambodia,



4. Veasna Duong
"Understanding dengue asymptomatic infection"
Institut Pasteur du Cambodge, Cambodia

ECOMORE : ECONOMIC DEVELOPMENT, ECOSYSTEM CHANGES, AND EMERGING INFECTIOUS DISEASES RISKS EVALUATION IN SOUTHEAST ASIA

Anthony Cousien

Epidemiology & Public Health Unit, Institut Pasteur du Cambodge, Phnom Penh, Cambodia

ECOMORE ("Economic Development, Ecosystem Changes, and Emerging Infectious Diseases Risks Evaluation") is a project in 4 countries in the Southeast Asia Region: Cambodia, Laos, Myanmar and Vietnam. The objectives are 1. better understand anthropogenic ecological changes responsible for the emergence of infectious diseases; 2. measure the health risks for local communities as a result of improvement of surveillance systems and strengthening of national and regional cooperation. In Cambodia, ECOMORE focused on improving the national surveillance system of dengue and developing a sensor for the early detection of major seasonal outbreaks of the disease. In Laos, the project studied the relationship between rubber plantation development, variation of mosquito dynamic and its consequences on the transmission of vector-borne diseases. It showed a higher risk of dengue transmission for workers living in plantations compared with those living in villages (relative risk=5). The recent opening of Myanmar led to a major economic development, but also to a massive flow of visitors coming with their pathogens. In this country, the project focused on the improvement of diagnosis, early detection and surveillance of severe respiratory diseases among children. In Vietnam, the objective was to study the impact of the shift from traditional to more intensive agriculture on environment and health. It showed a high circulation of leptospirosis in pig farming zones (15 to 17.5% of the population with antibodies), and a higher prevalence of detectable antibodies for hepatitis E in populations living in intensive pig farming zones compared with traditional farming zones (25% vs. 15%).

SOUTHEAST ASIA ENCEPHALITIS PROJECT (SEAE)

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Olivier Lortholary[2],
Arnaud Tarantola[1], Patrice Piola[1],
Philippe Dussart[1],
Xavier de Lamballerie[3],
Philippe Buchy[1],
Véronique Chevalier[4],
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Meningoencephalitis (ME) can be severe in children or adults, especially in the tropical and low-resource setting. Despite extensive laboratory testing, majority of patients remain undiagnosed. Better understanding of ME causes is of crucial public health importance, in order to better inform immunization policies and guide clinical management. A clinical study is conducted in three referral hospitals in Hanoi, Phnom Penh and Vientiane. Between July 2013 and November 2016, patients with clinical acute encephalitis syndrome were prospectively enrolled. Laboratory diagnostics consisted of molecular and serological tests targeting ~70 ME-causative pathogens. Only pathogens identified in CSF or blood were considered as a possible etiology. Of 480 enrolled patients, 58% were male. Median age was 6.3 [0-76] years. When performed, MRI was abnormal in 98% of patients. No etiology was identified in 41.9% cases. Japanese encephalitis virus, M. tuberculosis and Human herpes simplex virus 1 were the most common pathogens detected, identified in 34.3%, 4.6% and 3.6% cases respectively. Outcome was fatal in 13.7% and neurological sequelae occurred in 37.6% patients. Focal neurological signs and shortness of breath on admission were significantly associated with death (p

Keywords: Encephalitis, CNS, Infection, Clinical

ARTEMISININ AND DRUG PARTNER RESISTANCE: FROM PHENOTYPE TO GENOTYPE

Didier Menard

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Across the globe, over 200 million annual malaria infections result in up to 660,000 deaths. Malaria deaths are prevented by using effective antimalarial drugs. Artemisinin derivatives are one of the few remaining compound classes that can be used to cure multidrug-resistant *Plasmodium falciparum* infections. Unfortunately, last reports from Southeast Asia are showing that artemisinin combined therapies (ACTs) are losing their efficacy, adding renewed urgency to the search for the genetic determinants of parasite resistance. In our talk, we will present approach that have led to an improved understanding of artemisinin resistance and the identification of resistance-conferring mutations in the *P. falciparum* K13 gene along with that currently being used to identify molecular markers of partner drug resistance (piperaquine), as an example of effective and successful collaborative works conducted both at IP Cambodia and IP Paris.

Keywords: Malaria, *Plasmodium falciparum*, ACT, drug

UNDERSTANDING DENGUE ASYMPTOMATIC INFECTION

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Louis Lambrechts[2], Sowath Ly[1],
Anavaj Sakuntabhai[3],
Etienne Simon-Lorière[3],
Tineke Cantaert[1],
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Dengue is the most prevalent arthropod-borne viral disease. Clinical symptoms of dengue virus (DENV) infection range from classical mild dengue fever to severe, life-threatening dengue shock syndrome. However, three-quarters of the estimated 390 million dengue virus infections each year are clinically inapparent. People with inapparent dengue virus (DENV) infections are generally considered dead-end hosts for transmission because they do not reach sufficiently high viremia levels to infect mosquitoes. Here, we show that, despite their lower average level of viremia, asymptomatic people can be infectious to mosquitoes. Moreover, at a given level of viremia, DENV-infected people with no detectable symptoms or before the onset of symptoms are significantly more infectious to mosquitoes than people with symptomatic infections. Additionally, with this unique opportunity, we have investigated the host immune responses leading to virus elimination without negative impact on asymptomatic DENV-infected individuals using an integrated approach of transcriptional profiling and immunological analysis. We have shown that symptom-free DENV infection is determined by increased activation of the adaptive immune compartment and proper immune control mechanisms leading to elimination of viral infection without excessive immune activation. Our data indicate that asymptomatic DENV-infected individuals have the potential to contribute significantly more to virus transmission to mosquitoes than previously recognized and understanding the immune response in these individuals provides a new insight for novel vaccine development strategies.

Keywords: Dengue, Mosquito, Asymptomatic, immune response

WEDNESDAY 7 DECEMBER 2016

14.00 - 15.30
Room C

S9: VECTOR BIOLOGY AND CONTROL: CHALLENGES FOR MALARIA ELIMINATION AND DENGUE CONTROL PROGRAMMES

Chairperson :

Narumon Komalamisra

Invited Speakers :

1. Alongkot Ponlawat
"Field evaluation of indoor thermal fog and ultra low volume applications for control of *Aedes aegypti* in Thailand"
AFRIMS, Thailand

2. Patchara Sriwichai
"Role of secondary vectors in malaria transmission and implication for malaria elimination in Thailand"
Faculty of Tropical Medicine, Mahidol University

3. Siv Sovannaroth
"The role of vector control for malaria elimination in Cambodia"
CNM, Cambodia

4. Vanney Keo
"Use of guppy fish (*Poecilia reticulata*) for Aedes control in Cambodia; challenges and opportunities for optimal intervention coverage"
Malaria Consortium Cambodia

FIELD EVALUATION OF INDOOR THERMAL FOG AND ULTRA LOW VOLUME APPLICATIONS FOR CONTROL OF *AEDES AEGYPTI* IN THAILAND

Alongkot Ponlawat [1], J F Harwood [2], J L Putnam [3], C Nitatsukprasert [1], A Pongsiri [1], U Kijchalao [1], K J Linthicum [4], D L Kline [5], G C Clark [4], P J Obenauer [2], C W Doud [2], P W McCardle [1], A G Richardson [2], D E Szumlas [3], J H Richardson [3]

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[2] *Navy Entomology Center of Excellence (NECE), Jacksonville, FL,*
[3] *Entomology Branch, Walter Reed Army Institute of Research (WRAIR), Silver Spring, MD,*
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Efficacies of a hand-held thermal fogger (PatriotTM) and a backpack ultra-low volume (ULV) sprayer (TwisterTM) with combinations of two different adulticides and an insect growth regulator (pyriproxyfen) were field tested and compared for their impact on reducing indoor *Aedes aegypti* populations in Thailand. The effectiveness of the indoor space sprays was evaluated by sampling the natural *Ae. aegypti* population in houses and determining their physiological status, by monitoring mortality of sentinel caged mosquitoes and by assessing larval mortality in laboratory bioassays using water exposed to the spray. In the current study, the total of 14,742 *Ae. aegypti* were collected from Biogents Sentinel traps. Results showed the combination of ULD® BP-300 (3% pyrethrin) and NyGuard® (10% pyriproxyfen) sprayed either by the Patriot or Twister significantly reduced *Ae. aegypti* populations up to 20 days post spray relative to the control clusters. The addition of pyriproxyfen to the adulticide significantly extended how long mosquito populations were suppressed. The Twister resulted in higher mortality of caged mosquitoes compared to the Patriot. However, neither machine was able to achieve high mortality *Ae. aegypti* placed in hidden cages. The larval bioassay results demonstrated that the Twister provided better adult emergence inhibition than the Patriot.

Keywords: Aedes aegypti, ULV, Thermal fogger

ROLE OF SECONDARY VECTORS IN MALARIA TRANSMISSION AND IMPLICATION FOR MALARIA ELIMINATION IN THAILAND

Patchara Sriwichai [1],
Jetsumon Sattabongkot [2],
Wej Choochote [3], Stephan Karl [4],
Atiporn Saeung [3]

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[4] *Population Health and Immunity Division, Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia*

Malaria transmission along Thai borders is an important problem for national control programs. Changing of proportion between Plasmodium falciparum and *P. vivax* prevalence has been observed in many endemic areas. We have investigated the malaria vectors that may contribute to this change along the borders. The social and environmental changes may impact on vector distribution. The secondary vectors found in the areas may increase their role for malaria transmission. Where the species of both primary and secondary vectors are co-exists, we found species replacement and/or overlap population among primary and secondary vectors related to malaria prevalent with specific periods and specific village environmental. Change of host seeking behavior in the areas that both human and animal are available may impact on vector composition such as the Barbirostris Complex in Thai-Cambodia border and *Anopheles culicifacies* in Thai-Myanmar border. *An. dirus* and *An. philippinensis* were collected and found to be infected with malaria. These two species may contribute to the recent outbreak of malaria in Ubon Ratchathani province. We found the potential of insecticide resistant in the secondary malaria vectors particularly in the areas that herbicide are used for agriculture. The Barbirostris Complex and the costal vector, An. subpictus, have been found to be less susceptible to the insecticides currently used. The change in species composition and malaria vector biology will be important for the national vector control program which will have to consider the method that can control all potential vectors and not only, known to be, primary vectors in each area.

Keywords: Secondary vector, malaria, transmission, Thai borders

THE ROLE OF VECTOR CONTROL FOR MALARIA ELIMINATION IN CAMBODIA

Sovannaroth Siv

CNM

Cambodia has significantly reduced malaria morbidity and mortality over the last 10 years and is on the path for elimination with a vision of a malaria-free country by 2025. In the past decade, the number of reported malaria cases (both confirmed and clinically diagnosed) have been reduced by half, from 113,855 cases in 2004 to 56,271 cases in 2014. The overall malaria mortality rate has also decreased from 0.98 per 100,000 in 2010 to 0.12 per 100,000 in 2014. Much of this success can be attributed to expanding access to early diagnosis and treatment and the broad provision of Long Lasting Insecticidal Nets (LLINs) to populations at risk. But as Cambodia shifts from a broad control strategy to an elimination strategy there is a need to adapt entomological surveillance protocols from sentinel sites to risk ar-ea stratification and foci investigation. Land use changes over the past decade in Cambodia has changed the malaria transmission ecology. *An. dirus* and *An. minimus* previously considered most important, now have declined significantly. *An. maculatus, An. hyrcanus* and *An. barbirostris* may be of increasing im-portance. It is imperative that the country expand and decentralize mosquito collections for vector identi-fication and mapping in this rapidly changing ecology. For insecticide resistance *An. dirus* still susceptible; *An. minimus* and *An. maculatus* may have some pyrethroid resistance. Significant resistance in *An. barbirostris.* The CNM has developed an insectary in Phnom Penh with the core function of supporting bioassays for insecticide susceptibility for both Aedes and Anopheles vectors. The insectary also con-ducts bioassays for residual efficacy of insecticide treated materials. In the future the program intends to use the insectary for infection studies to determine the competence of local vectors to Plasmodium spp., for training and for the evaluation of new vector control tools. Vector control still relies mainly on LLINs. Moving to elimination the program will need to improve targeting through better use of GIS as well as Remote Sensing for environmental determinants of malaria transmission to complement epidemiological information. The migrant and mobile populations also presents a challenge as the country moves towards elimination. The first step is to identify malaria transmission risk in those locations where the mobile migrant populations. The second step is then to identify the most appropriate personal protection and vector control options. Entomological, geographical and ecological information is the key to targeting vector control and personal protecton interventions for the remaining at risk-populations

Keyword : CNM

USE OF GUPPY FISH (*POECILIA RETICULATA*) FOR *AEDES* CONTROL IN CAMBODIA; CHALLENGES AND OPPORTUNITIES FOR OPTIMAL INTERVENTION COVERAGE

Vanney Keo[1], John Hustedt[1],
Dyna Doum[1], Ly Sokha[2],
Chan Vibol[3], Neal Alexander[4],
John Bradley[4],
Didot Budi Prasetyo[5],
Agus Rachmat[5],
Muhammad Shafique[1],
Sergio Lopes[1], Leang Rithea[2],
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[5] *Naval Army Research Unit (NAMRU 2)*

In rural Cambodia, more than 80% of the Aedes mosquito breeding occurs in key containers exceeding 400 L which are mainly used for domestic purposes. A cluster randomized trial was used for the evaluation of guppy fish (*Poecilia reticulata*) distributed to water containers greater than 50 litres in intervention villages in one arm. Community health workers (CHW) and health centre (HC) staff established guppy banks and a system for mass distribution of guppies to the community. Entomology surveys showed a decrease in the number of adult female Aedes per house: 0.22 mosquitoes/house at baseline vs 0.17 mosquitoes/house three months after intervention start. Although high level of coverage (above 80%) was attained during the first six months, continued public sector support for CHWs is in doubt. Other challenges affecting efficacy and coverage include the effects of predaceous frogs and "elephant" fish; high water temperature during the dry season; flushing of guppy during heavy rain downpour; children removing fish; and use of mouldy rice husks for feeding guppies. To mitigate these challenges, CHW monthly meetings were conducted to discuss appropriate solutions, onsite training and support was provided to CHWs and Health Centre staff including for structural modifications to guppy farms. CHWs improved their colonization skills and coverage had remained high. Although guppy fish could be an important tool for Aedes control, local resources and solutions should address operational difficulties, particularly the lack of facilities and expertise in mass rearing, and the need to frequently re-introduce these agents into container habitats.

Keywords: Integrated Vector Management, Guppy Fish

WEDNESDAY 7 DECEMBER 2016

14.00 - 15.30
Room D

S10: TURBO TALK I

Chairpersons :

1.John Adams

2.Srivicha Krudsood

Speakers :

1. Muhammad Shafique
"Qualitative assessment to understand community's acceptance, preferences and sustainability of guppy fish (*Poecilia reticulata*), Pyriproxyfen (Sumilarv® 2MR), and community engagement for dengue control in Cambodia"
Malaria Consortium Asia, Bangkok

2. Dyna Doum
"The Correlation Between the Premise Condition Index and Presence of Adult *Aedes Aegypti* Mosquitoes in Kampong Cham, Cambodia"
Research Assistant, Cambodia

3. Om P Singh
"A New Knockdown Resistance (kdr) Mutation F1534L in *Aedes aegypti* Associated with Pyrethroid Resistance"
National Institute of Malaria Research , India

4. Akifumi Yamashita
"DGV: Dengue Genographic Viewer"
National Institute of Infectious Diseases, Japan

14.00 - 15.30
Room D

S10: TURBO TALK I (Continued)

Speakers:

5. Khadijah Chalermthai
"Development of rapid immunochromatography strip test for dengue virus"
Faculty of Tropical Medicine, Mahidol University

6. Mika Saito
"Risk assessment of Japanese encephalitis by phylogenetic analysis and high sensitive detection of viruses in Okinawa Island, Japan"
Graduate School of Medicine, University of the Ryukyus, Okinawa Japan

7. San Suwanmanee
"The infectivity of Zika virus in neuronal cell line: model to study Zika virus pathogenesis"
Faculty of Tropical Medicine, Mahidol University

8. Nahian Anjum Shejuti
"Evaluation of immunological status, acquisition risk factors and awareness regarding Hepatitis B Virus (HBV) infection among young healthy individuals in Bangladesh"
Department of Biochemistry & Microbiology, North South University, Bangladesh

9. Yuanita Mulyastuti
"Antimicrobial resistance changing of *Acinetobacter baumannii* in Intensive Care Unit of Dr.Saiful Anwar General Hospital during the years of 2009-2010 to 2014-2015"
Faculty of Medicine, Universitas Brawijaya, Indonesia

10. Chandresh Sharma
"Developing a Rapid Test For Improved Diagnosis of Typhoid Fever"
Centre for Bio-design & Diagnostics, Translational Health Science and Technology Institute, India

11. Witchakorn Trisukon
"*Blastocystis spp.* : A study of prevalence and associated factors in primary school children in a rural community, Central Thailand"
Phramongkutklao College of Medicine

12. Sarunporn Tandhavanant
"Functional characterization of two T3SS2-related proteins, VgpA and VgpB, of Vibrio parahaemolyticus"
Graduate School of Medicine, Osaka University, Japan

QUALITATIVE ASSESSMENT TO UNDERSTAND COMMUNITY'S ACCEPTANCE, PREFERENCES AND SUSTAINABILITY OF GUPPY FISH (*POECILIA RETICULATA*), PYRIPROXYFEN (SUMILARV® 2MR), AND COMMUNITY ENGAGEMENT FOR DENGUE CONTROL IN CAMBODIA

Muhammad Shafique[1], Dyna Doum[1], Vanney Keo[1], Ly Sokha[2], BunLeng Sam[2], Chan Vibol[3], Neal Alexander[4], John Bradley[4], Jeffrey Hii[1], Sergio Lopes[1], Leang Rithea[2], John Hustedt[1]

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A qualitative assessment was undertaken in August 2016, to explore the community's perceptions regarding acceptability, use, preferences and sustainability of guppy fish (*Poecilia reticulata*), a new controlled release pyriproxyfen (PPF) matrix (Sumilarv® 2MR), and community engagement. Using a purposive sampling technique, a total of 12 Focus Group Discussions (FGDs) and 8 in-depth interviews including free listing and pile sorting were conducted with key stakeholders at community and health facility level. A thematic analysis approach was adopted during data analysis. Majority of individuals preferred guppy fish over all other methods due to their ease of use and rearing, quick reproduction and propensity to eat larvae. FGD participants remarked "We love guppies as they are attractive, easy to keep and visibly clean the water from larvae." Many people liked PPF as well due to its long lasting effectiveness, convenience and easy maintenance. However, some showed concerns over the presence of larvae in the water despite its use. "We know PPF works well as fewer mosquitos are around, however, we are afraid the presence of larvae may contain parasites that can spread the disease". The findings suggest many participants were willing to travel to the guppy banks, pay for and collect the guppies in the future. They also indicate that sustained PPF use requires community sensitization on the way PPF works and the role of mosquito adults rather than larvae in disease transmission. As one community health worker intuitively remarked "the success should not be measured only by presence of guppies in jars, but through the high demand, participation and eagerness of communities for the guppies."

Sumilarv® is a registered trademark of Sumitomo Chemical Company, Tokyo, Japan.

Keywords: qualitative assessment, dengue, guppy fish

THE CORRELATION BETWEEN THE PREMISE CONDITION INDEX AND PRESENCE OF ADULT *AEDES AEGYPTI* MOSQUITOES IN KAMPONG CHAM, CAMBODIA

Dyna Doum

Malaria Consortium

Premise inspections and larval source management of container-breeding *Aedes aegypti* are laborious and resource-intensive. The Premise Condition Index (PCI) was developed as a rapid assessment tool to quickly predict household mosquito infestations. This study aims to assess the correlation between PCI scores or other housing variables and the presence of *Aedes aegypti* mosquitos in areas of Kampong Cham, Cambodia. Each house was scored from one to three on each of three categories: shade condition, house condition, and yard condition. PCI rapid assessments and detailed household questionnaires are being completed and samples of immature and adult mosquitoes are being collected from 1,200 households (40 randomized households in each of 30 clusters) every three months from October 2015 to October 2016. Preliminary results show that most houses were made of wood (76%), had ≥3 water containers (74%), and were raised on stilts (90.31%). In addition, the houses had an average of 5 people per house, with 85.9% having PCI scores between 5-7. Logistic and negative binomial regression models were used to examine the association between higher PCI scores or other housing variables and the presence or number of Aedes mosquitoes or immatures present in the household. Receiver Operating Characteristic curves were used to determine prediction accuracy.

Keywords: Cambodia, Dengue, Aedes, PCI, Entomology

A NEW KNOCKDOWN RESISTANCE (kdr) MUTATION F1534L IN *AEDES AEGYPTI* ASSOCIATED WITH PYRETHROID RESISTANCE

Om P Singh

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The control of several arboviral infections, mainly dengue, chikungunya and Zika virus solely relies on vector control methods in absence of specific drugs or vaccines against these infections. Emergence of pyrethroid resistance in vectors may pose a serious threat to the success of insecticide-based vector control programme. Here, for the first time, we report the presence of a new knockdown resistance (kdr) mutation F1534L in co-occurrence with another alternative mutation F1534C, which confer resistance to pyrethroids. DNA sequencing of partial domain III of the VGSC was performed on permethrin-resistant *Ae aegypti* collected from Bengaluru, India. It revealed the presence of two alternative kdr mutations F1534C and a new mutation F1534L resulting from T>G substitution on the second position of the codon and T>C substitution on the first position of the codon, respectively. PCR-RFLP based strategy was developed for genotyping of F1534L alongside F1534C and T1520I. Genotyping of field populations collected in the year 2014 and 2015 revealed a high frequency of F1534C (41-59%), moderate frequency of 1534L (10-35%) and absence of T1520I. The new mutation F1534L showed significant protection against permethrin and deltamethrin whereas F1534C showed protection against permethrin and DDT. This study, for the first time, reports the presence of a new kdr mutation F1534L in an *Ae. aegypti* population which is strongly associated with pyrethroid resistance. A highly specific PCR-RFLP was developed for the identification of this mutation. The presence of new mutations associated with pyrethroid resistance is of global importance and should be monitored worldwide.

Keywords: Knockdown resistance, Aedes aegypti, India

DGV: DENGUE GENOGRAPHIC VIEWER

Akifumi Yamashita[1],
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Tomohiko Takasaki[1],
Makoto Kuroda[1]

National Institute of Infectious Diseases, Japan

Dengue viruses (DENVs) and their vectors are widely distributed throughout the tropical and subtropical regions of the world. An autochthonous case of DENV was reported in Tokyo, Japan, in 2014, for the first time in 70 years. A comprehensive database of DENV sequences containing both serotype and genotype data and epidemiological data is crucial to trace DENV outbreak isolates and promptly respond to outbreaks. We constructed a DENV database containing the serotype, genotype, year and country/region of collection by collecting all publically available DENV sequence information from the National Center for Biotechnology Information (NCBI) and assigning genotype information. We also implemented the web service Dengue Genographic Viewer (DGV), which shows the geographical distribution of each DENV genotype in a user-specified time span. DGV also assigns the serotype and genotype to a user-specified sequence by performing a homology search against the curated DENV database, and shows its homologous sequences with the geographical position and year of collection. DGV also shows the distribution of DENV-infected entrants to Japan by plotting epidemiological data from the Infectious Agents Surveillance Report (IASR), Japan. This overview of the DENV genotype distribution may aid in planning for the control of DENV infections. DGV is freely available online at: (https://gph.niid.go.jp/geograph/dengue/content/genomemap).

Keywords: DENV, genotyping, web service

DEVELOPMENT OF RAPID IMMUNOCHROMATOGRAPHY STRIP TEST FOR DENGUE VIRUS

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Chonlatip Pipattanaboon[2],
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Dengue is a major public health issue in Thailand where one of the challenges in dengue management is unavailability of highly sensitive and reliable bed-side diagnostic test kits. This research aimed to develop rapid immunochromatography strip test for dengue virus detection using human monoclonal antibodies (HuMabs) which are cross reactive to all four serotypes of dengue virus and are specific to viral envelope protein. Twelve clones of HuMabs were previously produced by Setthapramote et al. (2012) in which two clones; HuMab 19 and HuMab 54 were selected based on dot blot analysis. The two HuMabs were prepared, purified, and determined for their binding ability by ELISA. The lateral flow strip tests were constructed using HuMab 54 as a gold conjugated antibody, while the captured antibody on the test and control line were HuMab 19 and goat anti-human antibody respectively. Finally, the constructed immunochromatography strip tests were tested with four serotypes of dengue virus obtained from culture fluid of infected C6/36 cell and later in spike human serum sample (pseudo positive samples) which were 2-fold serially diluted. Within 15 minutes, the strip tests showed specific detection to all four serotypes of dengue virus with no false positive reading. Similarly, with equal amount of virus in pseudo positive samples, the human serum at 1:32 dilution gave the best result. However, further studies and improvement is needed to enhance the detection efficiency of this in-house immunochromatography strip tests with pseudo positive samples and later may be used to evaluate with dengue patients samples.

Keywords: Dengue virus/ Human monoclonal antibodies/ immunochromatography strip test

RISK ASSESSMENT OF JAPANESE ENCEPHALITIS BY PHYLOGENETIC ANALYSIS AND HIGH SENSITIVE DETECTION OF VIRUSES IN OKINAWA ISLAND, JAPAN

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Tetsu Kinoshita [3], Yuka Kushida [2],
Daiji Endoh [4], Jun Kobayashi [5]

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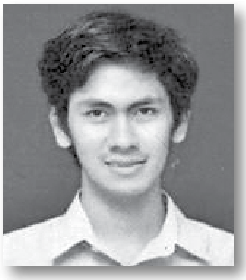
Japanese encephalitis virus (JEV) is an etiological agent of Japanese encephalitis (JE), one of the most severe infectious diseases in Asia and Oceania, and also single stranded RNA virus that is known as fast evolutionary rate. Despite the conventionally assessed risk decreased as the low prevalence of JEV antibodies in pigs and the low density of vector mosquitoes, recently Japanese encephalitis occurred in a human and pigs in succession, in wide range of Okinawa Island. Therefore risk assessment based on new strategy is required in Okinawa. Since 2015, we started research project on "development of control strategy for vector-borne diseases in Okinawa." We conducted risk assessment by A) phylogenetic analysis based on complete envelope region of 102 strains of JEV in Okinawa Island between 1971 and 2014, B) virus Isolation and comprehensive detection of viruses by PCR method using unique designed primers from field caught mosquitoes in Okinawa, in 2015. Phylogenetic analysis showed that a new cluster of JEV genotype 1 emerged on Okinawa Island since 2012 and seemed to be replaced. Evolutionary rates of cluster between 1998-2008 estimated by mean dN/dS is 2 to 5 times higher than those of clusters before 1993. Genomes of JEV were detected in 7 pools of wild mosquitoes, caught in suburban and farmland in wide range of the island, while no virus was isolated from the same samples. JE risk assessment in this study supports epidemiologic data that JEV distributed widely in Okinawa Island and suggests possibility of unknown ecology of JEV.

Keywords: Japanese encephalitis, risk assessment



THE INFECTIVITY OF ZIKA VIRUS IN NEURONAL CELL LINE: MODEL TO STUDY ZIKA VIRUS PATHOGENESIS

San Suwanmanee [1],
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Yong Poovorawan [4],
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[4] *Center of Excellence in Clinical Virology, Faculty of Medicine, Chulalongkorn University*

Zika virus infection is the one of current global concern with the increasing of epidemic during the last decade. Recent epidemiology studies shown the infection of this arbovirus virus related with the defect of fetal brain development and the neurons cell abnormality in adult. Interestingly, the exactly pathogenesis of this virus infection is not clearly understood and the standard effective cell line for in vitro study of this virus has not currently provided. In this study we shown the infectivity, cellular cytotoxicity, morphological change and the cell tropism of zika virus in neuroblastoma (SH-SY5Y) cell line. The results shown that the zika virus RNA could be early detect in 3 hour post infection with the highest intensity at day 3 post infection which taken together with viral titer detection. Hence, the cellular cytotoxicity shown the significantly decreased of cellular viability with increased of cellular cytotoxicity and the rapid morphological change correlated with the decreased of cell viability and the increased of viral titer. In conclusions, the zika virus is highly permissive and highly infectivity in neuroblastoma cell line rather than other primate cell. The results suggested that the neuroblastoma cell line can be used as the cell-based model for zika virus in vitro study in effectively. The further study of zika virus infection using neuroblastoma cell line to study neuropathogenesis in neuroblastoma cell line might be provide the valuable results to fulfillment the knowledge and development the vaccine and therapeutic method in nearly future

Keywords: Zika virus, Flavivirus, Neuroblastoma cell

EVALUATION OF IMMUNOLOGICAL STATUS, ACQUISITION RISK FACTORS AND AWARENESS REGARDING HEPATITIS B VIRUS (HBV) INFECTION AMONG YOUNG HEALTHY INDIVIDUALS IN BANGLADESH

Nahian Anjum Shejuti[1],
Tanzila Wasi[2],
Aniqa Afzal Esha[2],
Sohidul Islam[3],
Kazi Nadim Hasan[4]

[1] *Graduating Student,*
[2] *Graduated Student,*
[3] *Associate Professor, Department of Biochemistry & Microbiology, North South University,*
[4] *Professor, Department of Biochemistry & Microbiology, North South University*

Background: Once Bangladesh was recognized as intermediate prevalence of hepatitis B virus (HBV) infection; immunization at birth and awareness program had been initiated nationwide. The study aimed to determine the prevalence and exposure to HBV in young healthy individuals to evaluate the efficacy of the immunization program, HBV acquisition risk factors as well as awareness on a pilot basis.

Methods: The study comprised of 156 students of North South University of average age 21.08 ± 1.88 (Mean ± SD) who responded to a structured questionnaire. Blood sample analyses were performed for hepatitis B surface antigen (HBsAg), hepatitis B core antibody (HBcAb) and hepatitis B surface antibody (HBsAb) using third generation ELISA kit.

Results: The prevalence was 9.6% for HBcAb, 0% for HBsAg and 32.7% for HBsAb. Among HBV exposed individuals, 66.7 % (10/15) were found not to have protective antibody against HBV ($\chi2 = 19.35$, $p = < 0.001$). Among 156 subjects, only 28.2% were aware that they have been vaccinated against Hepatitis B, 47.4% were not vaccinated and 24.4% were not sure. Among 82 vaccinated individuals, 38% were found to be unprotected and 62% protected.

Conclusion: These results demonstrate the low prevalence of exposure to HBV in young healthy individuals however not having protective antibody against HBV. No prevalence of HBsAg might reveal the successful implementation of nationwide vaccination and awareness program. In order to reduce the prevalence of exposure to HBV, adequate program of active screening for HBcAb and vaccination with monitoring of HBV protection levels for adolescent and young adults should be implemented.

Keywords: Hepatitis B virus; Prevalence of HBV exposure, Immune status, Young healthy Bangladeshis

ANTIMICROBIAL RESISTANCE CHANGING OF *ACINETOBACTER BAUMANNII* IN INTENSIVE CARE UNIT DR.SAIFUL ANWAR GENERAL HOSPITAL DURING THE YEARS 2009-2010 TO 2014-2015

Yuanita Mulyastuti[1],
Siwipeni Irmawanti Rahayu[1],
Sanarto Santoso[2]

[1] *Department of Microbiology, Faculty of Medicine, Universitas Brawijaya,*
[2] *Department of Clinical Microbiology, dr. Saiful Anwar General Hospital*

Background : Infection caused by *Acinetobacter baumannii* is associated with increasing morbidity and mortality in patients treated in Intensive Care Unit (ICU). This study aimed to investigate the changes of antimicrobial resistance pattern among *Acinetobacter baumannii* during the year of 2009-2010 and 2014-2015.

Method : Retrospective study was performed on 388 and 3034 clinical specimens from January 2009 to December 2010, and January 2014 to December 2015 at Clinical Microbiology Department, dr. Saiful Anwar General Hospital, Malang, Indonesia. Clinical specimens including blood, sputum, urine and pus obtained from hospitalized at ICU. Antimicrobial susceptibility testing was performed and determined according to CLSI guidelines. Following antimicrobials were tested: ciprofloxacin, gentamicin, amikacin, meropenem, ceftriaxone, trimethoprim/sulfametoxazole, and tetracycline. Data was analyzed using ChiSquare test using SPSS.20.0 for Windows.

Result : We obtained 23 (12%) of 195 and 216 (16%) of 1388 *Acinetobacter baumannii* from positive clinical isolates in year of 2009 - 2010 and 2014 - 2015, respectively. The antimicrobial resistance of *Acinetobacter baumannii* was significantly increased.

Keywords: Antimicrobial resistance, *Acinetobacter baumannii*, ICU

DEVELOPING A RAPID TEST FOR IMPROVED DIAGNOSIS OF TYPHOID FEVER

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Tarang Sharma[1],
Susmita Chaudhuri[1],
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[3] *International Centre for Genetic Engineering & Biotechnology, New Delhi, India*
[4] *Experimental Medicine and Biotechnology Department, Postgraduate Institute of Medical Education and Research, Chandigarh, India.*
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Introduction: Typhoid fever is a significant global health problem with highest burden on the developing world. The severity of typhoid is often underestimated and currently available serological diagnostic assays are inadequate due to lack in requisite sensitivity and specificity. This underlines an absolute need to develop a reliable and accurate diagnostics that would benefit long-term disease control, treatment and to understand the real disease burden. Here we have utilized flagellin protein of S. *typhi* that is surface accessible, abundantly expressed, and highly immunogenic, for developing immuno-diagnostic tests.

Objective: To develop diagnostic assay for specific detection of *S. typhi* infection.

Methodology: Native *S. typhi* flagellin was isolated from large culture and recombinant flagellin was also purified using prokaryotic expression system. Monoclonal antibodies (mAbs) against the serovar specific middle region of flagellin were generated by hybridoma technology. Characterizations of mAbs were performed by immunoblotting, flowcytometry and ELISA.

Results: A panel of murine mAbs generated showed unique specificity and very high affinity towards *S. typhi* flagellin without showing any cross reactivity with other serovars. These antibodies also displayed stable binding in stringent reaction conditions for antigen–antibody interactions, like DMSO, urea, KSCN, guanidium HCl and extremes of pH. A sandwich ELISA based diagnostic assay was developed using these mAbs to detect soluble flagellin and validated using spiked serum.

Conclusion: In our study, binding of mAbs to flagellin, with high affinity, present on bacterial surface, as well as in soluble form, validates their potential use in developing improved diagnostics with significantly higher sensitivity and specificity.

Keywords: Flagellin, Typhoid, Diagnostics

BLASTOCYSTIS SPP. : THE STUDY OF PREVALENCE AND ASSOCIATED FACTORS IN PRIMARY SCHOOL CHILDREN IN RURAL COMMUNITY, CENTRAL THAILAND

Witchakorn Trisukon

Phramongkutklao College of Medicine

Background *Blastocystis* sp., an intestinal protozoan, is commonly identified in humans and animals worldwide, especially in developing countries. The evidence of Blastocystis sp. as a pathogen has been accumulated in recent years. *Blastocystis* sp. is transmitted by fecooral route. In Thailand, the prevalences of *Blastocystis* infection were different in each community and population. This study aimed to identify prevalence of *Blastocystis* infection among primary school students in a rural community and identify association factors of the infection.

Method: A crosssectional study was conducted. Stool examinations including wet preparation, and culture using Jones' medium were performed to detect *Blastocystis* infection. Kato, formalinethyl acetate concentration and agar plate techniques also were used to detect other intestinal parasitic infections. Standardized questionnaires were used to assess risk behaviors.

Result: Of 501 stool specimens, there are 64 specimens (12.8%) positive for *Blastocystis sp*. Other intestinal parasitic infections were founded including *Giardia duodenalis* (1.4%), *Entamoeba coli* (1.0%), *Opisthorchis viverrini* (0.8%), *Enterobius vermicularis* (0.6%), *Strongyloides stercoralis* (0.4%). Studying in some particular schools were associated with acquiring the infection.

Conclusion: Intestinal protozoa infections are predominant in this population. According to interview with school director, source of drinking are suspected environmental factor causing *Blastocystis sp*. infection. Quality of water should be further investigated.

Keywords: *Blastocystis* spp., Waterborne transmission

FUNCTIONAL CHARACTERIZATION OF TWO T3SS2-RELATED PROTEINS, VGPA AND VGPB, OF *VIBRIO PARAHAEMOLYTICUS*

Sarunporn Tandhavanant [1],
Toshio Kodama [2], Tetsuya Iida [2]

[1] *Graduate School of Medicine, Osaka University, Osaka, Japan,*
[2] *Department of Bacterial Infections, Research Institute for Microbial Diseases, Osaka University, Osaka, Japan*

Vibrio *parahaemolyticus*, a Gram-negative halophilic bacterium, is a causative agent of gastroenteritis via consumption of undercooked contaminated seafood. Type three secretion system (T3SS), a bacterial machinery for delivery of bacterial proteins into eukaryotic cytosol, plays a critical role in pathogenicity of *V. parahaemolyticus*. This study characterized the functions of 2 novel T3SS2-related proteins, VgpA and VgpB, in *V. parahaemolyticus* pathogenicity. vgpA and vgpB deletion mutants (ΔvgpA and ΔvgpB) highly secreted effector proteins while secretion of translocon proteins was diminished, which was contrary with the parental strain. The alteration of secretion pattern was a direct effect of vpgA or vpgB deletion. The transcriptional regulation of T3SS2 was consistently functional among VgpA, VgpB and parental strains. Besides, productions of T3SS2-related proteins were comparable among these strains. In addition, vgpA- or vgpB-defected *V. parahaemolyticus* extremely decreased the delivery of effectors into host cytosol, indicating that VpgA and VgpB is required for translocation process of T3SS2 function. Furthermore, ΔvgpA and VgpB dramatically decreased cytotoxic activity in Caco-2 cells infection as well as enterotoxicity in rabbit ileal loop test similar to infection with the T3SS2-deficient strain. Thus, these results indicate that VgpA and VgpB play a critical role in a regulation of T3SS2-related protein secretion and are essential proteins of T3SS2 for *V. parahaemolyticus* pathogenicity.

Keywords: *V. parahaemolyticus*, T3SS, Gastroenteritis, Foodborne disease

WEDNESDAY 7 DECEMBER 2016

14.00 - 15.30
Room E

S11: CHALLENGES OF INTRODUCING A NEW VACCINE

Chairperson :

Pratap Singhasivanon
Dean

Invited Speakers :

1. Jerome H Kim
"Cholera Vaccines: the agenda moving forward"
International Vaccine Institute, Korea

2. Suchada Jiamsiri
"Challenges in introduction of HPV vaccine into the Routine immunization program"
Division of Vaccine Preventable Disease, Department of Disease Control, MOPH
(Abstract not available)

3. Alain Bouckenooghe
"Implementation of dengue vaccination: perspectives and challenges"
Sanofi Pasteur
(Abstract not available)

CHOLERA VACCINES: THE AGENDA MOVING FORWARD

Jerome Kim [1]

[1] *International Vaccine Institute*

The disease we know as cholera was first described 200 years ago in India but was presumably known before then. It has caused 7 global pandemics and accounts for 80,000 deaths annually. Cholera is an explosive, toxin-mediated diarrheal disease that was feared because it could kill a man within 24 hours. Modern treatment with rehydration and antibiotics lowers the death rate to less than 1%. Since 2011, 2 new oral cholera vaccines (OCV) have been prequalified by WHO and a stockpile of cholera vaccine has been created by Gavi. In the past 5 years a tremendous amount of data on the efficacy, effectiveness, and cost effectiveness of OCV has been generated in the setting of outbreaks and in endemic disease settings. To date only 2.7M doses have been released from the stockpile. The availability of OCV and the use of OCV in conjunction with simple WASH (water, sanitation and hygiene) measures can have a significant impact on disease. As a case study we will look at Haiti, where introduction of V. cholera after the devastating earthquake of 2010, in a naïve population, was associated with a predictable outbreak, affecting 800,000 Haitians and resulting in nearly 10,000 deaths. After dropping substantially by 2014, in 2015 and 2016 the number of cases of cholera, prior to the hurricane, has consistently increased. The rainfall and wind damage associated with the hurricane substantially affected the established cholera treatment centers, fecally contaminated surface water was spread by flooding, and immediately, additional cases of cholera were presumptively diagnosed. Modeling suggests that vaccination and WASH might substantially control, and potentially "eliminate" cholera from Haiti. Nationwide vaccination holds substantial promise for the health of Haiti's people, and importantly could provide important scientific information on the utility of vaccination in the setting of endemic disease.

Keywords: cholera, vaccine, Haiti

WEDNESDAY 7 DECEMBER 2016

16.00 - 17.30
Room A

S12: MALARIA IN INDIA: PAST HISTORY AND FUTURE OPPORTUNITIES

Chairpersons :

1.Neena Valecha

2.Pradipsinh K. Rathod

Introduction: Malaria in India

Neena Valecha
Director, National Institute of Malaria Research, India
(Abstract not available)

Conclusion :

Pradipsinh K. Rathod
"Important questions to support the National Control Program"
Program Director, US NIH International Center of Excellence for Malaria Research (South Asia)
(Abstract not available)

Invited Speakers :

1. Ashwani Kumar
"Changing parasite-vector relationships in Southwest India"
National Institute of Malaria Research,Goa and the US NIH ICEMR
(Abstract not available)

2. Anupkumar R. Anvikar
"Diagnosis, pathogenesis, and treatment: The current scenario"
National Institute of Malaria Research,Delhi

3. Neelima Mishra
"Antimalarial Drug Sensitivity and Resistance in India"
National Institute of Malaria Research,Delhi

4. Pradyumna Kishore Mohapatra
"Prevalence and determinants of malaria in a tribal dominant population of Karbi Anglong district of Assam, India: A community survey approach"
Regional Medical Research Center,Assam & the US NIH ICEMR

DIAGNOSIS, PATHOGENESIS, AND TREATMENT: THE CURRENT SCENARIO

Anupkumar Anvikar[1],
Neelima Mishra[1],
Neena Valecha[1]

[1] *National Institute of Malaria Research, Sector 8, Dwarka, New Delhi, India*

Malaria is one of the major vector borne diseases in India with about One million cases reported annually. The strategy for malaria control includes early diagnosis, complete treatment and vector control. Since year 2007, the Indian national drug policy for malaria has switched over from presumptive therapy to treatment after confirmation and recommends investigating suspected malaria cases. Although microscopy is the preferred mode of diagnosis, due to various challenges, rapid diagnostic tests have are used for point of care diagnosis. Even the RDTs are not free from challenges. Their performance is affected by the storage / transport conditions, antigen variation, gene deletion, etc. However, India has a strong quality assurance programme for malaria RDTs. India has also witnessed change in clinical patterns of malaria. Cases of severe malaria and also deaths due to vivax malaria have also been reported from various parts of the country. The National Vector Borne Disease Control Programme recommends chloroquine for vivax malaria. For falciparum malaria, artemether lumefantrine is recommended in north eastern states, while artesunate+sulphadoxine-pyrimethamine is recommended in rest of India. Antimalarial therapy is also has many challenges like poor access, antimalarial drug resistance, artesunate SP being blister pack, poor compliance, irrational treatment practices, long antirelapse therapy, use of artemisinin monotherapy, etc. However, operational research is being carried out to help combat these challenges. The national programme is receptive and revises the policy taking note of research output.

Keywords: Malaria, Diagnosis, Treatment, India

ANTIMALARIAL DRUG SENSITIVITY AND RESISTANCE IN INDIA

Neelima Mishra [1]

[1] National Institute of Malaria Research (ICMR), Sector 8, Dwarka, New Delhi

Surveillance of antimalarial drugs is more urgent than it has ever been. Reduced sensitivity of *Plasmodium falciparum* to recommended antimalarial drugs impose an increasing burden on national malaria control programs in endemic countries. Thai-Cambodia border including Myanmar has recently witnessed artemisinin resistance in *Plasmodium falciparum*, which threatens to lessen the sensitivity of artemisinin combination therapies in the neighbouring countries including India. Since, malaria control efforts are geared up with the launch of Malaria elimination project in the India, monitoring emerging antimalarial drug resistance is the need of the hour. Monitoring of antimalarial drug resistance has been done in the past in the country. However, since 2009, Nation-wide sentinel site system has been developed in the country where systematic surveillance studies at 25 sentinel sites have been conducted during alternate years by National Institute of Malaria Research (NIMR) in collaboration with the National Programme (NVBDCP). This joint NIMR-NVBDCP surveillance system has been developed with several innovations so that judicious use of resources and finances can be utilized. New protocols updated and validated by World Health Organization (WHO) are being followed to study the therapeutic efficacy of first line antimalarials across sentinel sites in different states. Till date, more than six thousand patients have been enrolled. These include efficacy studies of artesunate plus sulphadoxine-pyremethamine (AS+SP), and artemether-lumefantrine (AL) in *Plasmodium falciparum* and chloroquine efficacy in P. *vivax* malaria in the country. Results of these studies have guided the national policy for malaria. Continuous monitoring of efficacy of ACTs is needed, as the partner drugs can endanger the efficacy due to high resistance rates, exposing the potent artemisinin derivatives to the development of resistance.

Keywords: Antimalarial drug resistance

PREVALENCE AND DETERMINANTS OF MALARIA IN A TRIBAL DOMINANT POPULATION OF KARBI ANGLONG DISTRICT OF ASSAM, INDIA: A COMMUNITY SURVEY APPROACH

Pradyumna Kishore Mohapatra[1],
Devojit Sharma[1],
Khukumoni Bora[1]

[1] *Regional Medical Research Centre, NE (ICMR), Dibrugarh, Assam, India*

Studies of *Plasmodium falciparum* malaria in a highly endemic area using a comprehensive and multidisciplinary approach in a well defined cohort provides important data about the epidemiology and dynamics of this complex disease. To achieve this a study was carried out in a cohort of seven villages in Karbi Anglong area of Assam from June 2015. We describe the methodology and our initial experience during the first 6 month of the project. All enrolled households were geo-referenced and mapped. A cohort was selected and administered a set of structured questionnaire to record clinical, physical and demographic parameters. Additionally, passive case detection was also carried out in individuals with febrile condition in between 2 active survey period. In the 1st survey 2275 out of 2331 individuals enrolled were screened for malaria among whom 152 (6.7%) were found to be malaria positive. A higher asymptomatic case load of 68.7% was observed specifically among the higher age group of greater than 15 years (63.3%) . In the 2nd mass survey 50 out of 2239 enrolled individuals (2.23%) were found to be malaria positive. During the non survey period, 16.1% (71 out of 440) febrile individuals were found malaria positive. Significant spatial clusters of malaria cases were detected during first survey. 93.6% individuals were using bed nets, however, only 8.47% used ITBN. This preliminary results of the survey provides information on the epidemiology of malaria and establishes a framework to use a multidisciplinary approach to the investigation of malaria distribution and determinants in a dynamic cohort.

