JOINT INTERNATIONAL TROPICAL MEDICINE MEETING 2015 (JITMM 2015)

"Tropical Diseases Post 2015: New Threats or Towards Sustainable Success"

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

Abstracts

ORAL PRESENTATIONS

2-4 December 2015

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 2nd DECEMBER 2015

09.30-10.00
Watergate Ballroom

OPENING SESSION

Opening Ceremony By Organizers and Co-organizers

Welcome Address

Dr. Sombat Thanphasertsuk

Senior Expert in Prevention Medicine, Ministry of Public Health, Thailand

Prof. Nicholas Day

Director, Mahidol-Oxford Tropical Medicine Research Unit, Thailand

Assoc. Prof.Pratap Singhasivanon

Secretary General/Coordinator of SEAMEO TROPMED Network, Bangkok, Thailand
Associate Professor, Department of Tropical Hygiene, Faculty of Tropical Medicine
Mahidol University, Bangkok, Thailand

Opening Address

Prof. Dr. Yaowalark Sukthana

Chair, Organizing Committee; Dean, Faculty of Tropical Medicine, Mahidol University, Thailand

TROPMED ALUMNI AWARD PRESENTATION

Presented by Professor Emeritus Arunee Sabchareon

President, Tropmed Alumni Association

AWARD RECIPIENTS:

1) **Prof. Dr. Yaowalark Sukthana**
Dean, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand
Centre, Director, SEAMEO TROPMED Regional Centre for Tropical Medicine

2) **Dr.Syahril Pasaribu**
Rector, University of Sumatera Utara, Indonesia
President , Indonesia Rectors Forum
Head , Infection/Tropical Disease Division,
Pediatrics Department, Faculty of Medicine, University of Sumatera Utara

3) **Prof Dr. Gias Uddin Ashsan**
Dean, School of Health and Life Science, North South University, Dhaka, Bangladesh
Chairman, Department of Public Health, North South University

WEDNESDAY 2nd DECEMBER 2015

10.30 – 12.00

Watergate Ballroom

S1 THE 21ST CHAMLONG-TRANAKCHIT HARINASUTA LECTURE
"TROPICAL DISEASES POST 2015: NEW THREATS OR TOWARDS SUSTAINABLE SUCCESS"

Chairperson :

Prof. Yaowalark Sukthana
Chair, Organizing Committee;
Dean, Faculty of Tropical Medicine, Mahidol University, Thailand

Keynote Speakers :

1 Prof. John Eu-Li Wong
Chief Executive,
National University Health System,
National University of Singapore

2 Clin. Prof. Udom Kachintorn
President of Mahidol University,
Thailand

3 Dr. Jurai Wongsawat
Medical Physician - Advisory Level,
Ministry of Public Health, Thailand

TROPICAL DISEASES POST 2015:
NEW THREATS OR TOWARDS SUSTAINABLE SUCCESS

Plenary Keynote Session:

After December 2015, ten countries in the Southeast Asian region will become ONE ASEAN, ONE COMMUNITY and ONE IDENTITY. 2016 is also the starting point of the new chapter in UN development goals, moving from the eight Millennium Development Goals to the new 17 Sustainable Development Goals.

Additionally, there are five global megatrends : 1) Demographic and Social Change, 2) Shift in Economic Power, 3) Rapid Urbanization, 4) Climate Change and Resources Scarcity and 5) Technological Breakthroughs, which are large, transformative forces that will further define the future of the Southeast Asian region.

What we can expect are not only opportunities and advantages but also threats and challenges.

This plenary keynote session will focus on healthcare systems, their practice and their workforce and how they may be affected by the previously mentioned changes and factors.

In the diverse ASEAN community, there are many shades of democracy, various religions and different economies across the country members. Healthcare systems are not an exception to this diversity.

For example, maternal and child mortality is higher in the CLMV countries (Cambodia, Laos Myanmar and Vietnam) than elsewhere. There has been substantial reduction in these mortality rates since 1990, but this progress has been uneven across countries and provinces .

In the middle income countries such as Indonesia, Malaysia, the Philippines and Thailand there is the dual problem of both infectious disease and chronic non communicable diseases..

Non communicable diseases are a major public health problem in Southeast Asia, accounting for 54 % of all deaths. And this is projected to increase by 21% over the next 10 years. Slowing this increase is likely to require behavioral solutions and interventions.

The current average age in the ASEAN population is younger than that of Europe and North America, however, the rapidly growing ageing populations in Singapore and Thailand is an alarming sign.

In high income countries such as Singapore, health technological breakthroughs such as reduced-cost personal genome sequencing, has resulted in an increasing focus on personalized medicine approaches.

As in other regions, many countries in Southeast Asia suffer from problems in the healthcare workforce - these include shortages of skilled staff, skill mix imbalances, and mal-distribution of skilled staff.

The global megatrend of a shift in economic power to Asia plus the free movement of skilled healthcare personnel through ASEAN as well as the free movement of populations will shape the healthcare personnel environment. ASEAN countries will be both producing and accepting healthcare professionals. Travelling for work or leisure will expand, therefore, travel medicine will grow and be prioritized as an area of medicine.

Additionally, climate change, limited resources, food insecurity and safety, emerging/re-emerging infectious diseases and the cost of universal healthcare coverage, especially for migrants, are other challenges which will be encountered.

As is the ASEAN way, we must enjoy and use our diversity to form a strong network, share information and step forward, together, to reach sustainable healthcare successes and become a healthy ONE ASEAN, ONE COMMUNITY and ONE IDENTITY.

HEALTH IN ASEAN: THE NEXT LAP

John Wong

Chief Executive of the National University Health System (NUHS) Singapore; Senior Vice President (Health Affairs) at the National University of Singapore

The ASEAN Community 2015 (AC15) is comprised of three pillars, namely the Asian Economic Community (AEC), ASEAN Political-Security Community (APSC) and ASEAN Socio-Cultural Community (ASCC). Each pillar has its own blueprint, and together with the Initiative for ASEAN Integration (IAI) Strategic Framework and IAI Workplan Phase II, form the 2009-2015 roadmap for AC15.

2015 will be an important year as we review what we have accomplished and work towards the ASEAN Community Post-2015 Vision aimed at enhancing and strengthening our community even further.

In healthcare, access to care, food security and safety, and threats from new and re- emerging infectious diseases remain key concerns. ASEAN will greatly benefit from building strong networks to share information, enhance surveillance, and coordinate responses to infectious disease outbreaks.

To ensure the prosperity of the region, we must accelerate development of innovative, value-driven and sustainable healthcare. It is hoped that AC15 will no longer be a slogan, but a major step forward in building a better future for our population and generations to come.

WEDNESDAY 2nd DECEMBER 2015

13.00 – 14.30

Room A

S2- ADVANCING DENGUE VACCINE TO EARLY CLINICAL PHASES (SPONSORED BY NVI)

Chairpersons :

Punnee Pitisuttithum

Charung Muangchana

Speakers :

1 Alain Bouckenooghe

"Challenges in dengue vaccine research and development : Industrial perspective"

2 In-Kyu Yoon

"Challenges in dengue vaccine research and development : DVI perspective and US Army experiences"

3 Sutee Yoksan

"Challenges in preclinical development of dengue vaccine in Thailand"

(Abstract not available)

4 Arunee Sabchareon

"Challenges and lesson learnt in conducting phase I dengue vaccine and beyond"

(Abstract not available)

CHALLENGES IN DENGUE VACCINE RESEARCH AND DEVELOPMENT : INDUSTRIAL PERSPECTIVE

Alain Bouckenooghe

Sanofi Pasteur, Singapore

A candidate tetravalent dengue vaccine is being assessed in three clinical trials involving more than 35,000 children between the ages of 2 and 16 years in Asian–Pacific and Latin American countries. We report the results of long-term follow-up interim analyses and integrated efficacy analyses.

Methods: We are assessing the incidence of hospitalization for virologically confirmed dengue as a surrogate safety end point during follow-up in years 3 to 6 of two phase 3 trials, CYD14 and CYD15, and a phase 2b trial, CYD23/57. We estimated vaccine efficacy using pooled data from the first 25 months of CYD14 and CYD15.

Results: Follow-up data were available for 10,165 of 10,275 participants (99%) in CYD14 and 19,898 of 20,869 participants (95%) in CYD15. Data were available for 3203 of the 4002 participants (80%) in the CYD23 trial included in CYD57. During year 3 in the CYD14, CYD15, and CYD57 trials combined, hospitalization for virologically confirmed dengue occurred in 65 of 22,177 participants in the vaccine group and 39 of 11,089 participants in the control group. Pooled relative risks of hospitalization for dengue were 0.84 (95% confidence interval [CI], 0.56 to 1.24) among all participants, 1.58 (95% CI, 0.83 to 3.02) among those under the age of 9 years, and 0.50 (95% CI, 0.29 to 0.86) among those 9 years of age or older. During year 3, hospitalization for severe dengue, as defined by the independent data monitoring committee criteria, occurred in 18 of 22,177 participants in the vaccine group and 6 of 11,089 participants in the control group. Pooled rates of efficacy for symptomatic dengue during the first 25 months were 60.3% (95% CI, 55.7 to 64.5) for all participants, 65.6% (95% CI, 60.7 to 69.9) for those 9 years of age or older, and 44.6% (95% CI, 31.6 to 55.0) for those younger than 9 years of age.

Conclusions: Although the unexplained higher incidence of hospitalization for dengue in year 3 among children younger than 9 years of age needs to be carefully monitored during long-term follow-up, the risk among children 2 to 16 years of age was lower in the vaccine group than in the control group.

Keywords: dengue vaccine, efficacy

CHALLENGES IN DENGUE VACCINE RESEARCH AND DEVELOPMENT : DVI PERSPECTIVE AND US ARMY EXPERIENCES

In-Kyu Yoon

Dengue Vaccine Initiative, International Vaccine Institute, Seoul, Korea

Dengue virus (DENV) is the leading cause of vector-borne viral disease globally with an estimated 390 million infections per year of which approximately 96 million lead to symptomatic disease. The burden of dengue has been increasing over the past few decades presumed to be due to increased urbanization, ease of global travel, ecological changes, and perhaps climate effects. Severe forms of dengue which were rare outside of Southeast Asia in the 1970's are now more commonly seen in dengue endemic countries as these areas become hyperendemic with more than one DENV serotype. Vector control measures have been implemented in some form in most affected countries, but the impact of such efforts have been limited. The general consensus is that an integrated approach involving both vector control and vaccine introduction will be needed to reverse the dengue pandemic. Currently, six different dengue vaccine candidates are in active human clinical trials. The most advanced candidate, CYD-TDV, sponsored by Sanofi Pasteur, is a live attenuated tetravalent chimeric vaccine consisting of a 17D yellow fever backbone with DENV pre-membrane and envelope proteins from the four different DENV serotypes. CYD-TDV has undergone phase IIb and III clinical trials in Asia and Latin America with mixed results. In particular, the vaccine had poor efficacy against serotype-2 and marginal efficacy against serotype-1 despite having good immunogenicity to all four serotypes based on neutralizing antibody assays. In addition, an increased risk of dengue hospitalization was noted in very young vaccinated children during the third year of the Asian phase III trial. Nevertheless, the vaccine appeared to have greater overall efficacy against more severe disease with no apparent safety signal among older vaccinated children. This has led to the possibility of vaccine introduction in older children and adults in some dengue endemic countries. Questions linger about the reasons for the suboptimal efficacy and safety signal in very young children which may have implications not only for CYD-TDV but also for other vaccine candidates. Two other dengue vaccine candidates in addition to CYD-TDV are close to entering phase III clinical trials. TDV, sponsored by Takeda, is a live attenuated chimeric vaccine that uses a DENV-2 backbone with pre-membrane and envelope proteins from the other serotypes. TV003/TV005, developed by U.S. NIH, are two different formulations of a live attenuated tetravalent vaccine which has undergone direct mutagenesis of three serotypes while the fourth serotype consists of a DENV-DENV chimera. Whether these and other vaccine candidates in development will have different results from CYD-TDV is unclear. However, understanding the reasons for the performance of CYD-TDV will help to inform the further development of all dengue vaccines.

WEDNESDAY 2nd DECEMBER 2015

13.00 – 14.30
Room B

S3 - UPDATE ON ECTOPARASITES IN THAILAND (*Sponsored by PTAT*)

Chairpersons :


Padet Siriyasatien


Sonthaya Tiawsirisup

Invited Speakers :


1 Padet Siriyasatien
"Molecular survey of head louse in Thailand"
(Abstract not available)


2 Kanyarat Kraivichain
Title - TBA
(Abstract not available)


3 Jariyanart Gaywee
"Arthropod-borne bacterial pathogens: survey in Thailand"

ARTHROPOD-BORNE BACTERIAL PATHOGENS: SURVEY IN THAILAND

Jariyanart Gaywee

Armed Forces Research Institute of Medical Sciences, (AFRIMS) Thailand

Arthropod-borne diseases become major health problem throughout the world including military areas of operation (AOs) along Thai borders. In response to this concern, we have conducted a surveillance program aiming to assess the distribution of 5 arthropod-borne bacteria; *Rickettsia*, *Ehrlichia*, *Anaplasma*, *Coxiella*, and *Borrelia* in AOs along Thai Borders. During November 2007 to May 2012, 780 pools of arthropod composed of 273 tick, 456 flea and 51 louse pools were collected from 219 survey sites along Thai borders. Arthropods were evaluated for the presence of 5 bacterial genus using Realtime PCR. Total 273 tick pools, 34.8% were positive for rickettsiae, 15% for *E. chaffeensis*, 1.8% for *Coxeilla* and 0.4% for*Borrelia spp.* Only rickettsial and *Ehrichia* DNA, but not other pathogens were detected in 95% and 70.6% of 456 flea pools, respectively. Of 51 louse pools, 25.5% and 13.7% were positive for rickettsiae and *Ehrlichia.* Risk areas of 5 pathogens were mapped using Geographical Informatic System. Ecological niche model to predict endemic areas was developed, ground truthing and adjusted accordingly. The presence of arthropod vectors for rickettsiae,*Erhlichia*, *Borrelia* and *Coxeilla* suggest the potential risk areas for infections. Fact sheet, health education, the use of insect repellant and caution activity in these risk areas are advised to prevent infections.

Keywords: Arthropod-borne diseases, GIS map

WEDNESDAY 2nd DECEMBER 2015

13.00 – 14.30
Room C

S4 - BIOINFORMATICS AND HEALTH INFORMATICS IN THE NEW CHALLENGES OF PRECISION MEDICINE

Chairpersons :

Jaranit Kaewkungwal

Saranath Lawpoolsri Niyom

Invited Speakers :

1 Santi Maneewatchararangsri
"Genome-wide in-silico secretomic analysis of *Leptospira* spp.: Focuses on virulent-associated secretome"

2 Bhoom Suktitipat
"Mining whole genome sequencing data for predictive genomic medicine"

3 Veerasak Kritsanapraphan
"Bioinformatics and health informatics in the new challenges of precision medicine"

GENOME-WIDE IN-SILICO SECRETOMIC ANALYSIS OF *LEPTOSPIRA* SPP.: FOCUSES ON VIRULENT-ASSOCIATED SECRETOME

Leptospirosis remains one of the most common zoonosis worldwide, especially in subtropical and tropical regions including Thailand, caused by pathogenic Leptospira infections. In Thailand, the leptospirosis is regarded as a re-emerging disease as the incidence has increased markedly during the past 15 years with mortality rates up to 5%. Extracellular protein (Secretome) plays important roles for bacterial biology, i.e. cell-to-cell communication, host interaction, detoxification, cellular process, and pathogenesis. In this research, whole secretomes from the representative pathogenic Leptospria interrograns serovar Lai and saprophytic Leptospira biflexa serovar Patoc genomes have been computational analyzed and identified by using our established secreted protein algorithms scheme. Predicted Leptospira virulent-associated secretomes were comparatively analyzed from the whole secretomes and the virulence annotations have been categorized.

Santi Maneewatchararangsri[1],
Ngamphol Soonthornworasiri[2],
Onrapak Reamtong[1],
Usa Boonyeun[3],
Piengchan Sonthayanon[1],
Pornpan Pumirat[4],
Muthita Vanaporn[4],
Urai Chaisri[5],
Direk Limmathurotsakul[2],
Poom Adisakwattana[6],
Sumate Ampawong[7],
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MINING WHOLE GENOME SEQUENCING DATA FOR PREDICTIVE GENOMIC MEDICINE

Bhoom Suktitipat

Department of Biochemistry, Faculty of Medicine Siriraj Hospital, and Integrative Computational BioScience Center, Mahidol University
Email: bhoom.suk@mahidol.ac.th, Tel: +662-419-9146

The cost of whole genome sequencing (WGS) has reduced from 100 millions USD in 2001 to under 10,000 dollars in 2013 with next-generation sequencing (NGS) technology. The most excited field that benefits from NGS is precision medicine. NGS allows clinicians to screen multiple genes simultaneously for suspected genetic causes. Furthermore, genetic markers have been used to predict the risk of many late onset, preventable diseases such as coronary artery disease, stroke, diabetes, etc. The population with higher risks than general can be identified since birth, and the appropriate intervention or management can be started prior to developing chronic conditions such as hypertension or dyslipidemia. Genetic information awareness have been shown to benefit patients and influence the change of their lifestyle towards a more healthy behavior. We present our early experience of applying WGS in two families consisting of five patients with Anderson-Tawil syndrome (ATS). WGS were performed using Illumina HiSeq-X (Macrogen Corp, Korea). The primary aim was to confirm the diagnosis of ATS in these families. The secondary aim was to identify clinically actionable incidental variants recommended for reporting by American College of Medical Genetics. Clinically important variants were confirmed using Sanger sequencing. As an example, genetic risk prediction of coronary artery disease in these families were investigated together with their pharmacogenomic profiles. The challenges and hurdles in the application of whole genome sequencing in Thailand are also covered in the discussion.

Keywords: whole genome sequencing, precision medicine

BIOINFORMATICS AND HEALTH INFORMATICS IN THE NEW CHALLENGES OF PRECISION MEDICINE

Veerasak Kritsanapraphan

Bangkok Hospital Group, Thailand

The hope of precision medicine that we will give treatments to the individual and not to the masses. To be able to achieve this non one sized fit all, we need a resilience framework in handling Bioinfomatics and Health Informatics. In this talk, we would like to present you challenges and some alternatives to tackle those challenges in preparing your healthcare practice and data in order to archive the ultimate precision medicine. ✤

Keywords: Bioinfomatics, Precision medicine

WEDNESDAY 2nd DECEMBER 2015

13.00 – 14.30
Room D

S5 - VECTORS OF TROPICAL DISEASES

Chairpersons :

Rutcharin Potiwat

Ronald Enrique Morales Vargas

Invited Speakers :

1 Patchara Sriwichai
“Evaluation of CDC light traps for mosquito surveillance in a malaria endemic area on the Thai-Myanmar border”

2 Stephan Karl
“Mathematical modelling of transmission of *Plasmodium falciparum* and *Plasmodium vivax* on the Thai/Myanmar border: Impact of cross-border migration”

3 Suchada Sumruayphol
“Morphometric and genetic diagnosis within closely related species of dengue and chikungunya vectors in Thailand: *Ae. aegypti, Ae. albopictus, Ae. Scutellaris*”

4 Shota Takagi
“Utilization of vector mosquitoes for a novel live-attenuated tetravalent Dengue vaccine”

EVALUATION OF CDC LIGHT TRAPS FOR MOSQUITO SURVEILLANCE IN A MALARIA ENDEMIC AREA ON THE THAI-MYANMAR BORDER

Patchara Sriwichai[1],
Stephan Karl[2],
Yudthana Samung[1],
Suchada Sumruayphol[1],
Kirakorn Kiattibutr[1,5],
Anon Payakkapol[1],
Ivo Mueller[2], Guiyun Yan[3],
Liwang Cui[4],
Jetsumon Sattabongkot[5]

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[2] Population Health and Immunity Division, Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia
[3] Program in Public Health, University of California, Irvine, CA, USA
[4] Department of Entomology, Pennsylvania State University, University Park, PA, USA.
[5] Mahidol Vivax Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

Background: Centers for Disease Control and Prevention miniature light traps (CDC-LT) baited with CO_2 are a routine tool for adult mosquito sampling used in entomological surveys, and for monitoring and surveillance of disease vectors. The present study was aimed at evaluating the performance of baited and unbaited CDC-LT for indoor and outdoor trapping of endemic mosquito species in northwestern Thailand.

Methods: CDC-LT (n=112) with and without dry ice baits were set both indoors and outdoors in 88 selected houses for stretches of 5 consecutive nights per month in 7 villages in Tha Song Yang district, Tak province between January 2011 and March 2013. Mosquitoes were identified by morphological characteristics. Absolute mosquito numbers were converted to capture rates (i.e., mosquitoes per trap and year). Capture rates were compared using multilevel negative binomial regression to account for multiple trap placements and adjust for regional and seasonal differences.