Keywords: Cohort, Epidemiology, Malaria, Survey, Pf

WEDNESDAY 7 DECEMBER 2016

16.00 - 17.30
Room B

S13: THAILAND AND ASTMH – A SHARED VISION IN TROPICAL MEDICINE

Chairpersons :

1.Patricia Walker

2. Watcharapong Piyaphanee

Invited Speakers :

1. Christopher Plowe
" The science and politics of malaria elimination in the Greater Mekong Subregion"
Institute for Global Health at the University of Maryland School of Medicine, USA

2. Patricia Walker
"Human Mobility and Health"
Professor of Medicine, University of Minnesota Medical Director, HealthPartners Travel and Tropical Medicine Center President, American Society of Tropical Medicine and Hygiene, USA

3. Karen Goraleski
"ASTMH: Leveraging the Voices of Scientists for Change"
American Society of Tropical Medicine and Hygiene, USA

THE SCIENCE AND POLITICS OF MALARIA ELIMINATION IN THE GREATER MEKONG SUBREGION

Christopher Plowe

[1] *Institute for Global Health at the University of Maryland School of Medicine*

The initial response to the emergence in the Greater Mekong Subregion (GMS) of artemisinin resistant *Plasmodium falciparum* was to try to contain it, preventing its spread from western Cambodia to other countries in the GMS and beyond. In 2015 the World Health Organization recommended abandoning this containment strategy and the World Health Assembly endorsed the regional elimination of P. falciparum in the GMS, based on 1) genomic epidemiological evidence that artemisinin resistance was not only spreading from its site of origin in Cambodia, but independently emerging in other GMS countries; and 2) the emergence in Cambodia of partner drug resistance led to high rates of artemisinin-based combination treatment failures. Achieving this goal requires political will and cooperation not only at the national level, but across all sectors of complex societies in the GMS. To promote cross-sectoral cooperation on malaria elimination in Myanmar, the American Society of Tropical Medicine and Hygiene, the University of Maryland's Institute for Global Health, and the Center for Strategic and International Studies sponsored a conference on malaria elimination Myanmar. Three months before national elections, civilian and military government health officials, members of parliament from both the governing and opposition parties, officials from ethnic health organizations affiliated with armed militias then in conflict with the government, and international partners working on malaria control in Myanmar met in Washington DC. Mutual trust was established, common ground was reached, and the participants issued a joint statement of commitment to work together to eliminate malaria in Myanmar irrespective of political differences. This event provides an example of "global health diplomacy" that can serve as a model for promoting cooperation and political and community buy-in for malaria elimination in other complex settings.

Keywords: artemisinin resistance malaria elimination global health diplomacy ASTMH

Patricia Walker[1]

[1] *Professor of Medicine, University of Minnesota Medical Director, HealthPartners Travel and Tropical Medicine Center President, American Society of Tropical Medicine and Hygiene*

HUMAN MOBILITY AND HEALTH

Human Mobility and Health Human mobility impacts both individual health and population health in multiple ways. Millions of people move around the globe every year, and the advent of air travel has meant that infectious diseases can travel rapidly worldwide. Migrants, travelers and refugees are a group of particular interest in the context of human mobility and health. Thailand is no stranger to these issues, having been a host nation for refugees since the mid -1970s. In addition, Thailand is a major tourist travel destination. This lecture will highlight best practices in refugee screening, care for migrants and the visiting friends and relatives traveler.

ASTMH: LEVERAGING THE VOICES OF SCIENTISTS FOR CHANGE

Karen Goraleski [1]

[1] *American Society of Tropical Medicine and Hygiene*

Professional scientific membership societies in the United States play a unique role as compared with their counterparts in other parts of the world. Like all scientific membership organizations, education and training are the highest priority for the American Society of Tropical Medicine and Hygiene as evidenced by the society's peer-reviewed journal, the American Journal of Tropical Medicine and Hygiene and the Annual Meeting. ASTMH also recognizes that reaching out to the media, engaging the U.S. Congress through lobbying and advocacy, and science-diplomacy efforts are additional powerful tools in the fight to improve global health. In this session hear how ASTMH creates and takes advantage of opportunities to increase awareness of, and support for evidence-based tropical medicine policies and robust funding. ASTMH advocates on behalf of the U.S. National Institutes of Health, the U.S. Centers for Disease Control and Prevention and tropical medicine research conducted by the U.S. Army and the U.S. Navy. The society collaborates with NGOs and coalitions, and encourages individual members of ASTMH to contact their elected representatives in the U.S. Congress. The Executive Director will share examples, review what has been successful and discuss how the definition of success can and does shift.

Keywords: advocacy, NIH, CDC, media

WEDNESDAY 7 DECEMBER 2016

16.00 - 17.30
Room C

S14: DIETARY REFERENCE INTAKES FOR THAILAND 2016: PREVENTIVE MEDICINE

Chairpersons :

1. Karunee Kwanbunjan

2. Amornrat Aroonnual

Invited Speakers :

1. Umaporn Suthutvoravut
"Calcium, Vitamin D and Osteoperosis"
Department of Pediatrics, Faculty of Medicine Ramathibodi Hospital, Mahidol University
(Abstract not available)

2. Nalinee Chongviriyaphan
"Vitamin C: Vitamin antioxidant"
Department of Pediatrics, Faculty of Medicine Ramathibodi Hospital, Mahidol University
(Abstract not available)

3. Anadi Nitithamyong
"Fiber: Phytochemical roles in NCDs prevention"
Institute of Nutrition, Mahidol University

FIBER: PHYTOCHEMICAL ROLES IN NCDS PREVENTION

Anadi Nitithamyong [1]

[1] *Institute of Nutrition, Mahidol University*

Dietary fiber and phytochemicals are plant-based compounds that are abundant in the diet of human. There has been an increasing interest in the roles of those compounds in reducing the risk or lessen the symptoms of common non-chronic diseases such as obesity, diabetes, hyperlipidemia and certain types of cancer. The presentation will review the properties, functions and probable roles of dietary fiber and some groups of phytochemical, e.g. flavonoids, polyphenols, isoflavones, carotenoids, etc., generally found in the diet, particularly Thai and Asian diets.

Keywords: dietary fiber, phytochemicals, phytonutrients

WEDNESDAY 7 DECEMBER 2016

16.00 - 17.30
Room D

S15: TURBO TALK II

Chairpersons :

1.John Adams

2.Srivicha Krudsood

Speakers :

1. Suwalee Worakhunpiset
"Assessment of carcinogenic potential of chemicals from plastic food containers and packaging through cell transformation assay"
Faculty of Tropical Medicine, Mahidol University

2. Xin Hui Chan
"Using the Surface Electrocardiogram to Evaluate Arrhythmia Risk in Antimalarial Therapy - the case of Halofantrine"
Mahidol-Oxford Tropical Research Unit, Faculty of Tropical Medicine, Mahidol University

3. Borimas Hanboonkunupakarn
"Comparison of the electrocardiographic effects of chloroquine and piperaquine"
Faculty of Tropical Medicine, Mahidol University

4. Thunyapit Thita
"Phenotypic and genotypic characterization of *Plasmodium falciparum* isolated from Thai-Cambodia border after artemisinin containment project"
Faculty of Science, Mahidol University

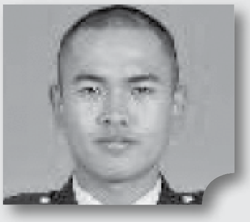
5. Thyl Miliya
"Invasive Bacterial Infections in Children Admitted to Angkor Hospital for Children and Satellite Clinic, 2013-2015"
Cambodia-Oxford Medical Research Unit, Cambodia

16.00 - 17.30

Room D

S15: TURBO TALK II *(Continued)*

Speakers :



6. Pongpisut Thakhampaeng
"Prevalence and risk factors of *Blastocystis* infection in a rural community, Central Thailand"
Phramongkutklao College of Medicine

7. Jipada Manomat
"Prevalence and associated risk factors of leishmaniasis among HIV/AIDS patients in Trang Province, southern Thailand"
Faculty of Science, Mahidol University

8. Dewi Masyithah Darlan
"Correlation behaviour, personal hygiene, home environment sanitation with prevalence of soil transmitted helminthes (STH) infection among public primary students in Medan"
Univeristy of Sumatera Utara, Indonesia

9. Abduljubbar Kariya
"Situation of intestinal parasitic infections in school-age children in Narathiwat: a southern border province in Thailand"
Faculty of Medicine, Princess of Naradhiwas University

10. Siraphop Malairatana
"Prevalence and risk factors of *Opisthorchis viverrini* infection in the Northeastern community located in Central Thailand"
Phramongkutklao College of Medicine

11. Picha Suwannahitatorn
"Infection dynamics of *Opisthorchis viverrini* infection: two-part model approach and age-prevalence-intensity relationship"
Phramongkutklao College of Medicine

12. Rie Takeuchi
"The gap of health education and the real situation of schistosomiasis --The situation of *Schistosoma mansoni* prevention and prevalence in Western Kenya"
Nagasaki University, Japan

13. Anthony Cousien
"An effecient tool for the detection of major denegue outbreaks in Cambodia"
Institut Pasteur du Cambodge, Cambodia

ASSESSMENT OF CARCINOGENIC POTENTIAL OF CHEMICALS FROM PLASTIC FOOD CONTAINERS AND PACKAGING THROUGH CELL TRANSFORMATION ASSAY

Suwalee Worakhunpiset [1],
Nathamon Kosoltanapiwat [2],
Ratchaneekorn Mingkhwan [1]

[1] *Department of Social and Environmental Medicine, Faculty of Tropical Medicine, Mahidol University,*
[2] *Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University*

Plastics play important role in our daily life. Several types of plastic have been produced by adding substances to a plastic during manufacture to create forms of plastics for intended uses, including for food storage and packaging. It is known that chemical components can migrate from plastic into food during use and may contribute adverse health effects to consumers. This study aimed to determine the carcinogenic potential of overall chemicals derived from plastic containers and food packaging using Bhas 42 cell transformation assay. The Bhas 42 cells were treated with test substances extracted from plastic containers using food stimulants for overall migration test for 4 days and 11 days in initiation and transformation assays, respectively. The results showed most of the test substances were negative for transformed foci while twenty-four samples of initiation assay and four samples of promotion assay were judged equivocal. Bhas42 cell treated with 95% ethanol gave the highest number of samples with equivocal results compared to other food stimulants. This indicated plastic containers should not use for storing fatty foods on account of the leached chemicals may have carcinogenic potential on both initiation and promotion stages. Besides, although most of the test substances gave negative results but many test substances exhibit the ability to induce transformed foci in both initiation and promotion stages. Further studies should be conducted to assess more fully assay, especially the samples that were judged equivocal.

Keywords: carcinogenic, plastic, cell transformation

USING THE SURFACE ELECTROCARDIOGRAM TO EVALUATE ARRHYTHMIA RISK IN ANTIMALARIAL THERAPY - THE CASE OF HALOFANTRINE

Xin Hui Chan[1],
Borimas Hanboonkunupakarn[1],
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Halofantrine has been associated with human ether-à-go-go-related gene (hERG) potassium channel blockade, significant QT prolongation, torsade de pointes (TdP) and over 30 reports of sudden cardiac death (SCD); it is no longer recommended by the WHO for treatment of malaria. The halofantrine experience informs contemporary concerns about piperaquine cardiotoxicity and the attention on appropriate markers for arrhythmia risk assessment in antimalarial therapy. QT interval prolongation on the surface electrocardiogram (ECG) is a well-known and sensitive risk factor for ventricular arrhythmias and SCD but has limited specificity. An alternative approach proposed is evaluation of multichannel block. Pure hERG potassium channel block is associated with higher TdP risk and has been shown to equally prolong J-Tpeak and Tpeak-Tend whereas additional inward current block is thought to lower TdP risk and preferentially shorten J-Tpeak. Tpeak-Tend/QT > 0.3 is another pro-arrhythmia risk marker. Halofantrine is a positive control to investigate the utility of ECG biomarkers for arrhythmia risk assessment in antimalarial therapy. We renalysed 20 ECGs of Karen patients with acute uncomplicated falciparum malaria who received halofantrine 8mg/kg three times a day in Shoklo refugee camp on the Thai-Burmese border 1992. We manually measured PR, QRS, QT, J-Tpeak, and Tpeak-Tend intervals in all complexes in lead II in traces with QTc > 530ms by either Bazett's or Fredericia's correction factor, and with any degree of heart block, compared to baseline. 1 patient had post-dose second degree heart block (Wenkebach), all others were in sinus rhythm. 2 patients (including the one who went into second degree heart block) had post-dose QT alternans. QTcF was the best correction factor compared with QTcB and QTc Karen. Mean QTcF at baseline and maximum prolongation were 399.4ms and 502.5ms respectively. Median increase in QTcF, QRS, J-Tpeakc, and Tpeak-Tend was 100.2ms, 6.6ms, 60.6ms, and 17.1ms respectively. No complexes had Tpeak-Tend/QT > 0.3. These findings underscore the importance of a population appropriate correction factor in QT measurement. While not entirely consistent with the multichannel block paradigm, they support the need for further electrophysiological studies to better characterise the cardiac action potential in pro-arrhythmia risk assessment.

Keywords: Malaria, antimalarials, cardiotoxicity, halofantrine, piperaquine

COMPARISON OF THE ELECTROCARDIOGRAPHIC EFFECTS OF CHLOROQUINE AND PIPERAQUINE

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Chloroquine and piperaquine are the two widely used antimalarial drugs. Both share basic structures and have effects on ventricular depolarization and repolarization. While there are not many concerns over the use of oral chloroquine, regulatory authorities have suggested restrictions on the use of piperaquine because of cardiovascular effects. Interestingly, animal studies suggest that chloroquine is more cardiotoxic than piperaquine. We have recently completed a series of cross-over clinical and pharmacokinetic evaluations of chloroquine, piperaquine, and primaquine in healthy subjects. All drugs were well tolerated. Four subjects were in two studies, thus received both chloroquine and piperaquine. We therefore aimed to compare the electrocardiographic effects of chloroquine and piperaquine in the same subjects by recruiting more subjects who have received either piperaquine (in form of 120/960 mg dihydroartemisinin-piperaquine) or a single dose of 600 mg chloroquine and administer the other drug, exactly as in the earlier subject study. Overall, 18 healthy Thai adults (12 female, 6 male) aged between 18 and 60 years were enrolled at the Pharmacokinetic Unit Faculty of Tropical Medicine, Mahidol University. Electrocardiography was done at predose, then at 1, 2, 4, 8, 12 and 24 hours postdose. QTc intervals were corrected using Fridericia's formula. Predose QTc intervals were comparable in both groups. Median of maximum QTc interval was higher after chloroquine than after piperaquine administration (437.48 vs. 430.16 msec). Median % Changes of QTc intervals from baseline values were significantly higher in chloroquine than piperaquine (5.57% vs. 1.72%, p = 0.0002). These results reassured the safety of piperaquine to be used in antimalarial treatment.

Keywords: Chloroquine, piperaquine, cardiotoxic, QT interval prolongation

PHENOTYPIC AND GENOTYPIC CHARACTERIZATION OF *PLASMODIUM FALCIPARUM* ISOLATED FROM THAI-CAMBODIA BORDER AFTER ARTEMISININ CONTAINMENT PROJECT

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Malaria is the one of the most important parasitic diseases threatens human being. Multidrug resistance is the major problems for elimination malaria. Due to antimalarial resistance, WHO has recommended artemisinin-based combination therapy (ACT) for treating uncomplicated falciparum malaria. However, the evidences of artemisinin resistance have been reported especially in Southeast Asian countries. Malarone®, a combination of atovaquone–proguanil, has been used to cease artemisinin pressure in some areas of Thai-Camboder border since 2009. We aimed to determine genotypes and phenotypes of *P. falciparum* isolated from Thai-Cambodia border after artemisinin containment project. *P. falciparum* isolates collected during 1988-2014 were characterized for K13 propeller domain, pfcrt, pfmdr1 gene. Our study shows the increasing percentage of the K13 C580Y in the isolates collected from and after 2009 indicating that the containment project might not be able to control the spreading of artemisinin-resistant genotype. Parasite isolates collected from and after 2009 contained the pfmdr1 184F allele and exhibited mefloquine resistance. New antimalarials should overcome these resistant genotype and phenotypes. In addition, we found no atovaquone resistance genotypes and phenotypes in the parasite isolates collected after the containment project.

Keywords: Malaria, ACT

INVASIVE BACTERIAL INFECTIONS IN CHILDREN ADMITTED TO ANGKOR HOSPITAL FOR CHILDREN AND SATELLITE CLINICS, 2013-2015

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Objective: To describe the clinical characteristics and pathogens associated with invasive bacterial infection in Cambodian children. In addition, to characterise the antimicrobial resistance (AMR) profiles of these pathogens and to describe the geographic distribution of cases.

Methods: A three-year prospective surveillance study of invasive bacterial infections in patients admitted to Angkor Hospital for Children and its Satellite Clinic, Siem Reap.

Result: Between 1st January 2013 and 31st December 2015, there was 463 patient episodes where blood cultures grew pathogens included in the following analyses. Community-acquired infections (CAI) accounted for 77% of these cases. The top 10 pathogens isolated were *Staphylococcus aureus, Streptococcus pneumoniae, Salmonella typhi, Klebsiella pneumoniae*, miscellaneous coliforms, non-fermenter Gram negative bacilli, *Burkholderia pseudomallei, Escherichia coli, Acinetobacter baumannii* and *Salmonella Paratyphi* A. Antimicrobial resistance was common. For example, 100% of *Salmonella typhi* isolates were multi-drug resistant and non-susceptible to fluoroquinolones. The most frequent hospital-acquired infection (HAI) isolates were Klebsiella pneumoniae, Escherichia coli and miscellaneous coliforms. These were frequently resistant to 3rd generation cephalosporins; however, carbapenem resistance was rare. The overall mortality rate was 17%, but higher in neonates and in children with hospital acquired infection.

Conclusion: This study demonstrates that there is already a high prevalence of antimicrobial resistance in invasive bacterial isolates from Cambodian children. The results clearly show the need for action to reduce infections by antimicrobial resistant organisms, for example increasing antibiotic stewardship, strengthening infection control to prevent HAI, and on-going surveillance to monitor trends in pathogens and AMR profiles.

Keywords: Invasive, bacteria, antimicrobial resistance, Children, Cambodia

PREVALENCE AND RISK FACTORS OF *BLASTOCYSTIS* INFECTION IN A RURAL COMMUNITY, CENTRAL THAILAND

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Blastocystis *sp.* is one of the most common intestinal protozoa detected in both human and animals. *Blastocystis sp.* is now considered as a pathogen causing gastrointestinal illnesses. The study aimed to determine prevalence and risk factors of Blastocystis infection in a community, SaKaeo, Thailand. A cross-sectional study was conducted in this community which consisted of 4 villages in February 2016. Data were collected by a standardized electronic questionnaire. Blastocystis sp. was identified by in vitro cultivation using Jones' medium. A total of 1008 villagers were enrolled in this study. The overall prevalence of Blastocystis infection was 11.8%. Multivariate analysis showed that those who lived in a particular village (OR = 2.9; 95% CI, 1.7-5.0), were farmers (OR = 1.7; 95% CI, 1.0-2.8),and had chickens at home (OR = 2.3; 95% CI, 1.1-4.8) were associated with Blastocystis infection. Predominant prevalence of Blastocystis infection in a particular village might indicate waterborne transmission since water supply of each village was from different resources and treatments. Having chickens at home as a significant risk may indicate zoonotic transmission. Both zoonotic and waterborne transmission might explain the high risk of Blastocystis infection in farmers since they exposed to animals, agricultural and environmental water. Further proof is to identify and determine subtype of *Blastocystis sp.* in those animals and water resources. Improvement of hygienic practices and the quality of water supply should be implemented in order to prevent and control Blastocystis infection.

Keywords: *Blastocystis*, Prevalence, Water, Intestinal protozoa

PREVALENCE AND ASSOCIATED RISK FACTORS OF LEISHMANIASIS AMONG HIV/AIDS PATIENTS IN TRANG PROVINCE, SOUTHERN THAILAND

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Leishmaniasis is one of opportunistic infectious diseases. Co-infection of visceral leishmaniasis and HIV results in high mortality rate, high relapse and treatment failure. In Thailand, leishmaniasis is a sporadic emerging disease which information regarding the prevalence and risk factors are still limited. Our study aimed to determine the prevalence and risk factors of leishmaniasis among HIV/AIDS patients in Trang Province, southern Thailand. A cross-sectional study of 324 HIV-infected participants was conducted to investigate Leishmania infection from February 2015-February 2016. Participants were screened for specific antibodies in plasma using Direct Agglutination Test (DAT) and DNA detection of the Leishmania in buffy coat using PCR. Demographic and behavioral data were collected using standardized questionnaire. Logistic regression analysis was used to investigate risk factors associated with leishmaniasis prevalence. Prevalence of leishmaniasis was 17.9% (58/324). After adjusting for potential confounders, an independent risk factor for leishmaniasis prevalence was having low CD4 level. The adjusted odds ratio and 95% confidence interval of CD4 = 200-350 cell/mm3 was 2.18 (1.01-4.69) and CD4 < 200 cell/mm3 was 2.95 (1.14-7.64) when compare with CD4 > 500 cell/mm3. This study highlighted that the prevalence of leishmaniasis among HIV/AIDS patients in southern Thailand was high. Individuals who had lower immunity were more likely to get the infection. Urgent need for effective intervention and prevention methods to control leishmaniasis in Thailand is very crucial.

Keywords: Leishmaniasis, HIV/AIDS, Risk factor, Thailand

CORRELATION BEHAVIOUR, PERSONAL HYGIENE, HOME ENVIRONMENT SANITATION WITH PREVALENCE OF SOIL TRANSMITTED HELMINTHES (STH) INFECTION AMONG PUBLIC PRIMARY STUDENTS IN MEDAN

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Prevalence of STH infection among primary school students in Indonesia is still high. Factor causing the high number of the prevalence of STH is the poor awareness in hygiene and inadequate enviromental condition. The purpose of this study was to examine the correlation of behavior personal hygiene and home environment santitation with prevalence of STH infection among public primary students in Medan and the total sample is 114 person. The number of sample is 80 person who are determined based on inclusion and exclusion criteria. Kato-katz method was employed for detecting worm eggs on feces. The result showed that prevalenced of STH infection were 40%. Questionnaire showed good knowledge 62.5%, good attitude 68.75%, good personal hygiene 75%, good home environment 67.5%,. Chi-square test showed for knowledge p=0.00, attitude p=0.003, personal hygiene p=0.008, home sanitation p=0.006. There is a significant correlation between behaviour, personal hygiene, and home environment sanitation with prevalence of STH infection among public primary student in Medan.

Keywords: Behaviour, Personal-hygiene, Sanitation, STH-infection, Students

SITUATION OF INTESTINAL PARASITIC INFECTIONS IN SCHOOL-AGE CHILDREN IN NARATHIWAT: A SOUTHERN BORDER PROVINCE IN THAILAND

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[1] Princess of Naradhiwas University

Intestinal parasitic infections remain a major health problem in Thailand for decades which reflects lack of proper hygiene and sanitation in some particular area. Infections could potentially affect childhood development. Narathiwat province is one of the southern border provinces which is considerably distant. Therefore, lack of epidemiological data of intestinal parasitic infections could result in healthcare planning issue. This study aimed to explore prevalence of intestinal parasitic infections including soil-transmitted helminths (STHs) and intestinal protozoa. Stool specimen was collected from students with 1 – 15 years of age in 3 primary schools; most of them were Islamic. Specimens underwent 3 microscopic-based examinations; simple smear, modified Kato-Katz and FECT. From 562 specimens, prevalence of STH infection was 17.4% (95% CI, 14.3 – 20.6) which were *Ascaris lumbricoides* 11.9% (95% CI, 9.2 – 14.6), *Trichuris trichiura* 7.5% (95% CI, 5.3 – 9.7) and hookworm 1.6% (95% CI, 0.6 – 2.6). Prevalence of intestinal protozoa was 20.0% (95% CI, 16.7 – 23.5) which were *Blastocystis sp.* 16.0% (95% CI, 13.0 – 19.1) and *Giardia intestinalis* 6.4% (95% CI, 4.3 – 8.4). Some students carried more than 1 organism. The results potentially reflect hygiene and sanitation problems in school-age children which requires immediate response including risk factor identification, treatment and further prevention and control program.

Keywords: Intestinal parasitic infections, STH, protozoa

PREVALENCE AND RISK FACTORS OF *OPISTHORCHIS VIVERRINI* INFECTION IN THE NORTHEASTERN COMMUNITY LOCATED IN CENTRAL THAILAND

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Opisthorchis *viverrini* infection is a major zoonotic parasitic infection in Thailand caused by consumption of undercooked cyprinoid fish containing infective metacercariae. Opisthorchiasis is mainly asymptomatic which subsequently progress to cholangiocarcinoma; an aggressive and incurable cancer within bile duct. National survey in 2001 shows that infection is geographically distributed; particularly in the North and Northeastern where local undercooked freshwater fish menu is favored. A study conducted in Baan Na-yao; Northeastern descendant community in Central Thailand, during 2002 – 2014 revealed that the area was manifested with prevalence over 20% of infection in early years and local menu Koi pla was determined as a potential risk. After providing multiple stool examinations and treatments, prevalence decreased to 7% in 2014. This study aimed to explore prevalence and risk factors of the infection in Baan Sai-tong, a neighboring area sharing same demographic background; Northeastern ethnic, to Baan Na-yao. Unlike Baan Na-yao, the area had never been examined for parasitic infection before. Prevalence of Opisthorchis viverrini infection was 19.8% (17.3 – 22.3, 95% CI) and consumption of Koi pla increased risk for acquiring the infection; OR = 2.2 (1.3 – 3.6, 95% CI). The study shows that the infection is still prevalent where risk behavior is presented. Therefore, active surveillance might be considerably useful in high risk area where risk behaviors could be preliminary identified.

Keywords: Opisthorchis viverrini, zoonosis, prevalence

INFECTION DYNAMICS OF *OPISTHORCHIS VIVERRINI* INFECTION: TWO-PART MODEL APPROACH AND AGE-PREVALENCE-INTENSITY RELATIONSHIP

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Opisthorchis viverrini infection is caused by food-borne trematode where transmission to humans occurs through the consumption of uncooked fish containing infective stage metacercariae leading to infection within the hepato-biliary system. Chronic infection is strongly associated with cholangiocarcinoma. This study aimed to measure prevalence and intensity of the infection. Stool examination was conducted with 3 methods; direct smear, modified Kato-Katz and FECT in Baan Na-ngam and Baan Na-isarn in Central Thailand. Infection intensity was determined to reflect the infection burden through eggs per gram. Regression models for count outcome were used to examine patterns of intensity distribution including Poisson and negative binomial distributions. Compound model, zero-inflated and hurdle models were formulated to incorporate over-dispersed and zero excess data. The prevalence of infection was 7.85% (95% CI, 4.96 – 10.75) in Baan Na-isarn and 9.29% (95% CI, 6.64 – 11.93) in Baan Na-ngam. The infection intensity data were over-dispersed, suggesting that the use of negative binomial distribution was more appropriate than Poisson distribution. A negative binomial hurdle (NBLH) model was the model of choice for zero excess and over-dispersed count data in this study. The results demonstrated that consumption of Koi pla was a potential risk factor for acquiring the infection and also increased infection intensity. The age-prevalence-intensity relationship indicated that prevalence linearly increased with age; intensity tended to increase and the parasite spread more equally. Up-to-date information on infection dynamics has a potential impact on public health and further ongoing extensive research in this field is essential to provide effective public health management.

Keywords: *Opisthorchis viverrini* Overdispersion Hurdle Zero-inflated

THE GAP OF HEALTH EDUCATION AND THE REAL SITUATION OF SCHISTOSOMIASIS --THE SITUATION OF *SCHISTOSOMA MANSONI* PREVENTION AND PREVALENCE IN WESTERN KENYA

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Despite of preventive measures such as mass drug administration, prevalence of *Schistosoma mansoni* remains high in Mbita located in the shore of Lake Victoria, western Kenya. This study aims to analyze the situation of Schistosomiasis, including its prevalence, health education, and water use in the schools. Four primary schools were selected as target schools and pupils in class six and seven were recruited as study samples. The prevalence of *Schistosoma mansoni* and *Schistosoma haematobium* were examined by Kato-Katz 3-day method and urine filtration method, respectively. Simultaneously, knowledge, attitude and practice test toward Schistosomiasis was conducted to same pupils. The contents of health education were extracted from textbooks. All primary schools in Mbita were surveyed how to secure water in schools using a questionnaire. The prevalence of *Schistosoma mansoni* was 56%. According to the science textbook, "avoid contact with contaminated water" is the way to prevent Schistosoma infection, however, 66% of schools order to pupils to fetch and bring water from Lake Victoria. School children are taught to avoid contact with contaminated water, on the other hand, they are ordered to fetch water from the lake. The water for domestic use in this area depends on Lake Victoria, thus fetching water is essential for their lives, and the lifestyle cannot be changed as long as infrastructure such as water supply would be improved. In addition, it is unfortunate that mass drug administration did not show expected outcome because of intermittent implementation caused by lack of budget. The alternative measures are necessary.

Keywords: school health helminth infection

AN EFFICIENT TOOL FOR THE DETECTION OF MAJOR DENGUE OUTBREAKS IN CAMBODIA

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Introduction: Dengue is endemic in Cambodia, with annual outbreaks of varying amplitude. Thanks to the ECOMORE project, we developed an early warning tool to inform healthcare stakeholders of largescale outbreaks and massive influx of patients. Method: We used data from the National Dengue Control Program (NDCP) dengue surveillance system. These data are routinely obtained through passive surveillance of dengue-like pediatric inpatients reported by public hospitals and a sentinel, pediatric hospital-based active surveillance system. We compared 4 existing algorithms to detect outbreaks using count data time series, comparing the current count to an expected distribution obtained from observations of past years. We selected the algorithm with maximum specificity and sensitivity for large outbreaks detection in 8 Cambodian provinces during 2008-2015.

Results: The analyses included 86,471 patients with dengue-like syndromes. Based on a Bayesian approach, the selected algorithm had an overall sensitivity and specificity of 73% and 97%, respectively, for the detection of large outbreaks during 2008-2015. Depending on the province, sensitivity and specificity ranged from 50% to 100% and 75% to 100%, respectively.

Conclusion: Cambodian hospital staff requested an early warning tool to prepare for important outbreaks. This tool can be easily implemented. It is an effective response to their request.

Keywords: Dengue, outbreak, early warning, Cambodia

WEDNESDAY 7 DECEMBER 2016

16.00 - 17.30
RoomE

S16: BEST STUDENT PRESENTATION AWARD

Chairperson :


Jaranit Kaewkungwal

Speakers :


1. Clovis Hugues Seumen Tiogang
" Reduced antimalarial total IgG associated with concurrent ascariasis in school aged children of two endemic areas in Cameroon"
The Biotechnology Center/ University of Yaounde I, Cameroon


2. Nabilah Amelia Mohammad
"Genetic heterogeneity of blastocystis from different hosts: amplification of small subunit ribosomal RNA gene"
Universiti Teknologi Mara, Malaysia


3. An-Ting Liou
"A new animal model containing human SCARB2 and lacking stat-1 is highly susceptible to EV71"
TIGP, Academia Sinica, Taiwan


4. Haruhiko Ishioka
" Impact of restrictive fluid management on acute kidney injury and plasma lactate in severe falciparum malaria"
Department of clinical tropical medicine, Faculty of Tropical Medicine, Mahidol University


5. Maria Karmella Apaya
" Pharmacological modulation of bioactive lipid mediators in sepsis and related infection-related inflammation"
Taiwan International Graduate Program, Taiwan

REDUCED ANTIMALARIAL TOTAL IGG ASSOCIATED WITH CONCURRENT ASCARIASIS IN SCHOOL AGED CHILDREN OF TWO ENDEMIC AREAS IN CAMEROON

Clovis Hugues Seumen Tiogang [1]

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Malaria infection and ascariasis are common in developing countries. An interaction, at any level, between both parasites would be of considerable public health significance. This study aimed at investigating variation in anti-malarial total IgG in school aged children of two endemic areas in Cameroon. A total of 643 children aged 2-16 years were recruited in Mfou and Nkolbisson. Presence of malaria parasites, parasites densities and species were determined by microscopy and confirmed using nested PCR. Ascaris eggs were identified and quantified with the Kato Katz technique. Immunoglobulin gamma level against three asexual stage recombinant plasmodial antigens (MSP142, AMA1 3D7, EBA175) and crude antigens were measured by ELISA. In all, 148 (23.01%), 141(21.9%) and 46 (7.15%) had malaria infection only, ascaris infection only and co-infection respectively. *P. falciparum* was the most present malaria parasite. The majority of malaria infected children (75%) were classified as higher anti-malarial total IgG producers. The mean anti-malarial total IgG was reduced in co-infected children compared to malaria mono-infected children. However, this difference was not statistically significant. Also, the IgG level was not affected the intensity of ascaris infection but slightly by the area. These findings reveal that malaria/ ascariasis co-infection have no effect on the production of antimalarial total IgG in the studied population. However, there is a need to examine the effect of malaria/helminths co-infections on antimalarial IgG subclasses.

Keywords: Malaria, Ascariasis, IgG, Children

GENETIC HETEROGENEITY OF BLASTOCYSTIS FROM DIFFERENT HOSTS: AMPLIFICATION OF SMALL SUBUNIT RIBOSOMAL RNA GENE

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Introduction: Blastocystis is genetically diverse parasite that currently classified into 17 subtypes (STs). Human Blastocystis isolates were limited into subtypes 1 to 9. Mixed infection with genotypic homology animals isolates were also demonstrated in all of these 9 subtypes. Hence, this study aimed to assess the genetic variation of Blastocystis subtypes recovered from humans and domestic animals from the aboriginal settlements by analysing the partial sequence of small subunit ribosomal RNA (SSU rRNA) gene.

Method: DNA polymorphism of Blastocystis from humans (167) and domestic animals (33) isolates were amplified by PCR assay. A fragment of 550 to 585-bp of the SSU rRNA was considered positive. The Blastocystis-positive amplicons were purified and sequenced. Phylogenetic tree of positive isolates, reference strains and outgroup were constructed using maximum likelihood method based on Hasegawa.Kishino.Yano+G+I model.

Results: The overall prevalence of Blastocystis infection in humans and domestic animals were 18.6% and 3.0%, respectively. Through molecular phylogeny, 31 isolates could be separated into 3 clusters contained isolates from both hosts. Among humans isolates, ST3 (10.2%) was the predominant subtype, followed by ST1 (4.8%) and ST2 (3.6%). ST2 was also observed in macaque (3.0%), the domestic animal.

Conclusion: To the best of our knowledge, this is the first study that conclusively demonstrated the genetic diversity of Blastocystis in humans and domestic animals in such population in Malaysia. One sequence from animal isolate was closely related to humans, indicating zoonotic risks. Therefore, it is extremely important to maintain good sanitary condition by avoiding sharing indoor and outdoor areas with domestic animals to curb the future expansion of this parasite via zoonotic route.

Keywords: Blastocystis, small subunit ribosomal RNA, subtypes, genetic variation, Malaysia

A NEW ANIMAL MODEL CONTAINING HUMAN SCARB2 AND LACKING STAT-1 IS HIGHLY SUSCEPTIBLE TO EV71

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Enterovirus 71 (EV71) is a major threat to children worldwide. Children infected with EV71 could develop subclinical infection and hand-foot-and -mouth disease (HFMD). In severe cases, patients could develop encephalitis, paralysis, pulmonary edema, and death. A more user-friendly and robust animal model is essential to investigating EV71 pathogenesis. Here, we established a hybrid (hSCARB2+/+/stat-1−/−) mouse strain from crossbreeding SCARB2 transgenic and stat-1 KO mice, and compared the susceptibilities to EV71 infection and pathogenesis between parental and hybrid mice. Virus-encoded VP1 protein can be detected in the streaking nerve fibers in brain and spinal cord. This hybrid mouse strain at 2-week-old age can still be infected with different genotypes of EV71 at 1000 fold lower titer via an ip route. Infected hybrid mice developed earlier onset of CNS disease, paralysis, and death at a higher incidence. These advantages of this novel model meet the urgent need from the scientific community in basic and preclinical research in therapeutics and pathogenesis.

Keywords: EV 71

IMPACT OF RESTRICTIVE FLUID MANAGEMENT ON ACUTE KIDNEY INJURY AND PLASMA LACTATE IN SEVERE FALCIPARUM MALARIA

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Purpose. Since liberal fluid resuscitation is harmful in adults with severe malaria, the appropriate volume of fluid administration should be defined. Methods. We conducted a prospective observational study in adults with severe falciparum malaria in Bangladesh and India. Conventional fluid management was provided by the treating physician. Where feasible transpulmonary thermodilution measurements were performed. We evaluated the association between fluid intake and Δcreatinine or Δlactate, and the incidence of hypotension or pulmonary edema. Results. Twenty-nine patients were evaluated of which 5 died. The median total fluid intake was 3.3 mL/kg/hour (interquartile range, IQR: 1.9–4.1) during the first 6 hours (n = 27) and 2.3 mL/kg/hour (IQR: 2.0–3.3) during the first 24 hours from enrolment (n = 28). The median global end-diastolic volume index at first measurement was 560 mL/m2 (IQR: 505–629), indicating hypovolemia (n = 9). Fluid intake during the first 6 hours was not correlated with Δcreatinine at 24 hours (rs = −0.06; P = 0.774) or Δlactate at 6 hours (rs = 0.08; P = 0.710) (n = 24). Similar results were observed considering fluid intake over the first 24 hours. One patient had shock and 5 had pulmonary edema on enrolment, but afterwards neither of the complications was documented during hospitalization. Conclusion. Restrictive fluid management did not affect measures of kidney function, tissue perfusion, or blood pressure. Our results support the recommendation for restrictive fluid management of 2–4 mL/kg/hour during the first 6 hours, followed by 2–3 mL/kg/hour of crystalloid in adults with severe malaria.

Keywords: Severe malaria *Plasmodium falciparum* Fluid management Acute Kidney Lactate

PHARMACOLOGICAL MODULATION OF BIOACTIVE LIPID MEDIATORS IN SEPSIS AND RELATED INFECTION-RELATED INFLAMMATION

Maria Karmella L. Apaya[1,2,3] and Lie-Fen Shyur[2,4]

[1]Molecular and Biological Agricultural Sciences Program, Taiwan International Graduate Program, Academia Sinica, Taipei, Taiwan; [2]Agricultural Biotechnology Research Center, Academia Sinica, Taipei, Taiwan; [3]Graduate Institute of Biotechnology, National Chung Hsing University, Taichung, Taiwan; [4]Biotechnology Center, National Chung Hsing University, Taichung, Taiwan

Traditional medicine and ethnopharmacology are rich and sustainable sources of bioactive phytochemicals in disease prevention and treatment. Discovery-oriented research on phytomedicine and pathophysiology is much-needed especially in the tropical regions where infections, chronic inflammation and cancer are huge economic and healthcare burden. Sepsis, an acute inflammatory condition associated with life-threatening bacterial infections and a major complication to malaria, HIV/AIDS, diabetes and cancer deaths, is one condition wherein strategies for cost-effective intervention in resource-constrained settings are crucial. In this work, we use a metabolomics approach to demonstrate the systemic role of bioactive lipid mediators in the progression of sepsis. We identify endogenous derivatives of arachidonic acid (AA), linoleic acid (LA) and dietary polyunsaturated fatty acids, including eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) which are important in preventing septic shock-induced multiple organ damage in murine models. We show the systemic and organ-specific efficacy of plant-derived compounds in modulating the levels of these key molecular mediators. Our results provide insights on the dynamic nature of the lipid metabolome in inflammation and related conditions and show current and future applications of bioactive lipid profiling in pathobiology and drug-discovery.

Keywords: Sepsis; Bioactive Lipids; Metabolomics; Inflammation

THURSDAY 8 DECEMBER 2016

9.00 - 10.30
Room A

S17: PROGRESS ON MALARIA VACCINES

Chairpersons :

1. Sathit Pichyangkul

2. Wang Nguitragool

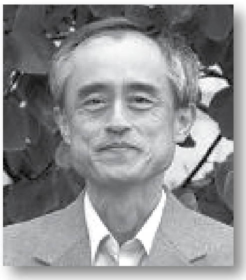
Invited Speakers :

1. Takafumi Tsuboi
"Post-genome malaria vaccine candidate discovery by wheat germ cell-free system"
Division of Malaria Research Proteo-Science Center Ehime University, Japan

2. Sathit Pichyangkul
"Chemoprophylaxis with sporozoites in *P. knowlesi* rhesus monkeys confers protection and elicits sporozoite-specific memory T cells in the liver expressing CCR5, CXCR6 and tissue-resident memory T cell marker CD69"
Armed Forces Research Institute of Medical Sciences (AFRIMS), Bangkok, Thailand

3. Noah Sather
" Development of novel antigens to elicit protective antibody responses against pre-erythrocytic malaria"
Center for Infectious Disease Research, USA

4. Toshihiro Horii
"What's new with BK-SE36, a blood-stage malaria vaccine candidate"
Department of Molecular Protozoology, Research Institute for Microbial Diseases, Osaka University, Japan



POST-GENOME MALARIA VACCINE CANDIDATE DISCOVERY BY WHEAT GERM CELL-FREE SYSTEM

Takafumi Tsuboi [1],
Eizo Takashima [1],
Masayuki Morita [1],
Edward H. Ntege [1],
Hikaru Nagaoka [1]

[1] *Division of Malaria Research, Proteo-Science Center, Ehime University, Matsuyama, Japan*

Malaria, caused by protozoan parasite of genus Plasmodium, is one of the leading global public health problems. It presents a major suppressor of social and economic development of many countries particularly in the tropical regions. The emergence of drug-resistant parasites and insecticide-resistant mosquito vectors has greatly hampered malaria control. This highlights the critical need for development of effective malaria vaccines. However, not even a single licensed malaria vaccine has been developed to date. These considerations galvanize us to expand the arsenal of discovery of promising malaria vaccine candidate antigens to be included in the next generation subunit malaria vaccine. We can now comprehensively exploit the genomic data by two post-genomic approaches for identification of novel malaria vaccine candidates: 1) immunoscreening approach and 2) functional approach. The success of these approaches depends heavily on the synthesis of quality recombinant parasite proteins. We previously demonstrated that the wheat germ cell-free protein synthesis system (WGCFS: an eukaryotic system), rather than Escherichia coli (a prokaryotic system), is a highly effective tools for synthesis of quality malaria proteins and hence the identification of novel malaria vaccine candidates. This presentation will review our current progress in post-genome malaria vaccine research.

Keywords: Malaria vaccine

CHEMOPROPHYLAXIS WITH SPOROZOITES IN *P. KNOWLESI* RHESUS MONKEYS CONFERS PROTECTION AND ELICITS SPOROZOITE-SPECIFIC MEMORY T CELLS IN THE LIVER EXPRESSING CCR5, CXCR6 AND TISSUE-RESIDENT MEMORY T CELL MARKER CD69

Sathit Pichyangkul[1]*,
Michele D. Spring[1],
Kosol Yongvanitchit[1], Utaiwan Kum-Arb[1],
Amporn Limsalakpetch[1],
Rawiwan Im-Erbsin[1],
Ratawan Ubalee[1],
Pattaraporn Vanachayangkul[1],
Edmond J. Remarque[2],
Evelina Angov[3], Philip L. Smith[1],
David L. Saunders[1]

[1] *Armed Forces Research Institute of Medical Sciences (AFRIMS), Bangkok, Thailand*
[2] *Biomedical Primate Research Centre, Rijswijk, The Netherlands*
[3] *Walter Reed Army Institute of Research, Silver Spring, MD, USA*

Whole malaria sporozoite vaccine regimens are promising new strategies and some candidates have demonstrated high rates of durable clinical protection associated with memory T cell responses. Little is known about the anatomical distribution of memory T cells following whole sporozoite vaccines, and immunization of nonhuman primates can be used as a relevant model for humans. We conducted a chemoprophylaxis with sporozoite (CPS) immunization in *P. knowlesi* rhesus monkeys and challenged via mosquito bites. Half of CPS immunized animals developed complete protection, with a marked delay in parasitemia demonstrated in the other half. Antibody responses to whole sporozoites, CSP and AMA1 but not CelTOS were detected. Peripheral blood T cell responses to whole sporozoites, but not CSP and AMA1 peptides were observed. Unlike peripheral blood, there was a high frequency of sporozoite-specific memory T cells observed in the liver and bone marrow. Interestingly, sporozoite-specific $CD4^+$ and $CD8^+$ memory T cells in the liver highly expressed chemokine receptors CCR5 and CXCR6, both of which are known for liver sinusoid homing. The majority of liver sporozoite-specific memory T cells expressed CD69, a phenotypic marker of tissue-resident memory (T_{RM}) cells, which are well positioned to rapidly control liver-stage infection. Vaccine strategies that aim to elicit large number of liver T_{RM} cells may efficiently increase the efficacy and durability of response against pre-erythrocytic parasites.

DEVELOPMENT OF NOVEL ANTIGENS TO ELICIT PROTECTIVE ANTIBODY RESPONSES AGAINST PRE-ERYTHROCYTIC MALARIA

Noah Sather[1]

[1] *Center for Infectious Disease Research, Seattle WA USA*

The pre-erythrocytic stage of malaria provides a window of opportunity for vaccine-induced antibody responses to prevent productive infection. The most clinically advanced anti-malaria vaccine (RTS,S) targets this stage and is able to mediate 30-50% protection from severe disease in several human clinical trials. However, there are considerable challenges in targeting this stage by antibody-inducing vaccines. These include a short duration of time from the injection of sporozoites into the skin until the invasion of the liver, the presence of a dominant antigen, and the likely need for the maintenance of high antibody titers to maintain protection. Further, the lack of defined surface-displayed antibody targets on the surface of the sporozoite in addition to the immunodominant Circumsporozoite protein (CSP) has hampered efforts to develop next generation vaccines. Our goal is to develop new vaccine immunogens derived from proteins that were recently found to make up the surface proteome of the Plasmodium sporozoite and to test their ability to induce infection-blocking antibodies by vaccination. To this end, we have developed a comprehensive pre-clinical vaccine pipeline for development and testing of new vaccine candidates. The pipeline includes recombinant protein production, immunizations, and recovery of antisera and monoclonal antibodies for further validation studies and dissection of the mechanisms of protection. Here we showcase our recent progress on developing new vaccine antigens in the Plasmodium yoelii model system. In addition, we highlight our early efforts to apply our preclinical developmental program to induce protective antibodies against *Plasmodium vivax*.

WHAT'S NEW WITH BK-SE36, A BLOOD-STAGE MALARIA VACCINE CANDIDATE

Toshihiro Horii [1]

[1] *Department of Molecular Protozoology, Research Institute for Microbial Diseases, Osaka University, Japan*

Malaria remains a leading cause of ill health, especially in African children. Key interventions currently in use have changed the epidemiology of malaria, yet a vaccine remains necessary to reduce mortality and deaths. Up to now, no effective vaccine has been licensed. As clinical illness occurs during blood-stage infection, a blood-stage vaccine would have an important impact from a health care perspective. We have been developing BK-SE36 based from Plasmodium falciparum serine repeat antigen-5 (SERA5) as a blood-stage vaccine. SERA5 is an essential antigen abundantly secreted in the parasitophorous vacuole by the malaria parasite; implicated for parasite egress, with high anti-SERA5 titers inversely correlating with malaria symptoms and severityreviewed in 1. As a vaccine candidate, SERA5 may likely overcome challenges with regards to extensive polymorphism2 and strict structural requirement of protective epitopes3. BK-SE36 animal pharmacology and pre-clinical toxicity studies show the vaccine is immunogenic, is effective against challenge studies, and safe, with no signs of systemic toxicity. In randomized trials with malaria naïve adults and volunteers from malaria endemic areas, BK-SE36 has been demonstrated to be a promising blood-stage vaccine candidate4,5. Suggestive efficacy obtained from a follow-up study after the phase Ib trial in Uganda showed that the vaccine afforded 72% protection against malaria episodes with ≥5000 parasites/µL blood + fever (axillary temperature ≥37.5 °C) 130-365 days post-second vaccination5. Furthermore, analysis of sera5 polymorphism of infecting parasites suggests that BK-SE36 does not show allele-specific efficacy; its protective efficacy is also not influenced by African HLAII haplotype6 and the immune response can be boosted by natural malaria infection7. In parallel with the BK-SE36 Phase Ib studies, a second formulation with CpG oligodeoxynucleotides (CpG ODN) have just completed the first-in-man clinical trials in malaria naïve Japanese adults, with the aim to improve immunogenicity, broaden and elicit longer-lasting vaccine immune response. References: 1Palacpac, et al. Vaccine 29, 5837-5845 (2011). 2Tanabe, K. *et al.* Vaccine 30, 1583-1593 (2012). 3Yagi, M. *et al.* PLoS ONE 9, e98460 (2014). 4Horii, T. et al. Parasitol. Int. 59, 380-386 (2010). 5Palacpac, N.M.Q. et al. PLoS ONE 8, e64073 (2013). 6Tougan, T et al. Parasitol. Int. 65, 455-458 (2016). 7Yagi, M et al. Sci. Rep. (in press 2016). Funding: Funds for integrated promotion of social system reform and research and development, MEXT (15651988) Grant for Translational Research Network Program (AMED) Global Health Innovative Technology Fund (G2013-105) (G2014-109)

Keywords: Malaria vaccine

THURSDAY 8 DECEMBER 2016

9.00 - 10.30
Room B

S18: HIV VACCINES AND OTHER PREVENTIVE STRATEGIES

Chairpersons :

1. Punnee Pitisuttithum

2. Robert J. O'Connell

Invited Speakers :

1. Punnee Pitisuttithum
"HIV vaccine Update"
Department of Clinical of Medicine, Mahidol University
(Abstract not available)

2. Eileen Dunne
"Microbicides for HIV prevention"
CDC/OID/NCHHSTP, HIV/STD Research Program, Thailand MOPH – CDC Collaboration, Bangkok, Thailand

3. Nittaya Phanuphak
"Strategic use of antiretroviral drugs for HIV prevention"
The Thai Red Cross AIDS and Research Center

MICROBICIDES FOR HIV PREVENTION

Eileen Dunne [1]

[1] *Thailand MOPH US CDC Collaboration (TUC)*

Different biomedical prevention interventions offer advantages and choices for HIV prevention. Microbicides, or compounds that can be used in the vagina or rectum to prevent viral STIs and HIV, are one type of product for HIV prevention. There are different ways microbicides act which including providing a physical barrier to infection, enhancing natural defenses against infection, or preventing replication. The advantages to microbicides is that they may be used by individuals at risk, they may be used in combination with other approaches, and they could be a more cost-effective approach. For females, microbicides include vaginal rings, vaginal gels, and other vaginal products. For men who have sex with men (MSM), microbicides include rectal gels, and other rectal products. Innovative types of microbicides include combined contraceptive and HIV prevention microbicides for females, and suppository, tablet, douche or other modalities for MSM. Novel nonotechnology-based systems that alter drug solubility, stability, and targetting could improve microbicide efficacy. Acceptability of microbicides is a challenge and feasible and convenient microbicide options are required for product success. This presentation will explore promising microbicides for HIV prevention and the opportunities and challenges for these tools.

Keywords: HIV prevention, Microbicides

Nittaya Phanuphak [1]

[1] *Prevention Department, Thai Red Cross AIDS Research Centre*

STRATEGIC USE OF ANTIRETROVIRAL DRUGS FOR HIV PREVENTION

Strategic use of antiretroviral drugs (ARV) for HIV prevention includes the use of ARV among HIV-uninfected individuals as pre-exposure prophylaxis (PrEP) and post-exposure prophylaxis (PEP) and the use among HIV-infected individuals to lower HIV viral burden in the body which translates into reduced risk of HIV transmission to others. WHO and several National Guidelines in the Asia Pacific region, including Thailand, now recommend antiretroviral treatment (ART) initiation for all people living with HIV regardless of their immune status since strong evidences have demonstrated both clinical and prevention benefits of early ART. PrEP and PEP are evidence-based biomedical HIV prevention interventions for people at risk for HIV infection. PrEP is the continuous use of ARV, prior to potential HIV exposure, to prepare enough drug levels in the body to reduce risk of HIV acquisition. PrEP is suitable for those who have confirmed HIV-uninfected status, foresee themselves to practice high risk behaviors for a certain period of time, and desire to take PrEP as part of their comprehensive HIV prevention package. PEP is an emergency ARV regimen, to be taken as soon as possible and within 72 hours after potential HIV exposure, to prevent the establishment of HIV infection. However, low awareness of PrEP and PEP and inadequate service delivery models to enhance HIV testing and uptake of these interventions remain key challenges to overcome. Innovative models such as community-led health services and online platforms have high potential to enable the achievement of UNAIDS 90-90-90 targets and the maximum use of comprehensive HIV prevention package.

Keywords: PrEP, PEP, treatment as prevention

THURSDAY 8 DECEMBER 2016

9.00 - 10.30
Room C

S19: ZOONOSES FROM WILD AND DOMESTIC ANIMALS (PTAT)

Chairpersons :

1. Padet Siriyasatien

2. Sonthaya Tiawsirisup

Invited Speakers :

1. Tawin Inpankaew
" Zoonotic parasites of domestic animals"
Department of Parasitology, Faculty of Veterinary Medicine, Kasetsart University

2. Sonthaya Tiawsirisup
"Update on wildlife zoonotic diseases in Thailand"
Parasitology Unit, Department of Veterinary Science, Chulalongkorn University, Bangkok, Thailand

3. Sangchai Yinsakmongkon
"Molecular characterization of coronaviruses in Lyle's flying fox (*Pteropus lylei*) in Thailand"
WHO-CC for Research and Training on Viral Zoonoses
King Chulalongkorn Memorial Hospital, Bangkok, Thailand
Faculty of Medicine Chulalongkorn University

ZOONOTIC PARASITES OF DOMESTIC ANIMALS

Tawin Inpankaew [1]

[1] *Department of Parasitology, Faculty of Veterinary Medicine, Kasetsart University, Bangkok, Thailand*

Domestic animals, particularly dogs and cats are susceptible to and excellent carriers for several species of helminthes and protozoa that can cause zoonotic diseases in humans. These parasites include trematode (*Opisthorchis viverrini*, *Schistosoma mekongi*), nematode (*Toxocara canis*, *T. cati*, *Ancylostoma caninum*, *A. ceylanicum*, *A. braziliense*, *Strongyloides sp*, *Gnathostoma spinigerum*, *Ascaris lumbricoides*), cestode (*Echinococcus granulosus*, *Taenia taeniaeformis*, *Spirometra mansoni*) and protozoa (*Giardia duodenalis*, *Cryptosporidium sp*, *Toxoplasma gondii*, *Sarcocystis sp*, *Entamoeba histolytica*, *Blastocystis sp*). Many of these parasites, especially in the larval stage, are capable of invading human tissues causing diseases such as visceral larva migrans and ocular larva migrans. Prominently, dogs and cats may also act as definitive reservoir hosts for the adult stages of zoonotic parasites. This review describes the main parasitic zoonoses in Southeast Asia particularly Thailand related to domestic animals (dogs and cats), with particular highlighting on their current epidemiology and evidence for zoonotic transmission. Preventing and controlling zoonotic parasitic infections from domestic animals involves an incorporated multidisciplinary 'One Health' approach requiring cooperation between medical doctor and veterinarian, public health officers and policy makers.

Keywords: zoonotic parasites, domestic animals, dogs, cats, human

UPDATE ON WILDLIFE ZOONOTIC DISEASES IN THAILAND

Sonthaya Tiawsirisup [1]

[1] *Animal Vector-Borne Disease Research Group, Parasitology Unit, Department of Veterinary Pathology, Faculty of Veterinary Science, Chulalongkorn University, Bangkok, Thailand*

Zoonotic diseases are diseases and infections which are naturally transmitted between vertebrate animals and humans. Wildlife serves as important amplifying or reservoir host involved in the outbreak and transmission cycle of zoonotic diseases. Arthropod vectors also play important roles in the ecology of vector-borne zoonotic diseases. Japanese encephalitis virus (JEV) is important *Flavivirus* found worldwide, including Thailand. Mosquito distribution and virus infection were investigated in different areas in Thailand. *Culex tritaeniorhynchus* were the most collected mosquitoes from the bird nested area in Pathumthani province from March 2008 to January 2009, and all of them were negative for JEV. *Cx. quinquefasciatus* were the most collected mosquitoes from the bat cave and surrounding area in Lopburi province from May 2009 to April 2010, and all of them were negative for JEV. *Cx. tritaeniorhynchus* were the most collected mosquitoes from the bat habitat and swine farms in Chonburi province from August 2011 to October 2012, and all of them were negative for *Flavivirus*. *Cx. tritaeniorhynchus* were the most collected mosquitoes from duck farms in Sing Buri and Ang Thong province from September 2015 to July 2016, and one mosquito pool was positive for Tembusu virus which is the virus member of the genus *Flavivirus*. Other important arthropod vectors are ticks – important vectors in the transmission cycle of various zoonotic diseases. *Haemaphysalis lagrangei*, *H. wellingtoni*, and *Rhipicephalus* (*Boophilus*) *microplus* were collected from Khao Chi-on non-hunting area and Banglamung wildlife breeding center, Chonburi province in 2015. *Anaplasma bovis*, *Anaplasma*, *Babesia*, *Ehrlichia*, and *Theileria* were found in these collected ticks.

Keywords: Zoonosis, Wildlife, Vector, Thailand

MOLECULAR CHARACTERIZATION OF CORONAVIRUSES IN LYLE'S FLYING FOX (*PTEROPUS LYLEI*) IN THAILAND

Supaporn Wacharapluesadee [1],
Prateep Duengkae [2],
Sangchai Yinsakmongkon [2],
Thongchai Kaewpom [1],
Apaporn Rodparn [1],
Pattarapol Maneeorn [3],
Thiravat Hemachudha [1]

[1] *World Health Organization Collaborating Centre for Research and Training on Viral Zoonoses, Faculty of Medicine, Chulalongkorn University,*
[2] *Kasetsart University,*
[3] *Department of National Parks, Wildlife and Plant Conservation*

The reported Middle East respiratory syndrome coronavirus and severe acute respiratory syndrome are phylogenetically closely related to the bat coronaviruses (BatCoVs). However, most of BtCoVs were reported from insectivorous bats. The surveillance of BtCoVs in Lyle's flying fox (*Pteropus lylei*) was conducted to characterize strain of CoV and evaluate the risk of transmission to human. *P. lylei* bats were captured monthly during January - December 2012 for detection of BtCoV at three closed areas of Chonburi province, Thailand. BtCoV were detected by nested RT-PCR of RNA-dependent RNA polymerase (RdRp) from rectal swabs of *P. lylei* bats. Sequencing and phylogenetic analysis were performed from positive specimens. From 370 *P. lylei* bats, 69 CoVs were detected, 18.6% prevalence. CoV was detected eight months in a year of the study. Highest recovery of CoV was observed in May and June with 41.0% (16 of 39) and 48.4% (15 of 31) positivity, respectively. Phylogenetic analysis of conserved RdRp gene revealed that detected BtCoV belonged to BetaCoV group D (n=65) and alpha-CoV (n=4). There is no evidence at this time to suggest these viruses pose a threat to human health. Further studied are necessary in order to clearly understand pathogenicity to human or other animals.

Keyworda: Coronavirus, Bat

THURSDAY 8 DECEMBER 2016

9.00 - 10.30
Room D

S20: LEGAL INTERVENTION FOR DISEASE CONTROL IN THE REGION: CASE STUDY IN THAILAND (THE COMMUNICABLE DISEASES ACT) ORGANIZED BY MOPH

Chairperson :

1. Krisada Mahotarn
Department of Disease Control, MOPH

Speakers :

1. Sombat Thanprasertsuk
"Development of the Communicable Diseases Act and Its Enforcement"
Medical Physician, Advisory Level, Department of Disease Control, MOPH
(Abstract not available)

2. Sombat Thanprasertsuk
"Disease Prevention, Detection and Response by using the Communicable Diseases Act"
Medical Physician, Advisory Level, Department of Disease Control, MOPH
(Abstract not available)

3. Rungrueng Kitphati
"Implementation of the Communicable Diseases Act at National and Regional Levels and at Point of Entry (POE)"
Director of Bureau of General Communicable Diseases, Department of Disease Control, MOPH
(Abstract not available)

4. Suthinee Manosamoot
"Development of Subordinate Legislation for Disease Control"
Legal Officer, Practitioner Level Law Center, Department of Disease Control, MOPH
(Abstract not available)

THURSDAY 8 DECEMBER 2016

9.00 - 10.30
Room E

S21: NEW TOOLS IN MEDICAL ENTOMOLOGY

Chairpersons :

1. Ronald Enrique Morales Vargas

2. Jiraporn Ruangsittichai

Invited Speaker :

1. Yutaka Suzuki
" Nanopore sequencing for genotyping pathogens of tropical diseases"
University of Tokyo, Japan

2. Rawadee Kumlert
"Microlandscape of chigger mite on wild rodent ear leaves"
Department of Medical Entomology, Faculty of Tropical Medicine, Mahidol University

3. Noppawan Phumala Morales
"Geographic profile of salivary gland proteins of *Aedes* species and its implications for understanding dengue and chikungunya transmission"
Department of Pharmacology, Faculty of Science, Mahidol University

4. Stephan Karl
"Fine scale mapping of mosquito abundance and its relationship to malaria infections"
Walter and Eliza Hall Institute of Medical Research, Australia

5. Jean Piere Dujardin
"The maximum likelihood identification based on morphometric data"
Directeur de Recherches IRD, CIRAD, France

6. Sebastian Dujardin
"True Online Morphometrics - TOM"
École des Technologies Numériques Appliquées, France

NANOPORE SEQUENCING FOR GENOTYPING PATHOGENS OF TROPICAL DISEASES

Yutaka Suzuki [1]

[1] *University of Tokyo*

Nanopore sequencer, MinION, has enabled sequencing analysis without pre-installation of expensive conventional sequencers or pre-requisite of specific skills in biological experiments. Even electric supply is not always necessary, by connecting MinION to a laptop PC. These features of MinION have opened the opportunity to enable precise genotyping of pathogens in tropical diseases in a developing country even in its filed areas. In this study, we attempted genotyping Dengue viruses regarding their serotypes (types 1-4). We directly used serum samples of Indonesian Dengue patients, from which viral genomes were directly amplified by the reverse-transcription-LAMP method in an isothermal reaction condition. We directly used the amplified templates for MinION sequencing allocating one flow cell per sample. We found, although the overall sequencing quality was low (82% sequence identify to the reference genome and the quality value of QV= 10 on average), thereby obtained sequence data could discriminate different serotypes of the viruses, whose genome sequences were diverged with the sequence similarity of 70%, with the overall accuracy of 98%. To further examine whether MinION sequencing can be also applied for detecting SNVs, we conducted genotyping of presumed drug resistance-causing SNVs in malaria parasites, *Plasmodium falciparum*. We similarly subjected ten PCR amplicon-mixes covering these SNVs to the MinION sequencing. In spite that the sequence alignments generated by representative alignment programs showed that the average sequence identity was 80%, we found that the mutations at a particular position could be called by the accuracy of 90%, when all the reads covering the corresponding positions were collectively evaluated. Taken together, we provide the first simple experimental and analytical MinION sequencing procedure, which can be easily followed in a developing country to effectively genotype pathogens of tropical diseases.

Keywords: On-site sequencing Genome technology Genotyping of pathogens

MICROLANDSCAPE OF CHIGGER MITE ON WILD RODENT EAR LEAVES

Rawadee Kumlert[1],
Chamnarn Apiwathnasorn[1],
Suchada Sumruayphol[1],
Piengchan Sonthayanon[2],
Anchana Prasartwit[3],
Daniel H Paris[4],
Tippawan Anantatat[4], Ivo Elliott[5],
Paul Newton[5], Serge Morand[6],
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[6] *Institut des Sciences de l'Evolution de Montpellier (ISEM), Université de Montpellier, 163 rue Auguste Broussonnet, Montpellier, 34090, France*

Wild rodents are the major natural hosts of chigger mites, the vector of scrub typhus disease. Rodent trapping is the main method of chigger survey because it can reveal the species diversity and population density of chigger mite in the surveillance area. Either much or less, a number of chigger are usually found on the rodent ear leaves causing some questions to inter- and intraspecific interaction among the chigger mite species on micro-landscape of the ears which might relate to potential of horizontal transmission of pathogen among chigger mite individuals. This study was used 18 rodent ear leaves which obtained from a rodent collection from Vientiane, Laos. All ear leaves has naturally attached chigger mites. The micro-landscape image had been processed by using the combination set of high magnified stereo microscope (400X), multilayer photography and picture merging software. The micro-landscape of rodent ear leaf was classified to 3 zones as; 1) Outer zone comprised of helix, antihelix, and lobule, 2) Middle zone comprised of bridge, and concha, and 3) Inner zone comprised of supratragus, tragus, intertragic incisures and external auditory canal. Each ear leaf, about fourteen chigger mites were stratified selected for species identification according to 3 zones ear leaf. Diversity and specific micro-landscape of the species was analyzed. The result showed that there were 10 species of chigger mites, those were; *Ascoschoengastia indica*, *Blankaartia acoscutellaris*, *Gahrliepia elbeli*, *G. marshi*, *Walchia alpestris*, *W. ewingi lupella*, *W. isonychia*, *W. micropelta*, *Leptotrombidium deliense* and *Schoengastia kanhaensis*. The chigger mite attached to ear leaf with 2 characters, individually and clustered. The chigger mites were usually clustered attached on ear leaf. Among 222 studied chiggers, there were 123 chiggers which same species of chigger mite were attached together whereas the other 23 chiggers were composed of difference species. The clustered attachment behavior of chigger mites might relate to presenting of mite islands in rodent foraging areas or might be clustered after settlement on host. The future study in host attached behavior of chigger mite is needed.

Keywords: chigger mite, landscape, rodent ear

GEOGRAPHIC PROFILE OF SALIVARY GLAND PROTEINS OF *AEDES* SPECIES AND ITS IMPLICATIONS FOR UNDERSTANDING DENGUE AND CHIKUNGUNYA TRANSMISSION

Noppawan Morales [1],
Ronald Enrique Morales Vargas[2],
Natthinee Jiraphan [1],
Yutthana Samang [2]

[1] *Department of Pharmacology, Faculty of Science, Mahidol University,*
[2] *Department of Medical Entomology, Faculty of Tropical Medicine, Mahidol University*

Salivary gland and salivary protein components of mosquitoes have been implicated in blood feeding behavior and the capacity of virus transmission. The Aedes species are important vector for dengue, chikungunya and other arboviruses. Therefore, in this study, the component of salivary gland extracts from 3 major species of Aedes species; *Ae. aegypti*, *Ae. albopictus* and *Ae. scutellaris* in several geographic regions of Thailand were studied. One hundred salivary glands were extracted and separated using one dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Protein bands were in-gel digested by trypsin. The peptides extracted from the gel were analyzed through liquid chromatography-tandem mass spectrometry (LC-MS/MS) followed by performing, the MASCOT search engine to identify proteins with NCBI database. All of the 3 species presented 3 protein bands with high abundance at 27 kDa, 35 kDa and 63 kDa, which were identified as proteins involved in antagonizing the host's hemostasis and immune system. The other proteins bands were different in term of quality and quantity among species, for example, high intensity protein band of 48 kDa was detected in Ae. aegypti, but not in Ae. scutellaris. In general, the salivary gland protein bands in the same species were conserved. However, the salivary gland protein of Ae. aegypti in the Southern part of Thailand are distinctive. The implications of the salivary gland protein profile on virus transmission will be discussed.

Keywords: *Aedes* species, salivary gland protein

FINE SCALE MAPPING OF MOSQUITO ABUNDANCE AND ITS RELATIONSHIP TO MALARIA INFECTIONS

<u>Stephan Karl</u>[1,2,3], Patchara Sriwichai[4], Wuelton Marcelo[5], Yudthana Samung, Vanderson Sampaio[5], Such ada Sumruayphol, Joabi Nascimento[5], Kirakorn Kiattibutr, Marcus Lacerda[5], Liwang Cui, Jetsumon Sattabongkot[6], Ivo Mueller1 [3]

[1] *Population Health and Immunity Division, Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia.*
[2] *Vector-borne Diseases Unit, Papua New Guinea Institute of Medical Research, Madang, Papua New Guinea*
[3] *Department of Medical Biology, Melbourne University, Melbourne, Australia.*
[4] *Mahidol, Department of Medical Entomology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand.*
[5] *Fundação de Medicina Tropical Doutor Heitor Vieira Dourado, Manaus, Brazil*
[6] *Mahidol Vivax Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand.*

This study was aimed at associating peri-domestic mosquito capture rates with concurrently occurring malaria parasite infections in two different transmission settings i) a village on the Thai-Myanmar Border and ii) three suburbs in Manaus in the Brazilian Amazon. In both transmission settings *P.vivax* is the dominant species, and occupational exposure is believed to be the main source of infection. The importance of peri-domestic transmission in these settings is unclear, yet has significant implications on the effect of various malaria control strategies. This study was intended to gain some insight into the associations between peri-domestic mosquito abundance and infection, and simultaneously occurring infections in humans. The studies differed substantially in methodology. In Thailand, an extensive longitudinal malaria survey was conducted; however, only clinical, symptomatic malaria cases (n=…) were recorded between 2011 and 2015. Mosquitoes were collected longitudinally in households in the same village using CDC light traps. In Brazil all individuals enrolled in a longitudinal cohort (n=1214) were screened for infection on a monthly basis for 13 months in 2013 and 2014 using PCR techniques. Mosquitoes were collected once in the majority of study households during this time. Strong spatial clustering of malaria cases was evident in both sites. However, peri-domestic mosquito abundance was in general not spatially correlated with clinical malaria infections both, in Thailand and in Brazil, although there was a clear overall seasonal association between peri-domestic *Anopheles spp*. (but not *Culex spp*.) abundance and incidence of clinical infections in Thailand. In contrast, asymptomatic malaria infections were significantly spatially correlated with mosquito positivity in Brazil. In particular, parasites detected in blood-fed *Culex spp*. mosquitoes were a good proxy for asymptomatic infections in the same and neighbouring households. The present study analysed entomology and epidemiology data, collected at the same time. from 2 different transmission settings. We present evidence for peridomestic transmission in both settings. In addition, mosquito surveillance, in particular the approach to screen the bloodmeals of non-malaria transmitting species (i.e., Culex), may offer a promising opportunity to complement epidemiological surveillance in the human population.

Keywords: malaria, mapping, transmission, Thailand, Brazil

THE MAXIMUM LIKELIHOOD IDENTIFICATION BASED ON MORPHOMETRIC DATA

Jean-Pierre Dujardin[1],
Sebastien Dujardin[2],
Dramane Kaba[3],
Soledad Santillan-Guayasamin[4],
Anita G. Villacis[4],
Sitha Piyaselakul[5],
Suchada Sumruayaphol[6],
Ronald Morales Vargas[6]

[1] *UMR 177, INTERTRYP, CIRAD-IRD, Baillarguet, France,*
[2] *ETNA,*
[3] *IPR, Bouake, Costa de Marfil,*
[4] *PUCE, Quito, Ecuador,*
[5] *Faculty of Medicine, Mahidol University, Bangkok, Thailand,*
[6] *Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand*

To distinguish species or populations using morphometric data is generally processed through multivariate analyses, in particular the discriminant analysis. We explored another approach based on the maximum likelihood method. Simple statistics based on the assumption of normal distribution at a single variable allows to compute the chance of observing a particular data (or sample) in a given reference group. When data are described by more than one variable, the maximum likelihood (MLi) approach allows to combine these chances to find the best fit for the data. Such approach assumes independence between variables. The assumptions of normal distribution of variables and independence between them are uncommon in morphometrics, but improvements may be obtained after some mathematical transformations. Provided there is strict anatomical correspondence of variables between unknown and reference data, the MLi classification produces consistent classification. We explored this approach using various input data, and compared validated classification scores with the ones obtained after the Mahalanobis distance-based classification. The simplicity of the method, its fast computation, performance and versatility, make it an interesting complement to other classification techniques.

Keywords: Morphometrics, Classification, Maximum likelihood, Mahalanobis distance

TRUE ONLINE MORPHOMETRICS - TOM

Dujardin Sebastien[1],
Charles Vienne[1],
Jean-Pierre Dujardin[2]

[1] *Ecole des Technologies Numériques Appliquées, Paris, France.,*
[2] *Institut de Recherches pour le Développement, INTERTRYP, Montpellier, France.*

Short Summary: TOM is a cross-platform Web Application that will give a 24/7 access to the complete geometric morphometric (GM) toolbox. No downloads, no configurations required. TOM presents at the moment 2D images import and online digitization procedure (landmarks and outlines). It runs mathematical analysis such as Procrustes superposition, Elliptic Fourier analyses, multivariate analyses, maximum likelihood classification, etc. It helps managing input and output data (edit, delete, export) and offers a forum in order to develop a community of GM users. Expected to be implemented soon are: an image bank, an automatic outlines digitization, computer assisted semi-landmarks digitization, and the ability for users to share and transfer their data publicly and among themselves.

Keywords: Geometric Morphometrics cloud web

THURSDAY 8 DECEMBER 2016

11.00 - 12.30
Room A

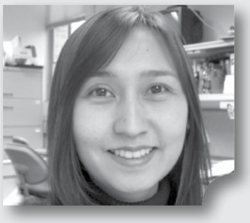
S22: PLASMODIUM VIVAX: LIVER STAGE CONSORTIUM ORGANIZE BY CENTER FOR INFECTIOUS DISEASE RESEARCH, USA

Chairpersons :

1.Sebastian Mikolajczak

2. Brice Campo

Invited Speakers :



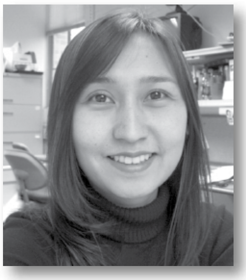
1. Rapatbhorn Patrapuvich
"Challenges for *P. vivax* liver stage study"
Mahidol Vivasx Research Unit (MVRU) Faculty of Tropical Medicine, Mahidol University

2. Rays H.Y. Jiang
"Swim, settle and move-on - using cutting edge genomics and bioengineering to uncover liver stage *P. vivax* infections"
(Abstract not available)

3. Nil Gural
"Deciphering the biology of *Plasmodium vivax* via an in vitro platform"
Harvard-MIT Department of Health Sciences and Technology, Institute for Medical Engineering and Science, Massachusetts Institute of Technology MIT

4. Erika Flannery
"Testing prophylactic and radical cure activity of drugs against liver-stage *Plasmodium vivax* and P. *falciparum* in a humanized mouse model"
Center for Infectious Disease Research, Seattle WA

CHALLENGES FOR *P. VIVAX* LIVER STAGE STUDY



Rapatbhorn Patrapuvich [1]

[1] *Mahidol Vivax Research Unit (MVRU) Faculty of Tropical Medicine, Mahidol University*

The most challenge for eliminating *P. vivax* malaria is developing interventions to eradicate the dormant hypnozoites. Although hypnozoites were first discovered in 1982, very few advancements have been made to understand their composition and biology. This is mainly due to the lack of a continuous in vitro culture system; unlike *P. falciparum*, research on *P. vivax* parasites requires 1) access to infected patients in endemic countries and 2) a regular supply of reticulocytes. Very limited supply of *P. vivax* sporozoites is also a major obstacle in developing hypnozoite model. With support from BMGF, several liver stage models have been developed, including a simple in vitro HC-04 cell line and primary human hepatocyte models (both in microfluidic bilayer device and in a micropatterned co-cultures, MPCC). However, long-term culture of primary human hepatocytes is still limited and required improvement to sustain hepatic functions in vitro. An in vivo humanized mouse model is another advancement of *P. vivax* liver stage study that also has been used to accelerate drug and vaccine discovery against *P. vivax* hypnozoites.

DECIPHERING THE BIOLOGY OF *PLASMODIUM VIVAX* VIA AN IN VITRO PLATFORM

Nil Gural[1], Sandra March[1,3],
Jetsumon Sattabongkot[2],
Sangeeta N. Bhatia [1,3,4]

[1] *Harvard-MIT Department of Health Sciences and Technology, Institute for Medical Engineering and Science, Massachusetts Institute of Technology (MIT)*
[2] *Mahidol Vivax Research Unit, Faculty of Tropical Medicine Mahidol University*
[3] *Broad Institute*
[4] *Howard Hughes Medical InstituteMIT*

Liver stage malaria is an attractive target for all Plasmodium species since it provides the opportunity to attack the parasite at an early, obligate, yet clinically silent stage. Of the 4 strains of malaria that infects humans, *Plasmodium vivax* (*P. vivax*) is the most frequent and widespread cause of human malaria and poses unique challenges to treatment and eradication because liver stage parasites can develop into dormant small forms, hypnozoites, that remain in this state for prolonged periods. This strain of malaria causes chronic,relapsing infection months to years after the initial infection via reactivation of hypnozoites. Drug discovery could be informed by targeting the hypnozoite stage, however the biology behind hypnozoite formation and reactivation remains to be elucidated. In vitro platforms for studying *P. vivax* are lacking because of challenges associated with keeping primary human hepatocytes phenotypically stable over the long periods of time required for studying dormant parasites. Benefiting from the longevity of our micropatterned primary human hepatocyte cultures, we were, for the first time, able to culture *P. vivax* hypnozoites in vitro. To validate the system as an in vitro surrogate for *P. vivax* biology applications, we have shown (1) complete *P. vivax* liver stage development, including release of merozoites and subsequent infection of overlaid reticulocytes and (2) formation, persistence and reactivation of hypnozoites. Using the system as a potential discovery tool, we presented evidence of differential drug sensitivity of schizonts and hypnozoites towards both clinically available and yet-indevelopment liver-acting drugs.

Keywords: malaria, vivax, liver stage, hypnozoite

Erika Flannery [1],
Niwat Kangwanrangsan [2],
Matthew Fishbaugher [1],
Mary Jane Navarro [1],
Sean Murphy [3],
Jetsumon Sattabongkot [2],
Sebastian Mikolajczak [1],
Stefan Kappe [1]

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[3] *University of Washington, Division of Infectious Diseases, Seattle WA*

TESTING PROPHYLACTIC AND RADICAL CURE ACTIVITY OF DRUGS AGAINST LIVER-STAGE *PLASMODIUM VIVAX* AND *P. FALCIPARUM* IN A HUMANIZED MOUSE MODEL

The liver-stage of the malaria parasite is an extreme bottleneck in the Plasmodium life cycle. Only a few parasites infect the liver, proceed to develop through schizogony and produce tens of thousands of parasites that can invade the blood stream. Targeting the liver-stage of the malaria life cycle averts blood-stage infection and thereby prevents disease, parasite transmission and decreases the threat of drug resistance. Additionally, elimination of the persistent P. vivax liver form, the hypnozoite, prevents relapse of infection. Currently pre-clinical compounds are tested in the rodent malaria chemoprophylactic model, which modestly predicts efficacy against the human malaria parasites *P. vivax* and *P. falciparum* and cannot test activity against persistent hypnozoites. Thus, to enable studies with the human malarias we used an immunocompromised and fumarylacetoacetate hydrolase-deficient mouse which allows for human hepatocyte engraftment (FRG huHEP) to test drug efficacy against *P. vivax* and *P. falciparum*. The FRG huHEP model supports complete liver-stage development similar to human infection. P. vivax hypnozoites develop and persist in this model and subsequent asexual blood-stage infection can be achieved in both species. In this model, single-dose primaquine treatment at one day after sporozoite inoculation results in complete ablation of liver infection by hypnozoites and replicating schizonts. Yet, single-dose treatment at day 4 only decreases the number of replicating liver-stage schizonts present by 2- or 7 -fold for *P. falciparum* and *P. vivax*, respectively. In *P. vivax* the number of hypnozoites are reduced by 1.2-fold. These data highlight the importance of compound stage of action and parasite clearance for prospective antimalarials. To test compounds for radical cure activity we established a long term persistence model for *P. vivax* hypnozoites. Five day treatment with primaquine clears established hypnozoites, demonstrating radical cure activity. Testing of new drugs in the FRG huHEP model is ongoing and will be discussed.Therefore, the FRG huHEP model can be used to identify prophylactic compounds that prevent liver-stage Plasmodium infection as well as radical cure compounds that clear the persistent hypnozoites of *P. vivax*. The model also allows for testing stage of action of these compounds to assist in the evaluation of potential antimalarial combination therapies.

Keywords: *Plasmodium vivax* falciparum liver drug

THURSDAY 8 DECEMBER 2016

11.00 - 12.30
Room B

S23: VECTOR BORNE DISEASES & OTHER TROPICAL DISEASES (FREE PAPER)

Chairpersons :

1. Weerapong Phumratanaprapin

2. Pornsawan Leaungwutiwong

Speakers :

1. Alexandra Wharton-Smith
"The challenges of managing dengue: an ethnographic study to explore how clinical practice guidelines are used at a hospital in Malaysia"
London School of Hygiene & Tropical Medicine, UK

2. Howoo Nam
"Development of RDT kit to detect anti-Zika virus antibody using monoclonal antibodies to the envelope and non-structural protein 1 of Zika virus"
College of Medicine, Catholic University of Korea, Korea

3. Suradej Siripattanapipong
"The study of recombinant proteins for the development of Leishmania martiniquensis diagnostic tool"
Faculty of Science, Mahidol University, Thailand

4. Sindhuprava Rana
"Computational 3-D QSAR Pharmacophore model of Novel Lead against Leishmania cathepsin-B like cysteine protease (CPC)"
RMRIMS (ICMR), India

5. Vianney Tricou
"Overview of Takeda's tetravalent dengue vaccine (TDV) candidate development program"
Takeda Vaccines Pte Ltd, Singapore

6. Toshio Hattori
"Increased incidence of HIV and drug resistant tuberculosis in the Philippines"
KIBI International University, Japan

THE CHALLENGES OF MANAGING DENGUE: AN ETHNOGRAPHIC STUDY TO EXPLORE HOW CLINICAL PRACTICE GUIDELINES ARE USED AT A HOSPITAL IN MALAYSIA

Alexandra Wharton-Smith [1],
Lucy Chai See Lum [2],
Ee Chin Loh [2], Loraine Bacchus [1],
Judith Green [3]

[1] *London School of Hygiene & Tropical Medicine,*
[2] *University of Malaya,*
[3] *King's College*

Background: Dengue is a major cause of morbidity and infectious disease mortality in Malaysia. The diagnosis and management of dengue remain a challenge; to date there is insufficient evidence to inform optimal clinical management; and existing World Health Organization and national guidelines are often not utilised.

Objectives: 1) To understand the current management of dengue at hospital in Malaysia; 2) To draw on implementation theories and empirical findings to design an intervention to facilitate improved case management; 3) To pilot the intervention and determine its feasibility and acceptability and 4) To make recommendations based on the findings that could enhance dengue case management.

Methods: The study site is an urban hospital in Malaysia that experiences high numbers of dengue cases. Doctors, nurses and other key hospital staff involved in managing dengue patients will be purposively sampled. Data collection, starting in September 2016, will draw on ethnographic, qualitative methods including direct observation, interviews and focus group discussions. Field notes and verbatim transcripts of the interviews and focus group discussions will be analysed using a modified thematic content analysis approach.

Conclusions: There is a need to understand how dengue case management occurs in practice and the role of guidelines, with attention to facilitators, barriers, and aspects of management which could be strengthened. The findings from this research could be applicable to other tertiary care settings.

Keywords: Dengue, clinical practice guidelines, Malaysia

DEVELOPMENT OF RDT KIT TO DETECT ANTI-ZIKA VIRUS ANTIBODY USING MONOCLONAL ANTIBODIES TO THE ENVELOPE AND NON-STRUCTURAL PROTEIN 1 OF ZIKA VIRUS

Howoo Nam [1], Hye-Jin Ahn [1],
Chom-Kyu Chong[2],
Pan Kee Bae[3], Tong-Soo Kim [4],
Sung-Jong Hong [5], Ronaldo Dias[6]

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[2] *Genbody Inc., Cheonan, Chungnam 330-714, Korea,*
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[4] *Dept of Parasitology, Inha University, Incheon 400-711, Korea,*
[5] *Dept of Medical Environmental Biology, Chung-Ang University, Seoul 156-756, Korea,*
[6] *BahiaFarma Diagnostics, Simoes, Bahia, Brazil*

The WHO has declared Zika virus (ZIKV) a global health emergency, underscoring an urgent need to diagnose the infection and manage the disease. Here, we present a development of highly sensitive and specific RDT to detect serum IgG and IgM against ZIKV. Nitrocellulose membrane of the kit was mounted serially with a buffer pad with a buffer applying hole, a conjugate pad of the complex of envelope and non-structural protein 1 of ZIKV with gold-conjugated mouse monoclonal anti-envelope/non-structural protein 1 antibodies, a sample loading hole, a test line of mouse monoclonal anti-human IgG or IgM antibodies, a control line of goat anti-mouse IgG antibody, and a absorbance pad. Comparing to the sera of the Anti-Zika Mixed Titer Performance Panel (BahiaFarma, Brazil) through ELISA and PRNT (plaque reduction neutralization test), RDT of this study showed 100% agreement with the result of the Panel in both IgG and IgM detection. Furthermore, applying patient sera of 300 IgG positive and 150 IgM positive to ZIKV by ELISA (from Hospital Gaffee e Guinle, Brazil) with 300 negative Korean, RDT showed sensitivity of 99.0% (297/300) and specificity of 99.3% (298/300) in IgG detection and sensitivity of 96.7% (145/150) and specificity of 98.7% (296/300) in IgM detection. This monoclonal antibody based RDT presents an utmost promising diagnostic method of ZIKV infection conveniently and economically.

Keywords: Zika virus, envelope- and non-structural protein 1- specific monoclonal antibodies, IgG/IgM RDT

THE STUDY OF RECOMBINANT PROTEINS FOR THE DEVELOPMENT OF *LEISHMANIA MARTINIQUENSIS* DIAGNOSTIC TOOL

Suradej Siripattanapipong[1],
Kato Hirotomo [2],
Peerapan Tan-ariya [1], Mathirut Mungthin [3],
Saovanee Leelayoova [3]

[1] *Department of Microbiology, Faculty of Science, Mahidol University, Thailand,*
[2] *Division of Medical Zoology, Department of Infection and Immunity, Jichi Medical University, Japan,*
[3] *Department of Parasitology, Phramongkutklao College of Medicine, Thailand*

Leishmania *martiniquensis* is a causative agent of cutaneous and visceral leishmaniasis in humans and animals. This organism was firstly reported in Martinique Island which has now been reported as an emerging infectious agent in Thailand and Myanmar. Symptomatic cases of L. martiniquensis infection in humans have been continuously increased. The possibility of asymptomatic infection of this novel species is being high which become seriously concerns from national public health policy. Due to the lack information of its biology and epidemiology, good surveillance systems and effective diagnostic tools are urgently needed for early detection, accurate case finding, and treatment. In this study, we determined the sequences of Kinesin 39 (K39), Heat-shock protein 70 (hsp70), Heat-shock protein 83 (hsp83), and Glycoprotein 63 (gp63) obtained from four target regions of *L. martiniquensis* and expressed recombinant proteins to evaluate the sensitivity and specificity for detecting antibody against *L. martiniquensis* in patient serum. Compared with *L. donovani*, the nucleic acid sequences similarity and amino acid sequences homology of these regions were 75.4%, 93.9%, 93.7%, 80% and 60.8%, 92.5%, 88.1%, 72.5%, respectively. The results from western blot analysis suggested that K39 recombinant protein is the most promising protein for further developing of *L. martiniquensis* diagnostic tool.

Keywords: Leishmaniasis Leishmania martiniquensis Diagnostic tool

COMPUTATIONAL 3-D QSAR PHARMACOPHORE MODEL OF NOVEL LEAD AGAINST LEISHMANIA CATHEPSIN-B LIKE CYSTEINE PROTEASE (CPC)

Sindhuprava Rana [1], Rani Mansuri [2], Ganesh Chandra Sahoo [1], Surendra Sarsaiya [3], Pradeep Das [1]

[1] *RMRIMS,*
[2] *NIPER,*
[3] *SSS University*

The treatment option of VL and PKDL patients in Bihar India is very limited since last 50 years the best treatment has been based on pentavalent antimonials but shown frequent protozoal resistance. Amphotericin B, paromomycin and miltefosine (second line drugs) are the other alternatives, but these drugs have also failed to the desired requirements of a safe drug. For this discovery of novel leads have to be developed to overcome this limitation. It is reported that cysteine protease activity was considerably greater in the mammalian amastigote form than the promastigote forms that live in the sand fly vector. This suggested that the cysteine proteases are important for survival of the parasite in the mammalian host. For this cathepsin-B like cysteine protease (CPC) has been targeted against different Leishmania strains as it is a major component of the lysosomal proteolytic repertoire and play an important role in intracellular protein degradation. The three dimensional structure of CPC was developed and verified. Then 3-D QSAR Pharmacophore model of collected drugs with their IC50 value was developed, out of 1024 candidates, 10 top pharmacophores selected. Then virtual screening was done by these features against available chemical databases i.e. Asinex, Zinc databases, Pubchem and natural compounds. Out of which 442 compounds were screened with similar features. Then these screened compounds were docked with the modeled and simulated proteins i.e. with CPA, CPB and CPC and best 10 hits showing stronger interaction were selected for In-vitro studies which could be new novel potential compounds act as inhibitors.

Keywords: Leishmania, Cysteine protease, QSAR, Pharmacophore, Inhibitor

OVERVIEW OF TAKEDA'S TETRAVALENT DENGUE VACCINE (TDV) CANDIDATE DEVELOPMENT PROGRAM

Vianney Tricou[1], Kwasi Amfo[1],
Astrid Borkowski [2],
Derek Wallace [2]

[1] *Takeda Vaccines Pte Ltd, Singapore,*
[2] *Takeda Pharmaceuticals International AG, Zurich, Switzerland*

Takeda is developing a live attenuated tetravalent dengue vaccine candidate (TDV) which contains a molecularly characterized attenuated dengue serotype 2 virus (TDV-2) and three recombinant viruses expressing pre-membrane (prM) and envelope (E) structural genes for serotypes 1, 3 and 4 in the attenuated TDV-2 backbone. To date, more than 3500 participants have been vaccinated using TDV in completed and on-going phase 1 and 2 clinical studies in both endemic and non-endemic countries. These studies have not raised any safety concerns. They have demonstrated that in vaccinated adults and children as young as 1.5 years a single dose of TDV or two doses 90 days apart induces robust neutralizing antibody responses against all four DENV, irrespective of prior dengue exposure. TDV also elicits cross-reactive T cell-mediated responses, which may contribute to protection against dengue. Different TDV candidate formulations have been shown to have acceptable safety and immunogenicity profiles which supports the continuing clinical development of TDV.

Keywords: live attenuated tetravalent dengue vaccine, children, immunogenicity, safety

INCREASED INCIDENCE OF HIV AND DRUG RESISTANT TUBERCULOSIS IN THE PHILIPPINES

Toshio Hattori [1]

[1] *KIBI International Univesrity*

In 2014, the incidence of TB in the Philippines is 288/100,000 and 2% of new cases and 21% of retreatment cases are multi-drug resistant TB (MDR-TB). The rate of HIV infection has been rising alarmingly over the past seven years in the subpopulation of men who have sex with men (MSM) in the Philippines. In June 2016, there were 841 new HIV antibody sero-positive individuals reported to the HIV/AIDS & ART registry of the Philippines. We successfully introduced Xpert MTB/RIF (GeneXpert) in San Lazaro Hospital (SLH), a government hospital for infectious diseases in Manila, since the later part of December 2011 up to the present. Cured rates among enrolled GeneXpert positive cases (Rifampicin resistant-TB, RR-TB) was 47% (84 among 179 cases) in 2012 and 46% (51 among 112 cases) in 2013, respectively. In 2015, total numbers of GeneXpert examined cases were 1052 cases, and 122 RR-DR cases (11.6%) were found. Among them, ninety cases (74%) were enrolled in the study. The reasons for non-enrollment were death (8%), refusal (9%) and lost (7%). During treatment, hypokalemia (2 cases) and behavior changes (1 case) were reported to FDA. In RR-TB patients, the number of HIV+ cases were 1 (2011), 6 (2012, 3), 11 (2014) and 14 (2015), respectively. Mortality rate is high ranging from 42%-66%. Lately, increasing rate of lost to follow-up was noted; the only reason identified was compounded adverse drug reactions of MDR-TB medications with antiretroviral drugs. Providing information on drug adverse reactions to patients as well as doctors is necessary.