Results: A total of 6,668 mosquitoes from 9 genera were collected from 576 individual CDC-LT placements. Culex was the predominant captured genus (46%), followed by anopheline mosquitoes (45%). Overall, CO_2 baited traps captured significantly more Culex (especially *Culex vishnui*) and *Anopheles* mosquitoes per unit time (adjusted capture rate ratio (aCRR) 1.64 and 1.38, respectively). *Armigeres* spp. mosquitoes were trapped in outdoor traps with significantly higher frequency (aCRR: 1.50), whereas *Aedes albopictus* had a tendency to be trapped more frequently indoors (aCRR: 1.89, p=0.07). Furthermore, capture rate ratios between CO_2 baited and non-baited CDC-LT were significantly influenced by seasonality and indoor vs. outdoor trap placement.

Discussion and Conclusion: This study shows significant differences in the capture efficiency of CDC-LT when placed indoors or outdoors and in different seasons. Our study thus provides important guidelines for more targeted future vector trapping studies on the Thai-Myanmar border, which is an important cross-border malaria transmission region in Thailand.

Keywords: CDC Light Trap, dry ice, mosquito, malaria, Anopheles

MATHEMATICAL MODELLING OF TRANSMISSION OF *PLASMODIUM FALCIPARUM* AND *PLASMODIUM VIVAX* ON THE THAI/MYANMAR BORDER: IMPACT OF CROSS-BORDER MIGRATION

Stephan Karl[1],
Patchara Sriwichai[2],
Yudthana Samung[2],
Suchada Sumroypol[2],
Kirakorn Kiattibutr[2],
Chalermpon Kumpitak[2],
Arnon Payakapon[2],
Jeeraphat Sirichaisinthop[3],
Ivo Mueller[1],
Guiyun Yan[4], Liwang Cui[5],
Jetsumon Sattabongkot Prachumsri[2]

[1] *Walter and Eliza Hall Institute of Medical Research, Australia*
[2] *Department of Medical Entomology, Mahidol University,Thailand*
[3] *Bureau of Vector Borne Diseases, Pra Phuttabhat, Saraburi, Thailand,*
[4] *University of California, Irvine,USA*
[5] *College of Agricultural Sciences, Pennsylvania State University, USA*

Cross-border malaria transmission in an important problem for national malaria control programs. Recent studies on the northern Thai/Myanmar border indicate that *P. falciparum* is sustained by importation, while *P.vivax* is locally transmitted. Here we present an individual-based, spatial mathematical simulation model of a Thai/Myanmar border village and explore a variety of control interventions targeted at eliminating malaria in this setting.

Case data were collected from local malaria clinics between 2011 and 2014. Demographic and migration data were collected in active case detection surveys. Infections were diagnosed by expert light microscopy. Mosquito trapping data were collected in 7 villages in the same region in a total of >2500 trap nights. The mathematical model includes mosquito population dynamics and flight, human migration, simultaneous transmission of *P. falciparum* and *P. vivax* and options for various control interventions.

The model was validated using the available data. It allows for a systematic evaluation of a variety of possible interventions. We show that migration substantially contributes to sustain malaria transmission locally. *P. vivax* is more resilient to elimination as compared to *P. falciparum* due to its hypnozoite reservoir. Eliminating the hypnozoite reservoir by primaquine is predicted to have a long-term benefit in averting cases (>12 months post intervention), whereas the effect on *P. falciparum* is restricted to the first few months after an intervention. Targeting the migrant population with malaria control is predicted to be very effective.

We have developed and validated a microscale mathematical simulation model for a Thai/Myanmar border village setting. Using this model we explored a variety of interventions. We show a long-term effect of primaquine-based interventions against *P.vivax*. Furthermore, we show that it is crucial when the intervention is conducted in relation to migration and transmission peaks.

Keywords: malaria transmission, migration, elimination

MORPHOMETRIC AND GENETIC DIAGNOSIS WITHIN CLOSELY RELATED SPECIES OF DENGUE AND CHIKUNGUNYA VECTORS IN THAILAND: *AEDES AEGYPTI, AEDES ALBOPICTUS* AND *AEDES SCUTELLARIS*

Suchada Sumruayphol[1], Chamnarn Apiwathnasorn[1], Jiraporn Ruangsittichai[1], Patchara Sriwichai[1], Siriluck Attrapadung[1], Yudthana Samung[1], Jean-Pierre Dujardin[2]

[1] *Department of Medical Entomology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand*
[2] *Unité Mixte de Recherche 177-Interactions Hôte-Vecteur-Parasite-Enrironnement dans les Maladies Tropicales Négligées dues aux Trypanosomatidés, Centre International de Recherches Agronomiques pour le Développement (CIRAD), Institut de Recherches pour le Développement (IRD), Campus international de Baillarguet, Montpellier, France*

Aedes aegypti, *Ae. albopictus* and *Ae. scutellaris* are important mosquito vectors of Dengue and Chikungunya viruses. They are morphologically similar and coexist in some places of their distribution so that the risk exists of wrong morphological identification. Any confusion could have a negative impact on epidemiological studies or on control strategies. We applied fast and inexpensive morphometric method to help morphological species determination and in parallel with DNA barcoding analysis.

Field specimens were classified according to morphological criteria. They were then submitted to genetic and morphometric analyses, the latter subdivided into landmark-based (392 specimens) and outline-based (317 specimens) techniques.

A subsample of the specimens examined for their wing metric properties was submitted to genetic analyses. This analysis, based on the 658 basepairs for 30 COI sequences, is the first one comparing *Ae. scutellaris* and *Ae. albopictus*. The total average interspecific divergence for the 3 species was 13.4%, ranging from 12.3% to 14.1%, while the average intraspecific divergence did not pass 0.4%.

The shape of the wing showed a different discriminating power according to the sex and the digitizing technique. *Ae. aegypti* could be easily separated from the two other species, with scores of correct classification higher for males (from 95% to 98% of correct classification according to the approaches) than for females (from 87% to 93%). To separate *Ae. scutellaris* from *Ae. albopictus*, scores were less satisfactory, except for the scores obtained through the outline-based technique applied on males (from 90 to 96%).

We conclude that geometric morphometrics technique can considerably increase the reliability of the morphological determination.

Keywords: *Aedes scutellaris*, *Ae. aegypti*, *Ae. albopictus*, landmark, outline, geometric morphometrics.

UTILIZATION OF VECTOR MOSQUITOES FOR A NOVEL LIVE-ATTENUATED TETRAVALENT DENGUE VACCINE

Shota Takagi

The Chemo-Sero-Therapeutic Research Institute, Kikuchi Research Center, Japan

Dengue is a mosquito-borne viral infection caused by four sero-types of dengue virus (DENV 1-4) and is one of the most widespread tropical diseases. The disease is endemic in over one hundred tropical and sub-tropical countries, and infects 100 million people every year. Of these, an estimated 500,000 people, mainly children, are hospitalized, and 12,500 die each year.

Despite an increase in the incidence of the disease there is currently no effective treatment or vaccine. Therefore, the dengue virus poses a threat to both residents and travelers to endemic regions, and is a major public health issue. For this reason there are high expectations for a safe and effective vaccine.

Responding to these expectations, The Chemo-Sero Therapeutic Research Institute (Kaketsuken) entered into a material and technology transfer agreement with Mahidol University in 2011, for the University's novel live-attenuated dengue vaccine seeds and related technology, and began developing a non-genetically modified vaccine. After favorable results from a candidate vaccine and non-clinical studies, including GLP studies, we are planning to enter clinical studies next year.

The development of our dengue vaccine follows the guidelines for development of live-attenuated tetravalent dengue vaccines issued by the World Health Organization, which describes a need to evaluate the replication of candidate vaccines in vector mosquitoes. However, the parameters of the mosquito model, such as the inoculation route, dose, age of mosquitoes, and evaluation method/timing are not clearly set. Therefore, we have begun developing an appropriate mosquito model to evaluate our novel live-attenuated dengue vaccine.

Keywords: dengue, vaccine, mosquito

WEDNESDAY 2nd DECEMBER 2015

14.30 – 16.00
Room A

S6 - BARRIERS AND FUTURE OPPORTUNITIES FOR DIAGNOSIS OF INFECTIOUS DISEASES

Chairpersons :

Yuvadee Mahakunkijcharoen

Thareerat Kalambahet

Invited Speakers :

1 Stuart D Blacksell
"Rickettsial diagnostics: Why are we stuck in the 20th century?"

2 Supaporn Wacharapluesadee
"Surveillance for and diversity of coronaviruses in bats from Eastern Thailand"

3 Narisara Chantratita
"Application of new technologies to the problem of bacterial infections and antibiotic resistance"

RICKETTSIAL DIAGNOSTICS: WHY ARE WE STUCK IN THE 20TH CENTURY?

Stuart Blacksell

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Despite significant advances in many areas of medicine and scientific research, the diagnosis of some tropical infectious diseases has lagged behind. This is especially the case with rickettsial infections where there is still a reliance on serology to make a definitive diagnosis. Examination using Bayesian analysis has allowed for the definition of revised serological diagnostic criteria nevertheless the underlying testing is very much based on 1960s immunofluorescence assay technology which has recognized inconsistencies. Frustratingly, the development of accurate commercial ELISAs for the sero- epidemiology screening and diagnosis of rickettsial infections has not yet been fully realized and the issues of local diagnostic cut-offs remains a problem. PCR technologies remain insensitive due to the pathophysiology of the diseases and their unique distribution of biomarkers throughout the body. Given that rickettsial infections have a significant burden throughout Asia and Southeast Asia it is exasperating that we are reliant on "legacy technologies" rather those provided by the cutting edge. There are possibilities in the use of non-specific essays such as those for C-reactive protein that may aid in patient management rather than provide a specific diagnosis of rickettsial illness.

Keywords : Rickettsia, diagnosis, technology, cut-off

SURVEILLANCE FOR AND DIVERSITY OF CORONAVIRUSES IN BATS FROM EASTERN THAILAND

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Pattarapol Maneeorn[3],
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Kevin Olival[4], Patrick J Blair[5],
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Thiravat Hemachudha[1]

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Bats are reservoirs for broad diversity of coronaviruses (CoVs), including those closely related to human pathogens such as Severe Acute Respiratory Syndrome CoV and Middle East Respiratory Syndrome CoV. Estimates suggest there are approximately 138 bat species in Thailand of which 116 are insectivorous and 21 are fruit bats. Given that CoVs have potential to spread from bats to humans and other mammal hosts, obtaining baseline surveillance data in order to plan for public health measures is essential. In this study, we sampled bat populations from 5 provinces in Eastern Thailand. A total of 626 bat individuals were sampled (84 faecal and 542 rectal swab) from 19 different bat species. CoV RNA was detected in 47 specimens (7.6%) from 13 different bat species, using degenerate PCR primers designed to detect all CoVs, with a detection rate of 1.4% to 100% per species. We identified 37 alpha (α)-CoVs; nine β-CoV group D and one β-CoV group B (SARS-CoV related). Five of β-CoV group D belonged to a new independent cluster closely related to HKU9 bat CoV. For the first time, we have found CoV in six bat species that have previously not been reported to harbor CoV, namely *Cynopterus sphinx*, *Taphozous melanopogon*, *Hipposideros lekaguli*, *Rhinolophus shameli*, *Scotophilus heathii*, and *Megaderma lyra*. Our phylogenetic data indicates high diversity and a complex ecology of CoVs in bats sampled from specific areas in eastern regions of Thailand. Further characterization of additional CoV genes may be useful to better describe the CoV divergence.

Keywords : coronavirus, bat, zoonoses

APPLICATION OF NEW TECHNOLOGIES TO THE PROBLEM OF BACTERIAL INFECTIONS AND ANTIBIOTIC RESISTANCE

Narisara Chantratita

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Antibiotic resistance is a growing challenge to the effective management of severe bacterial infections. The rate of multidrug-resistance of non-fermenter, methicillin-resistant *Staphylococcus aureus* (MRSA), carbapenem-resistant Enterobacteriaceae spp., vancomycin-resistant enterococci (VRE), and rifampicin- and isoniazid-resistant *Mycobacterium tuberculosis* is increasing worldwide. These bacteria are spreading rapidly, causing many outbreaks. The diagnosis and evaluation of antimicrobial resistance is currently based on bacteria culture and susceptibility testing, which are accurate but time-consuming, and exclude the identification of resistance mechanisms. Because few novel antibiotics are entering the market, therefore controlling bacterial spread is mostly based on rapid identification and prevention. Among molecular-based techniques, real-time PCR assays targeting clinically relevant genes are commercially available for routine laboratory use. The DNA microarray can now identify many antibiotic-resistant genes simultaneously. Matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF), a new technology based on mass fingerprint detection, is widely used to identify microorganisms. Recent studies have shown that MALDI-TOF can detect activity of carbapenenmases production from bacteria. New rapid, simple tests based on the biochemical activity of β-lactamases have recently been reported. Advances in high-throughput sequencing technologies (next-generation sequencing, NGS), have opened new pathways in the molecular epidemiology and diagnostics of antimicrobial resistance. With high-resolution, NGS is replacing conventional epidemiological tools such as pulsed-field gel electrophoresis and multilocus sequence typing. However, the use of these advanced technologies in developing countries remains limited.

Keywords: New technologies, bacterial infection

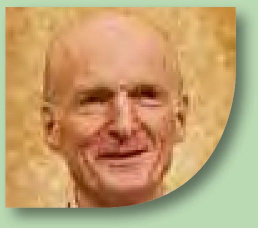
WEDNESDAY 2nd DECEMBER 2015

14.30 – 16.00
Room B

S7 - TURBO TALKS I (Please find abstracts in the Poster Presentations book)

Chairpersons :


Jetsumon Prachumsri


Nicholas J White

Speakers :

1 Sebastien Marcombe
"Vector bionomics and insecticide resistance in malaria vectors in Lao PDR: an update"
(p. 49 Poster)

2 Dagmara Poprawski
"Telemedicine: is there a place in tropical medicine for this novel approach to bring care closer to the patient" ***(p. 95 Poster)***

3 Nawaphat Somboonpoonpol
"Visceral leishmaniasis induced by newly emerged *Leishmania martiniquensis* in BALB/c mice using different routes of parasite inoculation"
(p. 30 Poster)

4 Jeffrey Hii
"Community-based program of larvivorous fish in domestic water containers and community mobilization for control of the dengue mosquito vector in Cambodia and Lao People's Democratic Republic: the Combating Dengue in ASEAN Study" ***(p. 50 Poster)***

5 Wanarit Jitsamai
"Seroprevalence of canine vector-borne infections in major regions of Bangkok, Thailand"
(p. 33 Poster)


6 Nutchavadee Vorasan
"Childhood malaria infection and school performance in children living in a malaria endemic area, western border of Thailand"
(p. 18 Poster)


7 Phubeth Ya-umphan
"Human antibody response to *Anopheles* salivary peptide as a biomarker to assess the risk of malaria transmission in the Thai-Myanmar border"
(p. 51 Poster)

14.30 – 16.00

Room B

S7 - TURBO TALKS I (Please find abstracts in the Poster Presentations book) (Continued)

Speakers :

8 Supawadee Poungsombat

"Capacity building for malaria and vector borne disease control programme for the sub district level Surveillance and Rapid Response Team (SRRT) in Thailand"

(p. 19 Poster)

9 Pimonwan Phokhaphan

"Molecular typing of Methicillin-resistant Staphylococcus aureus isolated from Thammasat University Hospital by Pulse-field gel electrophoresis"

(p. 70 Poster)

10 Natthida Sriboonvorakul

"Acids causing metabolic acidosis in patients with severe malaria (Assessing by novel method)"

(p. 20 Poster)

11 Kei Mikita

"Polymorphism in *Plasmodium falciparum* K13-propeller from Thai-Myanmar border in 1996-1997"

(p. 21 Poster)

12 Thomas Althaus

"How CRP rapid testing could impact antibiotics' prescriptions in developing countries"

(p. 80 Poster)

13 Win Mo Mo

"Warning signs to predict dengue severity in adult patients at the Hospital for Tropical Diseases, Thailand"

(p. 81 Poster)

14 Ian Gassiep

"Acute hepatitis in the setting of chronic *Schistosoma mansoni* infection and post- praziquantel therapy"

(p. 83 Poster)

15 Kittiyod Poovorawan

"Treatment coverage and allocation predict future burden of chronic hepatitis C in novel antiviral agent era, Thailand"

(p. 84 Poster)

16 Sirirat Lertpruek

"Acceptability of oral pre-exposure prophylaxis (PrEP) for HIV prevention among young men who have sex with men in Bangkok, Thailand"

(p. 87 Poster)

WEDNESDAY 2nd DECEMBER 2015

14.30 – 16.00

Room C

S8 - MALARIA I: ELIMINATION TOOLS: ANY DRUG(S) OF CHOICE

Chairperson :

Kesinee Chotivanich

Invited Speakers :

1 Arjen Dondorp
"Eliminating malaria in an era of MDR *Falciparum malaria*"
(Abstract not available)

2 Rob van der Pluijm
"Tracking resistance to artemisinins collaboration II"

3 Borimas Hanboonkunupakarn
"Therapeutic efficacy of OZ439 in patients with malaria infection"

4 Steve Ward
"Novel synthetic peroxides, Discovery and Development"

TRACKING RESISTANCE TO ARTEMISININS COLLABORATION II

Robertus van der Pluijm

Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University

The Tracking Resistance to Artemisinin Collaboration (TRAC) study confirmed that artemisinin resistant falciparum malaria has emerged and/or spread in all countries of the Greater Mekong Subregion (GMS). Predictably artemisinin resistance has been followed by emerging concomitant partner drug resistance in several parts of the GMS resulting in high rates of treatment failure with artemisinin combination therapies (ACTs). There is an urgent need to evaluate alternative treatments where standard courses of ACTs are failing, and to develop combinations of existing drugs which will not fall rapidly to resistance and can be deployed immediately. Triple artemisinin combination therapies (TACT) containing two partner drugs is likely to be an effective treatment of MDR malaria and triple or quadruple therapy might become the new paradigm for antimalarial treatment (as is already the case in HIV and TB treatment). TRACII will examine the safety, tolerability and efficacy of different TACT combinations in 17 sites in 8 countries in Asia and Africa. This will provide crucial information before TACT can be deployed at scale for the treatment of uncomplicated falciparum malaria in areas of artemisinin resistance, ACT failure and beyond.

Keywords: Malaria, Falciparum, Triple ACT

THERAPEUTIC EFFICACY OF OZ439 IN PATIENTS WITH MALARIA INFECTION

Borimas Hanboonkunupakan[1],
Podjanee Jittamala[2],
Aung Pyae Phyo[3,4],
François Henri Nosten[3,4], Sasithon Pukrittayakamee[1],
Mallika Imwong[5],
Nicholas J White[1,3],
Stephan Duparc[6],
Fiona Macintyre[6], Mark Baker[6]
and Jörg J. Möhrle[6]

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[4] *Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, UK.*
[5] *Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand*
[6] *Medicines for Malaria Venture, Geneva, Switzerland*

New antimalarial drugs are urgently in great demand due to the emergence of artemisinin-resistant *Plasmodium falciparum* that are spreading in Asia. OZ439 is a novel synthetic trioxolane that has been well tolerated in healthy volunteers. The good oral bioavailability, slower clearance, and increased metabolic stability of OZ439 may allow for single-dose cure in combination with suitable partner drugs. We report here a dose evaluation of OZ439 in acute malaria. A phase II open-label study of OZ439 given in single oral doses (200, 400, 800 and 1,200 mg) was conducted in adult patients with acute uncomplicated *P. falciparum* or *P. vivax* malaria at the Hospital for Tropical Diseases, Bangkok, and the Shoklo Malaria Research Unit, Thailand. Parasite clearance was assessed as a measure of antimalarial activity. All doses were equally effective in both *P. falciparum* and *P. vivax* malaria, with median parasite clearance half-lives of 4.1-5.6 h for *P. falciparum* and 2.3-3.2 h for *P. vivax*. Maximum plasma concentrations were reached at a median of 4 hours. The estimated elimination half-life ranged between 46 and 62 hours as previously observed in healthy volunteers. No serious drug-related adverse effects were observed in this study. Other adverse effects were generally mild and reversible. In conclusion, OZ439 is a new antimalarial drug with good efficacy against both *P. falciparum* and *P. vivax* malaria.

Keywords: antimalarials, clinical trial

NOVEL SYNTHETIC PEROXIDES, DISCOVERY AND DEVELOPMENT

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Reliance on semi-synthetic artemisinin derivatives with a single synthetic peroxide back-up class (OZ family) limits the ability of the community to respond to the malaria elimination challenge in terms of ensuring we have options in the face of potential resistance and the need to generate new drug combinations with a range of pharmacological and chemical characteristics going forward.

In order to address this concern we embarked on a discovery programme some ten years ago focusing on the tetraoxane pharmacophore. Over that time resistance or loss of susceptibility to artemisinins has become apparent. Mutations in pfKelch13, a primary marker of artemisinin resistance in *Plasmodium falciparum* is already threatening the long-term clinical utility of artemisinin based drug combinations, the cornerstone of modern day malaria treatment.

As a potential solution to this issue we have conducted a rational drug discovery programme that has delivered a novel fully synthetic peroxide tetraoxane based molecule, E209, through three generations of analogues, that meets the requirements of the Medicines for Malaria (MMV) target candidate profiles with potential for single exposure radical cure prophylaxis (SERCAP).