Keywords: Tuberculosis, HIV, drug-resistant, Rifampicin, GeneXpert

THURSDAY 8 DECEMBER 2016

11.00 - 12.30
Room C

S24: WHAT CAN WE LEARN FROM PROTEOMICS ANALYSIS BY MASS SPECTROMETRY?

Chairpersons :

1. Sasipa Tanyaratsrisakul

2. Supachai Topanurak

Invited Speakers :

1. Sittiruk Roytrakul
"Mass spectrophotometry for peptidome and proteome research"
National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency, Thailand
(Abstract not available)

2. Markus Winterberg
"A proteomics approach to scrub typhus"
University Oxford/Nuffield, Department of MedicineMahidol-Oxford Tropical Medicine, Research Unit Bangkok, Thailand

3. Duangnapa Kovanich
"Proteomics Meets Cellular Signaling"
Institute of Molecular Biosciences, Mahidol University

MASS SPECTROPHOTOMETRY FOR PEPTIDOME AND PROTEOME RESEARCH

Sittiruk Roytrakul[1]

[1] *Proteomics Research Laboratory, Genome Technology Research Unit, National Center for Genetics Engineering and Biotechnology*

The development of mass spectrometric tools and methods with improved dynamic range, resolution, sensitivity, and accuracy has driven the expansion in the field of peptidomics and proteomics research. Peptide mass fingerprint with high-throughput sample preparation and MALDI-TOF MS analysis allows the identifying peptidome signatures that are potentially useful in detection and classification of human diseases. High taxonomic resolution for microbiological research to the strain level by whole-cell MALDI-TOF MS has been reported. In addition, relative quantitative and subsequent identification of peptidome by nano-LC-MS/MS has been used to understand global peptidome dynamics in a cell, tissue or organism. Label-free relative quantitative approach including protein separation by SDS-PAGE, slicing gels, in-gel tryptic digestion of individual gel pieces and subsequent identification by nano-LC-MS/MS is used to compare protein abundance between samples. Shotgun proteomic analysis is now commonly used to identify protein localization, protein expression, protein complexes, and protein modifications in biological experiments. Additionally, the use of affinity purification to isolate protein complexes under native conditions, followed by mass spectrometry (AP-MS) can identify condition-specific interactions, allowing for a dynamic view of the interactome.

Keywords: Maldi-TOF MS, LC-MS, GeLC-MS, AP-MS, Interactome Supported by National Center for Genetics Engineering and Biotechnology

A PROTEOMICS APPROACH TO SCRUB TYPHUS

Markus Winterberg [1],
Tri Wangrangsimakul [2],
Joel Tarning [1], Daniel Paris [3]

[1] *Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, UK ; Mahidol-Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand,*

[2] *Chiangrai Clinical Research Unit, Chiangrai Prachanukroh Hospital, Chiangrai, Thailand,*

[3] *Mahidol-Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand ; Swiss Tropical and Public Health Institute, Basel, Switzerland*

The challenge for the management of tropical diseases is often not the treatment, but the diagnosis. In many cases, patients have nonspecific symptoms like fever, headache or rash, which can have their origin in bacterial or viral infections. Although the symptoms are similar, the treatment differs between pathogens. Conventionally used diagnostic tools like serology or microscopy may deliver reliable results, but are often only possible in later stages of the infection. Time consuming cultures of the pathogen and sophisticated equipment may be required to deliver a clear identification. Scrub typhus is an example of a disease that is often difficult to diagnose in patients. This zoonotic disease, transmitted by trombiculid mites, is caused by the obligate intracellular bacterium *Orientia tsutsugamushi*. Scrub typhus responds readily to antibiotic treatment but is difficult to differentiate in its early stage from other diseases with similar symptoms, such as dengue, murine typhus or leptospirosis. Using a proteomics approach, we were able to identify novel biomarkers for the diagnosis of scrub typhus. Such biomarkers might be used to develop a non-invasive, field-based rapid test, allowing for early and reliable identification of scrub typhus in patients. Furthermore, the applied proteomics approach enabled a deeper understanding of the underlying disease mechanisms and the immune response to the *Orientia tsutsugamushi* infection.

Keywords: Scrub Typhus, Proteomics, Biomarker

PROTEOMICS MEETS CELLULAR SIGNALING

Duangnapa Kovanich[1]

[1] *Institute of Molecular Biosciences*

Mass spectrometry-based proteomics has become an indispensable tool in the cellular life sciences. Recent advances in proteomics workflow from sample preparation to acquisition of massive amounts of data and bioinformatics analysis have enabled researchers to reveal dynamic and complex cellular signaling networks. We have employed several proteomics techniques to study cAMP signaling in the heart. Several aspects of cAMP signaling were investigated, including identification of cAMP interactome, its molecular environment, and phosphoproteome. Recently, we have integrated proteomics approaches in the study of flavivirus-host interplay. Interaction proteomics has been utilized to gain insight into virus-host protein-protein interactions and cellular signaling involving in virus replication and antiviral host responses.

Keywords: mass-spectrometry based proteomics cAMP signalling virus-host interaction

THURSDAY 8 DECEMBER 2016

11.00 - 12.30
Room D

S25: HEPATITIS B AND C (ORGANIZED BY MOPH)

Chairperson :

Suchada Jiamsiri

Speakers :

1. Mukta Sharma
"Global and Regional Strategy in Viral Hepatitis Prevention and Control"
WHO Country Office Thailand
(Abstract not available)

2. Suchada Jiamsiri
"Moderator, Country Situation and Strategy on Viral Hepatitis Prevention and Control"
Chief of Vaccine Program Development Section, Division of Vaccine Preventable Disease, Department of Disease Control, MOPH
(Abstract not available)

3. Tawesak Tanwandee
"Clinical and Guideline for Treatment for Viral Hepatitis in Thailand"
Department of Medicine, Siriraj Hospital, Mahidol University
(Abstract not available)

4. Kanitsak Chantrapipat
"Guideline on the Support from National Health Security Office for the Treatment of Viral Hepatitis including Access to Medication"
Director of Bureau of Medicine and Medical Supply Management, National Health Security office (NHSO)
(Abstract not available)

THURSDAY 8 DECEMBER 2016

11.00 - 12.30
Room E

S26: MALARIA ELIMINATION: MOBILE POPULATIONS AND BEHAVIOR CHANGES

Chairperson :

Muhammad Shafique

Invited Speakers :

1. Muhammad Shafique
"Malaria Elimination: mobile populations and behaviour changes"
Regional Behaviour Change Communication Specialist
Malaria Consortium, Faculty of Tropical Medicine, Mahidol University

2. Rungrawee Tipmontree
"Malaria Elimination: Mobile populations and behaviour changes, Thailand's perspective"
Bureau of Vector Borne Diseases, Department of Disease Control, MOPH

3. Shreehari Acharya
"Behavior change approach for mobile and migraine population"
Program Officer, Raks Thai Foundation, Thailand
(Abstract not available)

MALARIA ELIMINATION: MOBILE POPULATIONS AND BEHAVIOUR CHANGES

Muhammad Shafique [1]

[1] *Regional Behaviour Change Communication Specialist, Malaria Consortium*

As the malaria programme strategy in the Greater Mekong Sub-region shifts from control to elimination, it requires more effective and context specific behaviour change communication and community engagement approaches to reach out to the key target audience i.e. mobile and migrant populations effectively. For the malaria elimination, innovative and interpersonal communication methods such as positive deviance should be used in order to target the migrant populations who are mostly located in rural areas, work nocturnally and often in highly inaccessible locations. The qualitative assessments conducted by Malaria Consortium in the GMS region suggest that mobile and migrant populations should be targeted at various points/locations in order to engage them better in the malaria programme. Firstly, they need to be equipped with knowledge and preventive tools (mosquito nets) before they leave their point of origin; secondly, they should be targeted at their workplace through volunteers and employers to improve their access to malaria diagnosis and treatment services; and thirdly, those crossing from other countries should have easy access to malaria knowledge (bilingual messages), diagnosis and treatment services across the border. Easy access to health information and free and sufficient distribution of long lasting treated nets should be ensured for the migrant workers at the village or their workplace. Public-private partnerships should be also developed to engage private companies and farm owners to facilitate easy access to malaria services at their workplaces. As the interpersonal communication is the preferred and most appropriate method for migrants, we also need to develop context specific messages and materials to address misconceptions related to malaria and mobilise communities as active partners to ensure their enthusiasm at the wake of diminishing disease.

MALARIA ELIMINATION: MOBILE POPULATIONS AND BEHAVIOUR CHANGES, THAILAND'S PERSPECTIVE

Rungrawee Tipmontree[1]

[1] *Bureau of Vector Borne Diseases, Department of Disease Control, MoPH, Thailand*

With the tremendous progress of malaria control, Thailand has stepped up to eliminate malaria from the country. For Thailand's perspective, migrants and mobile populations have been considered as a vulnerable group to get malaria infection with many risks contributed from socio-economic factors to working and living environments. Considering their mobility behaviors, some interventions are crafted to deal with this group of population. Provision of malaria case management is extended through various activities such as establishment of malaria post and border malaria posts. Conducting of active case finding provides an additional opportunity to reach the service. Enrolling Village health volunteers is recognized as a form of community participation. They are expected to engage and mobilize communities to identify and report the cases in the malaria elimination phase. The interpersonal communication is a key intervention to deliver malaria key messages. Behavior change communication is implemented via tailor-made health education tools, methods, and materials with considering of cultural appropriateness. Bi-lingual tools and materials are developed to overcome language barriers in various forms such as Malaria corners were set up at a place where visibly seen by migrants and mobile population. More effort to overcome language barrier includes having migrant health volunteers to deliver malaria key messages. Since the cross-border activities tend to increase according to the progress of economic, hence cross-border collaboration should be considered as a key to better reach out to mobile and migrants in order to increase their access to malaria prevention and treatment services across the border.

Keywords: BCC, migrants, mobile population, malaria

THURSDAY 8 DECEMBER 2016

12.30 - 14.00
Room C

LOOP MEDIATED ISOTHERMAL AMPLIFICATION (LAMP) FOR TB AND MALARIA LUNCH SEMINAR BY MEDITOP CO.,LTD.

Speaker :

Yasuyoshi Mori
"Basic performance and it's applicatio of TB-LAMP and Malaria-LAMP"
General Manager R & D; eiken chemical

THURSDAY 8 DECEMBER 2016

14.00 - 15.30
Room A

S27: *PLASMODIUM KNOWLESI* : A CURRENT SITUATION IN THAILAND (IN THAI)

Chairpersons :

1. Porntip Petmitr

2. Jeeraphat Sirichaisinthop

Invited Speakers :

1. Somchai Jongwutiwes
"*Plasmodium knowlesi* in humans, Thailand"
Department of Parasitology, Faculty of Medicine, Chulalongkorn University

2. Chaturong Putaporntip
"*Plasmodium knowlesi* in macaques, Thailand"
Department of Parasitology, Faculty of Medicine, Chulalongkorn University

3. Srivicha Krudsood
"How to deal with *Plasmodium knowlesi*?: A Clinical Aspect"
Department of Tropical Hygiene, Faculty of Tropical Medicine, Mahidol University
(Abstract not available)

4. Theerayot Kob-asa
"Transmission and Control of *Plamodium knowlesi*"
Department of Disease Control, MOPH
(Abstract not available)

PLASMODIUM KNOWLESI IN HUMANS, THAILAND

Somchai Jongwutiwes [1], Chaturong Putaporntip [1]

[1] *Molecular Biology of Malaria and Opportunistic Parasites Research Unit, Department of Parasitology, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand*

Naturally acquired human infections with *Plasmodium knowlesi* are endemic in Southeast Asia. Our previous survey in 2006-2007 has shown a wide-spread and low prevalence of *P. knowlesi* in Thailand, accounting for 0.57% of all malaria cases identified. The follow-up study in the same endemic areas in 2008-2009 and a retrospective analysis of malaria species in patients' blood samples from one of these endemic areas collected in 1996 have shown that *P. knowlesi* contributed 0.67% and 0.48%, respectively, indicating that this simian malaria is not newly emergent human pathogen in Thailand. Sequence analysis of the complete merozoite surface protein-1 gene of *P. knowlesi* (Pkmsp-1) from human and macaque blood samples has revealed considerable genetic diversity among isolates. Importantly, the Pkmsp-1 sequence from one patient was identical to that from a pig-tailed macaque living in the same locality, suggesting potential cross-transmission of *P. knowlesi* from naturally infected macaques to humans. The number of haplotypes, haplotype diversity, nucleotide diversity and recombination sites of human-derived sequences exceeded that of monkey-derived sequences. Phylogenetic networks based on concatenated conserved sequences of Pkmsp-1 displayed a character pattern that could have arisen from sampling process or the presence of two independent routes of *P. knowlesi* transmission, i.e. from macaque to human and from human to human in Thailand. Importantly, recent life-threatening and fatal infections occurring in Thai patients have highlighted the clinical significance of this simian malaria in this country.

Keywords: *Plasmodium knowlesi*, Humans, Thailand

PLASMODIUM KNOWLESI IN MACAQUES, THAILAND

Chaturong Putaporntip [1],
Somchai Jongwutiwes [1]

[1] *Molecular Biology of Malaria and Opportunistic Parasites Research Unit, Department of Parasitology, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand*

The emergence of naturally acquired human infections caused by *Plasmodium knowlesi* in Southeast Asia has emphasized the public health importance of zoonotic malaria in this region. Both long-tailed *(Macaca fascicularis*) and pig-tailed *(M. nemestrina*) macaques that are prevalent in Southeast Asian countries including Thailand serve as main natural hosts for P. knowlesi. To explore the potential risk of macaques as reservoir hosts of nonhuman primate malaria potentially transmissible to humans, it is crucial to know the prevalence of this simian malaria parasite and those potentially causing human infections among these macaques in Thailand. Because morphological diagnosis of nonhuman primate malaria can be presumptive and some may not be unequivocally determined, we analyzed both the mitochondrial cytochrome b gene sequences and the small subunit ribosomal RNA genes of 297 malaria/Hepatocystis-positive isolates obtained from 987 monkeys comprising 351 long-tailed and 636 pig-tailed macaques. Species assignment is determined from phylogentic tree construction using known sequences of primate malaria available in the GenBank database. All simian malaria parasites known to circulate among these macaques were detected in this study, i.e. *P. knowlesi, P. cynomolgi*, *P. coatneyi*, *P. inui* and *P. fieldi*. A low prevalence of *P. knowlesi* in both macaque species was observed, mainly clustering in southern Thailand. It is interesting to note that *P. knowlesi* and *P. cynomolgi* are known to be transmissible to humans under natural infection. Hence, some risks emerge for those living in vicinity of or encroach upon macaques' natural habitats in this region where anopheline vectors are abundant.

Keywords: *Plasmodium knowlesi*, Macaques, Thailand

THURSDAY 8 DECEMBER 2016

14.00 - 15.30

Room B

S28: TRANSLATIONAL RESEARCH: CHALLENGES AND SUCCESSES

Chairperson :

Pongrama Ramasoota

Invited Speakers :

1. Jiro Yasuda
"Development of rapid and portable diagnostic assays for ebola and zika virus diseases"
Department of Emerging Infectious Diseases, Institute of Tropical Medicine, Nagasaki University, Japan

2. Pongrama Ramasoota
"Therapeutic human antibodies against 4 serotypes of Dengue virus"
Department of Social and Environmental Medicine, Faculty of Tropical Medicine, Mahidol University

3. Nat Malainual
"Public-Private-Partnership on Allergen Vaccine Development"
Department of Parasitology, Faculty of Medicine Siriraj Hospital, Mahidol University

(Abstract on pages 171)

DEVELOPMENT OF RAPID AND PORTABLE DIAGNOSTIC ASSAYS FOR EBOLA AND ZIKA VIRUS DISEASES

Jiro Yasuda[1]

[1] *Institute of Tropical Medicine, Nagasaki University*

From 2013 to 2016, the largest outbreak of Ebola virus disease (EVD) since the disease was first reported in 1976 occurred in West Africa. More than 28,000 cases were reported, and more than 11,000 people died from the disease, primarily in Guinea, Liberia, and Sierra Leone. During this outbreak, we developed the reverse transcription-loop mediated isothermal amplification (RT-LAMP) assay for EBOV using a portable device. The validation study in Guinea republic showed that the assay had comparable diagnostic accuracy to that of the reference real-time RT-PCR test for serum samples or oral swabs from suspected EVD cases. In Guinea, a mobile field laboratory with RT-LAMP testing facilities was deployed to improve the laboratory diagnostic abilities in remote areas. The RT-LAMP test can be conducted using a portable and battery-equipped detection system, making it practical for use in the field. Outbreaks of emerging viral diseases have been reported every year in anywhere of the world. Our assay system could be applied to diagnostics for other viral diseases. Currently, we are also developing the laboratory diagnostic test for Zika virus disease.

Keywords: Ebola, Zika, RT-LAMP

THERAPEUTIC HUMAN ANTIBODIES AGAINST 4 SEROTYPES OF DENGUE VIRUS

Pongrama Ramasoota [1,2],
Pannamthp Ptaksajjakul [1,2],
Chonlatip Pipattanaboon [1],
Surachet Benjatummaruk [1],
Khwanchit Boonha [1],
Tadahiro Sasaki [3],
Kazuyoshi Ikuta [3]

[1] *Center of Excellence for Antibody Research (CEAR), Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand,*
[2] *Department of Social & Environmental Medicine, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand,*
[3] *Research Institute for Microbial Diseases (RIMD), Osaka University, Osaka, Japan*

Dengue hemorrhagic fever (DHF) has become the world public health problem, caused 390 million infection patients annually. Until present, there has neither specific drug nor effective vaccine against all 4 serotypes of dengue virus (DENV). Neutralizing monoclonal antibodies (MAbs) against all 4 serotypes of DENV has been developed as one alternative for DENV treatment. Fully human MAb has been considered to be the best treatment in human comparing with mouse, chimeric and humanized MAbs. Using novel SPYMEG myeloma cell fused with peripheral blood mono nuclear cell (PBMC) from acute Dengue infected patients. Twenty hybridoma cells producing neutralizing fully human monoclonal antibody (NhuMAb) has been developed. All 20 NhuMAbs has 90-100 % neutralizing activity against all 4 serotypes of DENV. Three out of 20 NhuMAbs were selected as candidate for further neutralization tested with 20 clinical isolates DENV (5 isolates per each serotype), suckling mice and marmoset monkeys, respectively. All 3 NhuMAbs has neutralizing activity against all clinical isolates DENV better than those against laboratory strain. These 3 candidate NhuMAb could dramatically reduced the mortality of all suckling mice that prior intra-cranially injected DENV. Moreover, among marmoset monkeys that previously injected with 107 DENV, intra-peritoneally. Then 4 hours later, each NhuMAb was injected as DENV treatment to each monkey. Monkeys blood were collected at days 0, 1-7 and checked for amount of DENV. All 3 NhuMAbs could reduce the amount of DENV to be at zero within 2 days comparing with monkeys with no treatment that still has high amount of DENV. As reported by researcher that reducing DENV during viremia phase may reduce the followed severe manifestation of DENV. These 3 candidate NhuMAbs has now been producing in the form that Food and drug administration (FDA) accepted to use in human, by using IgG expression in stable expressed Chinese Hamster Ovary (CHO) mammalian cell. These expressed NhuMAb IgGs will be further clinical trial tested in healthy volunteers in the near future.

Keywords: Dengue virus, Neutralizing human monoclonal antibody, 4 serotypes

THURSDAY 8 DECEMBER 2016

14.00 - 15.30
Room C

S29: LIVER FLUKES AND CHOLANGIOCARCINOMA

Chairperson :

Banchob Sripa

Invited Speakers :

1. Banchob Sripa
"Recent advances in research and control of Liver Flukes and Cholangiocarcinoma"
Khon Kaen University
(Abstract on pages 176)

2. Sirikachorn Tangkawattana
"Animal reservoirs as a source of liver fluke transmission: Roles in control program"
Khon Kaen University
(Abstract on pages 175)

3. Narong Khuntikeo
"Cholangiocarcinoma Screening and Care Program (CASCAP): Health Innovation to Fight the Liver Fluke and Cholangiocarcinoma"
Khon Kaen University
(Abstract on pages 172)

THURSDAY 8 DECEMBER 2016

14.00 - 15.30
Room D

S30: SOUVENIRS FROM AEC

Chairperson :

Yupaporn Wattanagoon

Invited Speakers :

1. Wirongrong Chierakul
"TBA"
Department of Clinical Tropical Medicine, Mahidol University
(Abstract not available)

2. Jittima Dhitavat
"TBA"
Department of Clinical Tropical Medicine, Mahidol University
(Abstract not available)

THURSDAY 8 DECEMBER 2016

14.00 - 15.30
Room E

S31: GENOME EDITING IN TROPICAL MEDICINE

Chairpersons :

1. Thanat Chookajorn

2. Bunpote Siridechadilok

Invited Speakers :

1. Marcus Lee
"New genetic approaches to accelerate antimalarial target identification and validation"
The Wellcome Trust Sanger Institute, UK

2. Philip Shaw
"Application of the glmS riboswitch reverse genetic tool in *Plasmodium spp*"
National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand

3. Weerawat Runguphan
"Harnessing the CRISPR-Cas9 System for Production of Medicinal Compunds"
National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand
(Abstract not available)

GENOME EDITING IN TROPICAL MEDICINE

Genome editing technology has revolutionized research and medicine during the last few years. The ability to quickly manipulate genome with high efficiency allows developments of novel tools and reagents. The technology is on the rise with new techniques including CRISPR-Cas9, TALEN and riboswitch. The techniques have been used to modify key pathogens in Tropical Medicine. Even mosquitoes can be altered to block transmission. Rare and expensive drugs are synthesized inside living organisms based on the genome editing tools. This session aims to present latest genome editing technology and discoveries. Basic background on the technology will be introduced at the start of this session. The participants will learn how to apply the technology in various fields of Tropical Medicine.

NEW GENETIC APPROACHES TO ACCELERATE ANTIMALARIAL TARGET IDENTIFICATION AND VALIDATION

Marcus Lee [1]

[1] *Malaria Programme, Wellcome Trust Sanger Institute, Wellcome Genome Campus, Hinxton, UK*

Our ability to manipulate the genome of the malaria parasite is currently a bottleneck to systematic investigation of *Plasmodium* biology. Application of large-scale molecular genetics would permit rapid mechanistic analysis of novel drug targets, detailed characterization of specific genes and gene families, and would complement genome-wide association studies that pinpoint loci associated with drug resistance and clinical treatment failure. Methods to engineer the *P. falciparum* genome in particular have been hampered by limited tools and inefficiencies in transfection and integration. We are now adapting CRISPR-based systems to more efficiently modify or disrupt individual parasite genes. These approaches include the use of catalytically inactive Cas9 to conditionally regulate gene expression in parasites. CRISPR-interference, which may inhibit gene expression by hindering RNA PolII-mediated transcription, allows the modulation of target gene levels without an initial time-consuming step of integrating regulatable elements or tags at the genomic locus. In addition to simple obstruction of RNA polymerase, we are exploring using Cas9 as a platform to recruit a variety of transcription effector domains to potentiate transcriptional silencing or activation. Ultimately, we aim to better understand how the site of recruitment of the nuclease proteins and the fusion of regulatory domains can modulate gene expression, thereby establishing rules for efficient targeting of the parasite genome. Finally, we are also testing whether the recently described CRISPR enzyme Cpf1, with its [TTTN] PAM specificity, may be adapted for gene editing, increasing our coverage of the extremely AT-biased genome of *P. falciparum*.

Keywords: Malaria, Drug Resistance, CRISPR

APPLICATION OF THE GLMS RIBOSWITCH REVERSE GENETIC TOOL IN *PLASMODIUM SPP*.

Philip Shaw [1]

[1] *National Center for Genetic Engineering and Biotechnology*

Research into new drugs to combat malaria is hampered by the lack of suitable genetic tools for validating drug targets and identifying antimalarial compound mode of action. To address this need, we developed a reverse genetic tool for conditional attenuation of gene expression in *Plasmodium spp.* genes. The glmS riboswitch is a post-transcriptional regulatory element in bacteria that undergoes self-cleavage in a ligand-dependent manner. We applied the riboswitch as a tool by inserting the sequence in the 3¢ untranslated region of target genes by DNA transfection. Efficient, rapid and specific attenuation of target gene expression was observed in genetically modified transgenic parasites following treatment with the riboswitch inducer ligand, glucosamine. To demonstrate how the tool can be applied in antimalarial research, transgenic *P. falciparum* and *P. berghei* parasites lines were generated in which the expression of genes encoding dihydrofolate reductase-thymidylate synthase (DHFR-TS) is controlled by the riboswitch. The DHFR-TS attenuated parasites were specifically hyper-sensitized to antifolate antimalarials, but not other compounds with different modes of action. The riboswitch tool has been applied to study the functions of other *P. falciparum genes*, including novel drug targets (Plasmepsin V, PTEX150 and Falcipain 3) and genes with roles in parasite virulence (REX-1 and PTEX88). The data show that our experimental approach can be used to accelerate discovery of new drug targets and develop antimalarial drugs directed against them.

Keywords: glmS riboswitch; *Plasmodium*; malaria; reverse genetics

HARNESSING THE CRISPR-CAS9 SYSTEM FOR PRODUCTION OF MEDICINAL COMPOUNDS

Weerawat Runguphan[1],
Sutipa Tanapongpipat 1

[1] *Microbial Cell Factory Laboratory, Biodiversity and Biotechnological Resource Research Unit, National Center for Genetic Engineering and Biotechnology, Pathum Thani, Thailand*

Natural products have been exploited for medicinal purposes for thousands of years. Notable examples include the powerful antimalarial drug artemisinin from the sweet wormwood plant and the antiparasitic avermectin from the soil bacteria Steptomyces avermitilis. Recent advances in metabolic engineering and synthetic biology have enabled production of chemicals, including medicine for treatment of tropical diseases, in tractable microbial hosts. By reconstituting the biochemical pathways for the production of these medicinal compounds in a heterologous host, the corresponding compounds can be produced in a scalable manner under a controlled environment. Most famously, the partnership of Amyris and Sanofi has successfully demonstrated microbial production of 35 metric tons—roughly equivalent to 70 million doses—of artemisinin. Despite this unique outstanding success, microbial engineering to encode large biochemical pathways remains challenging. In the past three years, a robust and simple strategy to edit genome has emerged based on CRISPR (clustered regularly interspaced short palindromic repeats) and CRISPR-associated (Cas) genes, which are part of a recently discovered bacterial adaptive immune system. This talk will summarize the applications of the CRISPR-Cas9 system to edit the genomes of microbial production chasses for the production of medicinal compounds and other valuable chemicals.

THURSDAY 8 DECEMBER 2016

16.00 - 17.30
Room A

S32: MALARIA MANAGEMENT IN ASIA (IN THAI)

Chairperson :

Jeeraphat Sirichaisinthop

Invited Speakers :

1. Nipon Chinanonwait
“ประสบการณ์เชิงปัญหา และการแก้ไข”
Director Office of Diseases Prevention Control 1, MOPH
(Abstract not available)

2. Krongthong Thimasarn
“บทเรียนในการจัดการปัญหาไข้มาลาเรียในระดับโลกและภูมิภาคเอเชียอาคเนย์”
Medical Officer Malaria, WHO/ Myanmar

3. Suwich Thammapalo
“มุมมองของเขตสุขภาพ”
The Office of Disease Prevention and Control 12, Songkhla, MOPH
(Abstract not available)

4. Yuthapong Muernrat
“มุมมองจากพื้นที่”
The Office of Prevention and Control Disease Region 11, Nakhon Si Thammarat, MOPH
(Abstract not available)

บทเรียนในการจัดการปัญหาไข้มาลาเรียในระดับโลกและภูมิภาคเอเชียอาคเนย์

Krongthong Thimasarn [1]

[1] *Independent*

การควบคุมไข้มาลาเรียมีประวัติอันยาวนาน มีบทเรียนที่น่ารู้มากมายที่ใช้เป็นข้อคิดสำหรับการดำเนินการจัดการโรคนี้ในปัจจุบัน ในช่วงสงครามโลกครั้งที่ 2 (พ.ศ. 2484-2488) เป็นช่วงที่มาลาเรียคร่าชีวิตชาวโลกมากมาย จนกล่าวกันว่าอาจจะมากกว่าผู้เสียชีวิตจากสงครามก็ได้ ในช่วงนั้นระบบสาธารณสุขของประเทศต่างๆเสื่อมลง ขาดแคลนยา การคมนาคมถูกตัดขาด ฯลฯ นอกจากมาลาเรียแล้วยังมีโรคติดต่อสำคัญหลายโรคที่เป็นปัญหาใหญ่หลวงของมนุษยชาติ หลังสงครามโลกสงบลงมีการก่อตั้งองค์การสหประชาชาติ และต่อมาใน พ.ศ. 2491 องค์การอนามัยโลก (WHO) ถูกก่อตั้งขึ้น จึงได้มีการฟื้นฟูรณรงค์ควบคุมมาลาเรียอย่างจริงจังโดยใช้วิธีที่ทันสมัย (Modern Malaria Control) อาวุธที่ทรงอานุภาพในขณะนั้นได้แก่ ดีดีที (DDT) ที่ได้นำมาใช้สำหรับการพ่นฝาบ้านให้ออกฤทธิ์ตกค้าง (Indoor residual spraying – IRS) ร่วมกับการรักษาผู้ป่วยด้วยยาคลอโรควิน ซึ่งทั้งสองมาตรการได้ผลดีมาก ทุกประเทศพบว่าการป่วยตายจากโรคนี้ลดลงมากจนประเทศต่างๆเริ่มหวังที่จะขยายพื้นที่และมุ่งกวาดล้างไข้มาลาเรีย (Malaria Eradication) ให้หมดไปจากโลก มีการปรับเปลี่ยนยุทธศาสตร์และอบรมบุคลากรอย่างขนานใหญ่ แต่ต่อมาพบว่าโครงการกำจัดมาลาเรียไม่ประสบความสำเร็จตามที่คาด โลกได้เรียนรู้ความซับซ้อนของระบาดวิทยาของไข้มาลาเรีย การปรากฏตัวของเชื้อชนิด Falciparum ที่ดื้อต่อยาคลอโรควิน (ซึ่งในภายหลังยังดื้อต่อยาใหม่อื่น ๆอีกหลายขนาน) ยุงดื้อต่อดีดีทีและสารเคมีชนิดอื่นๆอีกด้วย หลายประเทศที่เคยควบคุมไข้มาลาเรียได้แล้วก็กลับมีมาลาเรียกลับมาระบาดรุนแรง องค์การอนามัยโลกร่วมกับประเทศสมาชิกจึงได้ปรับยุทธศาสตร์กลับมาเป็นโครงการควบคุมมาลาเรียในระยะยาว ในช่วงพ.ศ. 2520-2540 สถานการณ์โรคในประเทศต่าง ๆดีขึ้นบ้างแต่ค่อนข้างช้าเมื่อเทียบกับทศวรรษก่อนๆ โครงการควบคุมไข้มาลาเรียในหลายประเทศประสบปัญหาอุปสรรคคล้ายกันคือขาดแคลนงบประมาณ ขณะเดียวกันประเทศในภูมิภาคอัฟริกาเขตร้อน (Tropical Africa – Sub-sahara Africa) มีสถานการณ์โรคเลวร้ายมากลงมาก คาดว่ามีผู้เสียชีวิตจากมาลาเรียประมาณปีละ 1 ล้านคน ในจำนวนนี้ส่วนใหญ่เป็นเด็กเล็กต่ำกว่า 5 ปี และหญิงมีครรภ์ ในช่วงดังกล่าวมีการค้นพบเทคโนโลยีและวิธีการใหม่มากมาย ตัวอย่างเช่น มุ้งชุบด้วยสารเคมีฆ่าแมลง (insecticide-treated net) ซึ่งต่อมาพัฒนาเพิ่มเติมให้มีอายุใช้งานนานอย่างน้อย 3 ปีโดยไม่ต้องชุบมุ้งซ้ำ มีวิธีการตรวจโลหิตอย่างรวดเร็ว (ด้วย rapid diagnostic test – RDT) ยาผสมอนุพันธุ์อาร์ติมิซินิน (artemisinin-based combination therapy – ACT) แต่ความครอบคลุมของมาตรการเหล่านี้ต่ำมากเนื่องจากขาดงบประมาณ ทำให้ประชากรกลุ่มเสี่ยงต่อโรคมาลาเรียไม่สามารถเข้าถึงบริการได้ จึงไม่เห็นผลต่อสถานการณ์โรค จนถึงพ.ศ. 2541 องค์การอนามัยโลกประกาศเรียกร้องให้มีการระดมทุนเร่งรัดควบคุมไข้มาลาเรีย (Roll Back Malaria initiative) ซึ่งเน้นหนักที่อัฟริกา ต่อมาพ.ศ. 2545 มีการก่อตั้งกองทุนโลกเพื่อต่อสู้โรคเอดส์ วัณโรคและมาลาเรีย (GFATM) นับแต่นั้นมาประเทศต่าง ๆจึงสามารถเร่งรัดเพิ่มความครอบคลุมของมาตรการที่มีประสิทธิภาพเหล่านี้ได้ จากรายงาน World Malaria Report 2015 ขององค์การอนามัยโลกพบว่าในระดับโลกมีอัตราตายลดลง 60% และอัตราป่วยลดลง 37% ในช่วง 15 ปีที่ผ่านมา (พ.ศ. 2543-2558) แต่ในภูมิภาคเอเชียอาคเนย์ขององค์การอนามัยโลกอัตราป่วยและอัตราตายลดลงเพียง 49% ในอนุภูมิภาคลุ่มแม่น้ำโขง (Greater Mekong Sub-region - GMS) สถานการณ์ไข้มาลาเรียลดลงมาก แม้ในประเทศเมียนมาร์(พม่า) ซึ่งพบโรคชุกชุมมากที่สุด คิดเป็น 70% ของทั้งภูมิภาคก็พบสถานการณ์อุบัติการณ์โรคลดลงอย่างชัดเจนภายหลังจากได้รับทุนอุดหนุนอย่างมากจากกองทุนโลกและแหล่งทุนอื่นๆ อย่างไรก็ตามมีปัญหาที่รุนแรงซึ่งพบในภูมิภาคนี้คือ เชื้อฟัลซิปารัมดื้อยามาลาเรียหลายขนานและเริ่มดื้อต่อยา Artemisinin พบตั้งแต่ราวพ.ศ 2549-2550 และมีต้นกำเนิดที่บริเวณชายแดนไทย-กัมพูชา และกำลังแพร่กระจายไปอย่างรวดเร็วตามการเคลื่อนย้ายประชากร จากบทเรียนการแพร่เชื้อดื้อต่อยาคลอโรควินที่แพร่จากจุดกำเนิดเดียวกันนี้ไปแถบอื่นของโลก ทำให้หวั่นเกรงว่าจะเกิดประวัติศาสตร์ซ้ำรอย จึงเกิดแนวคิดที่จะเร่งรัดกวาดล้างเชื้อฟัลซิปารัมให้หมดไปอย่างเด็ดขาดซึ่งจะมีผลให้กำจัดกวาดล้างการแพร่โรคโดยเชื้อทุกชนิดไปพร้อม ๆกัน (Malaria Elimination) ด้วย ได้มีความพยายามดำเนินเรื่องนี้อย่างจริงจังเพื่อนำปัญหามาลาเรียขึ้นสู่ระดับผู้นำประเทศเพื่อให้เกิดเป็นข้อผูกพันในระดับรัฐบาล โดยในพ.ศ. 2557 ที่ประชุมสุดยอด East Asia Summit ครั้งที่ 9 ที่กรุงเนปิดอร์ เมียนมาร์ ผู้นำของ 18 ประเทศ (ซึ่งรวม 6 ประเทศลุ่มแม่น้ำโขงรวมถึงประเทศไทยด้วย) มีข้อตกลงร่วมกันเพื่อเร่งรัดกำจัดมาลาเรียภายใน พ.ศ. 2573 (ค.ศ. 2030) จากบทเรียนในอดีตแสดงให้เห็นว่ามาลาเรียมีลักษณะที่เปลี่ยนปลงอยู่ตลอดเวลาและมีปัจจัยเกี่ยวข้องมากมายทั้งสิ่งแวดล้อม และพฤติกรรมของกลุ่มเสี่ยงโรค ฯลฯ โครงการมาลาเรียในประเทศต่าง ๆ จึงต้องเข้าใจระบาดวิทยามาลาเรียอย่างลึกซึ้ง ปัญหาหนึ่งซึ่งจัดได้ว่าเป็นปัญหาโลกแตกที่ท้าทายสำหรับงานมาลาเรียในภูมิภาคนี้คือมาลาเรียที่ชายแดนประเทศซึ่งมีการข้ามแดนไปมาของกลุ่มอพยพและแรงงานต่างชาติซึ่งต้องอาศัยความร่วมมือที่ใกล้ชิดและจริงใจระหว่างประเทศ การกระจายงานและบูรณาการงานมาลาเรียซึ่งเดิมเป็นโครงการชำนัญพิเศษให้เข้าสู่ระบบสาธารณสุขทั่วไปก็เป็นเรื่องที่หลีกเลี่ยงไม่ได้ การบริหารให้มีงบประมาณที่พอเพียงและเจ้าหน้าที่ยังสามารถคงทักษะด้านมาลาเรียไว้ได้ในขณะที่ไข้มาลาเรียลดความสำคัญลงนั้นเป็นสิ่งท้าทายของโครงการมาลาเรียในทุกประเทศ

Keyword: Malaria SEA lessons learned

THURSDAY 8 DECEMBER 2016

16.00 - 17.30
Room B

S33: CHALLENGES IN TB ELIMINATION

Chairpersons :

1. Yupaporn Wattanagoon

2. Suparat Phuanukoonnon

Invited Speakers :

1. Lisa Stevens
"Global burden of tuberculosis and challenges to tuberculosis elimination"
FHI 360 Asia Pacific Regional Office, Bangkok

2. Jennifer Ho
"Engaging the communities in TB responese"
APCASO, Bangkok
(Abstract not available)

3. Phalin Kamolwat
"Challenges and Way Forward of TB Control in Thailand"
Bureau of Tuberculosis, Department of Disease Control, MOPH
(Abstract not available)

GLOBAL BURDEN OF TUBERCULOSIS AND CHALLENGES TO TUBERCULOSIS ELIMINATION

Lisa Stevens [1]

[1] *FHI 360 Asia Pacific Regional Office*

Background In 2015, 10.4 million people suffered from tuberculosis (TB), the leading infectious cause of death. Asia is home to the majority of global TB cases. The esclating multi-drug resistant (MDR) TB epidemic requires prolonged therapy, with frequent serious side effects and an unacceptabley low treatment success rate. Although TB control efforts have improved since the introduction of Directly Observed Treatment (DOTS), the current annual decline in incidence is insufficient to reach the END TB Strategy goal of TB elimination by 2035. Objective In this symposium we will discuss the challenges to finding and effectively treating all people with TB by examining the TB diagnosis and treatment cascade, along with TB prevention activities. Challenges include finding the missing TB cases, which in Asia is integrally related to the private health sector; the poor tolerability of current MDR-TB treatment regimens; the influence of concomitant diseases such as HIV and diabetes; infection control both in the community and in health facilities; the vast burden of latent TB infection and insufficient funding for an effective TB response. Strategies are needed for national TB programs to better target interventions. New tools are now available to overcome some of these barriers, including both diagnostics and new drugs and regimens. More are expected. Despite the compelling economic case for investment in TB control with its low cost and highly efficient treatment yielding substantial economic and health returns, TB remains a low financial priority for both donor and domestic financing in many high burden countries.

Keywords: Tuberculosis TB Diagnosis TB Treatment Barriers to care

THURSDAY 8 DECEMBER 2016

16.00 - 17.30
Room C

S34: RODENT-BORNE DISEASES AND THEIR IMPORTANCE IN SOUTHEAST ASIA

Chairpersons :

1. Akira Ito

2. Urusa Thaenkhom

Invited Speakers :

1. Kittipong Chaisiri
"Rodent-borne diseases: recent advances and challenges"
CNRS-CIRAD, Department of Department of Helminthology, Faculty of Tropical Medicine, Mahidol University

2. Kittipong Chaisiri
"Molecular ecology of chigger mites (*Acari: Trombiculidae*) and their associated bacteria in Thailand"
Department of Helminthology, Faculty of Tropical Medicine, Mahidol University

3. Urusa Thaenkham
"Updated evidence from biological studies of *Angiostrongylus* in Asia"
Department of Helminthology, Faculty of Tropical Medicine, Mahidol University

4. Sathaporn Jittapalapong
"Flooding effects on *Toxoplasma gondii* and *Anaplasma marginale* infections in rodents and surrounding animals"
Faculty of Veterinary Technology, Kasetsart University

RODENT-BORNE DISEASES: RECENT ADVANCES AND CHALLENGES

Serge Morand [1]

[1] *CNRS-CIRAD, Department of Helminythology Faculty of Tropical Medicine Mahidol University*

Here, we synthesize the knowledge and the challenges associated with the identification of habitat preferences of Southeast Asian murine rodents and associated rodent-borne diseases. The development of barcoding allows more accurate identification of rodents, specifically for complex species. Although the knowledge on the distribution and habitat specializations of many common murine rodents is still scarce, particularly regarding the specific habitat preferences of most synanthropic rodent species, new studies by analyzing the prevalence of major rodent-borne diseases help at identifying risky habitats of rodent zoonoses. Using information on current ecological and parasitological similarities among host species may help to predict the most likely pathways for future pathogen spillover. In particular network analysis can assess the relative epidemiological importance of rodent species and risky habitat. References: Bordes F, Caron A, Blasdell K, de Garine Wichatitsky M, Morand S (2016) Forecasting potential emergence of zoonotic diseases in South-East Asia: network analysis identifies key rodent hosts. Journal of Applied Ecology (DOI: 10.1111/1365-2664.12804) Blasdell K, Duong V, Eloit M, Chretien F, Ly S, Hul V, Deubel V, Morand S, Buchy P (2016) Evidence of human infection by new arenaviruses endemic to Southeast Asia. eLife 5: e13135.

Keywords: Rodent-borne diseases, Land Use, biodiversity

MOLECULAR ECOLOGY OF CHIGGER MITES (*ACARI: TROMBICULIDAE*) AND THEIR ASSOCIATED BACTERIA IN THAILAND

Kittipong Chaisiri [1],
Benjamin Makepeace [2],
Alexandr Stekolnikov [3],
John McGarry [4], Alistair Darby [5],
Christina Gill [5], Serge Morand [6]

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[2] *Department of Infection Biology, Institute of Infection and Global Health, University of Liverpool, UK,*
[3] *Zoological Institute of Russian Academy of Sciences, Universitetskaya Embankment 1, Saint Petersburg, Russia,*
[4] *School of Veterinary Science, University of Liverpool, UK,*
[5] *Institute of Integrative Biology, University of Liverpool, UK,*
[6] *Centre d'Infectiologie Christophe Mérieux du Laos, Vientiane, Lao PDR*

Chiggers are the tiny six-legged larval stage of mites in the family Trombiculidae. The larvae are the only parasitic stage, feeding on a variety of small mammals and incidentally on humans, whereas adults and nymphs live in soil and are predators of other arthropods. These mites, particularly the genus Leptotrombidium, act as important vectors of *Orientia tsutsugamushi*, the causative agent of scrub typhus disease in the Asia-Pacific region (including Thailand). Here, nationwide field sampling of small mammals revealed a high diversity of chigger mites. From 18 host species examined, 38 chigger species were found including three species new to science (i.e., *Trombiculindus kosapani n. sp.*, *Helenicula naresuani n. sp.* and *Walchia chavali n. sp.*) and 10 new records for the first time in the country. Most chigger species infest a broad host range, showing low host specificity, and this catholic feeding behaviour may increase the probability of people being bitten. The diversity of chiggers on small mammal hosts was influenced by host intrinsic (i.e., host phylogeny and maturity) and extrinsic factors (i.e., habitat and geographical location). Habitat alteration affected chigger diversity by reducing chigger species richness gradually from low human pressure (i.e., forests) to highly urbanized habitats such as human settlements. Linking the ecological study of chiggers with scrub typhus epidemiology, chigger species richness and host-chigger network connectance were found to be interrelated variables explaining human scrub typhus incidence in Thailand. Chigger-associated bacteria were investigated for the first time using an Illumina MiSeq 16S rRNA amplicon sequencing approach. DNA of *O. tsutsugamushi* was detected in the chigger population as expected. In addition to *O. tsutsugamushi*, Borrelia and Mycobacterium appeared as the potential pathogens of human and animals. Potential symbiotic bacteria of arthropods; e.g., Candidatus Cardinium, Pseudonocardia, Rickettsiella and Wolbachia were also discovered for the first time in chiggers. Some other dominant bacteria were presented such as Geobacillus, Corynebacterium, Staphylococcus and OTUs in the family Comamonadaceae and Neisseriaceae. These outcomes from the studies of chigger taxonomy and the ecology of host-chigger interactions, as well as the composition of the microbiome in chiggers, are of key importance to the chigger research field, providing essential information for disease epidemiology with vector control implications

Keywords: Chiggers; molecular ecology; microbiome; Thailand

UPDATED EVIDENCE FROM BIOLOGICAL STUDIES OF *ANGIOSTRONGYLUS* IN ASIA

Urusa Thaenkham[1],
Sirilak Dusitsitipon[1],
Kittipong Chaisiri[1],
Chalit Komalamisra[2]

[1] *Department of Helminthology, Faculty of Tropical Medicine, Mahidol University, Bangkok Thailand,* [2] *Bangkok School of Tropical Medicine, Mahidol University, Bangkok, Thailand*

Angiostrongylus is the well-known genus of the rat lung worm. Among the 21 valid species in this genus, 11 have been reported as rodent parasites, mostly distributed in Europe and America. However, only 3 species of these, i.e. *A. cantonensis, A. malaysiensis,* and *A. costaricensis*, can cause eosinophilic meningitis in humans. In Asia, *A. cantonensis* is a widely distributed species, while *A. malaysiensis* was believed to be distributed in the Malay Peninsula. Recently, *A. malaysiensis* has been found to be widely spread in Southeast Asia. Because of the morphological similarity between *A. cantonensis* and *A. malaysiensis,* mis-identification is frequently occurred. A phylogenetic relationship reconstruction, based on COX1, CYTB, and IT2 sequences, has indicated that they are closely related and diverged from each other about 3,800,000 years ago. In Southeast Asia, these two species have been found in overlapping areas, sharing the same species of snail intermediate hosts, and rodent definitive hosts. Experimental evidence of hybridization between these two species has reported the F1 generation. Parasite hybridization is an emerging public-health concern at the interface of infectious disease biology and evolution. Although information about the geographic distribution of *A. cantonensis* and *A. malaysiensis* has been updated, the percentage infection of rodents and snails, and co-infection data are needed. Hybridization evidence may be confirmed from natural parasite populations.

Keywords: *Angiostrongylus*; Morphology; Closely related species; Hybridization

FLOODING EFFECTS ON *TOXOPLASMA GONDII* AND *ANAPLASMA MARGINALE* INFECTIONS IN RODENTS AND SURROUNDING ANIMALS

Sathaporn Jittapalapong[1],
Aurelie Binot[2],
Stephane Herder[2],
Marc Desquesnes[2],
Serge Morand[2]

[1] faculty of Veterinary Technology, Kasetsart University,
[2] CIRAD-Bios

Thailand was influenced by climate changes for the past decade and this change was caused of more raining or drought in tropical atmosphere. Flooding has an impact on ecological modifications for pathogens, hosts, reservoirs, and vectors, which will vary on dynamic, densities, and interrelations with the environment. Consequences of floods influence the circulation and the incidence of some parasitic zoonoses such as toxoplasmosis, in ways which are hardly predictable and need data record and analyses. *Toxoplasma gondii* infections are directly transmitted via contaminated habitats and rodent reservoirs. Therefore, the changes of habitats and potential reservoirs will affect *T. gondii's* life cycle leading to unpredictable prevalence. One potential factor, rodents as reservoir hosts were forced to leave their habitats during the flooding period. The dry season might influence rodents to be more active for food and other activities leading to increasing prevalency. Anaplasmosis, caused by *Anaplasma marginale,* is majorly a vector-borne disease. The habitat modification of vectors resulting in the high incidences of disease in more animal reservoirs such as wildlife and small mammals. This wildlife will be served as accidental hosts or carriers in nature led to unbalance condition of anaplasmosis. This might be demonstrated as more virulent pathogens or emerging strains of pathogen. In conclusion, the wipe out by the flooding will create the new environment for pathogens and vectors so that we should understand the new chapter of old diseases to overcome the loss.

Keywords: *Anaplasma marginale*, flooding, rodents, *Toxoplasma gondii*

THURSDAY 8 DECEMBER 2016

16.00 - 17.30
Room D

S35: MICROBIOLOGY AND PARASITOLOGY (FREE PAPER)

Chairpersons :


1. Porntip Petmitr


2. Kesinee Chotivanich

Speakers :


1. Dar-Der Ji
" Surveillance of *Vittaforma corneae* parasite in hot springs in Taiwan"
National Yang-Ming Univeristy, Taiwan


2. Jinath Sultana Jime
"Isolation of vibrios in freshwater fishes of Bangladesh"
North South University, Bangladesh


3. Kazi Nadim Hasan
"Comparative evaluation of two Rapid Tests Devices and Real-time PCR for the detection of hepatitis B surface antigen in human plasma: implications in blood donation screening"
North South University, Bangladesh

4. Saiwasan Buathong
"Identification of metacercariae of fish-borne trematodes in freshwater fish in a rural community, Central Thailand"
Faculty of Science, Mahidol University

5. Siwipeni Irmawanti Rahayu
"Increasing resistance of *Burkholderia cepacia* toward antimicrobial agents used in Dr. Saiful Anwar General Hospital, Malang, Indonesia"
Faculty of Medicine, Universitas Brawijaya, Indonesia


6. Thanaphon Sripan
"Prevalence of anxiety disorders, depression, and associated risk factors among boarding high school students in Thailand: a cross-sectional study"
Faculty of Tropical Medicine, Mahidol University

SURVEILLANCE OF *VITTAFORMA CORNEAE* PARASITE IN HOT SPRINGS IN TAIWAN

Dar-Der Ji [1], Jung-Sheng Chen [2],
Bing-Mu Hsu [3], Men-Fang Shaio [4]

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Vittaforma *corneae* is an obligate intracellular parasite and can cause human ocular microsporidiosis. Although *V. corneae* has been found to cause keratoconjunctivitis in either healthy or immunocompromised persons, little is known about its epidemiology, such as transmission and infection pathways. In Taiwan, a study had shown that some cases of the microsporidial keratitis were infected through the hot springs exposure recently. Therefore, the survey and analysis for environmental *V. corneae* in hot springs was achieved. Sixty water samples from 6 hot springs recreation sites around Taiwan were analyzed. One liter of water from each sample site was filtered to recover parasites. The positive samples were detected by nested PCR using specific 18S rRNA gene primer pairs for *V. corneae*, and sequencing. Total 15 (25.0%) *V. corneae* like parasite isolates were identified. Among them, 5 isolates from recreation site B, C and D were highly close to a Taiwanese *V. corneae* keratitis strain. Cold water source had highest infection rate (50%) indicating hot springs might be contaminated by untreated water source. In comparison of the prevalent rate, the Eastern part of Taiwan (36.8%) was higher than Northern (25%), then Southern (20%), and then Central (13.2%). These observations add further evidence to support that new and appropriate control and regulations for hot springs recreational waters should be established to avoid health risks from this pathogen.

Keywords: *Vittaforma corneae*, Taiwan, keratitis, microsporidia, hot springs

ISOLATION OF VIBRIOS IN FRESHWATER FISHES OF BANGLADESH

Jinath Sultana Jime [1], Ashrafus Safa [2], Nayeema Bulbul [1], Kishwar Ifrit [3], Oshin Ghurnee [4], Sohidul Islam [1]

[1] Faculty of Dept. of Biochemistry and Microbiology, North South University, [2] Faculty of School of Life Sciences, Independent University Bangladesh, [3] Faculty of DDept. of Biochemistry and Microbiology, North South University, [4] Dept. of Biochemistry and Microbiology, North South University

Vibrios are Gram-negative γ-proteobacteria which is autochthonous to marine eco-system. Though Vibrios persevere as a natural element of the marine microbial flora, a large number of Vibrio species are pathogenic to humans. *Vibrio cholerae, V. parahaemolyticus, V. mimicus, V. vulnificus* and *V. alginolyticus* are the most remarkable human pathogens among members of Vibrio. Upon consumption, Vibrio causes gastroenteritis in humans, characterized by bloody or watery diarrhea with abdominal cramp, nausea, vomiting, headache, low-grade fever and chills. In rare cases, many members cause septicemia and wound infection, especially in immuno-compromised patients. The transmission of Vibrios in humans is mostly associated with consumption of contaminated water and foods i.e. seafood (Oysters, Shellfish, and Sea-weeds). However, the association of Vibrios with freshwater fishes and their transmission to humans through fresh water fishes has remained inexplicable. In the present study, we have examined locally available fresh water fishes (Reba carp, Mrigel, Tilapia, Silver Carp) for the presence of Vibrio spp. Our study revealed that the surface and gill of fresh water fishes harbor *V. vulnificus, V. parahaemolyticus* and *V. cholera*. Only *V. vulnificus* was able to form biofilm to the surface detected in the laboratory experimentally. This could be the survival strategy of *V. vulnificus* in freshwater environments.

Keywords: Vibrio, Freshwater fish, Biofilm

COMPARATIVE EVALUATION OF TWO RAPID TESTS DEVICES AND REAL-TIME PCR FOR THE DETECTION OF HEPATITIS B SURFACE ANTIGEN IN HUMAN PLASMA: IMPLICATIONS IN BLOOD DONATION SCREENING

Kazi Nadim Hasan [1],
Tanzila Wasi [2], Aniqa Afzal [3],
Nahian Anjum Shejuti [4],
Sohidul Islam [5]

[1] Professor, Department of Biochemistry & Microbiology, North South University, [2] Grduated student, [3] Graduated Student, [4] Graduating Student, [5] Associate Professor, Department of Biochemistry & Microbiology, North South University

Background and Aims: Hepatitis B Virus (HBV), a parenterally transmitted infectious virus, is one of the leading causes of hepatitis throughout the world. Screening for HBV infection is recommended before vaccination and blood transfusion in order to prevent its transmission. Immunochromatography (ICT) based rapid HBsAg kits are popular for the screening of HBV infection as they are faster, inexpensive and easier to perform than other methods. This study was aimed to evaluate two rapid HBsAg detection ICT kits for the screening of HBV infection by comparing with the gold standard real-time polymerase chain reaction (real-time PCR) system that quantifies HBV-DNA.

Materials and Methods: The study comprised of 203 samples, of which 103 had detectable and 100 had no detectable HBV-DNA by real time PCR. These samples were tested with ICT kits from two companies: OnSite HBsAg Rapid Test (CTK Biotech, Inc., USA) and HBsAg Test Device (EXCEL®, USA). Results: Sensitivity of CTK and EXCEL were found 97.1% and 95.1% respectively. Negative predictive value (NPV) of CTK and EXCEL were 97.1% and 95.2% respectively. Both kits showed 100% specificity and 100% positive predictive value (PPV). HBV-DNA status strongly correlated with CTK ($r = 0.971$, $p < 0.001$) and with EXCEL ($r = 0.952$, $p < 0.001$). Three and five moderate to high HBV load containing samples were undetected by CTK and EXCEL respectively.

Conclusions: The study results demonstrate that ICT based kits might not be considered suitable for screening of HBV infection, thereby necessitates the implementation of nucleic acid testing for hepatitis B virus (NAT-HBV) before vaccination and blood transfusion despite of showing high sensitivity.

Keywords: Hepatitis B Virus, Immunochromatography, Real-Time Polymerase Chain Reaction

IDENTIFICATION OF METACERCARIAE OF FISH-BORNE TREMATODES IN FRESHWATER FISH IN A RURAL COMMUNITY, CENTRAL THAILAND

Saiwasan Buathong [1]

[1] *Department of Microbiology, Faculty of Science, Mahidol University*

Introduction: Fish-borne trematode (FBT) infection is one of important parasitic infections reported in tropical and subtropical countries including Thailand. Little is known about their prevalences, intermediate hosts of FBT in central Thailand where they are still public health problem.

Objective: We aimed to study the prevalence of FBT in the metacercariae found in freshwater fish collected in the previously reported area of FBT infection, central Thailand. Methods: A total of 218 freshwater fish were collected from three villages; Na-Ngam, Na-Yao and Thoong-Heang, Chacherngsao Province, Central Thailand and investigated for the metacercariae using digestive solution. Metacercariae of FBT were identified using PCR amplifications of the ITS2 region of ribosomal RNA and cytochrome c oxidase subunit one (cox1) genes

Results: The amount of 201 metacercariae were observed and subjected to PCR assay targeting ITS2 region and cox1 of the metacercariae. The prevalence of metacercariae of FBT in infected cyprinoid fish was 5.04%. The ITS2 primers could identify the metacercariae of Haplorchis taichui in Na-Ngam village. The universal primer for amplification cox1 of trematode successfully amplified metacercariae DNA of two new haplotypes (bootstrap value >95%) of FBT from Na-Yao village. Two new haplotypes were detected from freshwater fish from villages of a rural community, central Thailand. Conclusion: More studies are required to investigate their life cycles and clarify their host specificity.

Keywords: Fish-borne trematode, metacercariae, cyprinoid fish, ITS2, cox1

INCREASING RESISTANCE OF *BURKHOLDERIA CEPACIA* TOWARD ANTIMICROBIAL AGENTS USED IN DR. SAIFUL ANWAR GENERAL HOSPITAL, MALANG, INDONESIA

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Yuanita Mulyastuti [1],
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[2] *Department of Clinical Microbiology, Dr. Saiful Anwar General Hospital Malang*

Infection of Burkholderia, including *Burkholderia cepacia* remains an overlooked threat in Indonesia, despite of its potency to cause significant problem in hospital. Report of *B. cepacia* infection is sporadically found in Indonesia, with even less report of its resistance profile. This bacteria exhibits wide range of resistance toward antimicrobial agents. In vitro sensitivity does not always match with in vivo potency, which poses as another challenge to treat infection of *B. cepacia.* We studied resistance profile of *B. cepacia* in Saiful Anwar General Hospital, Malang, Indonesia, toward three main antimicrobial agents that are generally used as drug of choice: trimethoprim-sulfamethoxazole, ceftazidime, and meropenem. Data was collected from report of 127 clinical specimen, composed of blood, sputum, pus and urine for five years (2011 to 2015) in Dr. Saiful Anwar General Hospital Malang, Indonesia. All collected data was subjected to statistical analysis using Chi-Square test. We found significant increase in resistance of ceftazidime from 2011 to 2015, from 47.4% to 54.8% ($p < 0.05$). Resistance of meropenem from 2011 to 2015 was also significantly increased, from 0% to 41.9% ($p < 0.05$). Interestingly, we found significant decrease in resistance of trimethoprim-sulfamethoxazole from 2011 to 2015, from 73.7% to 58% ($p < 0.05$). However, resistance pattern of the three tested antimicrobial agents showed dynamic pattern throughout the years. This dynamicity strongly requires continuous monitoring in resistance pattern, as well as surveillance of its emergence especially in Indonesia, since there is yet a universal guideline to treat infection of *B. cepacia.*

Keywords: *Burkholderia cepacia*, ceftazidime, meropenem, trimethoprim-sulfamethoxazole, resistance pattern.

PREVALENCE OF ANXIETY DISORDERS, DEPRESSION, AND ASSOCIATED RISK FACTORS AMONG BOARDING HIGH SCHOOL STUDENTS IN THAILAND: A CROSS-SECTIONAL STUDY

Thanaphon Sripan [1]

[1] *Department of Protozoology, Faculty of Tropical Medicine, Mahidol University*

Mental health problems are one of the most important public health issues worldwide. Untreated mental disorders were reported as a high prevalence of 13% of the total global burden of disease, according to World Health Organization. Mental disorders account for 33.5% and 25.3% of all age groups who lived with a disability in middle-and low-income countries, accordingly. The latest forecasts show that by 2030 depression will be the leading cause of disease burden worldwide. There are a few studies about the risk factors in young students regarding mental illness in school. This research aims to explore the prevalence and risk factors of depression and anxiety disorders among boarding high school students. The study is conducted as an analytical cross-sectional study design to determine prevalence and the risk factors or behaviors among high school students using anonymous self-reporting standardized test HADS score and structured questionnaires to evaluate prevalence and identify risk factors, respectively. The study included total of 387 high school students grade 10 to 12. The questionnaire are divided into 3 parts; personal information, risk factor (family, school, and personal factors), and lastly scale of anxiety and depression. There are total of 28.4% students who have anxiety, and 11.4% with depression. The major risk are being abused by their parents and/or teacher, aggressive behavior, learning difficulties etc. The results of this study may help raise awareness and development of prevention's policies, good advisory system and the good environment that could reduce the anxiety among high school students.

Keywords: Depression, Anxiety, Risk, High School

THURSDAY 8 DECEMBER 2016

16.00 - 17.30
Room E

S36: TROPICAL MEDICINE ACTIVITIES UNDER THE PROJECT OF HER ROYAL HIGHNESS PRINCESS MAHA CHAKRI SIRINDHORN

Introduction of the project :

Yaowalark Sukthana

Speakers :

1. Manachit Luangluexay
"The current situation of intestinal parasitic infections in Luangnamtha, Lao PDR"
Luangnamtha Provincial Hospital, Lao PDR

2. Senpasert Ormsub
"Prevalence and risk factors of intestinal helminthic infections in Khong District, Lao PDR"
Khong District Hospital, Lao PDR

Invited Speakers :

3. Teera Kusolsuk
"Intestinal parasitic infections among children in the border patrol police schools and villagers in rural areas, Thailand"
Faculty of Tropical Medicine, Mahidol University

Aongart Mahithikorn

THE CURRENT SITUATION OF INTESTINAL PARASITIC INFECTIONS IN LUANGNAMTHA, LAO PDR

Manachit Luangluexay [1],
Teera Kusolsuk [2],
Aongart Mahittikorn [3],
Emsri Pongponratn [4],
Yaowalark Sukthana [5]

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[2] *Department of Helminthology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand,*
[3] *Department of Protozoology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand,*
[4] *Department of Tropical Pathology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand,*
[5] *Department of Protozoology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand*

Background: More than one-third of the world's population is infected with one or more helminthes parasites. Intestinal parasitic infections are endemic worldwide and have been described as constituting the greatest single worldwide cause of illness and disease. Poverty, illiteracy, poor hygiene, lack of access to potable water and hot and humid tropical climate are the factors associated with intestinal parasitic infections. This study had shown the result of the prevalence of the intestinal infection among 3 villagers in Luangnamtha Province and the possible risk of intestinal parasitic infections of the villagers.

Objective: To evaluation health status and Intestinal Parasites infection among 3 villagers in Luangnamtha Province. Methods: A cross-sectional descriptive study was conducted with a total of 300 cases in 3 villagers in Luangnamtha District, Luangnamtha Province from August to September 2015. Using a questionnaire with demographical characteristics, we collected results of stool examination by the Kato-Katz thick smear and the simple smear technique.

Results: A total 300 cases were studied in 3 villagers. Most cases were female (56%). The proportion of intestinal parasitic infection was 38%. *Ascaris lumbricoides* was the most prevalent species 77% follow by *Trichuris trichiura* 16% and Hookworm 7%. Villagers who had poor hygiene and lack of access to potable water were high risk of intestinal parasitic infection. For the intestinal protozoa infections were rare. Conclusion: the prevalence of intestinal parasitic infection was high in Luangnamtha Province. Intervention to reduce and prevent parasitic infection must be introduced into this area.

Keywords: intestinal parasitic infection, intestinal protozoa infection, prevalence, risk factor

PREVALENCE AND RISK FACTORS OF INTESTINAL HELMINTHIC INFECTIONS IN KHONG DISTRICT, LAO PDR

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Aongart Mahittikorn [3],
Emsri Pongponratn [4],
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[4] *Department of Tropical Pathology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand*

The prevalence of parasitic infections was examined from OPD patients at Khong Hospital, Chumpasak Province Lao PDR by direct smear technique. The results shown 36.4% (24/66) were positive on parasites infected, *Opisthorchis viverrini* was the most common infection at 50% (12/24), followed by *Taenia spp.* at 21% (6/66), hookworm (3/66) and *Strongyloides stercularis* (3/66) infections. More than half of patients who parasites infection were accepted to consume raw or under cooked fresh water fish. Health education program to reduce parasitic infections was implemented to patient group, parasites mobile clinic need to perform by active service to patient's community for parasites identification in further.

Keywords: Parasitic infection, Kong district hospital Lao PDR, Health education program

INTESTINAL PARASITIC INFECTIONS AMONG CHILDREN IN THE BORDER PATROL POLICE SCHOOLS AND VILLAGERS IN RURAL AREAS, THAILAND

Teera Kusolsuk [2],
Aongart Mahittikorn [1],
Rapeepun Prasertbun[1],
Chantira Sutthikornchai[1],
Ruenruetai Udonsom[1],
Pongruj Rattaprasert[1],
Supaluk Popruk[1],
Surapol Sa-nguankiat[3],
Nirundorn Homsuwan[3], Akkarin Poodeepiyasawat[3], Supaporn Nuamtanong[3], Suntara Na Bangchang[4],
Rungson Praewanich[5],
Srisuchart Mongkolmoo[5],
Sumreng Promongkol[5],
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[4] *Hospital for Tropical Diseases,*
[5] *Mahidol - Bangkok School of Tropical Medicines*

Intestinal parasitic infections are one of the important infections in humans living in developing countries, particularly in among school aged children. Despite community-wide mass treatment of helminthic infections, the burden is still high among the poor sections of population in remote areas. In this study, more than 1,500 fecal samples from students in the border patrol police schools and people living nearby the schools in the northern, eastern, western, central and southern parts of Thailand were collected and analyzed for intestinal helminthes and protozoa by conventional (at the field sites) and/or molecular methods (PCR and direct sequencing). The current status, factors attributed to the infections and perspectives will be presented and discussed in this topic.

Keywords: Parasitic infections

FRIDAY 9 DECEMBER 2016

09.00 - 10.30
Room A

S37: WHAT'S NEW IN SEVERE MALARIA (ORGANIZED BY MORU)

Chairpersons :

1. Prakaykaew Charunwatthana

2. Arjen Dondorp

Invited Speakers :

1. Stije Leopold
"Acidosis in severe falciparum malaria"
Mahidol-Oxford Tropical Research Unit, Faculty of Tropical Medicine, Mahidol University
(Abstract not available)

2. Caterina Fanello
"Post-artesunate anaemia in paediatric severe malaria"
Mahidol-Oxford Tropical Research Unit, Faculty of Tropical Medicine, Mahidol University
(Abstract not available)

3. Arjen Dondorp
"Paracetamol and haem-mediated oxidative renal tubular injury in severe malaria"
Mahidol-Oxford Tropical Research Unit, Faculty of Tropical Medicine, Mahidol University
(Abstract not available)

FRIDAY 9 DECEMBER 2016

09.00 - 10.30
Room B

S38: PROTOZOAN INFECTIONS

Chairperson :

Yaowalark Sukthana

Invited Speakers :

1. Florence Robert-Gangneux
"Contrasting effects of il-33 in response to *Leishmania donovani* infection in the spleen according to genetic background"
Université de Rennes 1, Rennes University Hospital, France

2. Jean-Pierre Gangneux
"Visceral leishmaniasis : Distinct entities between Asia and Europe, and new therapeutic approaches"
Université de Rennes 1, Rennes University Hospital, France

3. Yoshifumi Nishikawa
"Brain manipulation by intracellular parasite, *Toxoplasma gondii*"
Obihiro University of Agriculture and Veterinary Medicine, JAPAN

CONTRASTING EFFECTS OF IL-33 IN RESPONSE TO *LEISHMANIA DONOVANI* INFECTION IN THE SPLEEN ACCORDING TO GENETIC BACKGROUND

Florence Robert-Gangneux [1],
A. Lamberet [1], O. Rostan [1],
A. Jan [1], C. Manuel [1],
Jp Gangneux [1]

[1] *Inserm U1085, University Rennes 1, University Hospital Of Rennes, France*

Little is known about the determinants leading either to progressive visceral Leishmaniasis (vl) or to asymptomatic carriage. We previously showed that il-33 had a deleterious effect on the hepatic immune response to l. Donovani. As the spleen is also a major target organ during vl and is often associated with clinical relapse, we aimed to describe the role of il-33 and its receptor st2 in this organ, using various mouse models. In several experiments, balb/c wild type (bwt) or balb/c st2-deficient (st2-/-) mice, c57bl/6 wild type (b6wt) or c57bl/6 il-33-deficient (il-33-/-) mice, bwt and b6wt treated with recombinant il-33 (bwt+ril-33 and b6wt+ril-33), or not treated (nt), were infected intraperitoneally with 108 l. Donovani promastigotes and sacrificed at day 15 (d15), d30 or d60 post-infection to collect spleen for histological and transcriptomic analysis. Both il-33 and st2 mrna were highly induced in bwt mice and peaked on d30 (x6.6 and x7.6, respectively, confirmed by immunohistochemistry), whereas they were only moderately induced in b6wt (x2.2 and x1.7, respectively). The kinetics of infection over time also differed, with increasing and decreasing parasite loads in bwt and b6wt, respectively. In both genetic backgrounds, parasite loads were lower in case of deficient il-33/st2 pathway (st2-/- or il-33-/-), compared to their wt counterparts, and this was associated with a trend towards higher expression of th1 cytokines (ifn-g, il-12) in deficient mice. Treatment with ril-33 had contrasting effects, with an early control of infection in b6wt+ril-33, but not in bwt+ril-33 ($p<0.01$ compared to nt bwt), and the opposite effect on d60, with higher parasite loads in b6wt+ril-33 ($p<0.05$) despite increased th1 response (ifn-g, il-12, cxcl10, il1-b), and decreasing parasite loads in bwt+ril-33 despite abolition of th1 response. Taken together, these results underline the complex interplay of the il-33 st2 axis in the immune response to l. Donovani according to genetic background, but confirm that the lack of il-33/st2 pathway warrants a better immune response during vl whatever the genetic background.

Keywords: *Leishmania donovani*

VISCERAL LEISHMANIASIS : DISTINCT ENTITIES BETWEEN ASIA AND EUROPE, AND NEW THERAPEUTIC APPROACHES

Jean-Pierre Gangneux[1]

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Université de Rennes 1 European Confederation of Medical Mycology, Laboratory of Parasitology and Mycology Biology Centre, Rennes Teaching Hospital*

Visceral leishmaniasis (VL) brings together 2 different entities according to geographical area and species. Leishmania infantum is endemic In South western Europe and is responsible for both VL and cutaneous leishmaniasis (CL). In Asia, VL is due to Leishmania donovani with major differences in terms of epidemiology and management. L. donovani VL is an anthroponotic infection with still high prevalence and mortality notably in India and Bangladesh. It is a disease associated to malnutrition and poverty, with a limited drug access. Besides, L. infantum VL is a zoonotic infection with dogs as principal reservoir. The majority of VL infections in Europe occur in children or adults who are immunocompromised such as HIV-infected adults. Sharing of needles by intravenous drug users (IVDUs) contributes not only to the spread of HIV but also greatly increases the risk of Leishmania infection and IVDUs constitute the population at greatest risk of Leishmania/HIV co-infection. Besides, other types of immunosuppression may favor VL such as solid organ transplantation, and the question of asymptomatic carriage remains opened. The importance and relevance of VL in Europe will be discussed further in this presentation, as well as its clinical management. Drug efficacy between Asia and Europe will be compared and new therapeutic approaches will be discussed.

Keywords: Leishmania infection

BRAIN MANIPULATION BY INTRACELLULAR PARASITE, *TOXOPLASMA GONDII*

Yoshifumi Nishikawa [1]

[1] *National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine*

Toxoplasma *gondii* is an obligate intracellular parasite that invades a wide range of vertebrate host cells. Chronic infections with *T. gondii* become established in the tissues of the central nervous system where the parasites may directly or indirectly modulate neuronal function. However, the mechanisms underlying parasite-induced neuronal disorder in the brain remain unclear. Our study evaluated host gene expression in mouse brain and behavioral changes following infection with *T. gondii.* Mice were infected with the *T. gondii,* and after one month of infection, histopathological lesions in the frontal lobe were found to be more severe than in other areas of the brain. Total RNA extracted from infected and uninfected mouse brain samples was subjected to transcriptome analysis using RNA sequencing. GOstat analysis predicted that *T. gondii* infection induced host immune responses and down-regulated neurological function. In the behavioral experiments, *T. gondii* infection impaired consolidation of conditioned fear memory. We measured neurotransmitter levels in the cortex and amygdala because these regions are involved in fear memory expression and found that the levels of cortical dopamine metabolites were associated with loss of the fear memory. Furthermore, we also confirmed that the depression-related behaviors in *T. gondii*-infected mice at the reactivation stage, but not in the chronic infection. This behavioral change was associated with enhanced tryptophan catabolic shunt and serotonin turnover. Our findings provide insight into the mechanisms underlying neurological changes during *T. gondii* infection. Here, I will also discuss how *T. gondii* infection should be controlled.

Keywords: *Toxoplasma gondii*, brain, behavioral change

FRIDAY 9 DECEMBER 2016

09.00 - 10.30
Room C

S39: MALARIA (FREE PAPER)

Chairpersons :

1. Srisin Khusmith

2. Srivicha Krudsood

Speakers :

1. Colin Ohrt
"Preparing for the next global threat– A call for targeted, decisive action now in Southeast Asia to prevent the next pandemic in Africa"
Consortium for Health Action

2. Erma Sulistyaningsih
"Expression of specific sequence in *Plasmodium falciparum* DBL domains associated with severe malaria outcome"
Faculty of Medicine, University of Jember, Indonesia

3. Kittiya Mahotorn
"*In vitro* pyronaridine susceptibility in Thai isolates of *Plasmodium falciparum*"
Faculty of Science, Silpakorn University

4. Kyaw Thura Tun
"Improved surveillance towards malaria elimination in Myanmar"
Malaria Consortium, Bangkok

5. Prayuth Sudathip
"Moving towards malaria elimination in Thailand"
Bureau of Vector-Borne Diseases, Disease Control Department, MOPH

6. Zin Zayar Win
"Molecular epidemiology of anti-malarial resistance in Myanmar"
Defense Services Medical Research Centre, Myanmar

PREPARING FOR THE NEXT GLOBAL THREAT– A CALL FOR TARGETED, DECISIVE ACTION NOW IN SOUTHEAST ASIA TO PREVENT THE NEXT PANDEMIC IN AFRICA

Colin Ohrt [1], Sara Canavati [2],
Jack Richards [2],
Duong Thanh Tran [3],
Thang Duc Ngo [3]

[1] *Consortium for Health Action, Ha Noi, Vietnam,*
[2] *Burnet Institute, Melbourne, Australia,*
[3] *National Institute of Malariology, Parasitology and Entomology (NIMPE), Ha Noi, Viet Nam*

A child still dies approximately every two minutes from malaria. Malaria control progress is again threatened by parasites from Cambodia. High treatment failure rates to both artemisinin derivatives and nearly all partner drugs are now widespread in Cambodia and in 2015, they crossed borders into Vietnam. Historically, the arrival the arrival of chloroquine-resistant parasites in Africa resulted in 2-6 fold increased mortality; with artemisinin combination therapy (ACT)-resistance the results could be the same, but evolution could be much faster in the era of globalization. With decisive action now, these strains can be eliminated near the 2020 target following available strategies, including those of World Health Organization and Bill Gates. A key Gates recommendation from "The Next Epidemic – Lessons from Ebola" is coordination should be by "a global institution that is given enough authority and funding to be effective…" He also noted militaries can help. A well-led military response targeting MDR malaria is urgent, as militaries are both part of the problem (a significant transmission reservoir) and part of the solution, especially in restricted, remote forested and border areas. Gates also called for a warning and response system that enables fast decision-making. Such a system targeting priority transmission foci must be rapidly implemented – an example will be presented. We are in the midst of public health emergency that could become among the worst pandemics in history over time, beginning when the new ACT-resistant strains reach Africa. Effectively targeting the current threat, in preparation for the next, should be a perfect fit for many partners in global health.

Keywords: malaria elimination leadership information system

EXPRESSION OF SPECIFIC SEQUENCE IN *PLASMODIUM FALCIPARUM* DBL DOMAINS ASSOCIATED WITH SEVERE MALARIA OUTCOME

Erma Sulistyaningsih[1],
Thomas Loescher[2],
Nicole Berens-Riha[3]

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[2] *Ludwig Maximilians University of Munich,*
[3] *Ludgwig Maximilians University of Munich*

The Duffy-binding like (DBL) domains in *Plasmodium falciparum*, which is found in two different protein families; Erythrocyte Binding Ligand (EBL) and PfEMP1, are believed play an important role in the pathogenesis of malaria during the blood stage of malaria infection. Previous study proposed the association of specific motif derived from DBL domain called var D gene with severe clinical outcome. In this study, blood samples from severe and uncomplicated falciparum malaria patients from Indonesia, were collected for DNA extraction. Blood filter papers were used for RNA extraction. DBL domains were amplified using UNIEBP primers and directly sequenced. Internal var D-like primers were designed based on the sequencing of the 550 bp band produced by UNIEBP primers. The nucleotide sequences were analyzed by NCBI BLAST. Amplification using UNIEBP primers resulted multiple bands ranging from 250 bp to 1 kb from gDNA in all samples. But, amplification of cDNA generated one to four bands ranging from 250 bp to 700 bp only from severe malaria. Sequencing of the 418 bp bands matched with the eba-175 gene, the 316 bp determined as DBL1a domain and 486 bp band matched with the DBLg domain isolated from Malawian woman with PAM. Reverse-transcription PCR of var D-like primers resulted a single band of 237 bp only from severe cases, implicated that the expression of var D-like gene is associate nd with the severe malaria in clinical Indonesian isolates. Further study on the var D-like gene with a larger sample size is required to draw a definite conclusion.

Keywords: DBL domains, *Plasmodium falciparum*, Severe malaria, Var D gene

IN VITRO PYRONARIDINE SUSCEPTIBILITY IN THAI ISOLATES OF *PLASMODIUM FALCIPARUM*

Kittiya Mahotorn[1],
Peerapan Tan-ariya[1],
Naruemon Sittichot[2],
Nantana Suwandittakul[3],
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[3] *Department of Helminthology, Faculty of Tropical Medicine, Mahidol University, 10400 Bangkok, Thailand*

Pyronaridine is a Mannich base antimalarial agent with a high activity against chloroquine-resistance Plasmodium falciparum. To date, Thailand has been known as an endemic area of multidrug-resistant *P. falciparum*. Artesunate-pyronaridine, an artemisinin derivative based combination therapy (ACT) could be one of the choices for treatment of uncomplicated falciparum malaria. However, parasites in this area have not been recently evaluated for in vitro pyronaridine susceptibility. The aim of this study was to determine in vitro susceptibility of pyronaridine against Thai isolates of *P. falciparum*. Cross resistance between pyronaridine and other antimalarial drugs was also evaluated. In addition, the influence of known resistance genes on in vitro pyronaridine susceptibility was determined. In vitro pyronaridine susceptibility of parasites isolated from Thai-Cambodia and Thai-Myanmar borders were examined by using the 3H-hypoxanthine uptake inhibition method. The mean IC50 of pyronaridine was 5.43.0 nM (range 0.2-15.4) with a significant positive correlation with mean IC50 of artesunate (r = 0.296, p = 0.001) and amodiaquine (r = 0.220, p = 0.042) and a significant negative correlation with mean IC50 of quinine (r = -0.248, p = 0.005). Polymorphisms of resistant genes were assessed using PCR techniques. Significantly differences were found between PRN susceptibilities and pfmdr1 mutations at codon N86Y and Y184F. However, artesunate-pyronaridine could be considered as the treatment of choice in multidrug-resistant areas of Thailand with the careful monitoring.

Keywords: *Plasmodium falciparum*, *In vitro* susceptibility, Pyronaridine, Artesunate, Resistant genes

IMPROVED SURVEILLANCE TOWARDS MALARIA ELIMINATION IN MYANMAR

Kyaw Thura Tun [1], Aung Thi [2],
Siddhi Aryal [1], Olivier Celhay [3]

[1] *Malaria Consortium,*
[2] *National Malaria Control Programme,*
[3] *Surveillance and Data Management Consultant*

Myanmar has set the ambitious objective to eliminate malaria in the country by 2030. To that effect, malaria surveillance is becoming a central intervention that will provide data needed to support control and elimination activities. Malaria Consortium provided technical assistance and capacity building support to the National Malaria Control Programme for setting up an ACCESS surveillance database as a new surveillance tool to strengthen data collection and linking reporting by basic health staff and community health workers to enable rapid response. It was tailored to the existing technology in Myanmar and could also be transitioned to more comprehensive databases. Piloted in two townships and one State at sub-national level in 2015, the database was subsequently rolled out in 106 townships in Myanmar, building capacity by training national staff and WHO's data assistants. A cloud-based data system, enabling national, sub-national and township level data sharing was incorporated into the design. A password-protected interactive dashboard using R/Shiny is used in the on-going rollout of the database to map all patients tested for malaria and confirmed malaria cases. Covering data entry, analysis, reporting, mapping of patient diagnosis and treatment data at different levels, the built-in functionality allows integrating existing data and inclusion of different types of data. The design facilitates additional sources of malaria data such as vector control, logistics, entomological and micro-stratification to provide a complete picture of progress and needs. It is important to extend this improved surveillance system in pre-elimination/elimination areas so patient level data is collected and used for real-time response.

Keywords: malaria, surveillance, elimination, Myanmar

MOVING TOWARDS MALARIA ELIMINATION IN THAILAND

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Nipon Chinanonwait [1],
Suravadee Kitchakarn [1],
Richard Reinthinger [2],
Surasak Sawang [2]

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[2] *RTI International, International Health, Washington DC, USA*

Thailand has reported a marked decrease of 73% in annual malaria cases from 2000-2015. This reduction coincides with a significant investment for implementation of highly efficacious interventions (including Long Lasting Insecticide-treated Nets, increased access to services including rapid diagnosis tests and effective antimalarial drugs, strong surveillance system, behavior change and communication, etc.). Despite these significant achievements in malaria control and prevention, malaria remains an important communicable disease in Thailand with a quarter of the population (16,892,506 out of 65,729,098 people) living in malaria-endemic areas and is at risk of infection and disease. Antimalarial drug resistance remains as a major concerning issue in the country. Malaria has a wide geographical distribution in Thailand with three profiles clearly defined: 1) Thai-Myanmar border; 2) Central Thailand and 3) Thai-Laos-Cambodia border. Between January and December 2015, a total 22297 malaria cases and 33 deaths were reported, corresponding to an annual parasite incidence of 0.38 per 1000 population at risk; of all cases, 6227(27.9%)were due to Plasmodium falciparum,14416(64.7%)P. vivax and 1654 (7.4%)other species. Most malaria cases are concentrated in profile 1 and 3where migrant and mobile populations play a significant role. There are5provinces that represent 72% of total cases in the country (Tak, UbonRatchathani, Sisaket, Yala and Kanchanaburi);34 provinces have reported 20 or fewer cases in 2015. Achieving malaria elimination will require adaption of existing interventions to better target key populations, especially along border areas. New strategies and challenges to achieve malaria elimination will be discussed.

Keywords: Malaria, Control, Elimination, Surveillance, Profile

MOLECULAR EPIDEMIOLOGY OF ANTI-MALARIAL RESISTANCE IN MYANMAR

Zin Zayar Win [1]

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Understanding the dynamics of *Plasmodium falciparum* parasite population in terms of drug resistance is of paramount importance especially in Myanmar, a country with increasing prevalence of artemisinin resistant malaria. Here, I attempt to clarify how change of drug treatment policy in Myanmar, particularly dramatic increase in artemisinin usage, affected population dynamics of P. falciparum. Blood samples from patients infected with P. falciparum were collected in two periods; before (2002-5) and after (2013), the official implementation of artemisinin combination therapies (ACTs) in Myanmar. Variants of kelch 13, pfcrt, pfmdr1, dhfr, and dhps were determined and microsatellite markers flanking above genes were assessed. A significant increase in the prevalence of parasites harboring kelch 13 mutation was observed from 8.6% in 2002-2005 to 24% in 2013 (p = 0.0031). One novel mutation (Y511H) was observed in the 14.8% of samples in 2013, suggesting potential selection after the ACTs initiation. Almost all fixation of pfcrt K76T and overwhelming of highly resistant types of dhfr and dhps mutant parasites persisted even after the withdrawal of official chloroquine and pyrimethamine/sulfadoxine usage. Lineages of chloroquine and pyrimethamine/sulfadoxine resistant parasites were shared between Myanmar and other endemic countries in Asia and Africa. This study suggests that artemisinin resistance arose independently and was selected in Myanmar, in sharp contrast to chloroquine and pyrimethamine/sulfadoxine resistance. Change of malaria treatment regime has not induced any sign of reduction of chloroquine and SP resistant *P. falciparum*.

Keywords: Malaria, *Plasmodium falciparum*, Drug resistance,

FRIDAY 9 DECEMBER 2016

09.00 - 10.30
Room D

S40: ENTERIC DISEASES

Chairpersons :

1. Yong Poovorawan

2. Nathamon Kosoltanapiwat

Invited speaker :

1. Toshio Kodama
"Functional analysis of *Vibrio parahaemolyticus* T3SS2 effectors"
Department of Bacterial Infections, Osaka University, Japan

2. Yong Poovorawan
"Human enterovirus infection in Thailand"
Faculty of Medicine, Chulalongkorn University
(Abstract on paes 177)

3. Leera Kittigul
"Molecular detection and characterization of enteric viruses in bivalve shellfish in Thailand"
Department of Microbiology, Faculty of Public Health, Mahidol University

FUNCTIONAL ANALYSIS OF *VIBRIO PARAHAEMOLYTICUS* T3SS2 EFFECTORS

Toshio Kodama[1], Tetsuya Iida[1],
Sarunporn Tandhavanant[1],
Shigeaki Matsuda[1],
Hirotaka Hiyoshi[1]

[1] *Department of Bacterial Infections, Research Institute for Microbial Diseases, Osaka University*

Vibrio *parahaemolyticus* is an important pathogen that causes food-borne gastroenteritis in humans. Most clinical isolates from patients with diarrhea possess two sets of genes for the type III secretion system (T3SS) on each chromosome (T3SS1 and T3SS2). T3SS is a protein secretion system that delivers effector proteins directly into eukaryotic cells. The translocated effectors then modify certain functions of the host cell by disrupting normal cell signaling processes. Several studies using animal infection model revealed that T3SS2 of *V. parahaemolyticus* plays a critical role in enterotoxicity. Therefore, T3SS2 has been considered to be closely related to human pathogenicity. Recent studies have elucidated the biological activities of several T3SS2 effectors and their roles in virulence. Many bacterial pathogens manipulate the actin cytoskeleton of mammalian cells to establish pathogenesis. T3SS2 also causes two dramatic changes in the actin cytoskeleton in infected cells: the accumulation of F-actin beneath bacterial microcolonies and the induction of actin stress fibers. At least four T3SS2 effectors have been identified as actin cytoskeleton modification effectors. Here, I will focus on T3SS2 effectors that specifically target the actin cytoskeleton of host cells.

Keywords: *Vibrio parahaemolyticus*, effector, T3SS, enterotxicity

MOLECULAR DETECTION AND CHARACTERIZATION OF ENTERIC VIRUSES IN BIVALVE SHELLFISH IN THAILAND

Leera Kittigul [1]

[1] *Department of Microbiology, Faculty of Public Health, Mahidol University, Bangkok, Thailand.*

Enteric viruses are an important cause of shellfish-associated outbreaks. A rapid method for concentrating viruses from bivalve shellfish was developed and used in combination with RT-nested PCR to detect norovirus, rotavirus, and hepatitis A virus. The method provided high sensitivity for the detection of known norovirus GII.4 in the range of 8.8 × 10-2 – 8.8 × 102 genome copies/g and group A rotavirus at 1.14 genome copies/g of digestive tissues from shellfish concentrates. From August 2011 to July 2012, a total of 300 shellfish samples, including each of 100 samples from oysters, cockles, and mussels were collected. Norovirus, hepatitis A virus, and rotavirus were detected in 12.3%, 8.3%, and 8.0% of shellfish samples, respectively. Mix-infections of two or three viruses were observed in 2.7%. Norovirus and rotavirus contamination at the highest detection rate was found in oysters, whereas the detection rate of hepatitis A virus was highest in cockles. Based on DNA sequencing and phylogenetic analysis, five different genotypes of norovirus GI (GI.2, GI.3, GI.4, GI.5, and GI.9) and four different genotypes of GII (GII.1, GII.2, GII.3, and GII.4) were identified. The rotaviruses detected were classified into G1, lineage II; G3: lineage I, lineage IIIc, lineage IIId, lineage IV; G9; and G12, lineage III. These findings indicate the prevalence and the identified genotypes of enteric viruses distributing in different shellfish species and contribute to the optimization of monitoring plans to improve the preventive strategies of viral foodborne infections.

Keywords: norovirus; rotavirus; hepatitis A virus;

FRIDAY 9 DECEMBER 2016

11.00 - 11.45
Watergate Ballroom

S41: CLOSING SESSION
SORNCHAI LOOAREESUWAN MEDAL LECTURE

Chairperson :

Pratap Singhasivanon
Dean, Faculty of Tropical Medicine

Keynote Speaker :

Stefan Hans Irmfried Kappe
"Challenges and opportunities in the pursuit of a protective malaria vaccine"
Director for Translational Science, Center of Infectious Disease Research (Seattle, USA)

11.45-12.30 Presentation of Awards and Closing Remarks

CHALLENGES AND OPPORTUNITIES IN THE PURSUIT OF A PROTECTIVE MALARIA VACCINE

Stefan H.I. Kappe[1]

[1] *Center for Infectious Disease Research and Department of Global Health, University of Washington Seattle WA, USA*

A highly efficacious malaria vaccine would be considered a milestone of modern Medicine, yet has so far eluted research and development efforts. This can be attributed to the extreme complexity of the malaria parasites, presenting with a multi-stage life cycle, high genome complexity and the parasites sophisticated immune evasion measures, particularly antigenic variation during pathogenic blood stage infection. However, the pre-erythrocytic (PE) early infection forms of the parasite exhibit relatively invariant proteomes, and are attractive vaccine targets as they offer multiple points of immune system attack. Humoral immune responses that produce antibodies can target the invasive PE sporozoite forms of the parasite and block their infection of the liver. Cellular immune responses, particularly CD8 T cells can eliminate the intracellular PE liver stage forms that develop from sporozoites after hepatocyte infection. The combination of these immune responses is critical to achieve complete protection against infection and is currently only attainable by immunization with whole viable attenuated sporozoites that infect the liver, develop as liver stages and cannot progress to blood stage infection. We find that the biological features of whole sporozoite vaccines dictate their potency and efficacy. I will describe our research efforts to develop a designed, genetically engineered, attenuated whole parasite (GAP) vaccine. I will discuss how we utilize new insights into the biology and immunology of PE infection to optimize the design of attenuated parasites in order to create a Plasmodium falciparum vaccine strain that is safe and retains optimal immunogenicity for vaccination in humans.