E209, has potent nanomolar activity against multiple strains of *P. falciparum* and *P._vivax in vitro* and against *P. falciparum* in *in vivo* experimental models, demonstrates a parasite reduction ratio equivalent to dihydroartemisinin and has pharmacokinetic and pharmacodynamics characteristics that are compatible with single dose cure treatment. Importantly, E209 retains full potency against parasites carrying mutations in pfKelch13. This data confirms for the first time that the mutations in pfKelch13 do not impact on the entire peroxide family of antimalarials and that the class retains significant therapeutic value.

WEDNESDAY 2nd DECEMBER 2015

14.30 – 16.00

Room D

S9 - VECTOR CONTROL AND PREVENTION

Chairpersons :

Narumon Komalamisra

Jiraporn Ruangsittichai

Invited Speakers :

1 Hamady Dieng

"Suggested Shift in mosquito control strategy: turning large-scale human carelessness into control tools"

2 Ryota Koizumi

"Development of a new method for evaluating spatial repellency against mosquitoes"

3 Sungsit Sunvornyothin

"Update of the giant mosquito research as the potential biological control agent for integrated vector control program of Dengue and Chigunkunya vectors"

(Abstract not available)

Hamady Dieng

Institute of Biodiversity and Environmental Conservation, Universiti Malaysia Sarawak

SUGGESTED SHIFT IN MOSQUITO CONTROL STRATEGY: TURNING LARGE-SCALE HUMAN CARELESSNESS INTO CONTROL TOOLS

Over 1 million people die from mosquito-borne diseases every year, and dengue affects more humans than any other arbovirus disease globally. Insecticides' use is one of the main strategies for containing vector populations. Apart from increased resistance to the main families of insecticides, environmental concerns and policies impede endeavors to control this illness. Thus, strategies that trigger potential variability in modes of action and limit environmental problems are needed. Annually, 4.5 trillion of smoked cigarettes end up tossed into our environment at time when the popularity of coffee and tea as drinks—*over five billions of cups consumed yearly worldwide*—tags along with the disposal of enormous amounts of waste into many natural ecosystems. With the growing consumption of these products, the accumulation of leftovers in the environment is forecast to increase markedly in the near future. Cigarettes, coffee and tea as well as their wastes are full of toxicants that occur naturally, during planting and manufacturing. Many of these chemicals are deadly to aquatic life and none of them have a history of resistance in mosquitoes. To anticipate their environmental impacts, find alternatives or additional disposal strategies, but also combat insecticide resistance and reduce cost associated to vector control, we explored the deterrence potentials of leachates from discarded cigarette butts, coffee and tea against the ovipositing, embryonic and immature stages of dengue vectors. When smoked cigarette butts are soaked in water: they readily kill young larvae while attracting egg-laying females. Oviposition activity increased steadily as cigarette butts steeped in water over ten days. Females that emerged from the butt-infused habitat were less fecund than their parents and had a shortened life span. Coffee acted both as an uninviting signal to gravid females and as a barrier to embryogenesis. In addition, the presence of only oviposition sites with coffee induced many females to retain most of their mature eggs within ovaries. Both fresh and used tea extracts were detrimental to the survival of young and old larvae when in competition with water. Exposure of larval stages to tea extracts increased larval development time and reduced pupation success, adult emergence and egg production. Taken together these observations suggest that cigarette, coffee and tea as well as their wastes may be useful in developing potent, low-cost and bio-rational mosquito control strategies. The observed butt waste toxicity to mosquito larvae opens new avenues for the identification of novel insecticide products. The observations that cigarette and coffee either repel or attract gravid females and inhibit larval eclosion provide novel possibilities in the search for novel oviposition deterrents/attractants and anti-larval eclosion agents. There are already far too many cigarette butts, unused grounds coffee and tea remnants being simply discarded; turning these common wastes into alternate control tools against mosquito vectors may represent a viable solution to the pollution problems they pose. This could sustainably decrease disease transmission and reduce the incidence of such toxic wastes in the environment as well as costs associated to vector control and debris removal.

DEVELOPMENT OF A NEW METHOD FOR EVALUATING SPATIAL REPELLENCY AGAINST MOSQUITOES

Ryota Koizumi

Kao Corporation, Kansei Science Research Lab, Japan

Female mosquitos require blood meal from humans or other animals to lay eggs. Due to its blood-feeding behavior, human beings are threatened by mosquito-borne diseases such as malaria and dengue fever, resulting in more than half of a billion of infections and millions of deaths each year. Its host-seeking behavior is dependent on their sensory system which detects multiple chemical signals released from their hosts through sensory receptors expressed on the antenna and maxillary palps. In a distance, CO2 is essential for mosquitoes to get activated and start flying toward their hosts. Therefore, the machinery to detect CO2 could be an ideal target for a development of a novel insect repellent which masks humans from mosquitoes. To achieve it, we constructed a new method for evaluating especially CO2-attracted behavior against mosquitoes in a laboratory. Using this method, our candidate materials, inhibitors of CO2-neural responses, showed stronger repellency than DEET, the most effective repellent in the market. It implies that blocking of CO2 reception in mosquitoes may provide a new method to reduce mosquito-borne diseases. ⁂

Keywords: mosquito, repellent, CO2

WEDNESDAY 2nd DECEMBER 2015

16.30 - 18.00
Room A

S10 - BEST STUDENT PRESENTATION AWARD

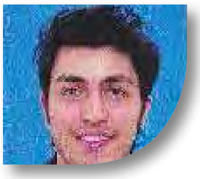
Chairpersons :

Sasithon Pukrittayakamee

Kasinee Buchachart

Speakers :

1 Maheshi Athapaththu
"Analysis of recombinant Chikungunya (CHIK) E1 and E2 antigens expressed in *Escherichia coli* and Pichia pastoris for the detection of anti-CHIK IgG antibodies in human serum samples"



2 Mohammad Behram Khan
"Immune response of Anopheles dirus during *Plasmodium falciparum* infection"

3 Palang Chotsiri
"Population pharmacokinetic and cardiotoxicity modeling of piperaquine"

4 Viswanathan Ramasamy
"A designer recombinant four-in-one dengue subunit vaccine candidate without the burden of disease enhancing antibodies"

5 Viriya Hantrakun
"A simple correction of under-reported notifiable disease cases in a resource-limited setting"

ANALYSIS OF RECOMBINANT CHIKUNGUNYA (CHIK) E1 AND E2 ANTIGENS EXPRESSED IN ESCHERICHIA COLI AND PICHIA PASTORIS FOR THE DETECTION OF ANTI-CHIK IGG ANTIBODIES IN HUMAN SERUM SAMPLES

Maheshi Athapaththu [1],
Naveen Khanna [2], S Inouve [3],
Sunethra Gunasena[4],
Wimaladharma Abeyewickreme[1],
Menaka Hapugoda [1]

[1] Molecular Medicine Unit, Faculty of Medicine, University of Kelaniya, Ragama, Sri Lanka,
[2] International Centre for Genetic Engineering and Biotechnology, New Delhi, India,
[3] 3WHO Collaborative Centre for Viral Reference and Research, Institute of Tropical Medicine, Nagasaki University, Japan ,
[4] Department of Virology, Medical Research Institute, Colombo 8, Sri Lanka

Introduction: Chikungunya (CHIK) is an important disease with explosive outbreaks occurring in Sri Lanka. A diagnostic intermediate using a single recombinant protein antigen to detect both Immunoglobulin (Ig) M and G antibodies of CHIK is important to overcome the problems associated with whole viral lysate antigen, in currently used ELISA. Overall objective of this study was to analyse and compare the sensitivity and specificity of the novel recombinant proteins developed using bacterial and yeast expression systems to detect anti-CHIK IgG antibodies.

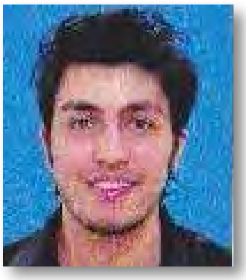
Method: Synthetic genes of CHIK named Envelope 1 (E1) and Envelope 2 (E2) were custom designed and chemically synthesized. The resulted proteins were expressed in both bacteria (*Escherichia coli*) and yeast (*Pichia pastoris*) vector expression systems and purified using a Ni- NTA columns. Novel developed recombinant proteins were evaluated to be used as a diagnostic intermediate, using panels of well characterized serum samples.

Results: For the detection of anti-CHIK IgG antibodies, the E1 recombinant protein expressed in *E. coli* showed 60 % (47/78) sensitivity and 64% (94/148) specificity while the E2 recombinant protein expressed in *E. coli* showed 83 % (65/78) sensitivity and 86% (195/227) specificity compared with the HAI test and indirect IgG ELISA using purified CHIKV. The E1 recombinant protein expressed in*P. pastoris* showed 86% (67/78) sensitivity and 61% (90/148) specificity and the E2 recombinant protein expressed in *P. pastoris*showed 76% (59/78) sensitivity and 81% (183/227) specificity compared with the HAI test and indirect IgG ELISA using purified CHIKV for the detection of IgG antibodies.

Conclusion: Recombinant CHIK-E2 protein antigen expressed in *E. coli* showed higher specificity and sensitivity in detection of IgG anti-CHIK antibodies.

Acknowledgement: International Centre for Genetic Engineering and Biotechnology (CRP/SRL08/02) and National Science Foundation, Sri Lanka (RG/2009/BT/01) for funding and International Atomic Energy Agency (TC/SRL/05/042) for technical co-operation.

Keywords: chikungunya, antigens, recombinants, ELISA, antibodies



IMMUNE RESPONSE OF ANOPHELES DIRUS DURING *PLASMODIUM FALCIPARUM* INFECTION

Mohammad Behram Khan

Department of Parasitology, University of Malaya

Malaria, one of the world's most threatening diseases is transmitted by *Anopheles* mosquitoes; *Anopheles dirus s.s* is one of the main vectors of malaria in South East Asia. The mosquitoes' innate immune response is the first line of defense against malaria parasites during its development. The IMD (immune deficiency) pathway, a conserved immune signaling pathway, influences anti-*Plasmodium falciparum* activity in *Anopheles gambiae*, *An. stephensi* and *An. albimanus*. In the present study, the *Rel2* gene, an IMD pathway-controlled NFkappaB transcription factor, of *An. dirus* was silenced using double stranded RNA (dsRNA) to deduce the role of *Rel2* during *Plasmodium falciparum* and bacterial infection (Gram-positive and Gram-negative). The infection study was performed by counting the oocysts for *P. falciparum* infected mosquitoes and conducting a survival analysis for bacterial infected mosquitoes. Our results suggest that *Rel2* is required for providing protection against *P. falciparum* and Gram-positive (*Micrococcus luteus*) bacteria with Lys-type peptidoglycan. This demonstrates that the IMD pathway could be manipulated to confer resistance to the vectors by overexpression or silencing the negative regulators of *Rel2* in an effort to restrict the malaria transmission cycle and develop vector based control strategies.

Keywords: Malaria, Anopheles dirus, *Plasmodium falciparum*

POPULATION PHARMACOKINETIC AND CARDIOTOXICITY MODELING OF PIPERAQUINE

Palang Chotsiri[1,2],
Thanaporn Wattanakul[1,2],
Borimas Hanboonkunupakarn[2],
Podjanee Jittamala[2],
Salwaluk Panapipat[1],
Richard Hoglund[1,3],
Daniel Blessborn[1,3],
Sasithon Pukrittayakamee[2],
Nicholas J. White[1,3],
Nicholas P.J. Day[1,3], and
Joel Tarning [1,3]

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[2] *Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand*
[3] *Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, United Kingdom*

Objective: The aim of this study was to evaluate the population pharmacokinetic properties of piperaquine and its cardiotoxicity outcome, i.e. the QT prolongation, in order to determine the safety of the antimalarial drug piperaquine.

Methods: Sixteen healthy volunteers were randomly administered primaquine, dihydroartemisinin-piperaquine or dihydroartemisinin-piperaquine plus primaquine. Piperaquine plasma concentrations were measured frequently using LC-MS/MS. Electrocardiographic (ECG) measurements were performed at screening and at 2, 4, 8, 12, and 24 h after drug dosing. Non-linear mixed effects modelling (NONMEM) was performed in order to characterize the pharmacokinetic and pharmacodynamic properties of piperaquine.

Results: Piperaquine plasma concentrations were accurately described using a three-compartment disposition model with two-transit absorption compartments. Double-delta Fredericia-corrected QT measurements (ΔΔQTcF) were modelled as a linear-direct response pharmacodynamic model. Thus, ΔΔQTcF increased linearly with respect to rising plasma concentrations of piperaquine. The final population pharmacokinetic-pharmacodynamic model was utilized for safety simulations. Peak piperaquine plasma concentrations below 850 ng/mL were suggested to show a safe cardiotoxic profile (below 60 millisecond) with 95% confidence.

Conclusions: A population pharmacokinetic and cardiotoxicity model of piperaquine was successful identified using the NONMEM. Simulations, using the final model, suggested that a standard 3-day dihydroartemisinin-piperaquine dose is safe.

Keywords: Piperaquine, pharmacokinetics, cardiotoxicity, prolonged QTcF interval, population pharmacokinetic-pharmacodynamic model

A DESIGNER RECOMBINANT FOUR-IN-ONE DENGUE SUBUNIT VACCINE CANDIDATE WITHOUT THE BURDEN OF DISEASE ENHANCING ANTIBODIES

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Upasana Arora[1], Ankur Poddar[1],
Raj Gokul[1], Rajendra Raut[2],
Ashiya Perween[1],
Poornima Tyagi[1],
Niyati Khetarpal[1],
Sathyamangalam Swaminathan[1],
Aravinda de Silva[2],
Laura White[3], Robert Johnston[3],
Siddhartha Bhaumik[4],
Murali Kaja[4],
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Dengue disease, caused by four antigenically distinct dengue viruses (DENVs), is a serious global health concern. It was estimated that DENVs infected ~400 million people globally in 2010, of whom 34% were people in India. Despite intensive efforts over the past three decades to develop a prophylactic vaccine for limiting the spread of disease, a licensed vaccine is still elusive.

Most dengue-specific antibodies in human immune sera are weakly neutralizing and bind to multiple DENV-serotypes, resulting in higher degree of cross-reactivity and disease exacerbation through antibody-dependent-enhancement. A recent study has reported that serotype-specificity of neutralizing antibodies is critical in conferring protection. Unfortunately, only a small fraction of human antibodies are serotype-specific. These serotype-specific antibodies are predominantly directed towards the DENV receptor binding envelope domain III (EDIII). Thus, dengue vaccines designed to skew the immune response towards highly neutralizing and serotype-specific epitopes of EDIII could be efficient in protecting against dengue and minimizing cross-reactive enhancement.

We have developed a tetravalent **D**engue **S**ubunit **V**LP (DSV^4) based vaccine candidate, expressed in *Pichia pastoris*. This four-in-one, tetravalent vaccine candidate incorporates EDIIIs of all four DENVs displayed on the surface of Hepatitis B surface Antigen virus-like-particles (VLPs). DSV^4 VLPs are immunogenic in mice and macaques, and elicit serotype-specific DENV neutralizing antibodies. Additionally, these antibodies have been found to exhibit breadth of genotype neutralization and are protective in AG129 mice. Moreover, non-manifestation of disease enhancement in AG129 mice by DSV4 antibodies is highly encouraging. Since this vaccine candidate is based on a non-replicating VLP platform presenting EDIIIs of all four DENVs in a single entity and uses the high capacity *P. pastoris*, we believe it has significant potential to emerge as a safe, efficacious and inexpensive dengue vaccine candidate without the burden of disease enhancement.

Keywords: Dengue, VLPs, EDIII, P.Pastoris

A SIMPLE CORRECTION OF UNDER-REPORTED NOTIFIABLE DISEASE CASES IN A RESOURCE-LIMITED SETTING

Viriya Hantrakun [1],
Sittikorn Rongsumlee [2],
Somkid Kongyu [3],
Punnarai Smithsuwan [3],
Yaowalark Sukthana [4],
Rungrueng Kitphati [3],
Nicholas PJ Day [5],
Soawapak Hinjoy [3],
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Although the national disease-surveillance system was developed for detecting and controlling outbreaks of communicable diseases, its data is commonly interpreted as representing the actual burden of infectious diseases by many who are not epidemiologists. In many tropical developing countries, data on notifiable diseases are often incomplete due to limited resources, and these data can be seriously misinterpreted. For example, melioidosis is a notifiable disease in Thailand, and researchers there estimate that there are >1,000 death due to this disease each year. However, only 15 deaths caused by meloidosis were reported to the Thailand disease-surveillance system in 2012. As a result, the burden of melioidosis is greatly underestimated.

A large retrospective study was conducted to obtain more accurate estimates of the number of cases and deaths caused by notifiable bacterial infectious diseases diagnosed in 2012 across Thailand. We combined multiple sources of routine surveillance data including microbiology databases and hospital admission databases from all provincial hospitals, and national death registry from Ministry of Interior, Thailand.

In the preliminary analysis, we found that 31, 38 and 162 patients died of culture-confirmed melioidosis diagnosed at 5, 4 and 2 provincial hospitals in east, central and northeast regions of Thailand. None of those cases were reported to the Thailand disease-surveillance system.

This study demonstrates that data from the national disease-surveillance system on notifiable bacterial infectious diseases could be rectified retrospectively by integrating information from readily available databases. This method could also be used for other notifiable infectious diseases such as dengue infection and leptospirosis, if databases of rapid diagnostic tests and serological diagnostic tests of each hospital is included.

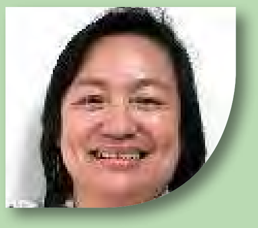
Keywords: melioidosis, surveillance system

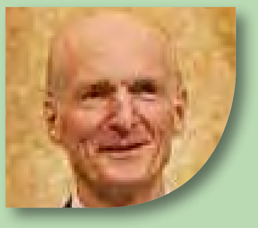
WEDNESDAY 2nd DECEMBER 2015

16.30 - 18.00
Room B

S11 - TURBO TALKS II (Please find abstracts in the Poster Presentations book)

Chairpersons :


Jetsumon Prachumsri


Nicholas J White

Speakers :

1 Hiroyuki Oku
Identification of a novel plasminogen-binding sequence in the loop region of *Plasmodium falciparum* enolase
(p. 7 Poster)

2 Ratana Somrongthong
"Community engagement in malaria prevention and control among ethnic minority groups in Ratanakiri and Mondolkiri province" ***(p. 9 Poster)***

3 Wanlapa Roobsoong
"Field based *in vitro* invasion inhibition assay of *Plasmodium vivax*"
(p. 11 Poster)

4 Moritoshi Iwagami
"Current malaria situation in Lao PDR based on DNA analysis by SATREPS project"
(p. 16 Poster)

5 Wilanee Dechkhajorn
"Third stage *Gnathostoma spinigerum* larva excretory secretory antigens alter function of Fc gamma Receptor I mediated monocytes in peripheral blood mononuclear cell culture"
(p. 37 Poster)

16.30 - 18.00
Room B

S11 - TURBO TALKS II (Please find abstracts in the Poster Presentations book) (Continued)

Speakers :

6 Prasert Saichua
"Seroprevalence of *Toxoplasma gondii* in free range chicken (*Gallus domesticus*) from Khon Kaen province" ***(p. 22 Poster)***

7 Aongart Mahittikorn
"Survey of intestinal protozoa in pigs and their in-contact humans in Nakhon Pathom Province, Thailand" ***(p. 23 Poster)***

8 Akkarin Poodeepiyasawat
"Molecular survey of parasitic filaria in domestic cats and potential vectors from Surat Thani, Thailand" ***(p. 23 Poster)***

9 Kevin Kobylinski
"Ivermectin inhibits the development of *Plasmodium vivax* in *Anopheles dirus* and *Anopheles minimus*" ***(p. 47 Poster)***

10 Oranicha Khamprapa
"New Insights on the Oviposition container type selection of *Aedes* mosquito species in dengue transmission foci of Bangkok, Thailand" ***(p. 48 Poster)***

11 Siriporn Phasomkusolsil
"Observations on the consumption and killing duration of *Toxorhynchites splendens* (Wiedemann) larvae on *Aedes aegypti* (L.) prey" ***(p. 57 Poster)***

12 Kuong Suy
"Pneumococcal colonisation in young Cambodian children shortly after introduction of pneumococcal conjugate vaccine" ***(p. 61 Poster)***

13 Tobias Brummaier
"Scrub typhus infection in pregnancy, review of the literature and a case study of a chloramphenicol averted maternal mortality in 3rd trimester" ***(p. 63 Poster)***

14 Suparat Giengkam
"Optimizing RNA extraction from fresh culture of *Orientia tsutsugamushi*" ***(p. 64 Poster)***

15 Sharanjeet Atwal
"Live imaging of the genetically intractable intracellular human pathogen *Orientia tsutsugamushi* using the fluorescent dye carboxyfluorescein succinimidyl ester" ***(p. 65 Poster)***

WEDNESDAY 2nd DECEMBER 2015

16.30 - 18.00
Room C

S12 - FREE PAPER - HELTHMINTHOLOGY & OTHER PARASITIC DISEASES

Chairpersons :

Aaron Jex

Poom Adisakwattana

Speakers :

1 Kesorn Thaewnongiew
"Liver fluke and cholangiocarcinoma prevention and control in 8th health service by four strategies"

2 Yukifumi Nawa
"Opisthorchis: How many species?"

3 Sirilak Dusitsittipon
"Genetic differentiation of *Angiostrongylus cantonensis* and its cryptic species (Nematoda: Angiostrongylidae) in Thailand by microsatellite markers and mitochondrial cytb sequences"

4 Howoo Nam
"Comparison of ELISA and RDT in the diagnosis of human toxoplasmosis"

5 Sasithon Tangsawad
"Prevalence and factor related to *Opistochis viverrini* infestation in high risk area, Thailand"

LIVER FLUKE AND CHOLANGIOCARCINOMA PREVENTION AND CONTROL IN 8TH HEALTH SERVICE BY FOUR STRATEGIES

Kesorn Thaewnongiew[1], Sasithorn Tangsawad[2], Nittaya Chudthaisong[3], Angsana Yospunya[4], Sayumporn Promjareet[5], Ngampis Sirivettumrong[6], Jongkon Tamiganon[7], Teerapong Pumpuang[8], Kornkum Ponwong[9]

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[2] Office of Disease Prevention and Control, Thailand
[3] Nongkai Provincial Health Office, Khon Kaen Province, Thailand
[4] Loei Provincial Health Office , Thailand
[5] Nongbualumphu Provincial Health Office , Thailand
[6] Udonthani Provincial Health Office, Thailand
[7] Nakonpranom Provincial Health Office, Thailand
[8] Sakonakon Provincial Health Office, Thailand
[9] Bungkan Provincial Health Office, Thailand

Background & Objective: Liver fluke and Cholangiocarcinoma (CCA) are main problems in Thailand. This serious problem leading to the four strategies to reduce CCA incidence rate by 50% in 3 years and liver fluke infection rate must be reduced to 5 % in 2016.