Add S5-1

QIAGEN'S SAMPLE TO INSIGHT FOR DETECTION OF INFECTIOUS DISEASES

Arun Buaklin [1]

[1] *QIAGEN Thailand (Senior Sales Application Specialist)*

Renowned for being the world's leading provider of innovative sample and assay technologies as well as having comprehensive product range, QIAGEN's automated Sample to Insight solutions offer standardization in every step of the workflow and deliver reproducible and high-quality data. QIAGEN provides seamless integrated solution for automation with optimized chemistries that helps to quickly convert biological samples into valuable molecular insights with a broad portfolio of molecular test to support research in life sciences, applied testing, and molecular diagnostics. Automation with the QIAsymphony RGQ, new era of automation, integrates automated sample preparation and assay setup with detection on the Rotor-Gene Q, giving versatile testing system and maximizing efficiency in detection. Complete validated workflows provide standardized and reliable solutions for routine testing, insight for healthcare application with profiling of infection, prevention of diseases, and setting standards in academic laboratories with cutting-edge technologies keeping with the QIAGEN goal of making improvements in life possible.

Keywords: QIAGEN's automation, Sample to Insight

Nat Malainual [1]

[1] *Department of Parasitology, Faculty of Medicine Siriraj Hospital, Mahidol University*

Add S28-3

PUBLIC-PRIVATE-PARTNERSHIP ON ALLERGEN VACCINE DEVELOPMENT

Prevalence of allergies in Thailand has been increasing nowadays. Approximately 30% of Thais, especially young children, is suffered from allergic symptoms. Not only the cost of medication but also the quality of life that patients are affected. To effectively treat the allergic patients, the known specific allergens have to be known in order to avoid the exposure or deviate the immune system by immunotherapy. At present, the allergenic extracts used in most allergic clinics are imported. Therefore, reseachers in Mahidol University in coperate with the pharmaceutical company (Greater Pharma, Co.,Ltd.) are developing the local allergenic reagents since 2008. Of which, these pharmaceutical products will be qualified by Thai FDA. Recently, all related documents have been submitted, whereas the industrial-scale production is also being improved. Talent Mobility program and funding run by the Ministry of Science and Technology, and Ministry of Education can enhance this collaboration into success. Expectedly, allergic patients in Thailand will be able to access to the lower cost of disease diagnosis and treatment soon.

Add S29-3

CHOLANGIOCARCINOMA SCREENING AND CARE PROGRAM (CASCAP): HEALTH INNOVATION TO FIGHT THE LIVER FLUKE AND CHOLANGIOCARCINOMA

Narong Khuntikeo[1,5,8],
Watcharin Loilome[2,5,8],
Bandit Thinkhamrop[6,7,8],
Paiboon Sitthithaworn[3,5,8],
Thidarut Boonmars[3,5,8],
Nittaya Chamadol[4,5,8],
Nisana Namwat[2,5,8] ,
Puangrat Yongvanit[5,8]

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Cholangiocarcinoma (CCA) is bile duct cancer caused by liver fluke *(Opisthorchis viverrini)* infection. It is an extremely aggressive, usually fatal disease. There are estimated 14,000 cases annually in the northeast Thailand. Khon Kaen University; the largest and leading research university in the northeast region of Thailand, has made it a priority to solve these problems and in the occasion of the 50th anniversary and "50 years of Social Devotion" have selected Cholangiocarcinoma Screening and Care Program (CASCAP) to take part in this mission. This program aims to promote disease prevention, screening, diagnosis and treatment, research, improving treatments and efficacy, and monitoring to evaluate the results of treatment. The CASCAP aims to resolve the problems of liver fluke and CCA from primary, secondary and tertiary levels. In the primary level, the diagnosis and treatment of liver fluke infection will be improved by the development of urine detection methods which can identify liver fluke antigens that are excreted in urine. In addition, the development of parasite-free fish with a standard process to ensure that fish which are produced can be safely used for cooking and processing. The primary level will also focus on parasite elimination in the intermediate hosts such as dogs and cats and improvements in sewerage sanitation systems. All of these things will help to cut off the life cycle of the liver fluke. Moreover, there are educational courses for children and youth to learn about liver fluke, cholangiocarcinoma, and practical procedures to avoid the disease. In the secondary level, the risk group screening and surveillance by ultrasonography is performed. In the tertiary level, CCA curative and palliative treatment as well as enabling patient's better access chemotherapeutic treatment will be developed. Moreover, a network for the diagnosis and referral for comprehensive treatment will be developed. These three levels are connected by the Isan Cohort database system which is able to extend data from the existing hospital network throughout the entire northeast region of Thailand. The diagnosis and treatment of high risk people and CCA patients can be monitored using the system and database supporting as many as 20 million people. Based on CASCAP work, The Cabinet of Thailand agreed to implement a 10-year Strategic Plan for the elimination of Liver Fluke Parasite and Cholangiocarcinoma (2016-2026) proposed by the Ministry of Public Health. Therefore, this work is an example of translational research which applies research results to solve the problems of the country.

Keywords: *Opisthorchis viverrini*, Cholangiocarcinoma, Cancer screening, Cancer registry, Cohort study

Add S2-2

MMV'S STRATEGY TO TACKLE ART RESISTANCE

Didier Leroy [1]

[1] *Medicines for Malaria Venture, Switzerland*

Medicines for Malaria Venture (MMV), a not-for-profit public-private partnership, was established as a foundation in Switzerland in 1999. Its mission is to reduce the burden of malaria in disease-endemic countries by discovering, developing and facilitating delivery of new, effective and affordable antimalarial drugs. MMV's vision is a world in which these innovative medicines will cure and protect the vulnerable and under-served populations at risk of malaria, and help to ultimately eradicate this terrible disease. MMV's drug research and development portfolio focuses specifically on medicines that will meet the following criteria: efficacy against drug-resistant strains of *Plasmodium falciparum*, potential for intermittent treatments (infants and pregnant women), safety in very young children, safety in pregnancy, efficacy against Plasmodium vivax (including radical cure), efficacy against severe malaria, and transmission-blocking properties. The presentation will describe the current combination therapies and new drug candidates that target the malaria eradication agenda in MMV's product portfolio, outlining their respective target product profiles and target candidate profiles. In particular, it will discuss current challenges to eradicating the disease and the urgent need to develop next-generation antimalarials that are expected to contain resistance to artemisinin and piperaquine in the Greater Mekong Subregion.

Add S5-2

AN INTRODUCTION TO QIAGEN'S SAMPLE TO INSIGHT SOLUTIONS FOR NGS

Andrea Wijeweera [1]

[1] *QIAGEN Singapore (Sales Application Specialist, BRC – SEA)*

Metagenomics and microbiome analysis are amongst two of the fastest growing applications in next generation sequencing. With the ability to profile and map genomes of complex microbial communities present within environmental, stool, oral, and other sample types – NGS offers a powerful new approach that enables researchers to gain insight into different areas of microbial and infectious disease research. However, to gain meaningful insights for any NGS experiment, efficient conversion of sample DNA to library without the introduction of sequence bias is important. This seminar will introduce innovative technologies in QIAGEN's QIAseq library preparation solutions for metagenomics and infectious disease research. Whether you're starting from single cells, 16s rRNA amplicons or gDNA for whole genome analysis, QIAseq technologies will enable the generation of high-quality libraries to capture genomic diversity of your samples in the most unbiased and streamlined way possible.

Add S29-2

ANIMAL RESERVOIRS AS A SOURCE OF LIVER FLUKE TRANSMISSION: ROLES IN CONTROL PROGRAM

Sirikachorn Tangkawattana[1,2]

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[2] *WHO Collaborating Centre for Research and Control of Opisthorchiasis (Southeast Asian liver fluke disease), Tropical Disease Research Center (TDRC), Khon Kaen University, Khon Kaen 40002, Thailand*

Liver fluke (*Opisthorchiasis*), caused by *Opisthorchis viverrini*, is one among the most important fish-borne diseases in Southeast Asian. The disease has been proven to be a major cause of cholangiocarcinoma. Although human is the definite host of the parasite, dog and cat have been described as the major reservoir hosts of this parasite. Comparatively, cat is confirmed to be the predominant animal reservoir, especially in the endemic areas locating in wetland complex. Pertaining to our investigation in the past years, those infected cats, which are feral or unowned cats in majority, rarely show clinical signs and abnormal hematological profile, regardless of infection severity. Since eggs of the parasite are passed into the environment with feces, significant role in disease transmission of the feline reservoir was attended. Multidisciplinary approach, participatory epidemiology, questionnaire using interviewing and GPS tracking on the reservoir animal were applied. The positive role in terms of spreading parasite eggs into their surroundings is confirmed. In addition, humidity or water, and intermediate hosts, such as Bithynia snails and Cyprinoid fish, are essential for the laid eggs to hatch and develop. It is a matter of fact that these essential elements are plenteously in the wetland. Thus, effective intervention for the elimination of this parasite in the environments should not conduct merely by lifting sanitary standard and giving effective and regular medical treatments in human patients, but also deworming in those reservoirs. In conclusion, effective control program of opisthorchiasis should perform concomitantly among human, environment and animal reservoirs.

Keywords: animal reservoir, liver fluke, Opisthorchiasis, control

Add S29-1

RECENT ADVANCES IN RESEARCH AND CONTROL OF LIVER FLUKES AND CHOLANGIOCARCINOMA

Banchob Sripa [1]

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Liver fluke infections caused by *Clonorchis sinensis* and *Opisthorchis viverrini* are major foodborne parasitic zoonotic diseases with over 30 million people infected. The infections are associated with several hepatobiliary diseases including cholangiocarcinoma (CCA), a fatal liver cancer arising from the bile duct epithelium. *Opisthorchiasis* caused by *Opisthorchis viverrini* infection is a major public health in Thailand and neighboring Mekong countries. The infection is associated with cholangitis, cholecystitis, gallstones, hepatomegaly, periductal fibrosis and cholangiocarcinoma (CCA). The rates of CCA in regions where the parasite is endemic are unprecedented. Host-parasite interaction by liver fluke's tegument and excretory-secretory products through endocytosis pathway drive biliary epithelial proliferation and production of inflammatory cytokines. This induces severe inflammation of the bile ducts, resulting in oxidative and nitrative DNA damage of the biliary epithelium. Opisthorchis specific pro-inflammatory cytokine/chemokine, specifically IL-6 and IL-8 production through biliary TLR4 activation was observed, supports inflammatory mechanism of the infected bile ducts. Elevation of IL-6 production is associated with advanced periductal fibrosis in infected individuals. IL-6 can induce inflammation, anti-apoptosis, cell transformation and eventually malignancy. Moreover, liver fluke excretory-secretory products can inhibit biliary cell apoptosis when cells underwent oxidative stress. These cells are thus stimulated to uncontrolled hyper-proliferate, providing an additional potential mechanism by which inflamed biliary epithelial cells become neoplastic in opisthorchiasis-associated CCA. For liver fluke control, extensive community-based control program using an EcoHealth/One Health approach was carried out at endemic Lawa Lake of Khon Kaen province with successful results. This program has been carried out for over 6 years using chemotherapy, novel intensive health education methods both in the communities and in schools, ecosystem monitoring and active community participation. As a result, the infection rate in the more than 10 villages surrounding the Lake has declined to more than one half of the average of 60% as estimated by a baseline survey. People in the area gained more knowledge of the liver fluke. Strikingly, the Cyprinid fish species, which are the intermediate host, now show less than 1% prevalence compared to a maximum of 70% during the baseline survey. This liver fluke control program, now named "Lawa model," has become recognized nationally and internationally. Lawa model is one of the two showcases of successful helminth control programs of WHO-NZD4 meeting. This integrated control program is being expanded to other parts of Thailand and, in the future, neighboring Mekong countries

Yong Poovorawan[1]

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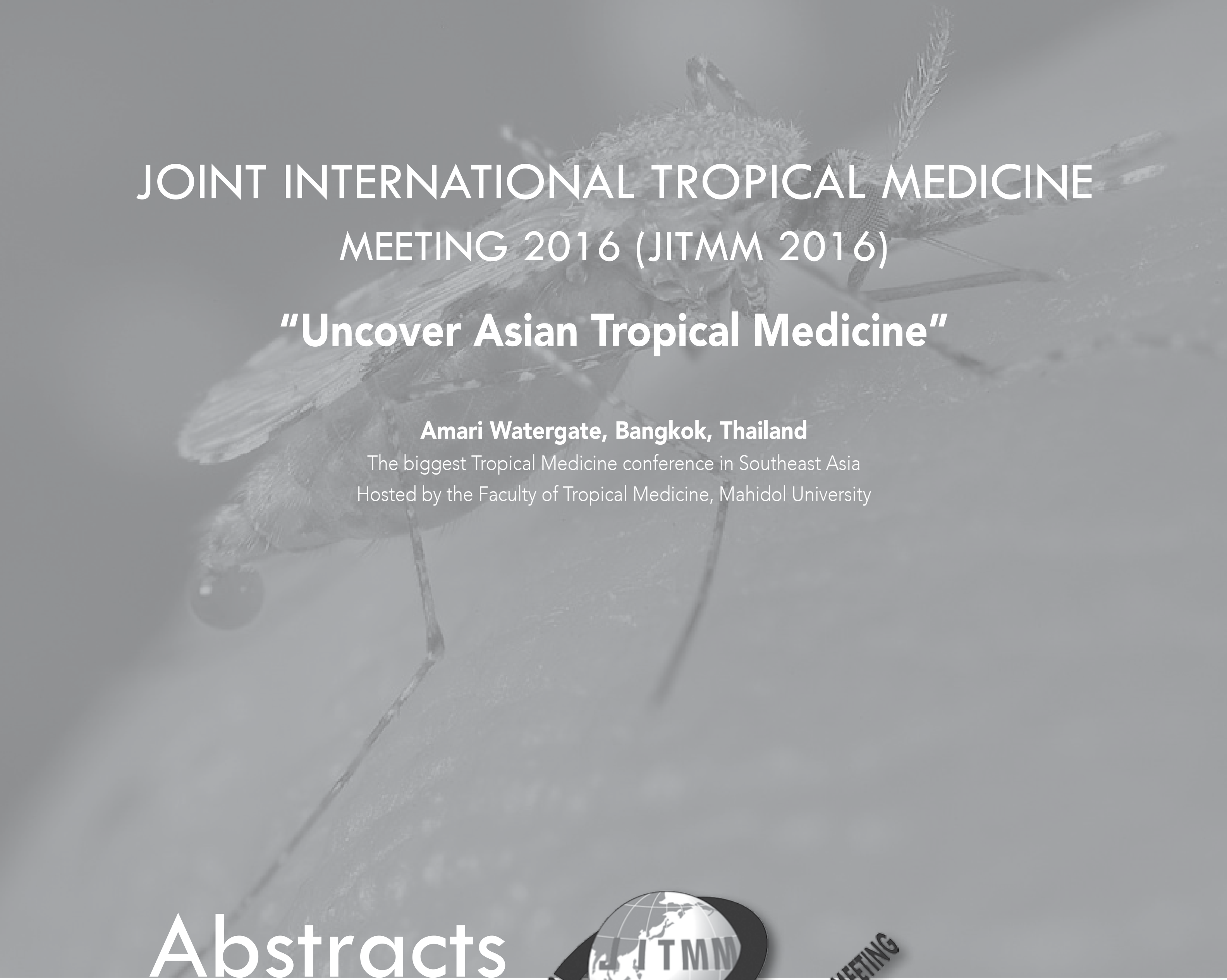
Add S40-2

HUMAN ENTEROVIRUS INFECTION IN THAILAND

Human enteroviruses (EV) are members of the family Picornaviridae and are comprised of 7 species: EV-A (25 types), EV-B (63 types), EV-C (23 types), EV-D (5 types) and human rhinovirus (HRV)-A (80 serotypes), HRV-B (32 serotypes) and HRV-C (55 serotypes). EV is a small non-enveloped virus ~30 nm in diameter). It possesses a positive single-stranded RNA genome of approximately ~7.5 kb in length encapsulated by a highly structured icosahedral capsid. EV is transmitted predominantly via oral-fecal route and contact with virus-contaminated oral secretions and vesicular fluid, surfaces and fomites. Transmission can also occur directly through patient's aerosolized respiratory droplets. Most infections are often asymptomatic, and even symptoms are mild. Clinical manifestations of human EV infection vary widely. Severe infection can involve the heart, pancreas, and the central nervous system, and systemic disease can be fatal or result in lasting organ dysfunction such as encephalitis and myocarditis. In Thailand, hand, foot and mouth disease and herpangina are the most common enterovirus infection in young children and are highly prevalent in the rainy season between June and September. In 2012, there was a large-scale outbreak caused by coxsackievirus A6 (CV-A6), although EV71 was also found in sporadic cases. Another enterovirus infection caused by CV-A24 resulted in an epidemic of acute hemorrhagic conjunctivitis (AHC) in 2014. Recently, an EV-D68 infection caused an outbreak in North America and resulted in clinical flaccid paralysis in some extreme cases. We detected EV-D68 in respiratory samples (2009-2015) from Thai patients with influenza-like illness and determined that the prevalence in Thailand was ~0.8-1.4%. None of the patients developed neurological complications. Additionally, human EVs such as HRV and poliovirus were detected in the stool of patients with acute gastroenteritis, although the polioviruses found were of vaccine strains types 1, 2, and 3. Although human EV infection can cause result in a wide spectrum of diseases, epidemiological data suggest that particular groups of human EVs are associated with specific diseases. The diverse genetic variability and emerging new variants of human EV will continue to present a challenge to the control, prevention, and the development of antivirals and vaccines shortly.

NOTES

NOTES



JOINT INTERNATIONAL TROPICAL MEDICINE MEETING 2016 (JITMM 2016)

"Uncover Asian Tropical Medicine"

Amari Watergate, Bangkok, Thailand
The biggest Tropical Medicine conference in Southeast Asia
Hosted by the Faculty of Tropical Medicine, Mahidol University

Abstracts

Poster PRESENTATIONS

7-9 December 2016

ORGANIZERS :

- Faculty of Tropical Medicine, Mahidol University
- SEAMEO TROPMED Network
- TROPMED Alumni Association
- The Parasitology and Tropical Medicine Association of Thailand

CO-ORGANIZERS :

- Department of Disease Control Ministry of Public Health (MOPH)
- Mahidol - Oxford Tropical Medicine Research Unit (MORU)

LIST OF Poster Presentations

Poster no.	Title	Presenter	Pages
1	Effects of freezer storage temperatures on the viability and infectivity of *Opisthorchis viverrini* metacercaria	*Wilawan Pumidonming*	**9**
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Poster No. 1

EFFECTS OF FREEZER STORAGE TEMPERATURES ON THE VIABILITY AND INFECTIVITY OF *OPISTHORCHIS VIVERRINI* METACERCARIA

Opisthorchiasis causes by *Opisthorchis viverrini* is an important food-borne parasitic zoonosis in South East Asian countries. Infection in humans occurs through consumption of raw or undercooked dishes made from cyprinid fish containing the viable metacercaria, infective stage of *O. viverrini*. Cooking processes to reduce viability and infectivity of *O. viverrini* metacercaria in the fish are required for prevention the infection in humans. In this study, we investigated effects of freezer storgae temperature on viability and infectivity of *O. viverrini* metacercaria. Cyprinid fish contained *O. viverrini* metacercaria were kept at 4°C, 0°C, -20°C for 12 hr, 48 hr. Then *O. viverrini* metacercaria were isolated and examined for viability under stereomicroscope and infectivity using hamsters. Results showed that complete and viable metacercaria were not found in the fish stored at 0°C and -20°C for 24 hr. Infectivity of *O. viverrini* metacercaria stored at 0°C and -20° C for atleast 24 hr was 0%. Result from this study can be used for cyprinid fish preparation for traditinal raw or undercooked dishes in endemic area to reduce O. viverrini infection.

Keywords: *Opisthorchis viverrini*, metacercariae, freezing temperature

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Poster no. 4

PRIMER DEVELOPMENT FOR DISCRIMATION OF LIVER FLUKES FAMILY OPISTHORCHIIDAE, USING POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT LENGTH POLYMORPHISM (PCR-RFLP)

Liver flukes in family Opisthorchiidae were a major public health problem in Southeast Asia. There were 2 species, *Opisthorchis viverrini* and *Clonorchis sinensis*, which were reported as the human pathogens. In the recent report, *Opisthorchis lobatus* was discovered in Lao PDR and had characteristics similar to *O.viverrini*. It was hardly to identify by morphological study. In this study, species-specific primers were developed for discriminate between species of liver flukes in family Opisthorchiidae. Adult worm of *O. viverrini*, *O. lobatus* and *C. sinensis* were extracting total genomic DNA. Designed primers (N-Ov-Cs-COI-F&R primers) amplified partial cytochrome *c* oxidase subunit I (COI) fragments of three worms. The genetic characters among of *O. viverrini*, *O. lobatus* and *C. sinensis* were distinguished by PCR-RFLP method. Polymerase chain reaction (PCR) amplicons were generated with low genomic DNA concentration ($\approx 10^{-6}$ng) at 50 ^{0}C annealing temperatures. Restriction site in COI sequences *O. viverrini*, *O. lobatus* and *C. sinensis* can be distinguished by enzyme BsrI. The BsrI restriction site profile obtained three fragment of 43, 162 and 219 bp from *O. viverrini*, two fragments of 43 and 381 bp from *O. lobatus*, two fragments of 102 and 322 bp from *C. sinensis*. The PCR-RFLP profile can use for diagnosing mixed of *O. viverrini*, *O. lobatus* and *C. sinensis* infections in endemic areas and can be applied to epidemiological studies.

Keywords: Opistherochiidae, *Opisthorchis viverrini*, Opisthorchis lobatus, Clonorchis sinensis, PCR-RFLP.

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Poster no. 5

NA+-TAUROCHOLATE CO-TRANSPORTING POLYPEPTIDE OF CLONORCHIS SINENSIS: 3D STRUCTURE AND FUNCTIONALITY

Na$^+$-Taurocholate Co-transporting Polypeptide (NTCP, SLC10A1) plays a key role in the bile acid recycling. The bile acids uptake activity of NTCP is electrogenically coupled with co-transport of sodium ion. When *Clonorchis sinensis* live in the bile duct, *C. sinensis* NTCP (CsNTCP) could play an important role for its physico-metabolism. Its cDNA 1,641 bp long encoded a putative polypeptide of 546 amino residues. Tertiary structure of CsNTCP was generated by homology modeling in region of 185-492 aa using a template, *Neisseria meningitidis* (PDB ID: 1zuy_A). Remaining regions were predicted to be disordered. The modeled structure was further refined and validated as a reliable model. CsNTCP had 10 transmembrane (TM) regions forming two domains: core domain consisted of TM3-5 and TM8-10 and panel domain formed with TM1, 2, 6 and 7. In the CsNTCP, substrate-binding sites for sodium and taurocholate were conserved. Compounds selectively docking to active pocket were selected through structure-based virtual screening. A chimeric polypeptide (24 kDa) of two antigenic and soluble was bacterially produced and used to immune mice. CsNTCP was localized in basement of tegument, basal membrane of intestine of epithelium, excretory bladder wall and mesenchymal tissues by using mouse-immune sera, contributing to bile acid transport. Taken together, these results provide information for deeper understanding on structural and functional characteristics of CsNTCP and homologues of flukes. Two compounds are proposed as putative inhibitors to CsNTCP and deserve further studies for anthelminthics.

Keywords: Na+-Taurocholate

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Poster no. 6

MOLECULAR AND MORPHOLOGICAL CHARACTERIZATION OF *FASCIOLA* SPP. ADULT WORMS COLLECTED FROM CATTLE SLAUGHTERED IN HANOI, NORTH VIETNAM

A total of 360 gall bladders from cows and buffaloes from slaughtered in Hanoi were examined for the presence of adults and/or eggs of *Fasciola* spp. The second internal transcribed spacer (ITS-2) of nuclear ribosomal DNA (rDNA) and mitochondrial genes (Cox1) were amplified from specimens belonging to 4 distinct phenotypes by polymerase chain reaction (PCR), and the representative amplicons were sequenced. A significant higher prevalence of *Fasciola* spp. infection was observed in cattle (63.53%; 216/340) in comparison with buffaloes (30%; 6/20) (Chi2=8.98; P-value=0.003). In a high proportion of gall bladders (38.3%; 138/360), only eggs were observed. Four different phenotypes were observed: type 1 (long-wide; 38.95±2.83 – 13.4±0.71), type 2 (long-narrow; 43.07±4.41– 11.01-1.15), type 3 (medium-narrow; 30.39±1.45– 7.86±0.70), and type 4 (medium-wide; 25.43±2.08– 11.7±1.4). Among them, type 4 presented a phenotype compatible with *Fasciola hepatica* while the others were compatible with *F. gigantica*. Molecular characterization based on Cox1 sequences indicated that all *Fasciola* types fall into *F. gigantica* cluster. However, ITS-2 sequences of *Fasciola* type 1, 2, 3 fall into *F. gigantica* cluster while Fasciola type 4 and Belgian isolate fall into *F. hepatica* cluster. *Fasciola* type 4 sequence showed two peaks at 207, 327 nucleotide positions. In addition, 7 different nucleotide positions between *Fasciola* type 4 and other types were observed. By morphometric and molecular analysis, we identified *Fasciola* type 4 as being a hybrid form of *F. gigantica* and *F. hepatica*.

Keywords: Fasciola gigantica, hybrid, phenotype, ITS-2, Cox1, slaughterhouse, Vietnam

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Poster no. 7

MOLECULAR IDENTIFICATION OF *FASCIOLA* SPP. FROM THAILAND BASED ON PCR-RFLP

Fasciola spp. is a large liver fluke in family Fasciolidae (Railliet, 1895), subfamily Fasciolinae (Stiles et Hassall, 1898). These parasites have been known as a pathogen of human and livestock. *Fasciola hepatica* Linnaeus, 1758 and *F. gigantica* Cobbold, 1855 are the cause of human fascioliasis. The infection of *Fasciola* has become increasingly important because of the recent widespread emergence related to climate change and human activity, while the disease has been overlooked. Currently, there were many reports of *Fasciola* intermediate form, genetically mixed between *F. gigantica* and *F. hepatica*. Although, many research areas to study in *Fasciola* spp. has been conducted, the accuracy to identify the *Fasciola* based on morphology has still been problematic. To solve this problem, many genetic markers have been applied to molecular identification such as the ribosomal internal transcribed spacer 1 and 2 (ITS1 and ITS2 rDNA) and mitochondrial gene sequences. Among the molecular markers, which used to apply for the molecular identification of *Fasciola* species, there is no information that what kind of markers are appropriate for. In this study, we aimed to evaluate the utility of such molecular markers, which have been used to identify the *Fasciola* spp. The PCR amplicons of ITS1, ITS2 and *COX*1 sequences were conducted and then studied based on PCR-RFLP method. The results indicated that digested ITS1 and ITS2 amplicon could show clearer band patterns than the digested *COX*1 amplicon. Therefore, this study concluded that the mitochondrial *COX*1 gene may not be the good genetic marker for molecular identification of *Fasciola* spp.

Keywords: *Fasciola* spp., Molecular identification, Molecular genetic marker, PCR-RFLP

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Poster no. 8

IDENTIFICATION OF *SCHISTOSOMA MEKONGI* EGG IMMUNOGENS BY AN IMMUNOPROTEOMICS APPROACH

Schistosomiasis is one of the most important human parasitic diseases caused by parasites in *Schistosoma* species. In Sounth-east Asia, *Schistosoma mekongi* is endemic in the lower Mekong river basin in Laos, Cambodia and northern Thailand. The major of symptoms of the disease is caused by the parasite eggs trapped in host tissues and formed granuloma formation resulted from the host induced immune response around the parasite eggs. The interaction between egg proteins and host immune system is important to be explored for further development of schistosomiasis diagnosis. In this study, crude egg antigens called soluble egg antigens (SEAs) were separated by one-dimension (1D) gel electrophoresis and analyzed by immunoblotting. Immunoglobulin IgG and IgM from uninfected and infected mouse sera at 2, 4 and 8 weeks after infection were used for schistosoma antigen detection. The evidence from this study suggested that only IgG at 4 and 8 weeks and IgM at 4 and 8 weeks were deteced the interaction between mouse immunoglobulin and parasite proteins using immunoblotting technique. Subsequently, tryptic digestion and LC-MS/MSanalysis were performed for protein identification. This study has found that mouse antibodies reacted with several *S. mekongi* egg proteins for example antioxidant proteins (thioredoxin peroxidase, 26kDa glutathione S- transferase (GST)), chaperone (70kDa heat shock protein) and major egg antigen. These findings enhance our understanding of host-parasite interaction. The obtained results are potential candidate proteins for *S. mekongi* infection diagnosis.

Keywords: Schistosoma mekongi, proteomic

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Poster no. 9

CRISPR/CAS9-BASED GENE EDITING IN SCHISTOSOMES

Schistosomiasis is the most important of the neglected tropical diseases caused by helminth parasites. Schistosomes live within the blood vessels of the human host. The hepatointestinal form of this debilitating disease results from a chronic infection with *Schistosoma mansoni*, *S. japonicum* and *S. mekongi* whereas infection with *S. haematobium* causes urogenital schistosomiasis. Events that lead to egg granuloma formation (the major cause of pathology) and other aspects pathogenesis remain poorly understood. We investigated the potential of the newly described CRISPR (clustered regularly interspaced short palindromic repeat)-Cas phenomena to edit the schistosome genome. Thus far we have targeted gene loci encoding major egg proteins, including omega-1, kappa 5 and Sm16, by introducing *Streptococcus pyogenes* Cas9-guide RNA ribonuclease complexes by square wave electroporation into developmental stages of *S. mansoni* in vitro. Quantitative PCRs used to estimate the insertion-deletion (INDEL) in the schistosome genome revealed gene knockout mutation rates ranging from 2-15% compared to control worms exposed to the Cas9 nuclease alone. Levels of messenger RNAs from the mutated genes were markedly reduced. In addition, using a donor single stranded oligoDNA that included homologous arms of ~50 nucleotides in length on both the 5' and the 3' side immediately adjacent the target double stranded break (DSB) site of the chromosome, along with a short tag region of 25 nt included between the two homology arms, we successfully epitope tagged the *omega-1* locus as demonstrated by PCRs. Together the findings revealed that both gene knockout, presumably mediated by non-homologous end joining (NHEJ) and gene knock-in mediated by homology directed repair (HDR) were active in these plathelminth

Keywords: gene editing, CRISPR, Cas 9

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Poster no. 11

IDENTIFYING VEGF-460 GENE POLYMORPHISMS IN FILARIASIS PATIENTS IN SOUTH BORNEO, INDONESIA

Secondary lymphoedema (LE) for filariasis are the most common and affects only a portion of the 120 million people infected with *Wuchereria bancrofti*, *Brugia malayi* and *Brugia timori*. Vascular endothelial growth factor (VEGF) was originally described as vascular permeability factor and is a relatively specific endothelial cell mitogen and chemotactic factor that is important in a wide variety of angiogenesis processes. Immune responses that are triggered by the filarial excretory-secretory product result in the activation of VEGF, thus promoting lymph vessel hyperplasia as a first step to lymphoedema development. The objective of this research was to study single nuclear polymorphism of VEGF-460 gene in filariasis patients in three endemic lymphatic filariasis (LF) villages, Balangan district, South Borneo, Indonesia. Blood samples taken by finger prick test from 50 acute filarial subjects were use to perform PCR and continued by sequencing. The microfilaria density count from 16 to 500 mf/60 µl blood and microfilaria (MF) rate in that district is 9%. PCR result in 50 samples obtained prevalence of heterozygous (C/T) 42%, homozygous variant (C/T) 42%, and homozygous variant (C/C) 8%. According to previous studies, polymorphisms of VEGF-460 gene were known associated with lymphoedema development in lymphatic filariasis. The study showed that plasma levels of VEGF-460 were significantly higher in subjects with the C/C genotype. In our study, C/C genotype was found only 8% from 50 patients with filariasis. Despite lower prevalence of C/C genotype, prevention is still needed to avoid filariasis and decreased morbidity.

Keywords: Lymphatic filariasis, VEFG-460 SNP

Poster no. 12

BRUGIA MALAYI MICROFILARIA PERIODICITY IN SOUTH BORNEO

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Brugia malayi, with prevalence more than 70% in Indonesia that cause the morbidity in lymphatic filariasis. The periodicity of *Brugia malayi* microfilaria also plays a vital role in the disease transmission and is related to the mosquitoes' blood sucking habit. The aim of this study is to see the periodicity of *Brugia malayi*. An observational, cross-sectional study was carried out in October 2014. There were 4 people that have been identified microfilaria positive were asked to join the study voluntarily. The finger blood approximately 1 cc were taken in 3 times a day as in 6 am, 1 pm and 11 pm. The measured blood samples of 60 mm^3 (20 mm^3/line) and stained with giemsa. The identification and counting of microfilaria was carried out. All of the volunteer were indigenous inhabitants who engaged at the rubber plantation site from 5 am to 12 pm. All of the subjects have physical contact directly with the vector as they did not have personal protective equipment. The microfilaria count in morning ranged from 9 mf to 121/60 mm^3 blood The microfilaria count in noon ranged from 14 mf to 121 mf/60 mm^3 blood. The microfilaria count in night ranged from 20 mf to 180/60 mm^3 blood.The periodicity of Brugia malayi is non periodic.

Keywords: *Brugia malayi* microfilaria, periodicity

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Poster no. 13

SELENIUM DEFICIENCY AMONG LYMPHATIC FILARIASIS IN INDONESIA

In Indonesia, *Brugia malayi* is the major species cause of filariasis and remains as a major public health issue. Based on Health National report (2015), microfilaria rate (mf) was high, 1-20%. Mass drug administration (MDA) anually for 5 years if mf rate in one district more than 1%. Infection of variety species of helminths in human host always induce the common pathway in immune response. Selenium (Se) as a micronutrient plays important role in immune system to fight against parasite. The aim of study was to explore selenium level among 65 Lymphatic filariasis (LF) subjects from October 2014 to May 2015. They were from 3 villages of Balangan district, South Borneo, with mf rate 9% and have not perfomed MDA until now. Selenium level was measured by ICP-MS procedure for hair sample. The median age were 45 years (range 16 to 65) and majority (71%) were mf positive. Among them, whose positive mf and Se deficiency were 63%, 0.3±0.05 μg/g compared to 26% deficiency (0.24±0.045μg/g) butmf negative. Good sources of selenium are seafood, organ and muscle meats, however rarely consumed by all of the subjects. On the contrary, they frequently have vegetables as a daily food, as fruits and vegetables are low in selenium, due to the poverty. Almost 90 % of all subjects were labor in rubber plantation with low income. Selenium supplementation can be considered to enhance selenium level to support the body's natural defence system due to filariasis infection.

Keywords: indonesia, lymphatic filariasis, selenium deficiency

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Poster no. 14

DETECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNP) CODON 200 BETA TUBULIN GENE IN *ASCARIS LUMBRICOIDES* AND *TRICHURIS TRICHIURA* FROM EAST NUSA TENGGARA, INDONESIA

Soil transmitted Helminth (STH) infection is still highly prevalent in Indonesia. The current national elimination strategy is mass administration of broad-spectrum anthelmintics as recomended by WHO. There is a concern that the repeated use of benzimidazole drugs in long term may cause resistance or decreasing of drug efficiency. Among the contributing factors is the presence of single nucleotide polymorphism (SNP) codon 200 beta tubulin gene of the worm which subtitutes phenylalanine to tyrosine (TTC to TAC). This is the first study in Indonesia aiming to determine the profile of beta tubulin gene codon 200 in *Ascaris lumbricoides (A. lumbricoides)* and *Trichuris trichiura (T. trichiura)* from a treatment naïve human population in East Nusa Tenggara, Indonesia. DNA from stool samples of infected individuals or from worm tissues were isolated, and subsequently amplified by PCR. Sanger sequencing was performed only on the successfull PCR result (two *A. lumbricoides* and one *T. trichiura* worms). Next the alignment of sequences with available references was done to obtain the bases of beta tubulin around codon 200. The bases in codon 200 beta tubulin gene from two *A. lumbricoides* and one *T. trichiura* worms were TTC. The result from this study showed that no SNP was detected from the two species of worms; however larger sample size will be needed to confirm the finding in the same worm population in East Nusa Tenggara, Indonesia.

Keywords: beta tubulin, SNP codon 200

Poster no. 15

LONGITUDINAL STUDY OF SOIL-TRANSMITTED HELMINTH INFECTIONS AMONG PRIMARY SCHOOL CHILDREN AT THA-PYAY-CHAUNG VILLAGE, NAY PYI TAW

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A longitudinal study of soil-transmitted helminth infections in primary school children at Tha-Pyay-Chaung village was conducted with the objectives to find out its prevalence, intensity, health and developmental consequences and effects of health knowledge, practice and preventive chemotherapy towards the burden. The study has been carrying out for more than four years upon 170 to 200 children. Modified Kato-Katz technique was used for parasitological analysis and hemoglobin level and blood film were examined for hematological analysis. Deworming with albendazole 400 mg was used as intervention. Children had high STH infection rate during initial assessment. Among various helminthes targeted in this study, *Ascaris lumbricoides* was found predominantly with the prevalence of 17.5% initially which fell to 2.02% at 48months after deworming. Hookworm was found only in one child during 36th month assessment and *Trichuris trichiura* was also found only in one child during final assessment. Reinfection rate after preventive chemotherapy was found to be high within first 24 months but it declined sharply after 30 months to reach 15.15% in final assessment. Present study showed only light intensity of helminth infection. Mean hemoglobin level of the children ranged between 9.2 g/dL and 14.1 g/dL during study period and found no effect due to deworming. However prevalence of children with anemia decreased from 48.67% to 11.61% within 48 months' assessment period. At initial assessment, underweight and stunting were found in more than 20% of children while wasting only in 10.6%. Prevalence decreased after deworming until it reached below 5% in all parameters. Socio-demographic factors including age, gender, school grade, family size, parents' occupation and income did not have any relationship with reinfection.

Keywords: Soil-transmitted helminth infection, Anemia, Growth, Primary school children

Poster no. 18

TREMATODE INFECTIONS IN THE ASSASSIN SNAIL, *CLEA (ANENTOME) HELENA* (NEOGASTROPODA; BUCCINIDAE) IN SURAT THANI PROVINCE OF THAILAND

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Clea (Anentome) helena Philippi 1847 is freshwater snail in the family Buccinidae. It was found in Cambodia, Indonesia, Lao PDR, Malaysia and Thailand. This gastropod is the predator of other snails. In Thailand, it distributes in every province. It can live in both running and stagnant water such as pond or reservoir. Although the previous studies showed that trematode infections in this snail was rarely observed, but it also had the medical importance. It could be the intermediate host of *Echinostoma revolutum*, *Apatemon gracilis* and *M. appendiculatus*. The aim of this study was to investigate the trematode infections of *C. helena* in Surat Thani Province, South of Thailand. The snails were collected from eight localities by hand picking and scooping method. The parasitic infections were examined by shedding and crushing methods. The trematode larvae were stained with 0.5% neutral red and studied the light microscope. In this study, cercariae were not obtained from shedding method. But in crushing method, sporocysts of *Podocotyle lepomis* and metacercariae of *Plagioporus (Caudotestis) sinizini* were observed. The overall infection rate of *C. helena* was 1.74% (3/172). The infection rates of *P. lepomis* and *P. sinizini* were 0.58 % (1/172) and 1.16% (2/172), respectively. This study showed the more species of parasite in *C. helena* than the previous studies. So, the susceptibility of *C. helena* to the trematodes should be more studied further.

Keywords: trematode, infection, Clea (Anentome) helena

Poster no. 19

TREMATODE INFECTIONS OF FRESHWATER SNAILS GENUS *CLEA* A. ADAMS, 1855 IN THE RESERVOIR OF LOWER NORTHEAST THAILAND.

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Trematode infections of freshwater snails genus *Clea* A. Adams, 1855 in the reservoir of lower northeast Thailand, were studied at 11 locations. The aim of this study was to evaluated the natural trematode infections of freshwater snail genus *Clea*. The snails were collected from four provinces (Nakhon Ratchasima, Buri Ram, Surin and Si Sa Ket) in March 2016. Five collectors picked the snails by hand for 10 minutes each station. The collected snails were observed for trematode infections by shedding and crushing methods. The infection rates was 1.92% (6/312). Cercariae were categorized by their morphological characteristics. Three types of cercariae were found. They were Furcocercous cercariae (tail forked), Cotylomicrocercous cercariae (cup-shaped tail with adhesive organ), and Cercariaeum cercariae (tail absent). The infection rates of these parasites were 0.64%, 0.96%, and 0.32%, respectively. Double infections were found with Cotylomicrocercous cercariae and Cercariaeum cercariae.

Keywords: Cercaria, Infection, Trematode, Genus Clea

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Poster no. 20

DISTRIBUTION OF *NEOTRICULA APERTA*, SNAIL INTERMEDIATE HOST OF BLOOD FLUKE *SCHISTOSOMA MEKONGI*, IN MEKONG RIVER, THAILAND

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The freshwater snail, *Neotricula aperta*, intermediate host for human blood fluke *Schistosoma mekongi*, was found in lower Mekong River and some of its tributaries in Lao, Cambodia and Thailand. The aim of this project is to study the distribution pattern and densities of *Netricula aperta* along Mekong River of Thailand and to investigate ecological condition of *N.aperta* habitat in Mekong River. The study sites cover 8 provinces in Northern and Northeastern Thailand including Chiang Rai, Loei, Nong Khai, Bueng Kan, Nakhon Panom, Mukdahan, Amnat Charoen and Ubon Ratchathani. The survey was carried out 2 times during November – December (after rainy season) and April-May (dry season). Total 44 sampling sites were selected to survey for the snail *N. aperta*. Eighteen *N.aperta* habitats were identify along Mekong River in Ubon Ratchathani (10 sites), Amnat Charoen (1 site), Nakhon Panom (1 site), Nong Khai (5 sites) and Loei (1 site). *N.aperta* densities range from 0.2-1577.2 snails/m^2. The snail distribution was mapping by GIS. The ecological conditions of each snail habitat and water quality parameters (water temperature, turbidity, dissolved oxygen, pH, hardness, salinity, ammonia, nitrate, nitrite, benthic diatom density and velocity) were recorded. The habitats of *N.aperta* in most sampling sites were in the islet of Mekong River. The bottom of the river or the islet type included bedrock, rock, pebble, sand, sandy soil, silt and muddy bottom. The substrates that *N.aperta* attached were natural rocks and also the rock that use for making river bank protection.

This study was supported by Research Grant from the Faculty of Tropical Medicine, Mahidol University, Fiscal Year 2013

Keywords: Neotricular aperta, Distribution, Mekong River

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Poster no. 21

CLONING AND SEQUENCING OF *PLASMODIUM FALCIPARUM* PHOSPHOETHANOLAMINE METHYLTRANSFERASE GENE AND VIRTUAL SCREENING TO IDENTIFY NOVEL INHIBITORS

The growing resistance to current antimalarial drugs is a major concern for global public health and pressing need for new potent antimalarial. The biological processes that regulate gametocytogenesis remain unknown. Thorough understanding of these processes is crucial to the development of a new generation of dual activity antimalarials that can inhibit both infection and transmission. SAM dependent *Plasmodium falciparum* Phosphoethanolamine methyltransferase (PfPMT) catalyzes three step methylation of phosphoethnolamine to synthesize Phosphatidylcholine (PC) from host seine, for rapid development of membranes in *Plasmodium* species at both asexual and sexual stages, is a promising target for research on a novel class of antimalarials.

Gene PfPMT was amplified and sequenced. Phylogenetic was done with orthologues of *Plasmodium* spp. as well other species. PfPMT protein was used for structure based inhibitor identification.

PfPMT gene Amplification, sequencing and phylogenetic analysis demonstrated that PfPMT (Indian) isolate is 100% conserved with PfPMT *3D7* and also domain is also found significantly conserved with other *Plasmodium* spp. and very closely related. Compounds inhibitors of PfPMT have been identified through virtual screening based on Lipinski rule of five, ADMET and docking of compounds with PfPMT. Selected compounds showed potential effect on cell viability by SYBR green 1 dye method and showed good inhibitory activity against PfPMT protein. Based on computational ADMET analysis selected compounds found noncarcinogenic, nonmutagenic, non heptotoxicity and have good ADME physicochemical properties. Hence the identified compound inhibitors may lead to potent anaimalarial and as a lead for ligand based drug designing to overcome the problem of multidrug resistance.

Keywords: Pfpmt, SAM, SDPM, ADMET, Virtual Screening

Poster no. 22

P. FALCIPARUM K-13 MUTATIONS AND TREATMENT RESPONSE IN PATIENTS IN HPA-PUN DISTRICT, NORTHERN KAYIN STATE, MYANMAR

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BACKGROUND: Artemisinin resistance has outpaced containment efforts in South East Asia. For national malaria control programs in the region, it is important to monitor the progression of K-13 polymorphisms and the allele diversity associated with the clinical phenotype.

METHODS: Parasite clearance half-lives were assessed in 35 patients with uncomplicated *P. falciparum* treated with artesunate monotherapy followed by 3-day ACT in an isolated area on the Thai-Myanmar border with relatively low artemisinin pressure. Molecular testing for K-13 mutations was performed on admission samples using dry blood spots.

RESULTS: The proportion of K-13 mutations in these patients was 41.7%, and only 5 alleles were detected: C580Y, I205T, M476I, R561H, and F446I. Of these, F446I was the most common, and was associated with a longer parasite clearance half-life (median) 4.1 (min-max 2.3-6.7) hours compared to 2.5 (min max 1.6-8.7) in wildtype (p=0·01). By contrast the proportions of K-13 mutants in another area of the border, 200 km south was 84% and 15 different alleles were detected, C580Y being the most common one.

CONCLUSIONS: This study provides evidence of artemisinin resistance in a remote part of eastern Myanmar. The prevalence of K-13 propeller mutations as well as allele diversity varies considerably across short distances, presumably related to historical patterns of artemisinin use and population movements.

Keywords: *Plasmodium falciparum* malaria, artemisinin, parasite clearance, K-13 mutation, drug resistance

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Poster no. 24

GENETIC DIVERSITY OF MSP3 BETA GENE IN *PLASMODIUM VIVAX* FROM TWO REGIONS IN SOUTHERN INDIA BY PCR/RFLP ANALYSIS

Introduction: *Plasmodium vivax*, the most widespread malaria parasite species across the globe and equally competes with *Plasmodium falciparum* as a cause of human malaria. As compared to *P. falciparum*, *P. vivax* is not much studied and least understood. Knowledge about PvMSP3β as an epidemiological marker is not available in the Indian context.

Objectives: This study aimed to genotype the PvMSP3β gene in populations from two regions of Southern India- Mangalore and Pondicherry.
Materials and Methods: A total of 100 *P. vivax* positive samples were detected by microscopy, QBC, and RDT. Further, it was confirmed by nested PCR. For genetic diversity study PCR-RFLP method was employed which targeted MSP3β gene.

Results: Out of 100 samples, Pondicherry contributed 31/100(31%) and Mangalore 69/100(69%). The alleles of the amplified DNA fragments were classified into Type A (1.5-2.0 kb) & Type B (<1.5 kb to 1 kb). Of the 100 *P.vivax*-positive samples, 49 (49%) belonged to Type A, 46(46%) to Type B and 5 (5%) showed mixed infections. Type A was predominant in Mangalore and Type B in Pondicherry.. Further, PvMSPβ gene was analysed using Pst-1 restriction enzyme and suballelic variants were found in both Type A (A1-A17) and Type B (B1-B12).

Conclusion: In consensus to existing studies, our findings also suggest that PCR/RFLP of PvMSP3β is a reliable, cost effective epidemiological marker for the genotyping.

Keywords: *Plasmodium vivax*, MSP3β gene, Genetic diversity, PCR-RFLP

Poster no. 25

IDENTIFICATION OF SMALL-MOLECULE INHIBITORS OF PLASMODIUM N-MYRISTOYLTRANSFERASE

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There is a desperate need for new antimalarial drugs due to the rise in resistance to current therapies which are small in number and have undesirable side effects. The enzyme *N*-myristoyltransferase (NMT) is a validated drug target in the causative agent of malaria, the single-celled eukaryote *Plasmodium*. NMT catalyzes the myristoylation of protein substrates, which is an essential lipid modification with roles in membrane targeting and cell signaling. As NMT is conserved among eukaryotes, it is crucial to identify inhibitors that act specifically against *Plasmodium* NMT without impacting the human homolog. Here, we used a biochemical assay in a 1536-well format to screen ~2 million small molecules from the GSK compound library against NMT of the most widespread human malaria parasite *P. vivax*. Confirmed hits were triaged based on potency and preferred physicochemical properties and were tested in a dose-dependent manner against *P. vivax* and *P. falciparum* NMT for their cross-species activity and against human NMTs to discard compounds with a selectivity index lower than 10. Chemical clustering of the most potent compounds resulted in 9 series and 22 singletons. Several of these inhibited the growth of the pathogenic blood stages of *P. falciparum* by more than 50% at a 2 μM compound concentration *in vitro*, and showed no to limited toxicity against the mammalian HepG2 cell line. These compounds represent good starting points for the development of new antimalarials.

Keywords: Malaria, drug discovery, high-throughput screening

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Poster no. 26

ACTIVE SURVEILLANCE MALARIA IN MILITARY ALONG THAI – MYANMAR AND THAI – CAMBODIA BORDERS

Thailand is still one of burden countries that impacted by malaria. In malaria endemic areas, especially along Thai borders, the border people including vigilant soldiers are the vulnerable groups take risk for malaria infection and transmission across Thai borders. This disease non-battle injury (DNBI) has been concerned and conducted an active surveillance among Thai military by Epidemiology section from RTA-AFRIMS for more than 20 years.

To survey and monitor the epidemiology evidence of malaria, active case detection along Thai-Myanmar and Thai-Cambodia borders has been performed using microscopic examination method and/or RDT. We also provided support for early detection and treatment at the troop level. In addition, monthly malaria case data from local public healthcare providers was integrated.

From October 2015 to June 2016, there is no malaria positive case in Thai-Myanmar border. In Thai-Cambodia AO, approximately 4,500 soldiers were screened for malaria infection and 151 cases (3.36%) were identified. The prevalence shown 1.22% *P. vivax*, 0.96% *P. falciparum* and 1.18% for mix infection of PV and PF. The annual prevalence was decreased for last few years; 2013-2016 (12.67, 7.45, 5.23 and 3.36 respectively). Interestingly, the prevalence of mix infection was increasing, meanwhile *P.vivax* infection prevalence was decreasing among malaria infected troop.

A trend of decreased prevalence implied that active surveillance strategy for reducing the burden of border malaria is substantial for malaria prevention and control among Thai military troops. The surveillance system would be further improved the coverage and expansion at the military operating base to the policy level to sustain malaria control toward progressive elimination.

Keywords: border malaria, active surveillance, military area of operation

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Poster no. 27

CURRENT MALARIA SITUATION IN FIVE SOUTHERN PROVINCES, LAO PDR – A STUDY BY THE SATREPS PROJECT

Morbidity and mortality of malaria in Lao PDR have decreased due to the continuous efforts of Lao Ministry of Health (MoH) with support of WHO, Global Fund and other developing partners. Presently, the Lao MoH has set a goal to eliminate malaria by 2030 in the country. To achieve this goal, we should know precise malaria situation in such high endemic Southern provinces such as, Savannakhet, Salavanh, Sekong, Champasak and Attapeu. In this study, 156 public health facilities in these provinces were selected and collected data on malaria suspected cases and positive cases. From June-October 2015, a total of 4,439 malaria suspected cases were recorded in the 156 public health facilities and 587 cases (13.2%) were diagnosed as malaria (133 *Plasmodium falciparum*, 196 *P. vivax*, 6 mixed-infection and 252 unknown species) by microscopy or rapid diagnostic test (RDT). When we analyzed the patients' data in each province, malaria positivity rate of male was significantly higher than that of female in the all provinces ($P < 0.01$) except Savannakhet. Moreover, 15-39 years old male population tended to be malaria positive, and most of their occupations were agriculture. These results suggest that malaria high-risk population in the 4 provinces was adult male population, and seemed to be associated with their working style, i.e. they routinely work in their farms, as well as in forests for collecting foods and woods. Current malaria elimination program is basically household-based approach. Our result suggests that job-based approach is also needed for malaria elimination in Lao PDR.

Keywords: SATREPS project, Lao PDR, Malaria

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Poster no. 28

COMPARATIVE STUDY OF WHEATLEY'S TRICHROME STAIN AND IN-VITRO CULTURE FOR THE DIAGNOSIS OF *BLASTOCYSTIS* SP. IN STOOL SAMPLES

Method of detection of *Blastocystis* sp. either by permanent stain or short-term *in-vitro* cultivation techniques remains controversial in term of their effectiveness. Hence, we evaluate the performance of routine permanent stain and cultivation method in comparison with PCR assay as the reference technique to detect *Blastocystis* sp. A total of 359 stool samples were examined using Wheatley's trichrome stain, *in-vitro* culture and PCR assay. Fifty-six (15.6%) samples were detected positive with *Blastocystis* sp. by Wheatley's trichrome stain and 73 (20.3%) by *in-vitro* culture, while PCR assay detected 71 (19.8%) positive samples. Our results confirmed that 28 microscopy-negative samples were positive by PCR assay. Detection rate of *Blastocystis* sp. was highest in combination techniques (27.9%). The sensitivity and specificity of Wheatley's trichrome staining and *in-vitro* culture techniques compared to PCR assay (reference technique) were 49.3% (95% CI: 37.2-61.4) and 92.7% (95% CI: 89.1-95.4) and 39.4% (95% CI: 28.0-51.8) and 84.4% (95% CI: 79.7-88.4), respectively. However, the sensitivity [60.6% (95% CI: 48.3-71.9)] of the method increased when both techniques were performed together but the specificity slightly decreased to 80.2% (95% CI: 75.1-84.7). The agreement between Wheatley's trichrome stain, *in-vitro* culture and combination techniques with PCR assay were statistically significant by Kappa statistics (Wheatley's trichrome stain: $K = 0.456$, $p<0.001$; *in-vitro* culture: $K = 0.236$, $p<0.001$ and combination techniques: $K = 0.353$, $p<0.001$). Hence, our results suggest combination techniques as a screening method in the diagnosis of *Blastocystis* infection either for clinical or epidemiological study to ensure better and accurate diagnosis. 💬

Keywords: Trichrome, culture, PCR, *Blastocystis*

Poster no. 29

MOLECULAR DETECTION OF *BLASTOCYSTIS*, *CRYPTOSPORIDIUM* SPP. AND *ENTEROCYTOZOON BIENEUSI* IN HUMANS AND PIGS IN NAKHON PATHOM PROVINCE, THAILAND

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Blastocystis, *Cryptosporidium* spp. and *Enterocytozoon bieneusi* are enteric protozoa in a wide range of vertebrate hosts, causing diarrheal diseases. In this study, a total of 142 human and 102 pig stool samples were collected from pig farms in Nakhon Pathom Province. Presence of the parasites was done using nested PCR. In human, 4/142 (2.8%) of *Blastocystis* and 13/142 (9.2%) of *E. bieneusi* were found while 32/102 (31.4%) of *Blastocystis* and 17/102 (16.7%) of *E. bieneusi* were found in pigs. No *Cryptosporidium* spp. (0%) was detected in both pig and human samples. In pigs, four *Blastocystis* subtypes, ST14, ST1, ST12, ST3, and eight *E. bieneusi* genotypes, EbpC, H, 6 new genotypes, were identified. In humans, *Blastocystis* ST1 and ST3 and 10 *E. bieneusi* genotypes were identified. Our study indicated the zoonotic potential transmission of *Blastocystis* and *E. bieneusi* in Nakhon Pathom, Thailand.

Keywords: Blastocystis/*Cryptosporidium*/*Enterocytozoon*/pig/human

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Poster no. 32

ANTIPROTOZOAL ACTIVITY OF ESSENTIAL OIL FROM THAI MEDICINAL PLANTS AGAINST *GIARDIA DUODENALIS*

Giardia duodenalis (synonyms: "*G. lamblia*" or "*G. intestinalis*") is a common flagellate protozoan that globally causes the diarrheal disease giardiasis. Most infections result from fecal-oral route. In Thailand, several herbs are used for medicinal purposes and in cooking to promote health and reduce antibiotic resistance. However, information on the effects of Thai herbs on intestinal protozoa are lacking. This study determined the effectiveness of Thai herbs-extracted essential oils (clove, ginger, galangal, litsea, star anise, indian ivy-rue, lemon, bergamot, orange, holy basil, and sweet basil) for inhibiting or killing *G. duodenalis.* The results showed that only 5 essential oils from lemon, litsea, galangal, clove and orange showed a significant inhibiting activity against *G. duodenalis* and IC_{50} values were 6.96±0.13, 60.66±0.82, 118.95±1.93, 138.10±3.21 and 650.73±6.25 μg/ml, respectively. In addition, IC_{50} value of metronidazole was 63.21±1.56 μg/ml, while the rest did not show inhibitive property. This is a pilot study to identify antiprotozoal essential oils, in which a further study will isolate the medicinal components for the development of herbal medication or products that will be used to treat giardiasis.

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Poster no. 33

GENOTYPE AND SUBGENOTYPE ANALYSES OF *CRYPTOSPORIDIUM PARVUM* AND *CRYPTOSPORIDIUM HOMINIS* ISOLATED FROM PHILIPPINE EDIBLE BIVALVES

In the Philippines, raw or lightly-cooked bivalve dishes are very common. Being filter feeders, these bivalves might be contaminated with pathogens which can cause diseases to humans. One common pathogen found in bivalves is the protozoan parasite of the genus *Cryptosporidium* (Phylum Apicomplexa) which causes human gastroenteritis in both developed and developing countries. In this study, oocysts of *C. parvum* and *C. hominis* were isolated from common edible bivalves using combination of sucrose flotation and immunomagnetic separation (IMS). They were identified by 18s rRNA gene sequence analysis and were subjected to genotype and subgenotype analyses using the 60 kDa glycoprotein gene. For *C. parvum*, genotype IIa was found in 30 out of 31 isolates with subgenotype IIaA15G2R1 as the dominant subgenotype (n=24) followed by subgenotype IIaA15G2R2 (n=3). One *C. parvum* isolate had very low BLAST matches and may indicate possibility of obtaining a new genotype. While for *C. hominis*, two genotypes were detected in nine isolates (1b and If), eight of which belonged to subgenotype 1fA19G1 and one isolate belonged to IbA10G2R2. All of these identified subgenotypes had been known to be involved in human cryptosporidiosis cases. Therefore, this study confirmed the presence of *C. parvum* and *C. hominis* genotypes and subgenotypes which are listed as common human pathogens. This study showed that humans ingesting contaminated shellfish are exposed to different *Cryptosporidiumge* notypes and subgenotypes of public health significance.

Keywords: *Cryptosporidium parvum*, *Cryptosporidium hominis*, bivalves

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Poster no. 34

SEROPREVALENCE OF *TOXOPLASMA GONDII* INFECTION IN REFUGEE AND MIGRANT PREGNANT WOMEN ALONG THE THAILAND-MYANMAR BORDER

Background: Primary infection with *Toxoplasma gondii* in pregnancy is associated with poor obstetric outcomes and congenital infection. Prevalence rates in pregnant women in Thailand are well documented (rates vary between 5.3-53.7%) but there is only one study from Myanmar reporting 30.7% (95%CI 27.9-37.2). This study aimed to determine the seroprevalence of *Toxoplasma* infection in pregnant migrant and refugee women on the Thailand-Myanmar border.

Material and methods: A random selection of 199 stored blood samples of women attending antenatal clinics over an 18 month period (Jan-14 to Jul-15) were tested for *Toxoplasma* IgG and IgM antibodies. Avidity testing discriminated between acute or past exposure to the parasite if IgM results were positive.

Results: Seroprevalence of *Toxoplasma* infection was 31.7 % (63/199) (95%CI 25.6-38.4). No acute infection was detected in the 3 positive IgM cases. A significant positive linear trend was seen with *Toxoplasma* exposure and increasing maternal age (p=0.036). Multiparity (≥ 3 children) was associated with a 2.46 aOR(95%CI 1.23-4.90, p=0.011) fold higher *Toxoplasma* seropositivity rate; while literacy, history of poor obstetric outcome, refugee status and ethnic group showed no significant associations. As expected, there was no association with poor outcomes in the current pregnancy as all results revealed past exposure.

Conclusion: Seroprevalence of *T. gondii* infection in pregnant migrants and refugees is similar to previously reported data in Myanmar and Thailand, and was only significantly associated with multiparity. *Toxoplasma* infection is important in pregnant women and is probably related to socioeconomic conditions. Nevertheless, in this marginalized population, this parasite infection may be given less priority, due to resource constraints in providing even the most basic components of safe motherhood programs.

Keywords: *Toxoplasma gondii*, TORCH, seroprevalence, congenital

Poster no. 36

TEMPORAL INCREASE IN PYRETHROID RESISTANCE AND FREQUENCY OF KDR MUTATIONS IN *AEDES AEGYPTI* FROM KOLKATA AN INDIAN METROPOLITAN CITY

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Emergence of pyrethroid resistance in *Aedes aegypti* is the main threat to worldwide dengue control programs. Knockdown resistance (*kdr*) is one of the mechanisms of resistance against DDT and pyrethroids resulting from non synonymous mutation(s) in voltage gated sodium channel (VGSC) gene-the target site of action for these insecticides. Emergence of pyrethroid resistance is reported worldwide but the status in Indian *Ae. aegypti* is limited. Thus, a pilot study for surveillance of insecticide susceptibility was conducted in *Ae. aegypti* from Kolkata city, India, which is a hot spot for dengue epidemic. Insecticide susceptibility was evaluated against DDT (4%), permethrin (0.75%) and deltamethrin (0.05%). Adult bioassays carried out in year 2012 and 2014 revealed increasing resistance against all three insecticides. Percentage mortalities against DDT, permethrin and deltamethrin in 2012 were 24%, 75%, 84% respectively which further reduced to 4%, 33%, 25% in 2014. DNA-sequencing of partial domain II, III and IV of the VGSC revealed two *kdr* mutations; first novel T1520I and another F1534C in domain III of VGSC whereas no *kdr* mutation was observed in other two domains. Further, PCR-RFLP assays were designed for genotyping of these mutations. Genotyping revealed increase in frequencies of both mutations in year 2014 as compared to year 2012. In 2012, no sample has T1520I mutation, whereas in 2014 its frequency increased to 0.6. Similarly, frequency of F1534C mutation increased from 0.25 in 2012 to 0.75 in 2014. This increase in *kdr* mutations with reduced insecticide susceptibility is alarming for vector control efforts.

Keywords: *Aedes aegypti*, insecticide resistance, *kdr*

Poster no. 37

EFFECT OF TEMPERATURE ON THREE PYRETHROID SUSCEPTIBILITY OF *AEDES AEGYPTI* IN NAKHONSAWAN AND RAYONG PROVINCES, THAILAND

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Background: Dengue fever is a mosquito-borne viral disease that found in tropical and sub-tropical areas of the world, mostly in urban and semi-urban areas. The bite of infected female *Aedes aegypti* is the effective route of dengue transmission. The use of the chemical insecticide is the common control measure of *Ae. aegypti*. Currently, In Thailand it had reported insecticide resistance of *Ae. aegypti*. Temperature is the external factor of insecticide susceptibility. Therefore, effects of temperature on insecticide susceptibility were studied in field population of *Ae. aegypti*.

Methodology: *Ae. aegypti* larvae were collected from Nakhonsawan and Rayong for two times during December 2015-January 2016 and April-May 2016. The unfed females of F1 progeny aged 3-5 days were used in the experiment. They were exposed at three temperatures (20±1°C, 25±1°C, and 30±1°C) for 4 hours prior to insecticide susceptibility test with three pyrethroids (Cyfluthrin, Deltamethrin, and Lambdacyhalothrin). Mortality was examined after 24 hr exposure.

Results: The mortality of 20°C pre-exposed groups were higher than 30°C pre-exposed ($P < 0.05$). The relationship between temperature and pyrethroid susceptibility was found negative relationship.

Conclusion: Temperature affected to pyrethroid susceptibility and exhibited a negative relationship between temperature and mortality of *Ae. aegypti* strains from Nakhonsawan and Rayong, Thailand.

Keywords: *Aedes aegypti*/ Temperature/ Insecticide susceptibility/ Thailand/ Pyrethroid

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Poster no. 38

COMPARATIVE REPELLENT ACTIVITY OF FIVE HERBAL ESSENTIAL OILS AGAINST *AEDES AEGYPTI*

The repellent activity of five herbal essential oils from bergamot (*Citrus bergamia*), basil (*Ocimum basilicum*), patchouli (*Pogostemon cablin*), anise (*Pimpinella anisum*) and coriander (*Coriandrum sativum*) against the *Aedes aegypti* mosquito was investigated. The undiluted essential oil was tested individually under laboratory conditions by arm-in-cage method. A sample of 0.1 mL of essential oil was applied to 3 x 10 cm area of exposed forearm skin of the volunteer. Subsequently, a test was conducted every 15 minutes. This involved exposing the treated arm to 250 *Aedes aegypti* female mosquitoes for 3 minutes. The experimental endpoint was at least 2 mosquitoes landing or biting on treated arm during testing period, which indicated the stop point of the protection time of the essential oil. Of the five essential oils tested, patchouli gave the longest protection time at 67.5 minutes, followed by anise, bergamot, coriander and basil at 51, 48, 36 and 16.5 minutes, respectively. Due to their potent activity, patchouli, anise and bergamot oil could be considered for development as an alternative mosquito repellent formulation.

Keywords: volatile oil, plant-based repellent, mosquitoes

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Poster no. 41

EFFECTS OF CONTAINER VARIATIONS ON PREDATION BY *TOXORHYNCHITES SPLENDENS* (DIPTERA: CULICIDAE)

The effect of container size on predation by fourth instar larvae of *Toxorhynchites splendens* was investigated in the laboratory. Experiments were conducted using containers with equal water volumes (500 ml) but different surface areas; small bowl (103.8 cm^2), big bowl (188.6 cm^2), small tray (300 cm^2) and big tray (638 cm^2). Also, three different water volumes were tested at 100, 300 and 500 ml. There were significant differences in prey consumed and killed among containers with different surface areas but there were no significant differences in prey consumed among containers of different volumes. The results showed that more prey were consumed in small bowls (615.5 larvae) than big bowls (486.9 larvae), small trays (442.1 larvae), or big trays (363.5 larvae). Fewer prey larvae were killed in the big trays than other containers. The daily mean consumption rate decreased over time but rates of killing (without consumption) increased as pupation approached. This study suggests that containers with small surface areas are most suitable for increasing consumption and killing by *Tx. splendens*.

Keywords: Toxorhynchites, prey, container, consumed, killed

Poster no. 42

EFFECT OF PREY DENSITY ON THE DEVELOPMENT TIME AND BODY SIZE OF MALE AND FEMALE PREDATORY MOSQUITOES *TOXORHYNCHITES SPLENDENS* (DIPTERA: CULICIDAE)

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The purpose of this study was to determine the effect of different prey densities on *Toxorhynchites splendens* development time and body size. Individual larvae were reared from 4th instars to adults in small plastic bowls and provided 4th instar *Aedes aegypti* larvae as prey at three different densities; 100, 200 and 300 larvae. The wing lengths of *Tx. splendens* adults were measured as an estimate of body size and the date of emergence and gender were recorded. There was a significant difference in the development times of *Tx. splendens* larvae and pupae when reared at different prey densities. The development times of larval and pupal stages were greater when reared at high prey densities (300 preys) compared to lower prey densities. The 4th instar predators consumed and killed significantly more prey at higher prey densities (300 preys) than low densities (200 and 100 preys). There were no significant differences between either gender in the amount of prey consumed and killed. However, prey density had a significant effect on male and female body size with larger adults emerging from tubs containing 300 preys (7.3 and 5.9 mm) compared to 200 preys (7.1 and 5.7 mm) and 100 preys (6.6 and 5.4 mm), respectively (*p*-value 0.000). The results show that high prey densities promote large adults that consume more prey, although they emerge slightly later.

Keywords: Toxorhynchites, prey, density, development, gender

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Poster no. 43

THE MORPHOLOGICAL STUDY OF *MUSCA DOMESTICA* (DIPTERA: MUSCIDAE) IN THIRD-INSTAR LARVA STAGE RECEIVING *STEMONA COLLINSIAE* ROOT EXTRACT

Musca domestica (House fly) is a synanthropic fly which is easily found in human community, restaurant including cattle. In Thailand, the population of *M. domestica* is found about 80-90 percent of all population of flies. *M. domestica* is a vector of pathogenic bacteria, virus, parasite and fungi which these pathogens are transmitted to human and animal via mechanical and propagating transmission. Synthetic-chemical insecticides are used for eliminating and preventing human or animal from vector-borne diseases. Due to accumulation in environment including human and animal body and long half-life of these synthetic-chemical insecticides, bio-pesticide which produces from plant and microorganisms is considered as a friendly environment, low toxicity to mammal and short degradation time. Many insecticidal plants are found in Thailand including *Stemona* plant.

Stemona collinsiae has been traditionally used as pesticide for plantation and food protector from fly. In this experiment, third-instar larvae of *M. domestica* were tested with 70 percent ethanolic crude extract from root of *S. collinsiae* using topical application method and a development of these larvae was studied comparing with negative control groups which received water. Physical appearances were detected using visible and SEM techniques. The third-instar larvae were able to develop to be pupae but physical appearance as segmental and curved body occurred instead of a barrel-liked shape which was a normal shape of *M. domestica* in pupal stage. The segmental body happened from a contractile of muscle and adult flies were not able to emerge from these abnormal pupae.

Keywords: Stemona collinsiae, Musca domestica, Housefly

Poster no. 44

ACTION AGAINST DENGUE IN THE SIXTH ASEAN DENGUE DAY CAMPAIGN 2016 IN THAILAND

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Dengue is a mosquito-borne viral disease problem among ASEAN countries which rapidly spread out to the other regions and become the global problem nowadays. Dengue is mostly found in tropical and subtropical climates worldwide and also in urban and semi-urban areas where they are the suitable places for spreading of the vectors (*Aedes aegypti* and *Aedes albopictus*). According to the report of the World Health Organization (WHO), 2015 was intense for dengue fever in many regions: the Philippines reported more than 169,000 cases, Malaysia had in excess of 111,000 cases and Vietnam reported some 80,000 where as Thailand reported more than 140,000 cases.

The Association of Southeast Asian Nations (ASEAN) designated 15th June in every year as the ASEAN Dengue Day to increase public awareness of dengue, to mobilize resources for its prevention and control and to demonstrate the region's commitment for tackling this disease. All ASEAN Member States agreed and supported the conduction of Annual Regional Observation of ASEAN Dengue Day as well as National ASEAN Dengue Day Campaign. ASEAN Dengue Day is an advocacy campaign that serves as a common platform for its 10 member-nations namely Brunei Darussalam, the Kingdom of Cambodia, the Republic of Indonesia, the Lao People's Democratic Republic, Malaysia, the Republic of the Union of Myanmar, the Republic of the Philippines, the Republic of Singapore, the Kingdom of Thailand and the Socialist Republic of Vietnam.

Action against *Dengue* in *the Sixth ASEAN Dengue Day* Campaign in 2016 was held on 14-15 June in Bangkok, Thailand under the theme "Community Empowerment: A Sustainable Success to Fight Dengue". This reflects the call for joint efforts from society to unite against the disease together as one community. The campaign has been organized in many community areas such as school, temple, houses and public spaces around community. Thailand has an outstanding profile in dengue prevention both the policy and implementation level. In 2015, the government stepped up efforts to reduce the number of dengue cases by convening the Memorandum of Understanding (MoU) signing ceremony among eight Ministries to work together to achieve the prevention goals. The morbidity rate is still high, but there are now very few deaths from the disease, with a mortality rate reduced to less than 0.1 percent.

Following the government officials' meeting, the Bangkok Call for Action in the Prevention and Control of Dengue has been launched and agreed upon by all member nations. Thailand would like to seek support from all ASEAN Member States for the proposed the conduction of Annual Regional Observation of ASEAN Dengue Day as well as National ASEAN Dengue Campaign and hope the implementation of the action plans in each ASEAN Member States will strengthen the community empowerment, social mobilization, public and private sectors engagement and participation for ensuring the effective dengue prevention and control as "Dengue Free Community" in this region.

Keywords: ASEAN, Dengue, Campaign

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Poster no. 45

ASSOCIATION OF CLINICAL MANIFESTATION AND LABORATORY CHARACTERISTICS WITH SEVERITY OF DENGUE VIRAL INFECTION IN CHILDREN IN DR. HASAN SADIKIN GENERAL HOSPITAL BANDUNG INDONESIA

Background: Dengue viral infection (DVI) is a major cause of morbidity and mortality in children. Indonesia has large amount of cases of dengue infection with 0.88% mortality rate. Unusual manifestation is commonly contributed to increasing mortality.

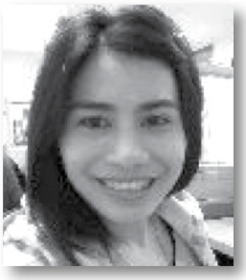
Objective: To describe association of clinical manifestation and laboratory characteristics of the confirmed DVI cases in children admitted to Dr. Hasan Sadikin General Hospital, Bandung, Indonesia with severity of disease.

Methods: All of the confirmed dengue viral infection cases from January 2014 to December 2015 were retrospectively studied. Data including patient demographic, initial symptoms, laboratory results, were collected. Severity of DVI is categorize as dengue fever (DF), dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS). Association between initial symptoms, blood count, and severity of disease was analyzed using Chi-square and one-way ANOVA ($p<0.05$ = significant).

Results: There were 192 confirmed cases of DVI, 89.58% using dengue IgG-IgM antibodies, while 10.42% using NS-1 antigen. The median age was 6.46 years. Initial symptoms of diaphoresis, epigastric pain, cold extremity, seizure were associated with more severe infection ($p<0.005$). Epistaxis was the most frequent hemorrhagic manifestation (19.79%). The mean leukocyte count in DF, DHF, DSS patients were respectively 6,069 mm^3, 4,196 mm^3, and 4,392 mm^3. While secondary infection in DF, DHF, DSS patients were respectively 22.8%, 58.8%, and 18.4%. The lower leukocyte count and secondary infection were associated with more severe infection ($p<0.001$).

Conclusion: Initial symptoms, leukocyte count, primary and secondary infection are associated with severity of DVI

Keywords: dengue, initial symptoms, leukocyte count, secondary infection, children



Poster no. 46

CHARACTERIZATION OF ANTI-DENGUE VIRUS NS1 HUMABS AGAINST DENGUE VIRUS

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Background: Dengue fever (DF) and its severe form, dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS) are one of the most important mosquito-borne tropical disease of public health throughout the world. The severe form of dengue disease was frequently hypothesized to be correlated with high viral titer and secondary infection with heterologous serotypes, so called ADE, that caused mostly by anti-E and anti-prM antibodies. Also, anti-NS1 antibodies were recently interested as one factor for severe dengue infection because of their cross-reactivity with human molecules, causing some severe symptoms like vascular leakage. However, information of anti-NS1 antibody, especially antibodies generated from human was still limited.

Methods: In this study, 5 anti-NS1 HuMAbs generated from our previous study were characterized. The hybridomas were cultured and re-cloned to obtain individual cells secreting HuMAb before proceeded to antibody gene cloning. Human variable heavy and light chain (VH and VL) were isolated from those hybridoma cells and analyzed by IMGT/V-QUEST database. HuMAbs were purified from collected culture supernatant for neutralizing activity test (NT).

Results: It was shown that most of the clones used the same parental germline sequence. As expected, for infection inhibition NT assay, studied on Vero cells, most of them showed moderate to weak neutralizing activities against DENV-2. Further studies on viral replication inhibition will be further performed. The results obtained from this study can be used as fundamental genetic information and neutralizing activity of the anti-NS1 HuMAbs, which can be used for further characterization of its enhancement mechanisms, epitope characterization, and their cross-reactivity.

Keywords: Human monoclonal antibody, Dengue virus Non- structural protein 1 (NS1), Germline, Neutralization activity

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Poster no. 47

LARGE SCALE PRODUCTION OF HUMAN THERAPEUTIC MABS AGAINST DENGUE VIRUS USING STABLE CHO CELL EXPRESSION

Using SPYMEG hybridoma cells, neutralizing human monoclonal antibodies (NhuMAbs) against 4 serotypes of Dengue virus (DENV) has been the world's first time established at CEAR. Two candidates NhuMAb (1B3B9 and 1G7C2). were successfully pre-clinically tested *in vitro* by 95-100 % neutralized all 20 clinical isolates DENV and *in vivo* by significantly decreased mortality of Dengue intra-cranially mice and eliminated DENV (from 10^{10} to be 0) in blood of Marmosets within two days. For further used in human, large scale production of NhuMAb using the Food and drug administration (FDA) accepted method namely Stable Chinese Hamster Ovary (CHO) cell expression, is needed. This study reports the establishment of stably expressed CHO cells for large scale production of NhuMAbs against 4 serotypes of DENV. To express DENV IgG, two plasmids containing heavy and light chains of anti-DENV IgG were transfected into CHO-K1 cells using lipofectamine 2000. Two antibiotics, hygromycin and puromycin, were used to select for anti-DENV IgG producing cells. Optimal concentrations of the antibiotics were determined to create stable CHO cells. The transfected cells were trypsinized and cloning of single cell by limiting dilution method. The wells with one colony were marked. Cell growth was observed, culture supernatants were harvested and NhuMAb concentration was measured using ELISA to screen for positive clones. Stably expressed CHO cells were successfully established for two candidate anti-DENV IgG NhuMAb. These CHO cells could stably express IgG NhuMAbs with the same neutralizing activity against 4 serotypes of DENV, as same as those from hybridoma cells. These expressed NhuMAb will be further clinical trial test in human in the near future.

Keywords: Stable Expression / Dengue Virus / Monoclonal Antibody / Mammalian Cell

Poster no. 48

PERCEPTIONS TOWARDS DENGUE HEMORRHAGIC FEVER ETHNIC MINORITY GROUPS IN RATTANAKIRI AND MONDOLKIRI PROVINCE : A RAPID ASSESSMENT

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Background: The Cambodia-Thailand Malaria Control project, was launched in 2007 in two eastern Cambodian provinces, Rattanakiri and Mondolkiri. The project aimed at malaria control among indigenous people belonging to several ethnic minorities. Presently malaria problem has been significantly reduced over the past several years. However, the public health threat of dengue has found in the project areas. This study aimed to describe the perceptions towards Dengue Hemorrhagic Fever (DHF) among the Ethnic Minority Groups in both Provinces.

Methodology: A rapid assessment was organized. Community and household environment observation were conducted. Sixteen participants were in-depth interviews. Content analysis was used for data analysis.

Results: Most of them (13/16) had ever heard about DHF. Among those, one half of them unable to describe about causes, signs/symptoms, prevention and control of DHF. More than half stated that headache and fever were main signs and symptoms of DHF. Less than half had known how to prevent and control DHF in the community. Most of participants perceived that their villages and they themselves were DHF at risk, "… there are a lot of mosquitoes in the villages and DHF cases were found in the villages". The observations found that very few households covering water jars/water containers and sleeping in mosquito nets in the day time.

Conclusion: The study, which is still underway, was undertaken to develop an improved, community-led socio-culturally sensitive approach to DHF prevention and control among the ethnic groups.

Keywords: perception, Dengue Hemorrhagic Fever, ethnic group

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Poster no. 53

MAN-MADE CONTAINER THE RISK OF DENGUE EPIDEMIC IN MONDULKIRI AND RATTANAKIRI, CAMBODIA

Entomological surveys were carried out from September 2014-January 2016 to investigate the presence of dengue vectors in man-made containers, discarded tires and artificial water containers in houses and peridomestic areas. A cross-sectional immature stage survey was done indoors and outdoors in 2-3 villages in Mondulkiri and Rattanakiri, Cambodia respectively. Larvae were identified morphologically, larval indices were also calculated, and key container were defined separately at each location. Mosquito larval sampling was conducted using pipette or dipper depending on container types.

Results showed *Aedes albopictus* was the predominant species found higher than *Aedes aegypti* in Rattanakiri and Mondulkiri province. Larval Indices were seasonally different among localities. HI in localities showed significant difference ($p<0.05$) between seasons: Dry (Dec) and Wet (May –October) of $X^2=80.45$ (df=4) and 4.98 (df=3) in Rattanakiri and Mondulikiri respectively. Both *Aedes aegypti* and *Aedes albopictus* are breeding in a wide range of artificial containers. However the key positive containers differed among each province, with 4 and 5 main breeding types in Mondukiri and Rattanakiri respectively. Used oil drums, water containers, used tires, and discarded containers were indicated as 'Key Containers' in Mondulkiri. While in Rattanakiri survey showed the same Key container, plus one additional type, large water jars. We suggest to achieve controlling these mosquitoes, the integration of different methods with community participatory should be taken into consideration.

Keywords: Dengue, Aedes vectors, key container

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Poster no. 55

RISK FACTORS FOR CHIKUNGUNYA INFECTION DURING A RE-EMERGED CHIKUNGUNYA OUTBREAK IN TAKBAI DISTRICT, NARATHIWAT PROVINCE DURING 2014-2015

In late November 2014, an outbreak of the Central East African chikungunya virus re-emerged in Takbai district, Narathiwat province. A serosurvey was conducted to investigate the clinical features and risk factors of infection. Sera from 208 volunteers aged more than 17 years had chikungunya IgM antibodies by Haemagglutination inhibition test and interviewed with structured questionnaire. Of 161 infected cases, 122 (58.6 %) had chikungunya-like-symptoms. The dominant symptoms reported were joint pain (99.2%), headache (94.3%), fever (87.7%) and rash (73.1%). Chikungunya infection was associated with no outdoor mosquito biting protection (adjusted odds ratio=3.13, 95%CI =1.27-7.67), having outdoor garbage pile (adjusted odds ratio=2.79, 95%CI =1.26-6.17) and illiteracy or lower primary school education (adjusted odds ratio=2.79, 95%CI =1.01-7.67). Therefore, self protection from outdoor mosquito biting and clearing of garbage piles should be promoted to residents during chikungunya outbreak.

Keywords: chikungunya, outbreak, risk factor

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Poster no. 57

DIFFERENTIAL VACCINIA VIRUS ENTRY AND INNATE IMMUNE SIGNALING IN MACROPHAGES

Previously, we showed that Vaccinia virus Western Reserve (WT-WR) contains A26 protein and enters HeLa cells through fluid phase endocytosis whereas a mutant, A26 deletion virus (WRDA26) enters through plasma membrane fusion. Now we extended this finding into the primary innate immune cells particularly macrophages to understand whether WT-WR and WRDA26 also enter immune cells through different pathways. Literatures showed that infection of WR in the human or mouse macrophages is not permissive, causing apoptosis of infected cells; however, the intracellular mechanism of restriction is unclear. We infected bone marrow derived macrophages (BMDM) with WT-WR and WRDA26 viruses and utilized microarray to analyze RNA harvested at 1, 2, 4 and 8 hours post-infection times. We found that WT-WR induced higher interferon and antiviral signaling compared to WRDA26. In addition, we generated recombinant viruses expressing fluorescence early Venus and late mCherry marker proteins to analyze for viral gene expression kinetics by live imaging and flow cytometry. We found that WRDA26 indeed expressed robust early and late proteins while WT-WR only expressed limited amounts of early proteins in BMDM. Further experiments to understand the molecular basis that contributes to differential viral gene expression due to different virus entry routes are currently underway and the results will be discussed.

Keywords: Vaccinia virus entry and interferon

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Poster no. 58

INCIDENCE OF *SALMONELLA* AND SEROTYPES WELTEVREDEN AND INFANTIS IN PORK PRODUCTS COLLECTED FROM SELECTED PUBLIC WET MARKETS IN METRO MANILA, PHILIPPINES

Salmonella is one of the most significant pathogens that cause food-borne diseases in the world. Although there are 2,659 identified *Salmonella* serovars, most human infections are caused by limited number of serotypes, which include Weltevreden and Infantis. Majority of *Salmonella* infections in humans are associated with the consumption of contaminated meat products, such as pork. Pork is the most widely produced and consumed meat products in the Philippines. The objectives of this study were to determine the incidence of *Salmonella*, its common O-serogroups, and serotypes Weltevreden and Infantis in pork. Five types of pork products, including ground pork (n=50), meatloaf *(embotido)* (n=50), ham (n=50), sausage *(longganisa)* (n=56), and cured pork meat *(tocino)* (n=50), were collected from five selected public markets in Metro Manila. Multi-step PCR assays were performed to determine the presence of *Salmonella*, and characterize the isolates according to their respective serogroups and serotypes. One hundred thirty-two out of 256 samples were found to be *Salmonella*-contaminated. All of the ground pork samples were found to be *Salmonella*-contaminated, while *embotido* and ham were the least contaminated (22.00%). Majority of *Salmonella* contaminants in pork samples were categorized to serogroup O:3,10 (66.67%), followed by O:4 (46.97%), O:6,7 (44.70%), O:8 (22.73%), others (6.06%), and O:9 (3.03). The low incidences of *S.* Weltevreden (14.39%) and *S.* Infantis (2.27%) detected in pork products were perhaps indicative of their low reports in clinical samples. This study provides baseline information regarding incidence of *Salmonella* and the distribution of its serogroups and serotypes in food, which is currently lacking in the Philippines.

Keywords: Salmonella Weltevreden Infantis Pork Philippines

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Poster no. 59

MOLECULAR DETECTION, CHARACTERIZATION, AND ANTIMICROBIAL PROFILING OF *SALMONELLA* SPECIES ISOLATED FROM SLAUGHTERED SWINE

Pork is one of the most commonly consumed meats worldwide. It is also considered as one of the main sources of salmonellosis which affects 93.8 million humans per year globally. In the Philippines, the swine industry contributes to the largest volume of livestock production. In the present study, we aimed to detect and characterize *Salmonella* spp. from slaughtered swine and screen the isolates for resistance genes. Tonsil and jejunum samples of freshly slaughtered swine were collected in three locally regulated meat establishments in Metro Manila. *Salmonella* spp. were isolated using conventional culture methods and confirmed by PCR amplification of the *invA* gene, a gene unique to *Salmonella* spp. which encodes for the protein involved in the invasion of the intestinal epithelium. Isolates were further characterized based on somatic antigen and presence of *bla* genes by multiplex PCR assays. Our findings reveal that out of 180 carcasses of slaughtered swine, 76 (42.22%) were contaminated with *Salmonella* spp. Majority (31.58%) of the contaminated carcasses carried *Salmonella* spp. under serogroup E1, and 21.05% carried multiple types of *Salmonella* spp. Twelve (15.79%) carcasses were contaminated with *Salmonella* spp. of unknown serogroup. Out of 132 **Salmonella** spp. isolates, 4 (3.03%) and 78 (59.09%) carried bla_{CTX-M} and bla_{TEM}, respectively. Co-carriage of the bla_{CTX-M} and bla_{TEM} genes was observed in three (2.27%) isolates. The gene bla_{SHV} was not found in any of the isolates. We report here the incidence of *Salmonella* spp. in Philippine swine and the characterization of the somatic antigen and resistance genes of the isolates.

Keywords: Antimicrobial resistance, pork, Salmonella, swine

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Poster no. 60

DEEP TUBE-WELL WATER USE AND MODERATE-TO-SEVERE CHILDHOOD DIARRHEA EPISODE DUE TO S. *SONNEI* INFECTIONS: A CROSS-SECTIONAL STUDY IN KUMUDINI WOMEN'S MEDICAL COLLEGE AND HOSPITAL, MIRZAPUR, BANGLADESH

Background and aim: The present study aimed to determine any association between drinking deep tube-well water and childhood diarrheal illness due to *S. sonnei* in rural Bangladesh.

Methods: A total of 1,394 children aged 0-59 months who presented with moderate-to-severe diarrhea in Kumudini Women's Medical College and Hospital for care from December 2007 to March 2011 were enrolled into the study.

Results: *Shigella* was the leading pathogen causing childhood moderate-to-severe diarrhea episodes. The isolation rates of *Shigella* spp. were similar from children belonging to those families who are using deep tube-well water as well as those from shallow tube-well water user families (41% vs. 44%). However, 13% of the children from deep tube-well water using families had *S. Sonnei* infection compared to 8% of the children from shallow tube-well water user families (OR 1.81, 95% CI 1.26-2.60, p<0.001). Usage of electricity was higher in deep tube well water users (OR ratio 1.38, 95% CI 1.10-1.71; p <0.004). Higher proportion of shallow tube-well water users treated drinking water compared to deep tube-well user families (7% vs. 2%, adjusted OR 0.26, 95% CI 0.14-0.47, p<0.000) and treatment method of filtering was through a cloth (OR 0.208, 95% CI 0.09-0.45, p<0.000).

Conclusion: It is well accepted that exposure to *P. shigelloides*, through contaminated drinking water, may immunize people to *S. sonnei* in developing countries. Increased and sustained access to safe drinking water and less exposure to contaminated water with presence of *P. shigelloides* that shares antigen with *S. sonnei* may have played a role in excess detection of *S. sonnei* in stool specimens of childhood moderate-to-severe illnesses as well as who are the users of deep tube-well water in this context.

Keywords: Bangladesh, diarrhea, tube well, Under-five children

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Poster no. 61

UNRAVELLING OF HOST SPECIFICITY OF *SALMONELLA* INFECTION BY COMPARATIVE SECRETOME PROFILING

Typhoid is an acute and life threatening febrile illness caused by *Salmonella* enterica serovar *typhi*. It is a major cause of morbidity and mortality worldwide and highly endemic in south Asian sub-continent. Despite ~90% genome similarity with *S.*Typhimurium, *S.* Typhi exclusively infects humans and causes systemic illness while *S.*Typhimurium does so in mice but only self-limiting gastroenteritis in humans. The exact mechanisms contributing to this host specificity are still unclear and the existing knowledge of *S.* typhi pathogenesis is based upon the *S.* Typhimurium infection in mice. Therefore, it is imperative to study *S.* Typhi pathogenesis through alternate models that could mimic *in vivo S.*Typhi infection in humans. We have utilized an *in vitro* model consisting of polarized intestinal epithelial cells (IEC) mimicking the gut to study *S. typhi* infection. To obtain a comprehensive overview of the contrast in the host secretory signatures post-infection amongst two closely related serovars, *S. typhi* or *S.* Typhimurium, we have used this IEC culture system wherein the Caco-2 cells were grown on porous inserts of trans-well plates. The monolayer integrity and polarity was determined through trans-epithelial electrical resistance measurement and the bacterial infection was carried out at 100 MOI. A comparative proteomic profiling of the basolateral secretome was carried out by LC-MS/MS and a total of 175 host proteins were identified of which 18 proteins were unique to *S.*Typhi and 12 proteins unique to *S.*Typhimurium infection with 14 common proteins. Identification of unique molecules and elucidation of their role would enable us to gain deeper insights and develop a better understanding of *Salmonella* pathogenesis. The study has important translational implications through identification and utilization of novel targets for rational design of typhoid diagnostics and therapeutics.

Keywords: Typhoid, proteomics, Salmonella typhi, typhimurium

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Poster no. 62

MOLECULAR CHARACTERIZATION OF SALMONELLA ENTERICA ISOLATES FROM MEAT PRODUCTS THROUGH ANTIMICROBIAL RESISTANCE AND VIRULENCE GENE PROFILING

This study aimed to examine the antimicrobial resistance and virulence profiles of *Salmonella enterica* isolates from raw and processed meat products. A total of 95 *S. enterica* isolates were characterized for virulence genes encoding for fimbriae, and beta-lactamase resistance genes. Antimicrobial susceptibility tests were performed for aztreonam, ceftazidime and cefotaxime. The results showed that 39 isolates were shown to be resistant to at least one antibiotic. Resistance to third generation cephalosporins ceftazidime (23%) and cefotaxime (15.8%) was most frequent.Among the three resistance genes examined, the bla_{TEM} gene was most common (67%). The long polar fimbriae (*lpfA*) gene was the most common virulence gene found *inSalmonella* isolates (34%). A strong positive correlation was observed between the *sefA* and *pefA* fimbrial genes, which were each found in 12% of the isolates. The results show that raw and processed meat products in Philippine wet markets act as salient reservoirs of *Salmonella* harboring virulent and resistance genes. Strong statistical associations were observed between the β-lactamase gene bla_{TEM} and the long polar fimbriae gene *lpfA.* This demonstrates that antimicrobial resistance genes and fimbrial genes can coexist in *Salmonella* isolates, and are selected through antimicrobial selective pressures. Thesefindings have significant implication with regard to the evolution and distribution of resistance and virulence genes, because selective pressures conferred by inconsistent use of antimicrobials lead to the emergence of new pathogens with increased virulence and resistance potential.