Method: Study design was research and development by four strategies to enhance people's potential.

Results: First Strategy: The new value "new Thai youth avoid eating raw fish" was a 8th health service area policy. Liver fluke and CCA knowledge was included in schools curriculum, executive board (54.1 %) of all schools was in the meeting. "Learning by doing" project to prevent liver fluke and CCA had expanded to the target district; "Stop eating raw fish" campaign had increase from 12 target sub-districts in 2013 to 218 target sub-district in 2015.

Second Strategies: Risk group was screening by health volunteer and 86.7% of the targets were similar to the policy "more screening, more findings". Risk group, patient, and mortality cases were analyzed to solving problem.

Third Strategies: There were 1,748,584 risk people who had CCA and 27,174 of them got Ultrasound. Sixty three of those was found having CCA. Then, referral system was set for appropriate treatment.

Fourth Strategies: The hospitals are cooperating to improve quality of patients' life. The patients gained better service with lover car fees and got treatment at home, 1,970 patients in 2013 and increased in 2015.

Conclusion: Four strategies are effective to prevent liver fluke and CCA.

Keywords: liver fluke, cholangiocarcinoma (CCA), four strategies.

OPISTHORCHIS: HOW MANY SPECIES?

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Doanh Pham Ngoc [2],
Natalya Yurlova [3]

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[2] Department of Parasitology, Institute of Ecology and Biological Resources, Viet Nam Academy of Science and Technology, Hanoi, Viet Nam
[3] Laboratory of Insect Pathology, Institute of Systematics and Ecology, Siberian Branch of Russian Academy of Science, Novosibirsk, Russia

Two species of *Opisthorchis*, *O. viverrini* and *O. felineus*, are, together with *Clonorchis sinensis*, known as the important pathogens causing serious hepatobiliary diseases, especially known as the causative agents for cholangio-carcinoma. However, little is known about the biodiversity of the genus *Opisthorchis*. We have made an extensive literature survey and found that 58 nominal species including several subspecies are supposed to be valid in the genus *Opisthorchis*. Among them, 33 species were parasites of birds, 15 of fish, 7 of mammals, and 1 each of molluscs, amphibians and reptiles. A majority of *Opisthorchis* were first found in India and Russia/Sibria, except for 3 species in Africa and 2 species in US. In particular, 13 out of 15 species recognized as fish parasites were found in India. Only one each were found from fish in China and Egypt. Except for the three human pathogens mentioned above, genetic data are not available for other *Opisthorchis* species. According to the recent data of ITS2 and cox I sequences of *O. lobatus* (Thaenkham et al. 2013), this avian *Opisthorchis* is rather closely related to *O. viverrini* and *O. felineus* is away from other 3 species. More genetic data should be accumulated to draw phylogenetic relationship of those diverse *Opisthorchis* species. ⁂

Keywords: Liver-fluke, Opisthorchis, Taxonomy, Phylogeny, Pathogen

GENETIC DIFFERENTIATION OF *ANGIOSTRONGYLUS CANTONENSIS* AND ITS CRYPTIC SPECIES (NEMATODA: ANGIOSTRONGYLIDAE) IN THAILAND BY MICROSATELLITE MARKERS AND MITOCHONDRIAL *CYTB* SEQUENCES

Sirilak Dusitsittipon[1],
Charles D. Criscione[2],
Serge Morand[3],
Chalit Komalamisra[1],
Urusa Thaenkham[1]

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Angiostrongylus cantonensis is a pulmonary parasitic nematode of rodents and carnivores. Accidental ingestion of some species can lead to eosinophilic meningitis in humans. Despite the fact that *A. cantonensis* has been reported globally, we have only a cursory knowledge of its lineage diversity and genetic connectivity among populations. This study aimed to reveal the genetic differentiation among worms of the genus *Angiostrongylus,* collected from 16 different geographical localities in Thailand, by using microsatellite marker and mitochondrial *cytb* sequences. 182 worms from these localities were studied for genetic diversity based on twelve microsatellite loci, while 157 worms underwent study based on their *cytb* sequences. The results showed congruency between the phylogenetic relationships revealed by both markers. There were two main monophyletic clades of Thai *Angiostrongylus*, composed of the clade *A. cantonensis* and the clade of its closely related species. The percentage genetic distance, based on the *cytb* sequence between the two clades, was 8.1 ±0.034. High haplotype diversity was detected in both *A. cantonensis* and its cryptic species populations. Interestingly, five haplotypes of the cryptic species were supposedly a pseudogene of the mitochondrial *cytb* gene. Moreover, the microsatellite results suggested evidence of hybridization between *A. cantonensis* and its cryptic form. ⁂

Keywords: *Angiostrongylus cantonensis*, Cryptic species, Genetic differentiation, Microsatellite markers, *cytb* gene

COMPARISON OF ELISA AND RDT IN THE DIAGNOSIS OF HUMAN TOXOPLASMOSIS

Howoo Nam[1], Hye-Jin Ahn[2],
Chom-Kyu Chong[3],
Tong-Soo Kim[4], Sung-Jong Hong[5]

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[5] *Department of Medical Environmental Biology, Chung-Ang University, Seoul 156-756, Korea*

ELISA has been used popularly in the diagnosis of toxoplasmosis, but for the time-consuming procedure and the need of skilled technician, it is now replaced gradually by a rapid diagnostic test (RDT), the universal trend of diagnosis. Here, we compared two methods in the survey of residents in an island located in the Yellow Sea nearby Incheon city, Korea. Routine IgG-ELISA with *Toxoplasma gondii* (RH strain) crude antigen and IgG/IgM RDT mounted with recombinant fragment of major surface antigen (SAG1), GST-linker-SAG1A, were applied to the sera from the residents for 4 years from 2010 to 2013 about 900 persons per year. In 2010, ELISA detected 135 positives among 921 (14.7%) and RDT detected more sensitively 202 positives (21.9%). But, RDT detected 87.4% (118 sera) of ELISA positives except for those sera of controversial OD just above the cut-off value, instead detected more positives in ELISA-negatives of 10.7% (84 sera). This pattern was maintained in 2011, 2012 and 2013 with the increasing seroprevalence of 23.3%, 23.6% and 32.1% by ELISA and 26.8%, 28.9% and 33.3% by RDT, respectively. IgM was detected in 3 sera in 2010, 1 in 2011, 7 in 2012 and 13 in 2013. This surgical increase in seroprevalence is suggested to be due to the organic agriculture in addition to eating behavior or pet loving of Korean.

Keywords: *Toxoplasma gondii*, toxoplasmosis, seroprevalence, IgG-ELISA, IgG/IgM RDT

PREVALENCE AND FACTOR RELATED TO *OPISTOCHIS VIVERRINI* INFESTATION IN HIGH RISK AREA, THAILAND

Sasithon Tangsawad,
Kesorn Thaewnongiew,
Orawan Jamjun, Seri Singtong

Office of Disease Prevention and Control, region 6, Khon Kaen Province,Thailand

Opisthochiasis is the Public health problem in the northestern part of Thailand. The policy has been implemented for long time but not yet decrease the prevalence rate. The objective of this crossectional analytic study was to find out the prevalence and factor related to *Opisthochis viverrini* infestation in Thailand. The 2,336 samples selected from the population 15 year and older in the public health region 7 by 30 cluster sampling technicque. Data collection by questionnare and Modified Kato′ s thick smear was used to stool examination. Descriptive and analytical statistic for factor related to Opistochis viverrini infestation by Odd ratio and multiple logistic regression. The results revealed that the prevalence of Opistochis viverrini infestation was 16.9% and the highest prevalence was 22.3% in Kalasin province. Female and male ratio was 1:1.1 . The highest prevalence found in 40-49 year age group. All age group except under 20 year had the prevalence more than 10%. The factor related to Opistochis viverrini infestation were age, occupation, conception for Opisthochis viverrini infestation, eating raw fish behavior. So, policy of changing raw fish consumption behavior by context of community is the strategy to control and decrease prevalence of Opistochiasis in the northestern part of Thailand.

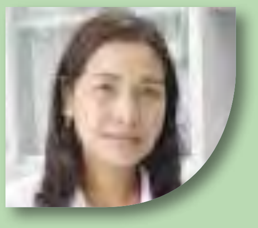
Keywords: Prevalence, Opisthochiasis, factor related to Opisthochis viverrini infestation

WEDNESDAY 2nd DECEMBER 2015

16.30 - 18.00
Room D

S13 - FREE PAPER - VECTOR BORNE DISEASES I

Chairpersons :



Pornsawan Leaungwutiwong

Jonas Schmidt-Chanasit

Speakers :

1 Alison Crawshaw
"Acceptability and effectiveness of insecticide-treated clothing for prevention of outdoor malaria transmission among rubber tappers in Myanmar"

2 Weerawat Phuklia
"Improving antibiotic susceptibility testing for *Orientia tsutsugamushi*"

3 Vianney Tricou
"Persistence of neutralizing antibodies one year after two doses of a candidate recombinant tetravalent dengue vaccine in subjects aged from 1.5 to 45 years"

4 Peeraya Ekchariyawat
"Inflammasome activation limits Chikungunya virus replication in primary human dermal fibroblasts"

5 Wipa Tangkananond
"Production of multiepitope E protein of Japanese encephalitis virus by using the HBcAg tandam loop gene in plants"

6 John Hustedt
"Determining the efficacy of guppies, community engagement, other new tools on dengue vectors in Cambodia: a cluster randomized trial"

7 Victor Chaumeau
"Impact of targeted malaria treatment on the transmission of *Plasmodium falciparum* along the Thai-Myanmar border"

ACCEPTABILITY AND EFFECTIVENESS OF INSECTICIDE-TREATED CLOTHING FOR PREVENTION OF OUTDOOR MALARIA TRANSMISSION AMONG RUBBER TAPPERS IN MYANMAR

The success of commercial factory insecticide treatment of clothing as a strategy against residual transmission of malaria hinges on acceptability, adherence and effectiveness, as there is limited information to inform policymakers on targeted distribution to mobile and migrant populations (MMPs). A cluster-randomized non-inferiority crossover trial was conducted to investigate acceptability and effectiveness of insecticide-treated clothing (ITC) in Mon State, Myanmar. 234 male and female rubber tappers in 16 rubber plantation clusters were enrolled in a two-arm trial (ITC versus non-treated clothing-NTC) and randomly allocated to the order of clothing distribution. Structured questionnaires and 32 focus group discussions were conducted at baseline and three follow-ups. Preliminary findings revealed high acceptability and adherence to ITC and NTC: 94.3% (95% CI: 92.1-97.3*) of respondents at follow-up 1 (FU1) and 96.0% [94.0-98.6] at FU2 reported liking the ITC/NTC overall, commenting: "[With ITC] no other measures are needed. It is perfect." Laboratory bioassays results on ITC and NTC at FU2 revealed that percentage mortality (1.3%) and knockdown rates (17.3%) of Anopheles dirus with worn ITC were statistically higher than NTC (0% for both outcomes, $p<0.05$) at high usage (75.0% of users wore every night) and washing (mean number of washes 5.88). Although ITC could be effective for outdoor malaria prevention among night-time workers, the washfastness of ITC is compromised by frequent laundering (99.5% of users washed the ITC/NTC at least once in the previous two weeks). More research in testing long-lasting formulation of insecticide with repellent properties is required. *CIs not adjusted for clustering.

Keywords: insecticide-treated material, acceptability, effectiveness

Alison Crawshaw [1],
Thae Maung Maung [2],
Myat Phone Kyaw [2],
Myo Win Tin [1], Nyan Sint [3],
Aung Ye Naung Win [2],
Olivier Celhay [4],
Sarala Nicholas [5],
Arantxa Roca-Feltrer [6],
Muhammad Shafique [4],
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IMPROVING ANTIBIOTIC SUSCEPTIBILITY TESTING FOR *ORIENTIA TSUTSUGAMUSHI*

Weerawat Phuklia[1,3],
Phonepasith Panyanivong[1],
Piengchan Sonthayanon[3,4]
Stuart D. Blacksell[2,4]
Daniel H. Paris[2,4],
Paul N. Newton[1,2],
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Antibiotic susceptibility testing for *Orientia tsutsugamushi* is labor intensive and difficult due to the intracellular nature of the pathogen. To improve antibiotic susceptibility testing for large sample sets, we aimed to develop a suitable screening assay using only one time point and a small number of antibiotics concentrations. To optimize the screening conditions, the best harvesting method, optimal multiplicity of infection (MOI), the best day for harvesting and the optimal antibiotic concentrations were investigated.

Mouse fibroblast cells (L929) were inoculated with *O. tsutsugamushi* strain Kato with different MOIs and cultured in 24-wells plate with azithromycin, chloramphenicol and doxycycline. Bacteria growth was quantified by qPCR. The optimized method was used to determine the Minimal inhibitory concentrations (MICs) in multiple strains to investigate strain variation.

Cells harvesting by trypsinization showed less variation than scraping. The bacteria growth peak was consistently observed at day 7/10 with MOI 1000:1 and 100:1 and the growth ratio between the two MOIs was similar. Therefore, we identified MOI 100:1, day 10 and trypsinization as optimal for screening. The MICs of azithromycin, chloramphenicol and doxycycline against Kato strain were 0.0067 (95%CI 0.0027-0.0170) µg/ml 1.005 (95%CI 0.3967-2.546) mg/ml, and 0.0761 (95%CI 0.0180-0.3214), mg/ml, respectively. The calculated MICs for 2 other strains were within the 95% confidence interval range of the Kato strain.

The MIC data will be used to determine screening concentrations to investigate antimicrobial susceptibility of *O. tsutsugamushi* in large populations.

Keywords: *Orientia tsutsugamushi*, Antibiotic, susceptibility testing

PERSISTENCE OF NEUTRALIZING ANTIBODIES ONE YEAR AFTER TWO DOSES OF A CANDIDATE RECOMBINANT TETRAVALENT DENGUE VACCINE IN SUBJECTS AGED FROM 1.5 TO 45 YEARS

Vianney Tricou, Derek Wallace

Takeda Vaccines Pte Ltd, Singapore

Takeda's live attenuated tetravalent dengue vaccine candidate (TDV) contains a molecularly characterized dengue serotype 2 virus (TDV-2) and three recombinant viruses expressing the pre-membrane (prM) and envelope (E) structural genes for serotypes 1, 3, and 4 in the TDV-2 genetic backbone. The safety and immunogenicity of TDV were previously demonstrated in two Phase 1 clinical trials in healthy, flavivirus-naïve adults aged 18–45 years. DEN-203 is a previously reported phase II placebo-controlled, multi-center trial (NCT 01511250) that assessed the safety, reactogenicity and immunogenicity of two doses of TDV or placebo, 90 days apart, in subjects living in dengue endemic areas (Puerto Rico, Colombia, Singapore or Thailand). Subjects were randomized 2:1 to receive TDV or placebo in an initial age-descending phase (four age cohorts: 21-45, 12-20, 6-11 and 1.5-5 years), and subsequent expansion phase (1.5-11 years). Here we present safety and immunogenicity results for this study including the persistence of antibodies to day 360 in vaccinees who were either dengue seropositive or seronegative at baseline and in the different age groups, compared with placebo. Vaccination was well tolerated with no safety signals in any age group. One dose of the candidate TDV vaccine elicited immune responses against the four DENV serotypes in initially seropositive and seronegative subjects from 1.5 to 45 years of age. There was little impact on antibody titers of a second dose administered at 90 days. Neutralizing activity persisted through 360 days irrespective of age or initial immune status.

Keywords: Dengue Vaccine, Tropical Diseases

INFLAMMASOME ACTIVATION LIMITS CHIKUNGUNYA VIRUS REPLICATION IN PRIMARY HUMAN DERMAL FIBROBLASTS

Peeraya Ekchariyawat[1, 2],
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Loïc Talignani[1],
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Philippe Desprès[6],
Laurence Briant[3],
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Global spread of arboviruses has been annually increasing. Alphaviruses and flaviviruses are the most arboviruses threaten humans. They are transmitted to vertebrates by the bite of infected arthropods. Early transmission to vertebrates is initiated by skin puncture and deposition of virus in this organ. Events at the bite site remain largely unknown. Here we demonstrate that, besides a common antiviral signature such as type-I interferon signaling pathway, Chikungunya virus (CHIKV), and West Nile virus (WNV) activate inflammasome program in primary human dermal fibroblasts. Both CHIKV and WNV induce maturation of caspase-1 and enhance IL -1β expression leading inflammasome activation. We also found that both CHIKV and WNV also upregulate the inflammasome AIM2 sensor in dermal fibroblasts. Depletion of caspase-1 and AIM2 expression by siRNA suppresses the IL-1β production in CHIKV- and WNV-infected cells. Finally, inhibition of the inflammasome via caspase-1 depletion was found to enhance CHIKV replication in dermal fibroblasts. Together, these results indicate that the skin contributes to the pro-inflammatory and anti-viral microenvironment via the activation of the inflammasome in the early stages following infection with arboviruses.

Keywords: Inflammasome, Caspase-1, AIM-2, Chikungunya, Arbovirus

PRODUCTION OF MULTIEPITOPE E PROTEIN OF JAPANESE ENCEPHALITIS VIRUS BY USING THE HBCAG TANDAM LOOP GENE IN PLANTS

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Hadrien Peyret[2],
Keith Saunders[2],
George P. Lomonossoff[2]

[1] *Department of Biotechnology, Faculty of Science and Technology, Thammasat University, Klongluang, Prathumtani 12121, Thailand*
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E protein protects Japanese encephalitis virus (JEV) nucleocapsid and its immune response protects against JEV infection. Previous researchers showed that only humoral immune response was elicited from immunised mice with inactivated JEV vaccine strain SA14-14-2 whereas both humoral and cellular immune responses were shown in immunised mice with recombinant multiepitope (MEP) peptide of JEV E protein expressed in *Escherichia coli*. Therefore, genetic engineering of JEV-MEP gene produced JEV-MEP protein in plants instead of culturing JEV in mice and animal tissue cultures, and expressing genetic engineered JEV-MEP protein in *E.coli*. Hence, this research is the pioneer for plant derived JE vaccine. The various steps were construction of JEV-MEP from six B cell and two T cell epitopes from E gene of JEV strain SA14 and vaccine strain SA14-14-2 and added the suitable promotor for cloning in *E. coli* and *Agrobacterium tumefaciens*. Second, *A. tumefaciens* was inoculated and expressed in *Nicotiana benthamiana* leaves using the pEAQ-HT-HBcAg-tEL vector. Then, the JEV-MEP with the core protein (HBc) of Hepatitis B virus (HBV) were shown the bands which were detected by chemiluminescence immunoassay. Finally, it will be characterized and purified for the plant based vaccine and its immune response will be investigated further.

Keywords: Japanese encephalitis virus, Hepatitis B virus, plant based vaccine, immune response

DETERMINING THE EFFICACY OF GUPPIES, COMMUNITY ENGAGEMENT, OTHER NEW TOOLS ON DENGUE VECTORS IN CAMBODIA: A CLUSTER RANDOMIZED TRIAL

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

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[2] *Cambodian National Dengue Control Program,*
[3] *World Health Organization,*

First identified in Cambodia in 1963, dengue is now endemic to the Greater Mekong sub-region. Vaccines, sterile insect techniques and the release of disease-refractory mosquitoes are years from operational roll-out and will be unlikely to provide universal protection from transmission. Due to the relatively high cost of the current vector control methods and widespread insecticide resistance there is an urgent need to find an alternative cost-effective solution for *Aedes* vector control that is operationally feasible by the National Dengue Control Program.