Keywords: Salmonella enterica, antimicrobial resistance, virulence

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Poster no. 63

DETECTION OF *SALMONELLA ENTERICA* FROM PORK SAMPLES USING LOOP-MEDIATED ISOTHERMAL AMPLIFICATION (LAMP)

In developing countries such as the Philippines, the risk of food poisoning due to the ingestion of food contaminated with pathogens such as *Salmonella enterica* has been a constant concern. Contamination may occur due to improper handling anywhere from the slaughter of the animals to delivery to handling for sale to consumers. Standards have been set in the Philippines that consider detection of 10^4 viable cells of *S. enterica* in 25 g of meat as unfit for consumption although this is not as stringent as in other countries. Turnover time between the slaughter of the animals and their sale to the general public is also short making efficient detection necessary. Loop-mediated isothermal amplification (LAMP) is an easy-to-use method with potential use for rapid and accurate detection of *S. enterica* in meat and meat products. In this study, LAMP was optimized and used to determine the efficiency of the method in detecting *S. enterica* of different serotypes and serogroups from meat products, specifically pork. The assay was found to be specific for different serogroups and serotypes of *S. enterica.* The sensitivity of the assay was found to be in the order of 2000 copies, the minimum tested amount of DNA. The assay was also found to be able to detect *S. enterica* from pork samples within 4 hours of pre-enrichment. LAMP was found to be an effective method for the detection of *S. enterica* from pork samples and it could present an efficient solution to increase health safety for the public.

Keywords: Salmonella LAMP Detection

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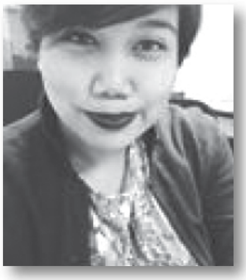
Poster no. 64

THE PREVALENCE OF *SALMONELLA* SPP. AND ASSOCIATED GASTROINTESTINAL PATHOGENS IN POULTRY BASED FOOD PRODUCTS IN DHAKA CITY

Nowadays safety of food is our main concern which is hampered by the presence of gastrointestinal pathogens like *Salmonella*. Present study reveals the presence of *Salmonella* and other potential pathogens in poultry based food products collected from different places in Dhaka. For pre-enrichment, Buffered Peptone Water and for selective enrichment, Rappaport-Vassiliadis Soya broth was used. Pure colonies were identified presumptively based on colony morphology and biochemical test results. The percentages of *Salmonella* on egg shells were 15%, the egg content had 5%; in grilled chicken, pudding and in mayonnaise- it was 30% and 20% for each of the latter two samples respectively. Isolated *Salmonella* strains were mostly resistant against Streptomycin, Nalidixic acid, Rifampicin, Kanamycin, Trimethoprim-sulfamethoxazole and Erythromycin and susceptible to Cefotaxime, Ciprofloxacin and Chloramphenicol. Amongst other gastrointestinal pathogens, higher percentages of *Shigella* in raw food (in egg shell 60% and egg content 25%) had been observed whereas, in cooked food samples, the percentages were lower (in grilled chicken 10%, in pudding and mayonnaise 0%). Other pathogens like *E.coli, Enterobacter, Klebsiella, Proteus, Citrobacter, Pseudomonas* had also been isolated in these samples. Additionally, higher numbers of *Bacillus* and *Staphylococcus* had been observed nearly in all of these samples. The presence of multi-drug resistant *Salmonella* and other potential pathogens are alarming and draw our concerns as poultry based products constitute a major part of the diet of children in our country, adequate measures must be taken to reduce the microbial load.

Keywords: Salmonella, poultry product, gastrointestinal pathogen



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Poster no. 65

SURVEY ON THE PRESENCE OF EXTENDED-SPECTRUM β-LACTAMASE (ESBL) PRODUCTION BY IDENTIFYING THE BLATEM GENE AMONG ESCHERICHIA COLI ISOLATES FROM DIFFERENT VEGETABLE PRODUCE IN SELECTED OPEN AIR MARKETS AND SUPER MARKETS IN THE PHILIPPINES

Foodborne illnesses may be accounted to the risk of microbial contamination that can be due to several factors such as irrigation waters, handling or processing. Bacterial contamination harbor antibiotic resistance conferred by enzymes like extended-spectrum β-lactamases (ESBLs), which can hydrolyze penicillins, cephalosphorins, and aztreonam, limiting options for treatment. Considering the possibility of transmission of antibiotic resistant bacteria through different sources and consequently fresh produce, ESBL production was evaluated in 12 *Escherichia coli* isolates from 132 vegetable samples in different open air and supermarkets in the Philippines. Initial and confirmatory screenings for ESBL production were conducted through disk diffusion method with ceftazidime and cefotaxime and through double disk synergy test, respectively. Polymerase chain reaction (PCR) testing was carriend out for $\mathit{bla}_{\mathrm{TEM}}$ ESBL genes. PCR testing showed blaTEM to be present in most of the confirmed ESBL-producing isolates. Presence of ESBL-producing bacteria in different readily eaten fresh produce suggests increased risk for publich health. Anthropogenic sources of antibiotic contaminants that promote the dissemination of antibiotic resistance accent the need for control of the release of contaminants into the environment.

Keywords: blaTEM, Escherichia coli, fresh produce

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Poster no. 66

DETECTION AND PREVALENCE OF ANTIMICROBIAL RESISTANCE PATTERNS OF *ESCHERICHIA COLI* ISOLATES FROM AGRICULTURAL IRRIGATION WATERS IN BULACAN, PHILIPPINES

Escherichia coli is an important cause of human illness in the Philippines, thus there have been numerous reports on water and food contamination which is associated with it. As *E. coli* is one of the reliable indicator of fecal pollution and an effective model for monitoring antimicrobial drug resistance, the study aims to detect and confirm the identity of the thermotolerant *E. coli* isolates in 10 different farming sites in Bulacan, Philippines using conventional and molecular methods and, to determine the patterns of antimicrobial resistance in confirmed *E. coli* isolates. From the 90 irrigation water samples, a total of 79 isolates were confirmed through PCR amplifying the *uidA* gene. Ten (10) antibiotics covering eight (8) different classes were used to determine the phenotypic resistance of the confirmed isolates. Forty-six out of 79 (58.23%) isolates were found to be multidrug resistant (MDR), which is the resistance to three or more classes of antibiotics tested. Highest resistance was observed in cephalothin (73.42%), followed by tetracycline (50.63%), streptomycin (49.37%), ampicillin (48.10%) trimethoprim (45.57%), nalidixic acid (35.44%), and chloramphenicol (25.32%). Least resistance, on the other hand, was observed in ciprofloxacin (5.06%) followed by cefotaxime (8.86%) and gentamicin (13.92%). Most common pattern observed was the combination of Chl-Nal-Tet-Amp-Cep-Strep-Tri (8.70%) and Tet-Amp-Tri (6.52%). Overall, the results imply that the agricultural water used in Bulacan is contaminated with fecal material of man or other animals present within the area and the MDR isolates detected in the study pose a potential threat to individuals exposed to the area.

Keywords: Antibiotics, E. coli, Multidrug resistance, PCR, uidA gene

Poster no. 69

PUTTING LIFE ON HOLD: A CLINIC BECOMES A COMMUNITY FOR TB PATIENTS

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While there has been some progress in case detection and treatment of tuberculosis (TB) and multi-drug resistant tuberculosis (MDR TB) globally, major challenges remain especially with regard to case holding and follow ups. These problems are exacerbated in highly mobile populations, such as those along the Thailand-Myanmar border. For example, treatment for MDR TB can take up to two years and is only provided by a limited number of centers, meaning a significant space-time commitment for people who are normally quite mobile. Conversely, persons with MDR TB who do not seek proper treatment and who are highly mobile may contribute to the geographic spread of the disease. MDR TB treatment therefore poses a difficult ethical conundrum. In 2009 Shoklo Malaria Research Unit (SMRU) established a TB detection and treatment program following an observed increase in TB cases presenting at clinics along the Thailand-Myanmar border. The program consists of two TB clinics, one on each side of the border, with a combined capacity of 220 patients and the provision of care and directly observed treatment for both drug sensitive and resistant TB. Most patients come from within a 30 kilometer radius of the clinics, while some are 100s of kilometers away from their home communities. Here we discuss the creation of a specific model of care in which TB infected migrants are given the opportunity to live on site for the duration of their treatment. We use patient and health provider stories and insights to highlight the challenges faced by both parties, together with obstacles and successes faced by the SMRU TB program, and some important ways forward for MDR TB treatment in the region.

Keywords: putting life on hold

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Poster no. 71

NEISSERIA MENINGITIDIS CARRIAGE AMONG MARCHING SOLDIERS

Neisseria meningitidis is the most deadly meningitis disease in the world. The disease is important because of its high case fatality rate, up to 50%, especially if the treatment is late. Different serotypes of meningococci are seen among various Asian countries although some countries do not give report and the others do not recently.

Meningococci is present in the throat of 10-20% of normal population. Although exact mechanism is unknown, meningitis occurs when the organism gains access into blood stream of the host. Carrier rate becomes higher in crowds and at the time of outbreaks. Transmission is through respiratory route and the crowded places like military camps and barrack become targets. Meningitis occurred at times with some incidences during 2006-2007 periods at Nay Pyi Taw military camp where troops were practicing for Armed Forces Day marching parade.

In this year 2016, in early March, meningococcal B disease outbreak occurred at Thazi township, 150 km north of Nay Pyi Taw, with 7 children hospitalized and 4 deaths. Therefore a study was done towards 200 marching soldiers at Nay Pyi Taw military camp practicing for 71st Arm Forces Day parade during March, 2016. Questionnaire concerning sociodemographic and behavioral factors were asked and oropharyngeal swabs were taken. Isolation of meningococci, bacterial identification and antimicrobial susceptibility tests were done using conventional solid culture, microscopy and Vitek 2 at Defence Services Medical Research Centre.

Among 200 soldiers tested, only 19 (9.5%) carried meningococci. Soldiers of age between 35 and 39 carried the most and over 40 the least. Association was seen with smoking and alcohol drinking but not with betel chewing. Resistance to Rifampicin and Penicillin showed 80% and almost 90% of isolates respectively. Isolates showed no resistance to Ciprofloxacin still keeping it as an effective chemoprophylaxis and treatment drug.

Keywords: Neisseria meningitidis, meningitis, soldiers, military camp, Myanmar

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Poster no. 72

MOLECULAR EPIDEMIOLOGY OF HUMAN LEPTOSPIROSIS WITH SEPSIS

Background: Leptospirosis is a zoonotic disease caused by pathogenic *Leptospira* species. The clinical manifestations of human leptospirosis range from sub-clinical symptoms to multi-organ involvement. Here, we aim to evaluate molecular epidemiology of *Leptospira* species causing sepsis in Southeast Asia.

Methods: Blood samples were obtained from "An Observational Study of the Causes, Management, and Outcomes of Community-acquired Sepsis and Severe Sepsis in Southeast Asia" (NCT02157259) conducted during 2013 to 2016 in 15 hospitals in Thailand, Vietnam, and Indonesia. Among the sepsis cases, leptospirosis was identified at 5.9%, 6.0%, and 7.6% for Thailand, Vietnam, and Indonesia, respectively. All blood samples with real-time PCR *Leptospira* positive results were used for identifying *Leptospira* species. The partial *rrs* gene was amplified using the nested PCR as described previously by Boonsilp *et al*. The amplicons were purified and sequenced. A phylogenetic tree of the 443-nucleotide *rrs* fragments was re-constructed prior to inferring *Leptospira* species.

Results: A total of 34 real-time PCR positive blood samples collected from 34 sepsis patients from Thailand were included in the study. Of overall, 30 (88.2%) were positive for the nested PCR. The remaining 4/34 (11.8%) were negative. *L. interrogans* and *L. weillii* were identified in 29 and 1 samples, respectively. Of 29 patients with blood sample on admission with nested PCR positive for *L. interrogans*, 19 (65%) had MAT positive, 7 (25%) were MAT negative with paired serum samples and 3 (10%) were MAT negative but without convalescent serum samples. The single patient PCR positive with *L. weilii* had MAT negative.

Conclusions: *L. interrogans* is a major cause of human leptospirosis with sepsis in Thailand.

Keywords: Leptospirosis, sepsis, L. interrogans, L. weillii, Southeast Asia

Poster no. 75

TRYPTOPHOL (QUORUM SENSING MOLECULES) INDUCED APOPTOSIS IN *CANDIDA ALBICANS*

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Quorum sensing molecules (QSMs) is referred to as auto-induction, microbial cell-cell communication. Various studied the role of QSMs (farnesol and tyrosol) in *Candida albicans* morphogenesis and program cell death. The other QSMs i.e. tryptophol do not know the biological effect on *C. albicans*. Therefore, we investigated the effect of tryptophol on *C. albicans* apoptosis pathway by observing apoptosis-related gene expression levels (CARD9, NOXa and BCL-2) after treated with tryptophol and farnesol. *C. albicans* were treated with farnesol and tryptophol for 2, 6 and 24hr. The level of apoptosis signalling gene expression was evaluated by qPCR. We found that the expression of CARD9 level was increased at 2, 6, and 24 h comparing with untreated cells. The highest expression level of CARD9 was seen after treated with tryptophol at 2 and 6 h whereas the expression level of CARD9 treated with farnesol was lower than farnesol but increasing at 24h. In NOXa, the expression level was increased at 6 and 24 h compared with untreated cells. Moreover, NOXa expressed the highest level in tryptophol treated-cells at 6 h, whereas in farnesol treated-cells at 24 h. Moreover, we found BCL-2 expressed the highest level at 2 h after treated farnesol and tryptophol compared with untreated cells. Although, BCL-2 expression level was decreased at 24h in tryptophol treated-cells but BCL-2 expression level was increased at each time point in farnesol treated-cells. Therefore, tryptophol plays some key role in apoptosis pathway in *C. albicans* but different mechanisms from farnesol. These molecules will be valuable in research field of the signaling pathways regulating the apoptosis and also may serve as starting points for potential new antifungal therapeutics.

Keywords: Tryptophol, Farnesol, Apoptosis, Candida albicans

Poster no. 76

APOPTOSIS OF *LOMENTOSPORA PROLIFICANS* AND *SCEDOSPORIUM BOYII* INDUCED BY FARNESOL

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Lomentospora prolificans (formerly *Scedosporium prolificans*) and *Scedosporium boydii* are important emerging fungal pathogens. These two pathogenic fungi cause severe infection in immunosuppressed individuals. Moreover, antifungal resistant of *L. prolificans* has been reported. Farnesol, a quorum sensing molecule firstly identified in eukaryotic organism; *Candida albicans*, has been studied in several fungi in terms of the effect of fungal morphology, biofilm development, conidia germination and apoptosis. However, the effect of farnesol on these two fungi has not been performed. Thus, the aim of this study was to investigate the effect of farnesol on apoptosis of *S. boydii* and *L. prolificans*. *S. boydii* CBS 120157 and *L. prolificans* CM324 were grown on Sabouraud Dextrose Agar slants at 37°C for 7 days. Conidia were collected and suspended in phosphate-buffered saline (PBS). Apoptotic cell investigation was performed by staining *S. boydii* CBS 120157 and *L. prolificans* CM324 with ethidium bromide (EB) and acridine orange (AO) and observed under a fluorescent microscope. Farnesol-treated *S. boydii* and *L. prolificans* showed organelle condensation and orange staining of the hyphae. This study provides a starting point for further investigation of the mechanism of the farnesol-induced apoptosis of these two pathogenic fungi .

Keywords: Farnesol, Quorum sensing molecule

Poster no. 77

DNA BARCODING FOR IDENTIFICATION OF *SCEDOSPORIUM APIOSPERMUM* SENSU STRICTO

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Scedosporium apiospermum sensu stricto is an important emerging fungal pathogens that have been frequently reported in immunocompromised patients and immunocopetent patient after near-downing. Nowadays, *Scedosporium apiospermum* sensu stricto was classified as member of *Scedosporium apiospermum* complex (together with other 5 species; *Scedosporium apiospermum, Scedosporium boydii, Scedosporium angusta, Scedosporium minutisporum, Scedosporium dehoogii,* and *Scedosporium aurantiacum*) by genetically relationship. Here, we assessed the utility of DNA barcoding for identification of *Scedosporium apiospermum* sensu stricto in Thailand based on sequence comparison of the DNA barcode region. Thirty environmental strains of *Scedosporium apiospermum* sensu stricto were used for the DNA barcoding study. DNA was extracted and the partial of ITS region of the rDNA gene cluster, ß-tubulin (TUB) and ß-tubulin (BT2) were amplified. The sequences were edited and subjected to pairwise alignment using BioEdit software. Edited sequences were compared with existing sequences in GenBank using BLASTn. Phylogenetic trees were constructed in MEGA7 a bootstrap analysis was conducted with 1,000 replications by individual loci and concatenated sequences. ITS region remain the best performance for identification in species level almost fungi. Our study consistency indicated that ß-tubulin (TUB) and ß-tubulin (BT2) showed a high threshold value and suitable for distinguishable within the *Scedosporium apiospermum* complex lineages than ITS region. Additional data from phylogenetic analysis, we provided the basis information for future monitoring of their populations in the Southeast Asian region.

Keywords: DNA barcoding, Scedosporium apiospermum sensu stricto

Poster no. 78

CLINICAL-MYCOLOGICAL STUDY OF DERMATOPHYTES FROM HOSPITAL FOR TROPICAL DISEASES, BANGKOK

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Dermatophytes comprising of the genera *Trichophyton, Microsporum* and *Epidermophyton* are also important cause of superficial mycoses. We not known the current situation of dermatophytes infections, precise size of infected patients and species distribution of these organisms. Therefore, the aim of this present study was to investigate the clinical pattern of dermatophytes infection patients and to identify the species of these dermatophytes from Hospital for Tropical Diseases, Bangkok. A total of 25 samples from 23 patients who diagnosis cases of dermatophytosis attending the skin out-patient clinic, Hospital for Tropical Diseases, Bangkok, period of September 2015-September 2016 were studied. Skin scrapings from the patients were direct examined the fungal element by 10% KOH. The other portion of the sample was used for the culture on sabourauds dextrose agar and dermasel (sabourauds dextrose agar with antibiotics and cycloheximide) and incubated at 25 °C. The agar were observed for 4 weeks. Any colony growth on the agar was observed morphology characteristic and did wet mount by using Lactophenol Cotton Blue, then examined under the light microscope for the looking of specific characteristic of dermatophytes species. Out of 23patients, Tinea corporis was the most common clinical type (52%) followed by tinea capitis, tinea facei, tinea cruris (12%) and tinea manuum, tinea pedis, tinea unguium (4%). Overall positivity by culture was 28 %. We found *Microsporum canis* 4 isolates, *Trichophyton* spp. 3 isolates, *Trichophyton verrucosum* 1 isolate and also found other non-dermatophytes i.e. *Candida albicans* 2 isolates and Dematiaceous fungi 1 isolate. Therefore, both direct microscopy and culture are important tools of diagnosis for help dermatophytes infection patients.

Keywords: Dermatophytes, Trichophyton, Microsporum, Epidermophytons

Poster no. 79

THE POTENTIAL ROLE OF FUNGAL QUORUM SENSING MOLECULES STUDY: *IN VIVO* PATHOGENESIS OF *CANDIDA ALBICANS* USING GALLERIA MELLONELLA MODEL

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The fungal quorum sensing molecules (QSMs) has been identified the role in various study, mostly for control the fungal biological activities and behaviors. Hence, the QSMs can caused programmed cell death and also play role in fungal virulence and pathogenicity. The potential role of fungal QSMs with pathogenicity has not been clearly understood in vivo. In this study we use the Candida albicans treated with tryptophol (QSMs) to identified the morphological and biological change and used the Galleria mellonella (wax worm) to study the pathogenesis and virulence of fungus after treated with QSMs. The results shown that the slow rate of hyphae development in tryptophol treated group rather than the without QSMs treated group significantly. In vivo study, the results shown the survival rate of Galleria mellonella in group of C. albicans infection without QSMs in day 1, 2, 3 after post infection are 66.66%, 66.66% and 0, respectively. In the group of C. albicans infection treated with QSMs, the survival rate of Galleria mellonella is 100% until 3 days post infection. The results suggested that the QSMs play the potential role in fungal biological activities and might be reduce the virulence of C. albicans in vivo. Further study the role of fungal QSMs need to determine to clarify the potential role of QSMs and further application development particularly in therapeutic and prevention.

Keywords: fungal quorum sensing molecule, Galleria mellonella, Candida albicans

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Poster no. 80

URETHRITIS IN MALE, YOUTH CLINIC, BANGRAK HOSPITAL

Urethritis is inflammation of the urethra and is either gonococcal or non-gonococcal or of mixed etiology which are the most common reported STI in youth. The prevalence and incidence of urethritis are higher in developing countries. The usual presentations are discharge with dysuria and it is diagnosed by Gram stain. The complications are rare. WHO recommended syndromic management guidelines of men with urethral discharge should be treated with both gonorrhoea and chlamydial.

A retrospective descriptive study of male urethritis was conducted at Youth clinic in Bangrak Hospital during the two fiscal years 2008 and 2009. The prevalence of male urethritis and percentage of risk factors, clinical features, diagnosis, treatment and treatment outcomes of GU and NGU were determined. Univariate analyses were applied to identify the association between the characteristics of urethral discharge and GU-NGU.

There were 75 cases and 116 episodes studied and the prevalence of male urethritis was 21.9% in fiscal year 2008, 18.4% in fiscal year 2009 and 19.8% in the two fiscal years. Forty four percentages of patients were students and 89.3% were single. On Gram staining, 72 patients positive for GU and 44 positive for NGU. After doing cultures, 67 patients were positive for GU. Three patients positive for *chlamydia trachomatis* (CT) among 72 GU patients and 7 patients were positive CT among 44 NGU. Dysuria with urethral discharge was the most common presenting symptom in both GU (74.7) and NGU (66.7%). Fifty patients were presenting with yellow and green color discharge and 25 patients with white color. Eleven patients had got heavy discharge. First symptom was occurred mostly in 3-5 days (36.6%) in GU and <3days (25.9%) and 3-5 days and ≥ 1 months (14.8% each) in NGU. Majority of the cases were treated with cefixime based regimen (59.7%) for 2 weeks duration (67.7%). In which 48.8% were cured and 7% were recurrent/persistent. Doxycycline based regimen (20.7%) for 2 weeks duration (54.8%) was usually used for NGU, the outcomes were cured (70.5%) and recurrent (12.5%). Complications of urethritis were found in 12 cases.

Prevalence of male urethritis in Youth clinic was determined and syndromic approach to the management of urethritis should be implemented to improve the outcomes of patients in Youth Clinic, Bangrak hospital.

Keywords: urethritis/male/youth/thailand/gonococcal/non-gonococcal

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Poster no. 81

SYNTHESIS AND ANTIMALARIAL ACTIVITY STUDY OF A SERIES OF NOVEL HYBRID DERIVATIVES OF 4-AMINOQUINOLINE AND MANNICH BASES

The emergence of resistance in parasites towards currently available antimalarial drugs has become a major health concern of the developing world. This resistance has necessitated an urgent awareness to constantly look for new chemotherapeutic agents for the treatment of malaria. The purpose of the present study was to develop new potential antimalarial agents.

A new series of hybrid derivatives from 4-aminoquinoline and Mannich bases were synthesized [1] by modifications at the side chain of chloroquine with *m*-phenylenediamine and pendent amino group with Mannich bases of substituted acetophenone without making alteration in 7-chloro-4-aminoquinoline nucleus. The structure of all the synthesized compounds were confirmed and characterized by using various spectral technique like IR, 1H NMR, 13C NMR and mass spectroscopy. All the synthesized compounds were evaluated for *in vitro* antimalarial activity [2] against 3D7 strain of *P. falciparum* and all the tested compounds exhibit moderate antimalarial activity at the tested dose. The Compound (2c) with significant *in vitro* activity was selected for *in vivo* antimalarial activity [3] against CQ-resistant N-67 Strain of *P. yoelii* in swiss mice at 100 mg/kg by oral route. This compound exhibits significant activity against CQ-resistant N-67 Strain of *P. yoelii* infections in mice.

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Keywords: 4-Aminoquinoline, Mannich bases, antimalarials

Poster no. 82

AN ASSESSMENT OF IRON FOLIC ACID SUPPLEMENTATION DURING PREGNANCY IN RURAL BANGLADESH

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Background: The World Health Organization (WHO) estimates that about half of the global maternal death due to anaemia occurs in South Asian countries, including Bangladesh. The most significant contributor to maternal mortality is iron deficiency anaemia (IDA). IDA during pregnancy is an important cause of restricted fetal growth leading to low-birth weight and preterm delivery as well as maternal illness and death. IDA has underlying significance for the achievement of Millennium Development Goals 4 & 5 to reduce child mortality and improve maternal health. In Bangladesh, 50% of pregnant women suffered IDA.

Objectives: To assess coverage and barriers of therapeutic supplementation of Iron-Folic Acid (IFA) tablet among women during pregnancy in a selected rural area of Bangladesh.

Methods: A combination of quantitative and qualitative methods was followed to address the objectives. A household survey was conducted with 114 women having at least one child ≤ 2 months of age, to capture their experience with IFA supplementation during their last pregnancy by using an adopted UNICEF questionnaire. The survey was supplemented by Focus Group Discussion (FGD) with selected mothers and was designed to explore the demand-side perspectives. Simple Random sampling techniques were used for the selection of the respondents. The facility assessment involved six health facilities in Kalai upazial of Joypurhat district. Key informant interviews (7), health facility inventory (6) and review of service statistics related to IFA supplementation during pregnancy over the year prior to the study, were conducted to reveal the supply-side perspectives. The Tanahasi framework was applied to identify coverage and barriers to coverage of IFA supplementation through its five tracer indicator e.g. availability, accessibility, utilization, adequate coverage and effective coverage.

Results: The IFA supplementation coverage in terms of availability, accessibility, utilization, adequate coverage and effective coverage was 100%, 80.7%, 67.4%, 13.3% and 2.1% respectively among the selected women during the reference period. The percentage of women who completed four ANC visits was only 37.7%. At about 37% of the respondents reported that they received more than 100 IFA tablet during their last pregnancy, while only 38% of mothers consumed more than 100 IFA tablets during their last pregnancy. A statistically significant relationship was found between the receipt of 100 IFA tablets and continuing use of ANC services. Supply-side barriers to IFA coverage revealed some important programmatic issues: lack of training, lack of job aid and IEC materials, shortage of workforce and high workload on the part of the service providers. Lack of consciousness, lack of proper knowledge about IFA, some side effects (bad smell, nausea) of the tablets and unpacked tablet were also identified as demand side barriers.

Conclusions & recommendations: The results of this study provided a better picture of coverage of IFA supplementation at different government service delivery points in Kalai upazila of Joypurhat district. At the same time, this study focused on understanding barriers of IFA supplementation and its determinants from both supply and demand sides. We strongly recommend to comprehensive training for service providers, a user friendly job aid, improved physical quality of IFA tablet and mass awareness raising campaign should be implemented.

Keywords: Iron folic acid, Pregnancy, Bangladesh

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Poster no. 83

EVALUATION OF THE PERFORMANCE OF A NEW SIMPLE OVITRAP WITH DIFFERENT ATTRACTANTS, STORAGE DURATIONS, AND COVER MATERIALS

Objective: This study was to evaluate performance of simple ovitrap and identify the affecting factors.

Methods: Using different attractants (rice hay infusion, weed grass hay infusion, well water, and tap water) and storing rice attractant for different durations (0, 12, 34, and 90 days), we assessed the effectiveness by comparing the number of eggs trapped and the percentage of eggs hatched. We compared the percentage of mosquitoes trapped between plastic mesh and nylon covers to evaluate its security.

Results: Rice hay infusion trapped most eggs, and the differences reached statistical significance in comparison with tap water and well water, but not with weed grass hay infusion. Rice hay infusion also had the lowest percentage of hatched egg, and the differences reached statistical significance in comparison with weed grass hay infusion and well water. This is supported by bacterial profile. Storage duration did not appear to be a significant factor affecting the number of eggs trapped or the percentage of eggs hatched. The less support from chemical profile indicate the role of others chemical factor. Using larva instars III, we found nylon was better than plastic mesh in terms of security.

Conclusions: The simple ovitrap is as efficient as the more complicated ones that were previously reported. Rice hay infusion was more efficient in trapping eggs than weed grass hay infusion, well water, and tap water. With rice hay infusion, storage duration did not affect the efficiency up to 90 days, and nylon cover was more secure than plastic mesh.

Keywords: Ovitrap, Aedes aegypti, egg, attractant, storage duration, hole size

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Poster no. 84

PREVENTION OF SEXUALLY TRANSMITTED DISEASES JEOPARDIZED BY DRINKING ALCOHOL IN TATKON CANTONMENT

A cross-sectional descriptive study was conducted among alcohol users in No.(4) Defence Industry and No.(2032) Air Defence Battalion in Tatkone Cantonment , Nay Pyi Taw Region. The main objective is to find out the prevention of Sexually Transmitted Diseases (STD) jeopardized by drinking alcohol among alcohol users. The study recruited 100 participants by using simple random sampling method. Pre-tested was done on 30 volunteers in Defence Services Medical Research Centre (DSMRC), Nay Pyin Taw . Study period was from September to October 2016. Data were collected by using the structured questionnaires. Each participant read and responded the survey questionnaire contained in an envelope except that the illiterates was aided by interviewer. The duration for each respondent was at least 30-45 minutes. After data collection, the data were cleaned, coded and entered by SPSS version 22. The entire data were maintained confidential. The participants were between 18 and 45 years. The

majority of participants were Bamar (99%) and all were Buddhist (100%). Regarding the educational status, there were illiterate (2%), read and write (1%), primary school level (3%), middle school level (40%), high school level (44%) and graduated (10%) respectively. The common reasons of initiation to alcohol use were social drinking (52%) and for pleasure (20%). In risky sexual behavior, there were oral sex (8%), anal sex(2%) and group sex (4%) respectively after alcohol drinking. According to results, we found that either increasing the frequency or the amount of alcohol drinking declined condom use with female sex workers. However, there was no significant association between the alcohol drinking and condom use for prevention of STD in this study (p=0.476).

Keywords: alcohol users, STD, risky sexual

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Poster no. 85

DATA QUALITY AND USERS' ATTITUDE TOWARD USING HIVINFO SOFTWARE IN VIET NAM

Objectives: The objective of this study are to (i) assess quality of data collected in HIVINFO 3.0 software used to manage HIV infected cases in Vietnam; and (ii) assess the users' attitude toward using this software. Methods: The study will be mixed design including retrospective study for the first objective and a descriptive cross sectional study for the second objective. The retrospective data from HIVINFOR will be collected to assess quality of data of HIVINFO 3.0 and questionnaire survey will be develop and send to HIVINFO 3.0 users to assess their attitude toward using this software. Results: Overall, the completeness of data was recorded highly in most variables (95.0% - 100%). The percentage of lacks information in mountain was higher than delta with 64.6% and 74.0% by region and in the large amount of patient was higher than small amount of patient with 59.8% and 79.8% by amount of patients. The timeliness of the data often delay in three lag time variables consist of HIV date; AIDS date; Dead date in the HIVINFO 3.0 and not satisfy the requirement as requests of Circular No 09/2012-BYT. The information collected from respondents on PEOU, PU, overall attitude, satisfaction also present high percentage of in all PCAs. Conclusion: This study provides an open platform of completeness and timeliness of data in the northern part of Vietnam. The level of data completeness and timeliness of software can confirm that the data quality is being used for these reports and research, and especially the reports to VAAC, Ministry of Health. Moreover, findings from a survey for HIVINFO 3.0 users' attitude was carried out in whole country to show the positive attitude and have high percentage to continue to use HIVINFO 3.0 software.

Keywords: Hivinfor 3.0/ Hivinfor Software/ Completeness/ Timeliness/ Users' Attitude

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Poster no. 86

PROTECTIVE EFFICACY OF DOXYCYCLINE ON MALARIA PROPHYLAXIS IN THE SOLDIERS DEPLOYED TO THE THAI-CAMBODIA BORDER

Background: Malaria has been a threatening disease to Royal Thai Army (RTA) troops who were deployed to borders, especially Thai-Cambodia border for decades. The incidence of malaria in the soldiers operating along Thai-Cambodia border in year 2010 was 25.36 %. Although there are supporting data from clinical trials that showed that daily 100 mg dose of doxycycline is an effective prophylactic agent for malaria but it has not been used for malaria prophylaxis in RTA Troops for around 10 years due to its gastrointestinal adverse symptoms. In the past, there was only hydrochloride form of doxycycline prescribed in Thailand. Now hyclate form of doxycycline is generally prescribed and there was evidence that it caused less gastrointestinal adverse symptoms than hydrochloride form. This brought to initiation to study protective efficacy, tolerability and compliance of doxycycline hyclate in RTA soldiers.

Objective: To study protective efficacy (PE) of doxycycline hyclate on prevention of malaria infection in RTA troops deployed to Thai-Cambodia border.

Methodology: A double-blind, placebo-controlled randomized field trial was designed. Eligible participants were male Royal Thai Army soldiers, 18-60 years old, deployed for at least 6 month period to the Thai-Cambodia border in Sisaket province of Thailand between October 2014 and September 2015. Blocked randomization with a block size of five was used to assign subjects to doxycycline hyclate capsule (DH, n=73), doxycycline hyclate film-coated tablet (DHFC, n=74) or placebo (n=37). Within each arm, subjects had to take daily, 100 mg of doxycycline hyclate or placebo for 3 months.

Result: Attack Rates (AR) of malaria in DH group, DHFC group and placebo group were 5.7% ,2.7 % and 15.0% respectively. Protective efficacy of DH was 62% and of DHFC was 82%. Results of survival analysis showed that Hazard Ratio (HR) in placebo group was 5.793 compared to DHFC group (p=0.031) and HR in DH group was 2.137 compared to DHFC group (p=0.381). Blood samples from two cases with *Plasmodium falciparum* were studied for immunomarkers. The results showed Plasmodium falciparum chloroquine resistance transporter (PfCRT) gene, Plasmodium falciparum multidrug resistance-1 (pfmdr-1) gene and gene mutation at K13 Propeller domain (C447R in one case and 580Y in both cases).

Conclusion: Doxycycline hyclate film-coated tablet was more efficacious than doxycycline hyclate capsule and placebo on malaria prophylaxis in Royal Thai Army soldiers deployed to Thai-Cambodia Border.

Keywords: doxycycline hyclate protective efficacy malaria prophylaxis

Poster no. 87

PRODUCT DEVELOPMENT : PASTEURIZED SUAEDA MARITIMA READY TO DRINK

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The research aimed to study *Suaeda maritima* extraction process, the standard formula for pasteurized. *Suaeda maritima* Ready To Drink and its shelf life based on physical quality, chemical composition, microorganism quantity, and sensory evaluation. It was found that 1,000 grams of *Suaeda maritima* fresh leaves when boiled and squeezed out the excess water, only 650 grams of the leaves were left. The leaves went through the extraction process in which the leaves were boiled in 105% of water weight per weight. The extract was then used as a raw material to create a standard formula for the RTD. One, 1 or 5 % of brown sugar was added into the extract. The extract with 5% brown sugar was most accepted in all aspects: appearance, color, flavor, taste, texture, and overall preference; the mean scores were 8.02, 7.95, 7.86, 8.07, 7.91, and 7.96, respectively. This indicated that the product was very much and most accepted. The lightness (L*), the greenness (a*), and the yellowness (b*) were at 18.34, -9.95 and 19.51. The soluble solid Brix was 6.85; the pH-alkalinity (pH) was 6.91. The total energy for 100 ml. of the product was 24 k. cal.; the beta - carotene and the phenolic compound of Alice were 1056 and 360 micrograms. The consumers' test result showed that most consumers accepted the product at the moderate level; and, they were interested in buying the product. The best price was 20 baht per 180 ml. of the product in a clear glass bottle. The product was best kept at 7 °C for not longer than 5 days when there was still no physical or chemical change. All the microorganisms found did not exceed the FAD Standard or OTOP *Indian pennywort* Drink Standard (163/2552).These confirmed that the product was safe to consume.

Keywords: Suaeda maritima , beta -carotene ,Phenolic compound, pasteurization.

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Poster no. 88

FACTORS RELATED TO STRESSES OF FOREIGNER STUDENTS IN TRADITIONAL CHINESE MEDICINE STUDENTS PROGRAM, GUANGZHOU UNIVERSITY OF CHINESE MEDICINE

This descriptive research aimed to study stresses and social supports of foreign students in Traditional Chinese Medicine program, Guangzhou University of Chinese Medicine, and to study factors related to the stresses. The subjects of this research were 193 1st – 5th year foreigner students selected by stratified random sampling method. The research instrument to collect the data was questionnaires.

Data was analyzed by mean, percentages and chi-square test. The findings showed that the majority of the foreign students were female (58.5%); aged 20-24 (53.4 %); 3rd year students (28.0%); earned less than 1,001 CNY a month (30.1); single (95.3); resided in the university's dormitories (74.6%); domiciled in Hong Kong (52.8%); and gained social supports from friends in the medium level (54.4%); were highly stressed (51.2%). There was a relation between the foreigner students' stresses and their genders, ages, collage years, monthly earnings, marital statuses, domiciles and social supports with statistically significant ($p<0.05$).

Keywords: stresses, social supports of students, foreign students

Poster no. 91

HEMOZOIN CORRELATES TO MALARIA-ASSOCIATED ACUTE RESPIRATORY DISTRESS SYNDROME THROUGH PNEUMOCYTIC APOPTOSIS MECHANISM

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Malaria stills a major global health problem especially in Tropical region including Thailand. Severe malaria can cause vital organ dysfunction and death in patients who infected with *Plasmodium falciparum*. Lung complication, pulmonary edema (PE) and acute respiratory distress syndrome (ARDS), is one of the clinical features in severe malaria that can be life threatening, however its mechanism is not well understood. Generally, the pathogenesis of PE and ARDS is closely connected to the integrity of blood-gas barrier, the composition of endothelium, basement membrane, and pneumocyte. One postulated mechanism may associate with hemozoin-induced barrier injury. In this study, lung histopathological and ultrastructural studies were examined in severe malaria patients with and without ARDS. In vitro co-culture model of pneumocyte (A549) and *P. falciparum* hemozoin was also performed to determine cellular-apoptotic effect. Apoptotic cell was characterized by pneumocytic-membrane, -cytoplasm, and -nuclear chromatin using Ethidium-bromide/Acridine-orange (EB/AO) staining. Caspase-recruitment-domain-containing-protein (CARD)-9, apoptosis regulator gene, was quantified using real-time polymerase chain reaction technique to confirm the level of existing apoptosis. The results revealed that the occurrence of deposited hemozoin pigment in the lung had positive correlation to hyaline membrane formation ($r=0.364$, $p=0.007$) and blood-gas barrier damaged score ($r=0.563$, $p=0.002$). In pneumocyte/hemozoin co-culture, early-phase of cellular apoptosis was significantly observed in all periods of time post induction (1, 6, 12, and 24 hours) relevant to the level of CARD-9 gene expression ($p<0.05$). The present study suggests that hemozoin relates to the pathogenesis of malaria-associated ARDS and damages lung epithelium verified by apoptotic gene expression.

Keywords: Malaria, Acute-Respiratory-Distress-Syndrome, Pneumocyte, Apoptosis, Hemozoin

Poster no. 92

REVIEW OF COMPARATIVE EFFICACY AND ACCEPTANCE OF INTERVENTIONS OF MONTHLY PROPHYLAXIS VS. SCREENING AND TREATMENT IN HIGH-RISK, MILITARY MOBILE POPULATIONS TO SUPPORT MALARIA ELIMINATION IN CAMBODIA

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The effectiveness of malaria elimination strategies in hard-to-reach mobile populations, including the military, is largely unknown. We conducted a two-arm, controlled, cluster-randomized, open-label pilot study to determine the effectiveness of monthly malaria prophylaxis (MMP), using dihydroartemisinin-piperaquine (DP) and weekly primaquine (22.5 mg), compared to focused monthly screening with microscopy and PCR and treatment (FSAT) of malaria positive volunteers according to the Cambodian national treatment guidelines. After 3 months of interventions, both arms were followed for 3 more months to assess malaria incidence in the rainy season when malaria usually peaks. Of 1,114 active duty military and dependents screened in Oddar Meanchey province near the Thai-Cambodian border, 1,050 volunteers were enrolled into 8 clusters. At the time of enrollment, the baseline prevalence of malaria was 17% (45 cases of *Plasmodium falciparum*, 39 cases of *P. vivax*, 8 cases of mixed) and 10% (39 cases of *P. falciparum*, 13 cases of *P. vivax*, 1 case mixed) in the MMP and FSAT arms, respectively. Transmission of *P. falciparum* malaria was interrupted with the prevalence of *P. falciparum* malaria reduced from 9.17% at enrollment to 0.62% on month 6 follow up visit, and from 7.75% down to 0.67%, for MMP and FSAT arms, respectively. *P. vivax* parasite positive rate was 2.52% at enrollment in FSAT arm, and 0.9% at month 6 follow up, compared to a higher 7.87% parasite positive rate at enrollment and 4.97% rate of *P. vivax* at month 6 in the MMP arm. The majority of *P. vivax* cases in the MMP group were detected in the last 3 months of follow up, possibly representing *P. vivax* relapses. Investigation into CYP450 2D6 polymorphisms in the study population, responsible for primaquine metabolism, may provide additional evidence for the cause of *P. vivax* recurrences in the MMP arm. Both interventions under study received overall favorable ratings among military and civilian study participants despite concerns over mass drug administrations for malaria in other reports.

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Poster no. 94

BACTERIAL AEROSOLS AND OCCUPATIONAL RISK IN A LANDFILL SITE IN METRO MANILA, PHILIPPINES

Payatas landfill site is one of the major dumpsites in Metro Manila, Philippines. It was converted in 2004 to utilize methane gas as an energy source, following the tragedy and closure in 2000. In this study, the landfill was evaluated based on the presence and concentration of pathogenic bacterial aerosols through culture and molecular techniques. Bioaerosols are biological airborne particles that may or may not cause diseases, though some may stay virulent for a long time. MAS-100 Air Sampler was used for sampling from both indoor and outdoor locations. Culture technique employed general and selective media in order to identify the organisms. To test the accuracy of the said technique, those that were presumptively identified as *Staphylococcus aureus* and *Klebsiella pneumoniae* using selective media were subjected to molecular analysis using 16s rRNA sequencing. As a result, those that were presumptively recognized as *S. aureus* were identified as ***S****. saprophyticus, S. hominis, S. kloosi, S. arlettae, Bacillus licheniformis, B. safensis, Enterococcus casseliflavus*, and *E. faecium;* while those that were presumptively identified as *K. pneumoniae* were identified as *Pseudomonas stutzeri, Agrobacterium larrymorei, Acinetobacter baumanii*, and *Enterobacter* sp. The exposure assessment done by interview showed matches between prevalent diseases caused by the identified bacterial species. Passive and active sampling were also compared based on aerobic plate count and active sampling showed more accuracy and efficiency. The results of this study can be used as basis for creating standards and regulations for workers' and residents' safety and health in the landfill site.

Keywords: bacterial aerosol, landfill site, active sampling, exposure assessment

Poster no. 95

PREVALENCE AND ASSOCIATED FACTORS FOR CHRONIC KIDNEY DISEASE IN THE THAI ELDERLY POPULATION IN BANGKOK, THAILAND

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Background: Chronic kidney disease (CKD) is one of the major public health problems in Thailand and worldwide. CKD is also a prominent problem in the elderly and is associated with a higher risk of kidney failure, cardiovascular complication, and mortality. This study aimed to determine the prevalence and associated factors for CKD in the elderly.

Methods: A community-based, prospective study was conducted during 2014-2016 in 7 (out of 50) randomly selected districts in Bangkok. Thai participants aged ≥ 60 years living in Bangkok were included. Participants who had fever or acute illness one week before screening were excluded. Medical and social histories, physical examinations, venous blood, and urine samples were collected. The prevalence of CKD and its 95%CI were calculated. Factors associated with CKD stages 3-5 compared with no CKD were measured by adjusted prevalence ratio (aPR), using multivariated Poisson regression performed in SAS version 9.1.

Results: The study included 1,058 participants. The mean age was 69.2 years (SE=6.7), and the age range was 60–95 years. The overall prevalence of CKD in the Thai elderly was 30.6% (95%CI, 27.9-33.4%) while the prevalence in males was 35.6% (29.4-41.3%) and the prevalence in females was 29.2% (26.1-32.3%). The prevalence of CKD stages I, II, III, IV, and V were 4.9%, 7.9%, 16.5%, 0.9 %, and 0.4%, respectively. Factors associated with CKD (stages 3-5) were older age comparing those aged 60-69 years (aPR =1.9 [1.4-2.8]) with those aged 70-79 and ≥80 years (aPR=3.2 [2.1-5.0]), hypertension (aPR=1.63 [1.2-2.3]), diabetes (aPR=1.5 [1.1-2.0]), and hyperuricemia (aPR=3.0 [2.2-4.2]).

Conclusions: The prevalence of CKD in the Thai elderly is still high. Appropriate monitoring and management of underlying diseases / associated factors will be beneficial in slowing the progression of CKD.

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Poster no. 96

MULTIPLEX PCR ASSAY FOR IDENTIFYING FORENSIC RELATED BLOW FLIES

Blow flies are commonly found with dead animals including those of humans. Information of these insects can be used in forensic investigation such as time or place of death. Two forensically related blow flies mostly found in Thailand are *Chrysomya megacephala* and *C. rufifacies.* Of which, the immature stages can be easily collected in the scene, however the identification of them by non-specialist is rather difficult and time consuming. Therefore, a PCR-based assay was developed in this study in order to overcome those disadvantages. After testing a number of primers, two sets of primer pairs which were designed from the genes *internal transcrice sapcer* 1 (ITS1) and ITS2 were selected and the PCR conditions were optimized. Finally, duplex PCR had been successfully developed, of which it can clearly identify DNA from those two blow fly species with the sensitivity and specificity at 90% and 100%, respectively. This assay is simpler than the morphological identification which requires microscope and it is more rapid and less laborious. It can be applied for the forecsic investigation work relating to the estimation time of death and/or determination place of death.

Keywords: Blow flies, molecular identification, ITS1, ITS2, Duplex PCR

First Announcement

Joint International Tropical Medicine Meeting 2017

(JITMM 2017)

December 2017

Bangkok, Thailand

Organized by:

- Faculty of Tropical Medicine, Mahidol University
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