Guppy fish (*Poecilia reticulata*) have been found to be a low cost, sustainable and effective approach to reduce dengue vector populations, and thus, reduce the risk of dengue transmission. It has also been shown that strong community involvement linked to a clear Communication for Behavioral Impact (COMBI) strategy is essential in maintaining coverage and efficacy. Miscellaneous containers, which are uninhabitable by guppies, must be dealt with through alternative interventions.

Although there is a plethora of evidence suggesting the use of guppy fish, recent reviews show there has never been a cluster randomized trial to evaluate their effectiveness nor a proper evaluation of their impact on adult mosquito densities. This cluster randomized trial, starting in September 2015, is the first to attempt this and has been designed to demonstrate community effectiveness of guppies with COMBI activities versus a control. The results of the study will be used to determine cost effectiveness and create policy recommendations.

Keywords: Dengue, Guppy, Vector Control, Cambodia

IMPACT OF TARGETED MALARIA TREATMENT ON THE TRANSMISSION OF *PLASMODIUM FALCIPARUM* ALONG THE THAI-MYANMAR BORDER

The emergence and spread of artemisinin resistance in *Plasmodium falciparum* (Pf) is challenging the efforts of malaria control and elimination in South East Asia. The Shoklo Malaria Research Unit through the support of the Welcome Trust and the Bill & Melinda Gates Foundation has implemented a pilot study in four villages along the Thai Myanmar border to assess whether Targeted Malaria Treatment (TMT) can eliminate the parasite reservoir and contain artemisinin-resistance. Entomological surveys using human landing catch technique were conducted in parallel to parasitological surveys to address the Pf-malaria transmission before and after intervention. One thousand two hundred and eighty two malaria vectors belonging to the Minimus, Maculatus and Dirus Groups were collected during baseline surveys (before TMT, during the rainy season). Bites of malaria vectors occur all night long but *An. maculatus s.l.* and *An. dirus s.l.* exhibit a peak in their biting behaviour during the early evening and a higher tendency to exophagy. An average of 267 bites of malaria vectors was received per person and per month (95% CI 226-309). Pf-sporozoitic index (Pf-SI) was 2.2 ‰ (95% CI 0.0-4.4, n=1,782 mosquitoes inspected) and we estimated that each person received an average of 0.6 (95% CI 0.02-1.18) Pf-infective bites per month (Pf-EIR). When analysing 9 months of collection, average Pf-SI was 0.9‰ (95% CI 0.4-1.4) and average Pf-EIR was 0.22 Pf-infective bites per month (95% CI 0.10-0.34). Half of the transmission occurred outside the premise (2 on 4 infective bites) and half of the transmission occurred between 5:00 and 06:00 a.m. (2 on 4 infective bites). Data on the impact of TMT on Pf transmission will be presented during the meeting. In conclusion, malaria transmission in the studied area involves early feeding and exophagic vectors that could maintain residual transmission (i.e. transmission that is not controlled by full coverage of the population with long lasting insecticide-treated bed-nets) after TMT. Therefore the development and evaluation of vector control tools adapted to malaria transmission settings in South-East Asia is needed in order to act in synergy with TMT and achieve artemisinin-resistance containment.

Keywords: Malaria, artemisinin resistance, targeted malaria elimination, anopheles, Thai-Myanmar border.

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JITMM2016

THURSDAY 3rd DECEMBER 2015

09.00- 10.30
Room A

S14 - TRAVEL MEDICINE

Chairperson :

Watcharapong Piyaphanee

Invited Speakers :

1 Prativa Pandey
"Expat living in the tropics: Relax or Risk?"

2 Rogelio López-Vélez
"Parasitic infections in travelers and migrants: Lesson Learned from Europe"

3 Yongjua Laosiritaworn
"EBOLA/MERS CoV :Threat to Asia"
(Abstract not available)

EXPAT LIVING IN THE TROPICS: RELAX OR RISK?

Prativa Pandey

Medical Director, CIWEC Hospital and Travel Medicine Center, Kathmandu, Nepal

An expatriate (or expat) by definition is a person temporarily or permanently residing in a country other than that of their citizenship. GeoSentinel network of the International Society of Travel Medicine defines expatriates as those living in a destination country with an independent residence, using mostly the infrastructure used by local residents of the same economic class, independent of duration of residence. People move for work, as staff of diplomatic and aid agencies, for relief or volunteer work, and as missionaries. Disease profile differs in expats depending mainly on destination e.g. whether expats are living in Africa, Asia, or South America. Disease profile also differs depending on the nature of work that people do, length of stay in the destination, and whether they sought pre-travel advice before leaving home country. While it is relaxing to be in the tropics with warm weather, beautiful ocean, jungle and mountains, diseases can occur that need to be dealt with in the country of residence of the expats. Cases will be presented that will highlight health problems in expatriates living in the tropics.

PARASITIC INFECTIONS IN TRAVELERS AND IMMIGRANTS

Rogelio López-Vélez

National Referral Unit for Tropical Diseases. Infectious Diseases Department. Ramón y Cajal University Hospital, Madrid, Spain

Travel and migration contribute to the emergence of certain parasites which may be imported into nonendemic areas. Importation of vectors may contribute to the emergence of protozoan infections in nonendemic countries. Climate change may affect arthropod distribution and facilitate the spread of protozoan vector-borne diseases. Noncontrolled importation of food products and animals may also contribute to the diagnosis of infections caused by helminths in nonendemic countries. Imported parasitic diseases which may be transmitted vertically or through blood transfusion/organ donation could become a public health priority in the near future.

Infections such as malaria are potentially fatal, especially in nonimmune patients, and outcome depends largely on timely diagnosis and treatment. Some helminth infections such as strongyloidiasis may be life-threatening, especially in immunocompromised patients, and outcome depends on correct diagnosis and treatment. Other helminth infections are neglected tropical diseases associated with chronic disease and/or disability.

Diagnosis/management of imported parasitic infections may be complex especially as some patients may have underlying immunosuppressive conditions such as HIV infection. Major challenges concern the development of improved diagnostic techniques, safer/more effective drug therapies and identification of biological markers of progression and response to treatment.

The study of these imported infections in travelers and immigrants may provide opportunities for research which may not be readily available in resource-poor endemic countries. Updated reviews and guidelines are necessary as new data become available.

THURSDAY 3rd DECEMBER 2015

09.00- 10.30

Room B

S15 - TRANSLATIONAL RESEARCH

Chairperson :

Pradip Rathod

Invited Speakers :

1 Nares Damrongchai

"Translational researches"

(Abstract not available)

2 Suradej Hongeng

"Research involving stem cell technology"

(Abstract not available)

3 Suparerk Borwornpinyo

"New platform for drugs development"

(Abstract not available)

4Ashley M. Vaughan

"Human-liver chimeric mice for experimental *Plasmodium falciparum* crosses"

HUMAN-LIVER CHIMERIC MICE FOR EXPERIMENTAL *PLASMODIUM FALCIPARUM* CROSSES

Ashley Vaughan,
Richard Pinapati,
Ian Cheeseman, Nelly Camargo,
Matthew Fishbaugher,
Lisa Checkley, Shalini Nair,
Carolyn Hutyra, François Nosten,
Timothy Anderson,
Michael Ferdig and
Stefan Kappe

*Center for Infectious Disease Research,
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98109, USA*

Genetic crosses of phenotypically distinct strains of the human malaria parasite *Plasmodium falciparum* are a powerful tool for identifying genes controlling drug resistance and other key phenotypes. Previous studies relied on the isolation of recombinant parasites from splenectomized chimpanzees, a research avenue that is no longer available.

Here, we demonstrate that human-liver chimeric mice support recovery of recombinant progeny for the identification of genetic determinants of parasite traits and adaptations. To date, we have carried out four genetic crosses. Whole genome sequencing of progeny from one cross has identified over 5000 SNPs that distinguish the parental strains. With regard to basic biology, experimental crosses will provide insight into strain compatibility as well as maternal inheritance patterns. An experimental cross pipeline will being great power to the field of malaria genetics and will be especially relevant for the tracking of artemisinin resistance in the field as well as assaying parasite resistance to new antimalarials.

Keywords: *Plasmodium falciparum*

THURSDAY 3rd DECEMBER 2015

09.00- 10.30
Room C

S16 - MALARIA II MALARIA ELIMINATION: THE ROLE OF FUTURE MALARIA VACCINES

Chairperson :

Wang Nguitragool

Invited Speakers :

1 Jessica Hostetler
"A library of *Plasmodium vivax* recombinant proteins reveals new vaccine candidates and protein-protein interactions"

2 Anjali Yadava
Title TBA

3 Sebastian Mikolajczak
Title TBA

4 Yaming Cao
"An unusual sulfhydryl oxidase from *Plasmodium berghei* as a malaria transmission-blocking vaccine candidate"

A LIBRARY OF *PLASMODIUM VIVAX* RECOMBINANT PROTEINS REVEALS NEW VACCINE CANDIDATES AND PROTEIN-PROTEIN INTERACTIONS

Jessica B. Hostetler[1,2],
Sumana Sharma[2,3],
S. Josefin Bartholdson[2,3],
Gavin J. Wright[2,3],
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[3] *Cell Surface Signalling Laboratory, Wellcome Trust Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridge CB10 1SA, United Kingdom*

A vaccine targeting *Plasmodium vivax* will be an essential component of any comprehensive malaria elimination program, but major gaps in our understanding of *P. vivax* biology, including the protein-protein interactions that mediate merozoite invasion of reticulocytes, hinder the search for candidate antigens. Only one ligand-receptor interaction has been identified, that between *P. vivax* Duffy Binding Protein (PvDBP) and the erythrocyte Duffy Antigen Receptor for Chemokines (DARC), and strain-specific immune responses to PvDBP make it a challenging vaccine target. To broaden the repertoire of *P. vivax* merozoite-stage vaccine targets, we initiated a large-scale study of *P. vivax* merozoite proteins that are potentially involved in reticulocyte binding and invasion. We selected 39 *P. vivax* proteins that are predicted to localize to the merozoite surface or invasive secretory organelles, some of which show homology to *P. falciparum* vaccine candidates. Of these, we were able to express 37 full-length protein ectodomains in a mammalian expression system, which has been used to express *P. falciparum* invasion ligands such as PfRH5 in previous studies. To establish whether the expressed proteins were correctly folded, we performed immunoreactivity screens using plasma from Cambodian patients with acute vivax malaria. IgG from these samples recognized 31 of 34 antigens tested, the majority of which showed heat-labile IgG immunoreactivity, suggesting the presence of conformation-sensitive epitopes, an indication of tertiary protein structure. Using a method specifically designed to detect low-affinity extracellular protein-protein interactions, we confirmed several known and predicted protein-protein interactions between ligands, including the *P. vivax* 6-cysteine proteins P12 and P41, which further suggests that the proteins are natively folded and functional. This screen also identified two novel protein-protein interactions, between P12 and PVX_110945, and between MSP3.10 and MSP7.1, the latter of which was confirmed by surface plasmon resonance. As well as identifying new interactions for biological follow-up studies, this library will be useful in identifying *P. vivax* proteins with vaccine potential, and studying *P. vivax* malaria pathogenesis and immunity.

Keyword: *Plasmodium vivax*

AN UNUSUAL SULFHYDRYL OXIDASE FROM *PLASMODIUM BERGHEI* AS A MALARIA TRANSMISSION-BLOCKING VACCINE CANDIDATE

Wenqi Zheng[1], Enjie Luo[1], Liwang Cui[2], Yaming Cao[1]

[1] College of Basic Medical Sciences, China Medical University, Shenyang 110001, China
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Quiescin sulfhydryl oxidases (QSOX) catalyze the facile direct insertion of disulfide bonds into unfolded reduced proteins with concomitant reduction of oxygen to hydrogen peroxide. They are present in a wide variety of eukaryotic species including metazoans and plants, but absent in fungi. We identified a QSOX in malaria parasites and characterized *Plasmodium berghei* QSOX (PbQSOX). The recombinant PbQSOX protein possessed notable oxidase activity using artificial substrates. PbQSOX is primarily expressed in the sexual stage and highly localized on the surface of ookinetes. Knockout of PbQSOX did not affect asexual stages, but affected exflagellation of male gametocytes and reduced the formation of ookinetes and oocysts. To assess the transmission-blocking potential of PbQSOX, anti-rPbQSOX serum was obtained from BALB/c mice that were immunized with purified rPbQSOX protein, and anti-PbQSOX monoclonal antibody (anti-PbQSOX mAb) was developed. Both anti-rPbQSOX serum and anti-PbQSOX mAb significantly inhibited ookinete and oocyst formation, indicating that PbQSOX could be a candidate for a transmission-blocking vaccine target. ⁂

THURSDAY 3rd DECEMBER 2015

09.00- 10.30
Room D

S17 - DIETARY REFERENCE INTAKE (DRI) FOR THAILAND 2015: A SUSTAINABLE HEALTH SUCCESS

Chairpersons :

Karunee Kwanbunjan

Pornrutsami Jintaridth

Invited Speakers :

1 Supranee Changbumrung
"DRI and new threats prevention: Macronutrients"

2 Karunee Kwanbunjan
"Folate intake recommendations for Thai: New adjustability"

3 Wantanee Kriengsinyos
"Systematic review on dietary sodium intake and hypertension: Maximal recommended doses"

DRI AND NEW THREATS PREVENTION: MACRONUTRIENTS

Supranee Changbumrung

Department of Tropical Nutrition and Food Science, Faculty of Tropical Medicine, Mahidol University

Dietary Reference Intake (DRI) is an important dietary guideline used to plan and assess the nutrient intakes of healthy people; it is calculated using data from Recommended Dietary Allowance (RDA) (the average daily dietary intake level sufficient to meet the nutrient requirement of nearly all (97-98%) healthy individuals in a group) and Adequate Intake (AI) (a value based on observed or experimentally determined approximations of nutrient intake by a group (or groups) of healthy people, used when an RDA cannot be determined), and has been gradually developed for individual countries. In Thailand, the first published RDA was issued in 1976. A second, revised RDA was issued in 1989, while the latest DRI was issued in 2003. A new DRI is currently being developed by an expert committee, which is expected to be finished by the end of this year. All of the daily macronutrient requirements (carbohydrate, protein, fat including energy intake) and important micronutrients (vitamins, minerals and trace elements) will be revised.

The revised DRI for macronutrients are described below:

Energy: Total energy intake per day consists of Resting Energy Expenditure (REE) and energy needed for all physical activities during the day. REE can be calculated from standard equations, which vary from sex, age and average weight. Sources of energy are mainly carbohydrates, fat and protein.

Carbohydrates: Daily carbohydrate requirement is 45-65 per cent of total energy intake. Carbohydrates are good source of energy. Complex carbohydrates (rice, wheat) are good sources of carbohydrates. Precautions should be taken with added sugar, of which 6 teaspoons (24 g) are allowed per day.

Protein: the DRI for protein is one gram per kilogram body weight. Various proteins are important for growth and maintenance of body function. If the total energy intake derived from carbohydrates and fat is insufficient, the body will utilize protein as the source of energy instead.

Fat: The requirement of fat per day is 20-35 per cent of the total energy intake. Intake fat includes fat from animals and cooking oils. Fat is a good source of immediate and stored energy. Furthermore, linoleic acid and alpha-linolenic acid are essential fatty acids. At the present time, there is considerable debate regarding the usefulness of mono-unsaturated fatty acids and polyunsaturated fatty acids in reducing the risk of coronary heart disease. The intake of saturated fat should be limited and avoiding the consumption of trans-fat is also recommended; as both can increase risk of coronary heart disease.

FOLATE INTAKE RECOMMENDATIONS FOR THAI ADULTS

Karunee Kwanbunjan

Department of Tropical Nutrition and Food Science, Faculty of Tropical Medicine, Mahidol University, Thailand

Folate is a generic term for a water-soluble B vitamin, which functions in single-carbon transfer reactions and exists in many chemical forms. Folate coenzymes are involved in deoxyribonucleic acid (DNA) synthesis, purine synthesis and the conversion of homocysteine to methionine. Folate serves as a major source of methionine for the synthesis of S-adenosyl-methionine, an important *in vivo* methylating agent. In 2003, the Dietary Reference Intake (DRI) of folate equivalents for Thai adults was set at 400 µg/d which was based on USA/Canada DRI 2000. This was arguably due to insufficient research in Thailand on the role of folate on neural tube defects and cardiovascular diseases prevention. Since that time, a number of studies have revealed that the preventive effect of folic acid intake on cardiovascular events was not supported by randomized controlled trials. Moreover, high folate intake may cause adverse effects whereas the intake of folate below 400 µg/d has been shown to result in a sufficient folate status. Thus, a reduction of the reference value to 300 µg/d for Thai adults is proposed.

SYSTEMATIC REVIEW ON DIETARY SODIUM INTAKE AND HYPERTENSION: MAXIMAL RECOMMENDED DOSES

Wantanee Kriengsinyos

Institute of Nutrition, Mahidol University

Sodium is essential for cellular homeostasis and physiological function. Excess dietary sodium has been linked to elevations in blood pressure (BP) along with increased risk of cardiovascular disease. The association between high sodium intake and hypertension was well documented in INTERSALT study, which reported a significant linear association between urinary sodium excretion and systolic BP. The same finding was found later in the European Prospective Investigation into Cancer in Norfolk study. It has also reported that population-based intervention on sodium intake reduction could decrease the incidence of stroke by 75% and coronary artery disease mortality by 80%. Based on these strong evidences, the intake of less than 2 g/day sodium or 5 g/day salt was recommended by the World Health Organization (WHO).

Presently, sodium intakes in Thai population exceed the WHO recommendation. Based on the first salt survey in 2009, an average daily consumption of salt was 10.8 g or 4.3 g sodium/day/person, which was approximately double of that recommended by WHO (2g/day). In addition, the 24-hour-dietary-recall data from the Thai National Health Examination Survey IV, 2008-2009 indicated that 67.6 % of populations consumed extra dietary sodium and thus exceeding the current Thai recommendations of 2400 mg/d. However, sodium reduction initiatives in Thailand actively work under “Low salt Thailand Network”, started in 2012 onward under the support of the Thai Health Promotion Foundation with the theme “Thais reduce salt by half, keep diseases far away”. Therefore, the cooperation from all partners and everyone is needed for the success to achieve the goal of salt reduction.

THURSDAY 3rd DECEMBER 2015

09.00- 10.30
Room E

S18- THE CONTAINMENT OF MERS – COV: THAILAND'S EXPERIENCE
(Sponsored by Ministry of Public Health, Thailand (MOPH))

Moderator :

Jurai Wongsawat

Speakers :

1 Yongjua Laosiritaworn
"Surveillance and risk assessments"
(Abstract not available)

2 Waraluk Tangkanakul
"MERS - CoV screening health measure at 4 airports for Hajj Pilgrim in Thailand 2015"
(Abstract available on page 136)

3 Chariya Sangsajja
"Case management and hospital infection control"
(Abstract not available)

THURSDAY 3rd DECEMBER 2015

11.00 – 12.30
Room A

S19 - APPROACH TOWARDS HEALTHY ELDERLY LIFE POST 2015

Chairperson :

Prof. Yaowalark Sukthana

Invited Speakers :

1 Sureeporn Punpuing
"Towards a healthy life for older adults post-2015 in light of thailand's demographic and social changes"

2 Puangpen Chanprasert
"Towards Healthy Ageing Post 2015"
(Abstract not available)

3 Additional speaker
To be announced
(Abstract not available)

TOWARDS A HEALTHY LIFE FOR OLDER ADULTS POST -2015 IN LIGHT OF THAILAND'S DEMOGRAPHIC AND SOCIAL CHANGES

Sureeporn Punpuing

Institute for Population and Social Research, Mahidol University, Thailand

Thailand has been classified as an aged society since 2005, and it is projected that in 2031, Thailand will be a "super aged" society, when the proportion of older adults aged 65+ reach 20 percent. This study explores the situation of older Thai adults in light of Thailand's demographic transition and social changes. National surveys of older adults by the National Statistical Office in 2011 and 2013 were employed. In 2013, there are about 10 million older adults (aged 60+) in the population, more females than males. Female older adults are more likely to be single and to live alone, and are less likely to work than male counterparts. In addition, females are likely to face more physical and mental health problems than males. Age, sex, marital status, and economic status are related to health status, economic situation and living arrangement among older adults in Thailand. This is partly because Thailand's low fertility since the 1970s, along with improvements in medical technology, have led to increases in both the number and proportion of older adults. On the other hand, social and economic changes encourage an increase in educational levels, labor force participation and the proportion of the population who are unmarried. This study suggests that to improve the "quality of ageing society", three aspects of security for older persons should be assured. First, security in health, in that all elderly have healthy and active lives; second, security in income, ensuring that all older persons have enough income for living; and third, security in living arrangements, so that all older persons live with care givers or in a care giving system.

THURSDAY 3rd DECEMBER 2015

11.00 – 12.30
Room B

S20 - GLOBAL HEALTH

Chairperson :

Kamolnetr Okanurak

Invited Speakers :

1 Bruce A Wilcox
"Social-ecological systems thinking in tropical disease research: A Global Health Imperative"

2 Suriya Wongkongkathep
"Thailand's strategy in a changing global health context"
(Abstract not available)

SOCIAL-ECOLOGICAL SYSTEMS THINKING IN TROPICAL DISEASE RESEARCH: A GLOBAL HEALTH IMPERATIVE

Bruce A. Wilcox

Global Health Asia Office, Faculty of Public Health, Mahidol University

A century ago, beginning mainly with discovery of the role of mosquitoes in malaria transmission, the field of tropical medicine emerged to address vector borne and other diseases originating in the world's tropics. The field has since contributed incalculably to the alleviation or prevention human suffering worldwide. Yet, malaria remains the leading cause of death and disability with dengue as the most significant re-emerging disease globally in terms of the rate of increase numbers of people at risk. A total of about half the world's 7 billion-plus population has been estimated to be at risk from these and other persistent vector borne diseases.

This situation was not anticipated by medical and public health sciences when attention and funding for infectious diseases was cut back and focused on cancer and other non-communicable diseases in the 1970s. This complacency, including divestment and decline in public health infrastructure - along with population growth, globalization and the accompanying social and environmental changes -has been described by many experts as a cause of increased emergence of new and resurgence of existing infectious diseases. With the emergence of HIV/AIDS, but also the resurgence of malaria, TB and persistence of neglected tropical diseases, complacency and divestment have ceased be factors. Yet the others remain and need to be factored more fully into tropical disease research and interventions.

In this paper I describe this challenge, focusing in particular on the need for systems thinking and the framing of infectious diseases prevention and control strategies that incorporates social and ecological perspectives. This requires research that is truly integrative - interdisciplinary and Transdisciplinary - and that recognizes that zoonotic and vector borne disease dynamics exist within social-ecological systems. This represents an entirely different type of research frame than as proven so effective in laboratory and clinical research for drugs, diagnostics, vaccines and therapeutics.

However, vector-borne disease transmission systems, or "complex episystems"; arguably obey a different set of laws and principles than operate in controlled and replicable laboratory conditions and typically suitable for most biomedical research models. To conclude I briefly describe the above framework, principles and applications. I use malaria as one example, in the context of climate change adaptation. This area represents an opportunity to develop a new, integrative science of tropical medicine that restores a balanced and complementary relationship of clinical and laboratory research with field and community-based research. ⁂

Keyword: Global Health

THURSDAY 3rd DECEMBER 2015

11.00 – 12.30
Room C

S21 - G6PD PREVALENCE AND TESTING FROM PUBLIC HEALTH PERSPECTIVES
(*Sponsored by ACCESS BIO, INC / WELLS BIO, INC*)

Chairperson :

Young S. Hong

Speakers :

1 Issarang Nuchprayoon
”Molecular genetics of G6PD deficiency in Southeast Asian populations”

2 Raja Zahratul Azma Raja Sabudin
“Diagnosis of G6PD deficiency in Malaysia”

3 Sovannaroth Siv
“G6PD performances, Cambodia”
(Abstract available on page 137)

MOLECULAR GENETICS OF G6PD DEFICIENCY IN SOUTHEAST ASIAN POPULATIONS

Issarang Nuchprayoon

Department of Parasitology, Faculty of Medicine, Chulalongkorn University, Thailand

Glucose-6-phosphate dehydrogenase (G6PD) deficiency is highly prevalent among Southeast Asians. The prevalence was consistently high among Cambodians (15-26%), Laotians (7%), Thais (11-12%), Burmese (10-22%), Mons (12%), Karen (24%) Vietnamese Khin (1.5-5%), Malays (4.6%) and oversea Chinese (6-7.2%). G6PD mutations are ethnic-specific, with G6PD Viangchan (871G>A), highly prevalent in people to the east of the peninsula, namely the Cambodians (allele frequency 12-21% in males), Laotians (7%), Thais (3%), Vietnamese Khin (3%), Malays (2%), rarely in Northern Thais (1%), Karens, but not in Burmese or Mons. The other common Southeast Asian allele, G6PD Mahidol, (487G>A), is highly prevalent in people in the West of peninsula, namely Karens (20%), Burmese (7-14%), Mons (7%), and less common alleles among Northern Thais (3%), Central Thais(<1%), but not found in Cambodians.

Evolutionarily, the G6PD Viangchan allele is an older mutations, while G6PD Mahidol is more recent and was shown to be positively selected by P vivax and not by P falciparum in Karen people. In the endemic region, people with G6PD Mahidol had lower parasitemia but no less frequent malaria infection. The selection by malaria could explain the high prevalence of G6PD deficiency in this region.

DIAGNOSIS OF G6PD DEFICIENCY IN MALAYSIA

Raja Zahratul Azma Raja Sabudin

Department of Pathology, Universiti Kebangsaan Malaysia, Malaysia

Glucose-6-phosphate dehydrogenase (G6PD) deficiency is one of the commonest causes of neonatal jaundice in Malaysia. Screening of cord blood for G6PD deficiency by fluorescent spot test (FST) is performed in Malaysia. However this method, being a qualitative test, detects only cases with severe G6PD deficiency, but miss cases of partial G6PD deficiency when the enzyme levels are more than 20% of the mean normal activity. Currently, screening G6PD deficient patients using quantitative method is only performed at UKM Medical Centre, Kuala Lumpur. In UKM Medical Centre, we use OSMMR-D kit assay to measure G6PD activity. Measurement using this method is rapid, easy to perform, less laborious and has good reproducibility. We established the normal ranges and the 60% and 20% cut-off points to be used for the diagnosis of G6PD deficiency. The partial deficiency ranges (20-60% of mean normal) for G6PD activity in neonates, paediatrics and adults were 2.5-7.4 U/gHb, 2.03 – 6.11 Ug/Hb and 1.84-5.52 U/gHb, respectively. All cord blood of deficient male (negative FST) and all female newborns in UKM Medical Centre will be subjected for G6PD activity measurement. We also received cord blood samples from other hospitals. From our recent study on G6PD stability in stored EDTA tube, we found that the maximum storage time was within 3 days if the samples stored at 2 – 8°C. Thus we had no problems in helping out analysed samples from other hospitals included those from Sabah and Sarawak. We also conducted a molecular analysis on our newborns with G6PD deficient. Molecular mutations were detected in 59.4% (85/143) of G6PD-deficient neonates. The mutations detected were Viangchan, Mahidol, Kaiping, Mediterranean and Canton.

THURSDAY 3rd DECEMBER 2015

11.00 – 12.30
Room D

S22 - FOOD SECURITY: THAI RICE 2015

Chairpersons :

Dumrongkiet Arthan

Amornrat Aroonual

Invited Speakers :

1 Pitipong Thobunluepop
“Global impact: Climate change and food productivity”
(Abstract not available)

2 Apichart Pongsrihadulchai
“Drought in Thailand: In-season rice field”

3 Apichart Vanavichit
“Drought and flood tolerant rice: Impact on world food supply”
(Abstract not available)

DROUGHT IN THAILAND : IN-SEASON RICE FIELD

Apichart Pongsrihadulchai

Thailand Organic Agriculture Foundation (TOAF)

The objectives of the presentation is to evaluate the impact of the drought on the current rice production in Thailand. The relative importance of rice to the national economy and national food security as well as definition and dimensions of food security as adopted by FAO will be described. The historic data on the level of water in major dams in Chaophya basin that are the major sources of water supply for rice producing in the central plane, the rice bowl of the county, are also included in the presentation. ✻

THURSDAY 3rd DECEMBER 2015

11.00 – 12.30
Room E

S23 - SUSTAINABLE DISEASE CONTROL IN THE MIGRANT POPULATION IN THAILAND

(Sponsored by Ministry of Public Health, Thailand (MOPH))

Moderator :

Wichai Satimai

Speakers :

1 Representative for WHO, Thailand

"The global perspective and related resolution of WHA in relation to disease control for migrants and how to sustain disease control activity among migrants"

(Abstract not available)

2 Chawetsan Namwat

"Prevention and control of tuberculosis in migrants"

(Abstract not available)

3 Monaiya Pruedthiphap

"Experience on disease control among migrants : Viewpoint from working in the field"

(Abstract not available)

4 Promboon Panitchapakdi

"NGO and their experience on disease control among migrants"

(Abstract not available)

THURSDAY 3rd DECEMBER 2015

12.30 - 13.15
Room A

LUNCH SEMINAR: Presentation of the new WHO Global Technical Strategy for Malaria, the accompanying Roll Back Malaria Partnership framework for investment and action 2016-2030, and the Asia Pacific's 2030 elimination plan

Chairperson :

Jetsumon Prachumsri

Sponsored by APMEN, APLMA and The Roll Back Malaria Partnership

Speakers :

Pru Smith
Roll Back Malaria Partnership

Benjamin Rolfe
Asia Pacific Leaders' Malaria Alliance

Maxine Whittaker
Asia Pacific Malaria Elimination Network

WHO represeantive
World Health Organization

PRESENTATION OF THE NEW WHO GLOBAL TECHNICAL STRATEGY FOR MALARIA, THE ACCOMPANYING ROLL BACK MALARIA PARTNERSHIP FRAMEWORK FOR INVESTMENT AND ACTION 2016-2030, AND THE ASIA PACIFIC'S 2030 ELIMINATION PLAN

RBM Ms. Pru Smith,
WHO (TBD),
APLMA Dr. Benjamin Rolfe,
APMEN Professor Maxine Whittaker

The new World Health Assembly endorsed *Global Technical Strategy for Malaria 2016-2030* and the Roll Back Malaria Partnership's *Action and Investment to defeat Malaria 2016-2030 (AIM) - for a malaria-free world* will be presented to regional malaria advocates and technical experts at the Joint International Tropical Medicine Meeting 2015 in Bangkok, Thailand.

Progress in the fight against malaria since 2000 has resulted in a 58% reduction in malaria mortality - with more than 6.2 million malaria deaths averted between 2001- 2015. However, malaria remains a major cause and consequence of poverty and inequity worldwide. It impedes economic development, reduces the productivity of businesses, and absorbs the capacity of national systems to respond effectively to health security threats. On the release of this comprehensive new vision, the United Nations Secretary-General, Ban-Ki-Moon noted: *"Reaching our 2030 global malaria goals will not only save millions of lives, it will reduce poverty and create healthier, more equitable societies. Ensuring the continued reduction and elimination of malaria will generate benefits for entire communities, businesses, agriculture, health systems and households."*

The result of worldwide expert consultation with regions, countries and affected communities, the complementary *Global Technical Strategy for Malaria* and AIM documents share the 2016-2030 timeline of the UN SDGs and provide milestones to measure progress. Together, the documents lay out the technical strategies required to continue driving down the burden of malaria, while charting the investment and collective actions needed to reach the 2030 malaria goals of reducing global malaria case incidence and deaths by 90% - compared to 2015 - and eliminating the disease in an additional 35 countries.

Comments on the implications of these two documents for the Asia Pacific Region in particular will be provided by the Asia Pacific Leaders malaria alliance (APLMA) and the Asia Pacific Malaria Elimination network (APMEN).

Acceleration toward malaria elimination will require increased financing by the international donor community, as well as increased domestic financing by affected countries. *"Investing to achieve the new 2030 malaria goals will avert nearly 3 billion malaria cases and save over 10 million lives. If we are able to reach these targets, the world stands to generate US $4 trillion of additional economic output across the 2016-2030 timeframe,"* said Dr. Fatoumata Nafo-Traoré, Executive Director of the Roll Back Malaria Partnership. *"Now, more than ever, we must re-focus our efforts and re-commit our budgets so we can continue saving lives and unlock economic potential in communities around the world."*

At a cost of US $5-8 per case averted, malaria has continually proven to be one of the most cost-effective investments in public health, with relatively low investments yielding high results even beyond the health sector, and experts estimate that the return will only continue growing as countries begin focusing on elimination targets. New analysis in AIM reveals that the global return on investment of achieving the 2030 malaria goals is 40:1. This reinforces the evidence that continued efforts to reduce the burden of malaria have the potential to stimulate transformative and inclusive growth, and give an entire generation given the chance to live healthy lives and grow into strong, contributing members of society.

THURSDAY 3rd DECEMBER 2015

14.00 – 15.30
Room A

S24 - CLINICAL TROPICAL MEDICINE: NEVER SAY 'NEVER' AGAIN - INTERACTIVE CASE DISCUSSION

Chairperson :

Yupaporn Wattanagoon

Invited Speakers :

1 Wirongrong Chierakul
Department of Clinical Tropical Medicine, Mahidol University, Thailand

2 Jittima Dhitavat
Department of Clinical Tropical Medicine, Mahidol University, Thailand

3 Chatporn Kittitrakul
Department of Clinical Tropical Medicine, Mahidol University, Thailand

4 Kittiyod Poovorawan
Department of Clinical Tropical Medicine, Mahidol University, Thailand

THURSDAY 3rd DECEMBER 2015

14.00 – 15.30
Room B

S25 - GLOBAL HEATH RESEARCH AND TRAINING IN TROPICAL INFECTIOUS DISEASES

Chairperson :

Vivek R. Nerurkar

Invited Speakers :

1 Vivek R. Nerurkar
"Global heath research and training in tropical infectious diseases"

2 Pornsawan Leaungwutiwong
"Tropical infectious disease research and training in Thailand for students and postdocs from non-endemic countries"

3 Herawati Sudoyo
"Laboratory capacity building on emerging viruses"

4 Petra Emmerich-Paloh
"Training procedures and seminars on bio-safety and bio-security when dealing with highly pathogenic infectious viruses (CCHFV and EbolaV) where no BSL4 Lab is available."

5 Nittaya Phanuphak
"Global heath research and training in tropical infectious diseases: HIV and HPV research in Thailand"

GLOBAL HEATH RESEARCH AND TRAINING IN TROPICAL INFECTIOUS DISEASES

Vivek R. Nerurkar

John A. Burns School of Medicine, University of Hawaii at Manoa, Hawaii

The Global Heath Research and Training in Tropical Infectious Diseases workshop will focus on opportunities for training, mentoring and capacity building to combat global infectious diseases threat, specifically in the Asia-Pacific. Dr. Vivek R. Nerurkar who is the PI and mentor for multiple global health related training grants from the US NIH Fogarty International Center (FIC) the Northern Pacific Global Health (NPGH) Fellows program and the Minority Health International Research Training (MHIRT) program will be joined by global infectious diseases trainers and mentors from Thailand, Indonesia, Germany, United Kingdom and United States to introduce global infectious diseases training and mentoring opportunities. Each of these training programs provide high school, undergraduate, medical and graduate students (US and non-US citizens) as well as post-doctoral fellows opportunities to conduct short term (2 months or 11 months) training at a number of international sites, including Thailand and Cameroon. Current research projects are in the fields of infectious tropical diseases, engineering and public health. The goal of these programs is to train and mentor scholars and fellows to conduct, i) global health infectious diseases research and ii) integrate and enhance communication between global health partners to reduce disease burden. Opportunities for Thailand-based students and post-docs include conducting laboratory- and field-based epidemiological and translational research in infectious diseases. Dr. Nerurkar will discuss his role as PI on these specific global health training grants, the current status of Thailand-based scholars and fellows, and discuss the future direction and opportunities for student and mentor participation.

TROPICAL INFECTIOUS DISEASE RESEARCH AND TRAINING IN THAILAND FOR STUDENTS AND POSTDOCS FROM NON-ENDEMIC COUNTRIES

Pornsawan Leaungwutiwong, [1]
Narin Thippornchai, [1]
James F Kelly, [1,2]
Vivek R. Nerurkar [1,2]

[1] Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand.
[2] Department of Tropical Medicine, Medical Microbiology and Pharmacology, University of Hawaii, John A. Burns School of Medicine, Hawaii, USA.

Emerging infectious diseases are a reoccurring threat to populations globally, especially in endemic countries throughout the tropics. In endemic and non-endemic countries alike, training a new generation of students and postdocs the necessary laboratory skills to prevent emerging diseases threats and contribute to the understanding of emerging infectious diseases are high priorities.

A number of university faculty members throughout Thailand, together with the support of their Head Departments and Faculty Deans have embraced the tenets of international collaboration and training for students and postdocs to gain experience in emerging infectious diseases research in an endemic setting. As the lead in-county coordinator for the Minority Health International Research Training (MHIRT) Program and Mentor for the Northern Pacific Global Health (NPGH) Fellowship Program, Dr. Pornsawan Leaungwutiwong of the Department of Microbiology and Immunology, Faculty of Tropical Medicine (FTM), Mahidol University has worked closely with leadership from the Department of Tropical Medicine, Medical Microbiology and Pharmacology, John A. Burns School of Medicine, University of Hawaii at Manoa (UHM), USA to coordinate and implement short-term (8-week) and long-term (1-2 yr) infectious disease research training programs for undergraduate, graduate students and postdocs.

Dr. Pornsawan has assisted 13 undergraduate MHIRT students receive training on a variety of emerging infectious diseases. In her lab, she has trained 5 students on arbovirus discovery, enteric viruses and dengue virus research and hepatitis E virus screening. In addition to gaining skills on scientific methodologies and hypothesis development, students underwent rigorous competency-level laboratory training, including mosquito dissection, RNA isolation, flow cytometry, PCR assay, and other skills. Also, FTM has contributed to the professional growth of two NPGH fellows. Dr. Pornsawan will discuss findings of the projects implemented under these MHIRT and NPGH programs and their implications for the public health and emerging infectious disease patterns in Thailand.

LABORATORY CAPACITY BUILDING ON EMERGING VIRUSES

Herawati Sudoyo

Eijkman Institute for Molecular Biology, Indonesia

The ongoing occurrence of emerging infectious diseases globally highlights the great need for laboratory training and capacity building in the region including Indonesia. Building laboratory capabilities and capacity is paramount for surveillance of endemic and emerging viruses as well as outbreak response. Emerging viruses has become the greatest disease threats as evidenced by Ebola, MERS, SARS, and Avian Influenza. In developing countries, viral identification capability is mainly limited to a few reference laboratories. The laboratory training is particularly important for these countries where a range of pathogenic agents are endemic and many yet to be recognized are presumed.

The Emerging Laboratory of Eijkman Institute for Molecular Biology (EVRU) has set up local and international training and workshops within the past 2 years for participants including researchers, laboratorians, clinicians and undergraduate/graduate students to increase knowledge of virological assays. The workshops involve intensive discussions and practical laboratory training on viral diagnostic techniques. Safety is the hallmark of laboratory operations and it is necessary to have a robust safety program. Additional training on biosafety and biosecurity is added to insure safe and quality sample handling, particularly for potential high consequence pathogens. We have also provided opportunities for the local technical staff to receive training in reference laboratories in the region as part of our capacity building initiatives.

The discussion will include an overview of the important viral AFI etiologies in the region and approach to training based on the country's need and networking. The preliminary discussions should establish a common foundation on how to best prepare for the future workshops. This will also form the foundation for more networking and research collaborations in the region. The goal would be to partner with relevant institutions in the region to initiate capacity development with shared benefits. ✻

Keywords: capacity building, virus, workshop, networking

TRAINING PROCEDURES AND SEMINARS ON BIO-SAFETY AND BIO-SECURITY WHEN DEALING WITH HIGHLY PATHOGENIC INFECTIOUS VIRUSES (CCHFV AND EBOLAV) WHERE NO BSL4 LAB IS AVAILABLE

Petra Emmerich- Paloh

Bernhard Nocht Institute for Tropical Medicine, German Reference Center for Imported Parasitic and Viral Infections, Germany

CCHF- and Ebola viruses are risk 4 viruses. Handling these viruses and conducting clinical diagnostics on them poses a major challenge for clinical and technical staff. The project "Diagnostics and Surveillance of Crimean-Congo Hemorrhagic Fever (CCHF) in Kosovo", which is financed by AA Germany, teaches doctors, laboratory staff, vets and students how to: deal with infected patients transport samples from hospital to laboratory deactivate human samples containing CCHFV conduct clinical diagnostics collect virus-carrying ticks and build up a forensic database use personal protective equipment (PPE) The deactivation of suspected Ebola and other Risk 4 samples is carried out in glove boxes in BSL3 labs at the BNI in Germany. Regular training seminars are arranged for local staff as well as for all those who work in mobile laboratories in Africa.

Keywords: Bio-safety, training, risk 4 virus

GLOBAL HEATH RESEARCH AND TRAINING IN TROPICAL INFECTIOUS DISEASES: HIV AND HPV RESEARCH IN THAILAND

Nittaya Phanuphak

Prevention Department, Thai Red Cross AIDS Research Centre, Thailand

The Thai Red Cross AIDS Research Centre (TRCARC) is an organization committed to improving access to HIV/AIDS prevention and care in Thailand and the Southeast Asia region through quality research and services on the basis of humanity. TRCARC has worked collaboratively with research, community and government organizations, both nationally and internationally, to generate research data relevant to the region and to actively translate research findings into practices.

Through collaboration with the University of Hawaii, TRCARC has hosted five NPGH and three MHIRT students over the past three years. Main research topics are those mutually interesting both for the students and TRCARC. These include HIV prevention among Thai men who have sex with men (MSM) and transgender women (TGW), which are currently key affected populations in Thailand, and human papillomavirus (HPV) and other sexual health concerns among MSM and TGW. Ongoing studies are looking at factors affecting post-exposure prophylaxis (PEP) uptake among MSM, correlation between anal HPV clearance and HIV acquisition among MSM and TGW, co-occurrence of HIV, hepatitis C and syphilis among MSM and TGW, and development of culturally relevant health records for TGW.

TRCARC has seen research studies conducted by NPGH and MHIRT students a very productive way of establishing collaborative works between Thai and US organizations. Students have developed skills to conduct high quality research studies within specific timeline while they also have experienced country-specific challenges related to regulatory policies and cultures in workplace and among research participants. These are valuable skills for those who will pursue their global health career.

THURSDAY 3rd DECEMBER 2015

14.00 – 15.30
Room C

S26 - DENGUE VACCINE: GLOBAL NEED AND CHALLENGES (*Sponsored by Sanofi-Pasteur*)

Chairperson :

Tawee Chotpitayasunondh

Speakers :

1 Pratap Singhasivanon
"Epidemiology and burden of dengue"
(Abstract not available)

2 Punnee Pitisuttithum
"Latest update on Sanofi vaccine candidate clinical trials"
(Abstract not available)

3 Usa Thisyakorn
"Public health value of dengue vaccine"

PUBLIC HEALTH VALUE OF DENGUE VACCINE

Usa Thisyakorn

Chulalongkorn University, Bangkok, Thailand

Dengue is the most rapidly spreading vector-borne disease impacting nearly half of the world's population, in all age groups and segments in society. It causes an estimated 390 million cases with 96 million symptomatic infections and 2 million hospitalizations each year. A major economic burden, estimated at US$6 billion annually, $2 billion in Southeast Asia. Despite these striking numbers, dengue remains a major neglected disease with most countries needing strengthened public health policy and response to control disease, particularly long term inter-epidemic strategies. Alongside sustainable vector control efforts, community mobilization and civil society engagement, an evidence based and well-implemented dengue vaccine program should contribute to the achievement of the WHO targets of reducing dengue mortality and morbidity by at least 50% and 25% respectively by 20201.

Pivotal phase III results demonstrated overall efficacy against symptomatic dengue (56.5% and 60.8%) in Asia and Latin America respectively, with efficacy against severe dengue (80% and 95%) and dengue hospitalization (67.2% and 80.3%) during 25 months follow-up. Mathematical modeling predicts that vaccinating routine and catch-up cohorts can rapidly reduce dengue burden, transmission and outbreaks. The Sanofi Pasteur dengue vaccine is a major advance in the armamentarium to combat dengue disease and would complement existing Dengue Integrated Management. Post-licensure evaluation of vaccination programs with active surveillance, assessment of vaccine effectiveness, and pharmacovigilance are crucial. Dengue should be considered as a pan-Asian and global priority and countries should redefine their road maps to align with WHO recommendations 2 demonstrate political will and commitment to control dengue.

THURSDAY 3rd DECEMBER 2015

14.00 – 15.30
Room D

S27 - FREE PAPER: VECTOR BORNE DISEASES II

Chairpersons :

Srisin Khusmith

Porntip Petmitr

Speakers :

1 Rhea Longley
"Asymptomatic *Plasmodium vivax* infections induce boosting of IGG responses to seven different proteins in a low-transmission region of Western Thailand"

2 Daniel Parker
"Complex spatial patterns in Southeast Asian falciparum malaria transmission mean that reactive case detection is unlikely to halt transmission"

3 Aung Pyae Phyo
"The declining efficacy of mefloquine-artesunate on the Thailand-Myanmar border and the relative roles of resistance genetic markers: A longitudinal study"

4 Toshio Hattori
"Elevated plasma levels of galectin-9 reflect disease severity in acute malaria infection"

5 Alexis Kaushansky
"Host-based prophylaxis targets dividing and non-dividing liver stage malaria parasites"

ASYMPTOMATIC *PLASMODIUM VIVAX* INFECTIONS INDUCE BOOSTING OF IGG RESPONSES TO SEVEN DIFFERENT PROTEINS IN A LOW-TRANSMISSION REGION OF WESTERN THAILAND

Rhea Longley[1], Camila France[2], Chalermpon Kumpitak[3], Patiwat Sa-angchai[4], Connie SN Li Wai Suen[5], Jakub Gruszczyk[6], Wai-Hong Tham[7], Jessica B Hostetler[8], Sumana Sherma[8], Rick M Fairhurst[9], Julian C Rayner[8], Gavin Wright[8], Anjali Yadava[10], Christopher L King[11], Wang Nguitragool[12], Jetsumon Sattabongkot[13], Ivo Mueller[5]

[1] *Walter & Eliza Hall Institute of Medical Research & Mahidol Vivax Research Unit,*
[2] *Walter & Eliza Hall Insitute of Medical Research,*
[3] *Mahidol Vivax Research Unit, Faculty of Tropical Medicine, Mahidol University,*
[4] *Department of Tropical Hygiene, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand,*
[5] *Division of Population Health and Immunity, Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia,*
[6] *Division of Infection and Immunity, Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia,*
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[8] *Malaria Programme, Wellcome Trust Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridge, UK,*
[9] *Laboratory of Malaria and Vector Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland, USA,*
[10] *Malaria Vaccine Branch, United States Military Malaria Research Program, Walter Reed Army Institute of Research, Silver Spring, Maryland, USA,*
[11] *Case Western Reserve University, Center for Global Health and Diseases, Cleveland, Ohio, USA,*
[12] *Department of Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand,*
[13] *Mahidol Vivax Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand*

Plasmodium vivax has now become the dominant species causing malaria within Thailand, and the country is aiming to eliminate all malaria species by the year 2024. A better understanding of immune responses to *P. vivax* in Thailand will be pivotal for developing new strategies for elimination, such as improved surveillance methods and vaccine development. We aimed to characterize IgG responses to seven unique *P. vivax* proteins in a village in Western Thailand, utilizing plasma samples from a cross-sectional survey conducted in 2012. Six of these proteins are thought to be involved in reticulocyte binding or invasion (ARP, HPZZ, GAMA, Pv41, Pv12 and the RBP family), and the seventh, CSP, is a leading pre-erythrocytic vaccine candidate. Overall, we found the highest relative antibody responses to the *P. vivax* proteins ARP and RBP1a. Significantly greater IgG responses were associated with individuals positive for *P. vivax* (as determined by blood-stage qPCR), despite all infected individuals being asymptomatic. Higher IgG levels were also associated with adults (more than 18 years of age) rather than children. For half of the proteins, higher IgG levels were associated with individuals living closer to the Myanmar border and further away from health services. In conclusion, all seven *P. vivax* proteins were recognized in individuals from a low-endemicity region of Western Thailand. IgG responses were of a greater relative magnitude in adults and malaria-infected volunteers, but even young children and currently uninfected volunteers were able to induce a detectable response. Future research will determine the relevance of these IgG responses as markers of exposure or markers of clinical protection.

Keywords: *Plasmodium vivax*; antibodies; malaria; immunity

COMPLEX SPATIAL PATTERNS IN SOUTHEAST ASIAN FALCIPARUM MALARIA TRANSMISSION MEAN THAT REACTIVE CASE DETECTION IS UNLIKELY TO HALT TRANSMISSION

Daniel Parker, Jordi Landier,
J. Wiladpaingern,
L. Kereecharoen, L. Maelankiri,
May Myo Thwin, Francois Nosten

Shoklo Malaria Research Unit, Mahidol Oxford Tropical Medicine Research Unit

Reactive case detection is a malaria screening approach in which the household members and neighbors of confirmed malaria patients are preemptively screened as an attempt to halt further transmission. Different spatial scales have been proposed for screening, ranging from immediate house members up to a 1 kilometer radius around a house (mostly based on studies from Africa). In this research we took retrospective data from a study village along the Myanmar-Thailand border in order to look at the potential effects of reactive screening and treatment on subsequent malaria infections. The study includes a demographic surveillance system, spatial coordinates for each house, and a malaria post to treat and record malaria cases. We created maps of all symptomatic falciparum cases for each month during the study period and enumerated the cases that would have been detected and treated in a given month, given different spatial scales of screening and treatment in the previous month. At the house level we would have reactively detected around 20% of all cases that occurred in the following month. At a radius of 80 meters around the house we would have reactively detected around half of all cases and would have tested approximately half of the total village population. At 250 meters radius we would have detected almost 90% of all cases and tested about 90% of the total village population. We take these results to indicate that screening and treatment at scales smaller than a typical village are unlikely to halt further transmission in this area. Furthermore, this pattern may indicate that some transmission is occurring outside of the village, complicating the spatial patterns of infectious disease that we may otherwise expect to find within a village.

Keywords: spatial ecology, reactive case detection

THE DECLINING EFFICACY OF MEFLOQUINE-ARTESUNATE ON THE THAILAND-MYANMAR BORDER AND THE RELATIVE ROLES OF RESISTANCE GENETIC MARKERS: A LONGITUDINAL STUDY

Aung Pyae Phyo[1],
Francois Nosten[2],
Nicholas White[2,3]

[1] Shoklo Malaria Research Unit, Thailand
[2] Mahidol Oxford Research Unit, Mahidol University, Bangkok, Thailand
[3] Centre for Tropical Medicine, Nuffield Department of Medicine, University of Oxford, Oxford

Background Mefloquine-artesunate treatment of *Plasmodium falciparum* malaria in the displaced population on the Thailand-Myanmar border led to a dramatic decline in transmission. Efficacy has fallen substantially in recent years, but the relative contribution of resistance to the individual drugs is unknown.

Methods Patients with uncomplicated *P. falciparum* malaria receiving supervised mefloquine-artesunate treatment were followed for 42 days. Molecular testing was undertaken to determine baseline *pfmdr1* copy number, *K13* genotype and discriminate recrudescences.

Findings 1005 patients were enrolled from 2003-2013, during which PCR-adjusted cure rate declined from 100% to 81·1%. The proportion of isolates with multiple *pfmdr1* copies rose from 32·4% to 64·7% while infections with *K13* mutation increased from 6·7% to 83·4%. *K13* propeller mutations predominated after 2009. The PCR-adjusted failure rate of infections with both amplified *pfmdr1* and *K13* propeller mutation was 42·2% and the adjusted hazard ratio was 14·05 ($p<0·001$). Even without *pfmdr1* amplification, *K13* propeller mutation was a strong risk factor for recrudescence (AHR=5·73, p=0·009). The combined population attributable fraction of recrudescence associated with *K13* mutation and *pfmdr1* amplification was 82%.

Interpretation *Pfmdr1* amplification and *K13* mutation act in combination to reduce the efficacy of mefloquine-artesunate but the rise in *K13* propeller mutations was the decisive factor in the fall in efficacy to unacceptable levels. These findings confirm the strong link between artemisinin resistance and ACT failure, and demonstrate the relatively short timeframe in which ACT efficacy can be lost once artemisinin resistance is present.

Funding Wellcome Trust–Mahidol University–Oxford Tropical Medicine Research Programme

Keywords: *Plasmodium falciparum* malaria, mefloquine-artesunate, *Pfmdr1*, *K13* mutation, drug resistance

ELEVATED PLASMA LEVELS OF GALECTIN-9 REFLECT DISEASE SEVERITY IN ACUTE MALARIA INFECTION

Toshio Hattori[1], Haorile Chagan-Yasutan[1], Bindongo PP Dembele[2], Toshiro Niki [3], Shigeyuki Kano[4], Srivicha Krudsood[5]

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[2] *Division of Emerging Infectious Diseases, Department of Internal Medicine, Graduate School of Medicine, Tohoku University, Sendai, Japan*
[3] *Department of Immunology and Immunopathology, Kagawa University, Takamatsu, Japan*
[4] *Department of Tropical Medicine and Malaria, Research Institute, National Center for Global Health and Medicine, Tokyo, Japan*
[5] *Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand*

Background and aim: Galectin-9 (Gal-9), a β-galactoside-binding lectin, is a glycoprotein with multiple immunoregulatory and inflammatory properties. Gal-9 is produced by immune cells such as kupffer cells and T cells. Here we examined the kinetics and activities of Gal-9 in malaria infection and its association with clinical status. Method: Plasma samples and clinical parameters were obtained from 50 acute malaria cases from Thailand at 3 time points (Day0, Day7 and Day28). Total 38 kinds of cytokine/chemokines (sCD40L, VEGF, TNF-β, TNF-α, TGF-α, MIP-1β, MIP-1α, MDC (CCL22), MCP-3, MCP-1, IP-10, IL-17, IL-15, IL-13, IL-12 (p70), IL-12 (p40), IL-10, IL-9, IL-8, IL-7, IL-6, IL-5, IL-4, IL-3, IL-2, IL-1ra, IL-1β, IL-1α, IFN-γ, IFN-α2, GRO, GM-CSF, G-CSF, Fractalkine, Flt-3 ligand, FGF-2, Eotaxin, EGF) were measured using bioplex assay (EMD Millipore, MA, USA). The levels of Gal-9 were determined by ELISA assay (Galpharma Co. Ltd, Takamatsu, Japan). Results: Gal-9 was higher at Day0 compared to Day7 and Day28 ($p<0.0001$). It was significantly associated with pro- and ant-inflammatory cytokines IFN-γ ($r=0.4235$), IL-1α ($r=0.3346$), TNF-α ($r=0.62$), IFN-α2 ($r=0.33$), IL-6 ($r=0.38$), IL-1RA ($r=0.41$) and IL-10 ($r=0.64$). With clinical laboratory findings, Gal-9 was significantly correlated with SGOT ($r=0.56$), creatinine ($r=0.5$), total bilirubin ($r=0.37$), sodium ($r=-0.47$) and platelets ($r=-0.46$). Those correlations were observed at day0 and the correlations were disappeared at day28. Gal-9 is sensitive to dehydration as revealed by its elevation in patients with BUN/creatinine^{3}20. Conclusion: These results revealed that the plasma levels of Gal-9 track the inflammation status during malaria infection and could be used as severity marker in acute phase of malaria infection.

Keywords: malaria, galectin 9, plasma, marker

HOST-BASED PROPHYLAXIS TARGETS DIVIDING AND NON-DIVIDING LIVER STAGE MALARIA PARASITE

Alexis Kaushansky[1],
Alyse Douglass[1], Heather Kain[1],
Niwat Kangwanrangsan[2],
Marian Abdullahi[1],
Nadia Arang[1], Stefan Kappe[1],
Sebastian Mikolajczak[1],
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Eliminating malaria parasites during the asymptomatic but obligate liver stages (LSs) of infection would stop disease and subsequent transmission. Unfortunately, only a single licensed drug that targets malaria parasites prophylactically and for radical cure, Primaquine, is available. Targeting host proteins might significantly expand the repertoire of drugs against malaria. Here, we demonstrate that both Bcl-2 inhibitors and P53 agonists dramatically reduce liver stages burden in a mouse malaria model in vitro and in vivo by altering the activity of key hepatocyte factors on which the parasite relies. Bcl-2 inhibitors act primarily by inducing apoptosis in infected hepatocytes, whereas P53 agonists eliminate parasites in an apoptosis-independent fashion. In combination, Bcl-2 inhibitors and P53 agonists act synergistically to delay, and in some cases completely prevent, the onset of blood stage disease. Both families of drugs are highly effective at doses that do not cause substantial hepatocyte cell death in vitro or liver damage in vivo. P53 agonists and Bcl-2 inhibitors were also effective when administered to humanized mice infected with *Plasmodium falciparum*. Preliminary data suggests that P53 agonists and Bcl-2 inhibitors were also effective against both developing schizonts and hypnozoites when administered to humanized mice infected with *Plasmodium vivax*. Together, our data demonstrate that host-based prophylaxis could be developed into an effective intervention strategy that eliminates LS parasites before the onset of clinical disease and thus opens a new avenue to prevent and cure malaria.

Keywords: liver, malaria, P53 BCL-2

THURSDAY 3rd DECEMBER 2015

14.00 – 15.30
Room E

S28 - A WORLD FREE OF MALARIA BY 2030: WHAT WILL IT TAKE?

Chairperson :

Bruce A Wilcox

Speakers :

1 Bruce A Wilcox
Global Health Asia Office, Faculty of Public Health, Mahidol University, Thailand

2 Gopinath Deyer
WR Office, Thailand

3 Sirinate Piyajitpirat
Cambodia-Thailand collaboration on malaria, dengue and other mosquito-borne disease control under the initiative of HRH Princess Maha Chakri Sirindhorn, Thailand

4 Valaikanya Plasai
Independent Consultant for Public Health, Thailand

A WORLD FREE OF MALARIA BY 2030: WHAT WILL IT TAKE?

D. Gopinath[1], BA Wilcox [2],
S. Piyajitpirat[3], and V. Plasai[4]

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The sixty-eighth World Health Assembly, in May 2015, endorsed the WHO's proposal to rid the world of suffering due to malaria by 2030. Worldwide, the endorsement was met with a mixed reception. Reservations about the prospects of achieving this laudable goal are understandable. The well-known failure of the 1955 to 1963 WHO Global Malaria Eradication Programme (GMEP), and heavily funded by the USAID and its predecessor, still looms large. The variable success since then in achieving sustainable control among regional and local initiatives reinforces concerns about setting overly-ambitious global, let alone regional, targets in the absence of critically analysis of previous failure (and successes). The international community seems to agree that we can learn from history.

While pushing for "a world free of malaria by 2030", the 68th WHA cautioned the global malaria elimination efforts to focus on sustainable incremental local gains. It emphasized the need to recognize the social, cultural, and ecological context of each locality, as well as factoring in the long-term political and financial commitments required. Thus, it appears that the Assembly is recommending that malaria elimination efforts to go beyond the predominantly biomedical approach that has long driven the framing, planning and execution of malaria control campaigns. This echoes concerns long expressed by many malariologists, parasitologists, ecologists, social scientists and others about the shortcomings of past strategies.

We introduce an approach to achieving a slow but firm progress towards malaria elimination that builds on the strengths of the biomedical approach yet is framed using the well-established social-ecological systems framework and its adaptive management methodology for planning and executing a malaria elimination. The approach considers malaria illnesses as a systemic challenge within the social and ecological contexts that necessitates strong participatory, interdisciplinary and equitability components as essential to a disease control programme. As case example, we describe a community life competence project being carried out in Ratnakiri and Mondulkiri provinces of Cambodia. The community life competence is a process to catalyze local responses or the set of actions that individuals and communities take by themselves to address their community challenges (malaria included), using first of all the resources within their reach. Service providers can then enhance these local responses. Finally, we describe a few critical skills for the effective implementation of WHO elimination strategies for the Greater Mekong Sub-region, particularly the subnational staff –being front line with the elimination efforts, but have long been left out in non-core technical capacity building plans. The new cadre of professionals, will be able to empower the community by building on local traditions, knowledge and culture, drawing conflict resolution, consensus building, fund raising, private sector engagement, non-health stakeholder engagement, political advocacy skills, just to name a few. In conclusion, a human resource development programme that aims at improving human performance which goes beyond training is necessary.

THURSDAY 3rd DECEMBER 2015

16.00 – 17.30
Room A

S29 - FREE PAPER TROPICAL MEDICINE

Chairpersons :


Jaranit Kaewkungwal


Suparat Phuanukoonnon

Speakers :


1 Sara E. Canavati
"Efficacy and safety of pyronaridine-artesunate for the treatment of *Plasmodium falciparum* malaria in western Cambodia in 2014"


2 Wike Astrid Cahayani
"Increased CD11b and hypoxia-inducible factors-1alpha (HIF-1α) expressions in the lung tissue and surfactant protein-D (SP-D) levels in serum are related with acute lung injury in severe malaria of C57BL/6 mice"

3 Frilasita Yudhaputri
"The discovery of Zika Virus in Jambi, Indonesia"


4 Neelima Mishra
"Tracking artemisinin resistance in falciparum malaria in north eastern regions of India"

5 Tawatchai Apidechkul
"Prevalence and risk factors of intestinal parasitic infections among hill tribe schoolchildren, Northern Thailand"

6 Thae Maung Maung
"Private drug outlets survey before artemisinin resistance containment in Myanmar: Availability and dispensing practices of anti-malaria drugs"

EFFICACY AND SAFETY OF PYRONARIDINE-ARTESUNATE FOR THE TREATMENT OF PLASMODIUM *FALCIPARUM MALARIA* IN WESTERN CAMBODIA IN 2014

Sara E Canavati[1], Rithea Leang[2], Nimol Khim[3], Saorin Kim[3], Denis Mey Bouth[4], Lasse Vestergaard[5], Pisal Heng[6], Bunkea Tol[6], Rekol Huy[6], Arjen M Dondorp[7], Didier Menard[3], Pascal Ringwald[8]

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Background. Pyronaridine-artesunate is an artemisinin-based combination therapy approved for *Plasmodium falciparum* and *P. vivax* malaria. Pyronaridine-artesunate efficacy in uncomplicated *P. falciparum* malaria was assessed in an area of artemisinin resistance in western Cambodia.

Methods. This non-randomized, single arm, observational study was conducted between July 2014 and March 2015 in Pailin, Pursat and Battambang provinces. Eligible patients were adults or children ≥20 kg body weight, with microscopically confirmed asexual *P. falciparum*infection and fever within the previous 24 h. Patients received pyronaridine-artesunate once daily for 3 days, dosed by body weight. The primary outcome was day-42 adequate clinical and parasitiological response (ACPR), adjusted to exclude reinfection (PCR-adjusted), estimated using Kaplan–Meier analysis.

Results. 123 patients were enrolled (60 Pursat, 55 Pailin, 8 Battambang). Kaplan–Meier estimates for day-42 PCR-adjusted ACPR were 89.8% (95%CI 78.8, 95.3) for Pursat and 84.0% (95%CI 70.6, 91.7) for Pailin (log-rank test p=0.353). Day-28 PCR-adjusted ACPR was 93.2% (95%CI 82.9, 97.4) and 88.1% (95%CI 75.3, 94.5), respectively. The proportion of patients achieving day-3 parasite clearance was significantly lower in Pailin (56.4% [95%CI 43.9, 69.6]) versus Pursat (86.7% [95%CI 76.8, 93.8]; p=0.0019). Fever clearance was also extended at Pailin versus Pursat (p<0.0001). Most patients (95.9% [116/121]) had the *P. falciparum kelch13* C580Y polymorphism. Pyronaridine-artesunate was well tolerated; safety data were consistent with previous reports.

Conclusions. Pyronaridine-artesunate did not meet efficacy criteria for the first-line treatment of *P. falciparum* malaria in western Cambodia, despite high efficacy in other countries in Asia and Africa.

Keywords: Pyronaridine-artesunate, *Plasmodium falciparum*, artemisinin, Cambodia, drug resistance

INCREASED CD11B AND HYPOXIA-INDUCIBLE FACTORS-1ALPHA (HIF-1α) EXPRESSIONS IN THE LUNG TISSUE AND SURFACTANT PROTEIN-D (SP-D) LEVELS IN SERUM ARE RELATED WITH ACUTE LUNG INJURY IN SEVERE MALARIA OF C57BL/6 MICE

Background: Severe malaria is a serious infectious disease and characterized with high cases of morbidity and mortality, especially if accompanied with acute lung injury (ALI). Until now, the pathogenesis of severe malaria-associated ALI is still not fully understood. This study aimed to reveal the role of CD11b and hypoxia-inducible factors-1alpha (HIF-1α) expressions on monocytes and alveolar macrophages of lung tissue, and also the levels of serum surfactant protein-D (SP-D) in severe malaria-associated acute lung injury (ALI).

Methods: The C57BL/6 mice were divided into control group, renal malaria group (inoculated with 106 Plasmodium berghei ANKA), and cerebral malaria group (inoculated with 107 P. berghei ANKA). The expressions of CD11b and HIF-1α in lung tissue were observed by immunohistochemistry, and serum SP-D levels were measured by ELISA.

Results: The CD11b expression on pulmonary tissue of renal and cerebral malaria mice were significantly higher than control mice (P=0.002; P=0.002), as well as the HIF-1α expression on pulmonary tissue (P=0.002; P=0.002). The level of serum SP-D in renal malaria and cerebral malaria mice were significantly higher than control mice (P=0.002; P=0.002). We found a strong correlation between the expression of CD11b and HIF-1α in lung tissue (r=0.937, P=0.000), as well as between CD11b expression and serum SP-D levels (r=0.907, P=0.000) and between HIF-1α expression and serum SP-D levels (r=0.913, P=0.000).

Conclusions: Severe malaria-associated ALI increased the expression of CD11b and HIF-1α in the lung tissue and increased serum SP-D levels of C57BL/6 mice significantly.

Keywords: acute lung injury, severe malaria, CD11b, HIF-1alpha, SP-D.

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THE DISCOVERY OF ZIKA VIRUS IN JAMBI, INDONESIA

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Chairin Nisa Maroef[1],
Ungke A. Jaya[3],
Benediktus Yohan[1],
Khin Saw Myint[1],
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Background: Arthropod-borne viruses are significant causes of human disease worldwide with great impact on public health throughout Asia. Zika virus (ZIKV) is one of the arboviruses that causes human illness but for which the impact is just being evaluated. ZIKV has been causing epidemics during the past 8 years throughout the Western and South Pacific and was recently discovered in Brazil. ZIKV is transmitted by *Aedes* species mosquito and is reported to be associated with mild and self-limited infection. However, it is often misdiagnosed as dengue (DEN) because of clinical similarities and cross-reactivity. In Asia, serological evidence of ZIKV infection has been reported from Pakistan, Thailand, Malaysia, Vietnam, Indonesia, Cambodia and Philippines. Other than serological detection, molecular detection and isolation of ZIKA in Indonesia has never been reported.

Findings: We have confirmed the cause of an undifferentiated febrile illness from Jambi, Sumatera as ZIKV. Samples of 103 cases negative for DEN (collected during our DEN molecular surveillance in December 2014-April 2015) were further screened for other viruses. One sample presenting with high fever, headache, myalgia, and arthralgia, was determined to be a flavivirus using family group primers in RT-PCR and was later identified as ZIKV by sequencing. In addition, virus isolation revealed the growth of ZIKV as evidenced by cytopathic effect in Vero cells. Whole genome sequencing using next generation sequencing is in progress.

Conclusion: Our finding confirms that ZIKV is circulating in Indonesia mimicking the symptoms of DEN and most likely contributing to a large neglected disease burden. It is essential that surveillance be implemented to evaluate and monitor the distribution ZIKV and its potential public health problems.

Keywords: Zika Virus, Indonesia, Arbovirus

TRACKING ARTEMISININ RESISTANCE IN FALCIPARUM MALARIA IN NORTH EASTERN REGIONS OF INDIA

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Background: Artemisinin resistance in *Plasmodium falciparum* has emerged in Southeast Asia and now poses a threat to malaria control and elimination in neighboring countries. Northeastern region of India is known to be the epicenter of drug resistance. Tracking artemisinin resistance is essential for evaluating the sensitivity of *P. falciparum* to artemisinins.

Methods: Between May 2013 and November 2013, 115 adults and children with acute uncomplicated falciparum malaria were enrolled in an open-label trial at 2 sites (Gomati district, Tripura state and Lunglei district, Mizoram state) of northeast India. Artesunate (4mg/kg) was given orally for 3 days, followed by standard 3-day course of ACT (artemether-lumefantrine) and primaquine (0.75 mg/kg) as per national drug policy. Peripheral blood parasite counts were measured 6-hourly and the parasite clearance half-life was determined.

Results: Majority of the subjects cleared parasite between 18-24 hours in Gomati district, Tripura and 24-30 hrs in Lunglei district, Mizoram. Median parasite clearance half-lives (PCt1/2) ranged from 3.0 hours in Lunglei to 2.9 at the Gomati. Gametocytemia at 0 hrs was observed only at Gomati district. A decreasing trend of gametocytemia was observed from 7% at day 0 to 5% at day 3 in Gomati district. The proportion of patients with slow parasite clearance half-lives (PCT1/2> 5 hrs) was 7.4% in Lunglei district whereas it was 23.4% in Gomati district. The treatment efficacy without PCR correction and with PCR correction (95% confidence interval) was found to be 96.9% and 98.2% in Lungle district, and 95.2% and 100% in Gomati district. The day 3 positivity was not observed at any study sites.

Conclusion: Artemisinin remains efficacious to *P. falciparum* at two study sites in northeastern India. Continuous surveillance and rationale treatment practices needs to be promoted to preserve the precious medicine for malaria treatment in the country.

Keywords: Artimisnin resistance, falciparum malaria

PREVALENCE AND RISK FACTORS OF INTESTINAL PARASITIC INFECTIONS AMONG HILL TRIBE SCHOOLCHILDREN, NORTHERN THAILAND

Tawatchai Apidechkul

School of Health Science, Mae fan Luang University

Objective: To study the prevalence and risk factors of intestinal parasitic infections among hill tribe schoolchildren who attended 10 border patrol police schools in 2012, Chiang Rai, Thailand.

Methods: A total of 339 subjects were recruited into the study from 2 194 children. Questionnaire was tested for validity and reliability before use. About 5 g stool specimens were collected and investigated for intestinal parasite infections by using cellophane-covered thick smear technique. Logistic regression at $\alpha = 0.05$ was used to test the associations between variables to find risk factors.

Results: There were 339 subjects of whom 51.9% were males and 66.1% were Buddhist; racially 31.2% were Akha and 30.4% were Kmong; mean age was 10.3 years old (minimum = 6, maximum = 16). The prevalence of parasitic infection was 9.7%. After controlling for age, sex, religion, parents' education levels and parents' occupations, the only factor that showed a statistically significant association with intestinal parasitic infection was the source of drinking water. The group of drinking mountain piped water had a greater risk of 8.22 times (adjusted odds ratio = 8.22, 95%; confidence interval: 1.07–63.18) compared to the drinking commercially bottled water group, while the group of drinking underground water had a greater risk of 9.83 times (adjusted odds ratio = 9.83, 95%; confidence interval: 0.93–104.12) compared to the drinking commercially bottled water group.

Conclusions: Drinking water contaminated by soil was shown to be an important risk factor for intestinal parasitic infection in hill tribe schoolchildren living in mountainous border areas in the northern part of Thailand. Safer alternative drinking water source should be provided along with health education for schools and villagers to be aware of the risk of intestinal parasites from drinking water sources such as mountain piped or underground wells. Such sources are likely to contain higher soil contents.

Keywords: Intestinal parasite infection, Prevalence, Risk factors, Schoolchildren, Hill tribe

PRIVATE DRUG OUTLETS SURVEY BEFORE ARTEMISININ RESISTANCE CONTAINMENT IN MYANMAR: AVAILABILITY AND DISPENSING PRACTICES OF ANTI-MALARIA DRUGS

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The occurrence of artemisinin resistance in Greater Mekong Sub-region due to irrational use of anti-malarial drugs is a great problem in the world. Although private drug outlets are considered as the main first contact point for malaria treatment, their knowledge and dispensing practice were still doubtful. This cross-sectional descriptive study was conducted in 120 drug outlet of 71 villages within tier 1 and 2 malaria areas in 2012 before artemisinin resistance containment project in Myanmar. Interview with structured questionnaires and observation check lists were used. About 42% of drug outlets did not have a license and 45% of drug outlets were general stores or shops. More than half of the providers did not have an appropriate training. Although the knowledge about malaria signs and symptoms was sufficient, only 16% of the respondents could correctly identify the recommended drug for uncomplicated *P. falciparum* malaria. Availability of artemisinin combination treatment (ACT) including Coartem was extremely low. Most dispended anti-malarial drugs sold were artesunate tablets, chloroquine and artemether. Irrational dispensing practices such as selling partial package (55.2%) and cocktail treatment (25%), found in 80% of drug outlets. About 20% of drug outlets sold malaria tests mainly rapid diagnostic tests (RDT) and Paracheck was mostly used. Customer demand (67%) was found as a main reason for selling anti-malarial drugs. Respondents' background education and experiences in malaria training workshops was significantly associated with correct knowledge and dispensing practices of the recommended anti-malarial drug. Intervention for private drug outlets is urgently needed for artemisinin resistance containment.

Keyword: Drug Outlet

THURSDAY 3rd DECEMBER 2015

16.00 – 17.30
Room B

S30 - IDENTIFICATION AND EVOLUTION OF HELMINTHS AND HELMINTHIASES

Chairpersons :

Akira Ito

Paron Dekumyoy

Invited Speakers :

1 Akira Ito
"Cestode zoonoses: the importance of molecular approach for identification of causative species"

2 Serge Morand
"Challenges in research on parasitic helminths: systematics, barcoding and ecology of neglected parasitic diseases"

3 Peter Odermatt
"Epidemiology and control of *Strongyloides stercoralis* in Cambodia"

CESTODE ZOONOSES: THE IMPORTANCE OF MOLECULAR APPROACH FOR IDENTIFICATION OF CAUSATIVE SPECIES

Ito, Akira[1], Yanagida, Tetsuya[2], Nakao, Minoru[1]

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Background: Cestode zoonoses including echinococcoses and cysticercosis are most neglected among the 17 NTDs. Recent molecular approaches for differentiation of the causative cestode species have revealed more number of independent species in *Echinococcus spp*. (from 4 to 9 species), two geographic genotypes of Taenia solium and their hybrids, hybrids of *Taenia saginata* and *Taenia asiatica* and increase in accidental cysticercosis cases due to non-human *Taenia* species.

Present Situation: (1) Echinococcoses: On alveolar echinococcosis (AE) caused by *Echinococcus multilocularis*, four geographic genotypes have been confirmed in the world. Through human and animal travels, European genotype has most recently been confirmed from Canada where historically American genotype had exclusively been distributed. All four genotypes have been confirmed from Russia. The majority of cystic echinococcosis (CE) in humans has been conceived to be caused by Echinococcus granulosus sensu stricto (G1). However, *Echinococcus canadensis* (G6/7) has also been found sympatrically distributed almost all over the world. (2) Cysticercosis: Two, Asian and Afro/American genotypes of *T. solium* and their hybrids have been confirmed in Madagascar. (3) Taeniases: When a third species of human *Taenia*, *T. asiatica*, was confirmed from Asia, it has been debated if *T. saginata* and *T. asiatica* are independent species or intra-species variants. Hybrids of adult tapeworms of these two species have been confirmed. (4) Cysticercosis due to non-*T. solium*: Molecular tools have revealed that cysticercosis suspected cases are caused not only by *T. solium* but also by other *Taenia* species which accidentally infect humans. Globalization with human and animal travels is causing more complicated situation of cestode zoonoses in 21st century.

Keywords: cestode zoonoses, cysticercosis, echinococcoses

CHALLENGES IN RESEARCH ON PARASITIC HELMINTHS: SYSTEMATICS, BARCODING AND ECOLOGY OF NEGLECTED PARASITIC DISEASES

Serge Morand

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Department of Helminthology, Faculty of Tropical Medicine, Mahidol University, Thailand

Neglected parasitic diseases include helminths, with many of them being zoonotic. After decades of control and eradication of these parasitic diseases, new insights in their biology and ecology have emerged. For instance, studies on polyparasitism or multi-infection have challenged several medical and veterinary paradigms such as how interactions between gut helminths and gut microbiome may lead to several disease symptoms. We identified at least three challenges in the field of helminthology. First, there is a need to maintain taxonomic expertise. Barcoding is one way to overcome the loss of expertise. Barcoding procedures include the development of: collection of voucher (or reference) specimens and/or biological materials and their management; molecular protocols (tools to get DNA barcode sequences or other molecular data); database (open library of geo-referenced traceable vouchers and their DNA barcode sequences); phylogenetic and molecular epidemiological analyses (identification of taxa and/or strains and their relationships). Barcoding is a key step to improve data management procedures and methods, multidisciplinary databases set-up, data sharing and traceability. The second challenge is to develop studies on evolutionary ecology of host-helminth interactions. Studies on wild animals give some examples how we can implement similar studies in animal models and even in humans, considering ethics. Third, helminths and microbes were important elements in the evolution of free-living animals and humans. The immune system and immunes responses have evolved facing multiparasitism, while dealing with the maintenance of the overall physiological homeostasis. Changes in parasite communities' or microbiome composition may have drastic effect on the immune responses leading to auto-immune diseases. The challenge is how to promote tolerance towards parasites and microbes but avoiding the dramatic effect of parasite burden on morbidity.

EPIDEMIOLOGY AND CONTROL OF *STRONGYLOIDES STERCORALIS* IN CAMBODIA

Peter Odermatt
for the Cambodian-Swiss research team

Swiss Tropical and Public Health Institute, Basel, Switzerland, P.O. Box, CH-4002 Basel, and University of Basel, Basel, Switzerland

Strongyloides stercoralis, endemic in tropical and temperate climates, is a most neglected tropical disease. Accurate information on its geographic distribution and global burden are lacking. The objectives of our project were (i) to validate existing diagnostic tools for field based use in point-of-care and surveillance services, (ii) to clarify the burden of infection and morbidity, and (iii) to study the impact of ivermectin treatment at individual and community levels in Cambodia.

Between 2009 and 2014 we have conducted a series of studies: We (i) validated currently used parasitological diagnostic techniques such as Baermann technique (BT) and Koga Agar plate culture (KAP) in schoolchildren, (ii) conducted large scale epidemiological studies in Preah Vihear and Takeo provinces to assess distribution of S. *stercoralis* infection and risk factors, (iii) diagnosed, treated and follow-up *S. stercoralis* patients and (iv) performed a community-based cohort study on *S. stercoralis* infection and re-infection after treatment. Stool samples were examined using BT and KAP. Bayesian spatial prediction was used to predict risk at non-surveyed locations in Preah Vihear.

Repeated stool sample examination proved to be a valid but labour-intense procedure to obtain sensitive *S. stercoralis* diagnosis. *S. stercoralis* infection prevalence among the general population was 44.7% and 21.0% in Preah Vihear and Takeo province, respectively. Age, sex and access to adequate water and sanitation facilities were most important risk factors identified. 39% of *S. stercoralis* infection could be prevented by adequate defecation habits. Infection risk significantly decreased with increasing rainfall and soil organic carbon content and it was associated rice farming. Ivermectin showed a high efficacy. Muscle pain and urticaria were associated with *S. stercoralis* infection.

S. stercoralis infection is highly prevalent in rural communities of Cambodia, in places where appropriate diagnosis and treatment do not exist. Personal hygiene, including latrines use, is a major predictor for strongyloidiasis. *S. stercoralis* infection should no longer be neglected in Cambodia.

THURSDAY 3rd DECEMBER 2015

16.00 – 17.30
Room C

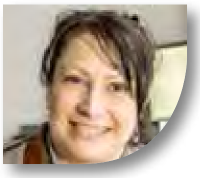
S31- APPROACHES TO RESEARCH IN TROPICAL MEDICINE: SPONSORED BY MORU

Chairperson :

Nicholas Day

Speakers :

1 Arjen M Dondorp
"Clinical Research in Tropical Medicine"
(Abstract not available)



2 Lisa White
"Mathematical Modelling in Tropical Medicine"

3 Joel Tarning
"A Pharmacometric Approach to Tropical Medicine Research"

MATHEMATICAL MODELLING IN TROPICAL MEDICINE

Lisa White

Mahidol-Oxford Tropical Medicine Research Unit, Mahidol University

The field of mathematical modelling in tropical medicine is undergoing rapid growth and attracting a number of researchers who are based in the tropics and who are interested in addressing pertinent public health questions in their countries. There are many preventable and treatable tropical diseases where mathematical modelling could be used to support the design of optimal integrated control strategy. For modellers to make a valid contribution an interdisciplinary approach is required where mathematicians work with clinical and veterinary epidemiologists, health economists, field and laboratory biologists, and policymakers. Tropical diseases often involve complex parasite life-cycles linked with non-trivial patterns of human contact with each other, animal reservoirs and the environment. This is coupled with the additional complexity of multiple sub-optimal interventions (e.g. vaccines with partial and/or short-lived protection and the emergence and spread of drug and insecticide resistance). Mathematical models can provide a framework that combines these complex systems with their corresponding data sources to support evidence-based intervention strategy design where uncertainty in the underlying system can be incorporated and explored. These frameworks can be used to extrapolate field trials of novel interventions to national level implementation with the corresponding logistical and economic constraints.

Keywords: Mathematical model, tropical medicine

A PHARMACOMETRIC APPROACH TO TROPICAL MEDICINE RESEARCH

Joel Tarning

Clinical Pharmacology, Mahidol-Oxford Tropical Medicine Research Unit,, Thailand

Malaria is the most important parasitic infection of humans and still kills approximately 2,000 people each day. Children <5 years of age in malaria-endemic countries are especially vulnerable to malaria and to the development of severe disease. Many of the antimalarial drugs used today were introduced at the wrong doses, particularly in young children and pregnant women. This has undoubtedly resulted in therapeutic failures and the development of drug resistance. It is therefore essential to optimise dosing in these vulnerable populations, so that the limited armamentarium of currently used antimalarial drugs maintains their excellent efficacy for as long as possible. This has recently been identified as a priority by the World Health Organization.

The only way to determine accurately the correct dose regimens for antimalarial treatment is to establish a dose-response relationship through pharmacokinetic-pharmacodynamic modelling. It is necessary to identify the different demographic, physiological, disease related, and pharmaceutical variables that influence drug concentrations and thereby outcomes. This powerful approach allows dose-optimisation in different patient groups, such as pregnant women and children, and it facilitates considerably the interpretation of clinical trials and pharmacological studies.

The work presented here discusses the applications and challenges of pharmacokinetic- pharmacodynamic modelling of antimalarial drugs.

THURSDAY 3rd DECEMBER 2015

16.00 – 17.30
Room D

S32 - FREE PAPER: GLOBAL HEALTH AND PARASITIC DISEASES

Chairpersons :


Kittiyod Poovorawan


Wanlapa Roobsoong

Speakers :


1 Jonas Schmidt-Chanasit
"Discovery of a novel zoonotic bornavirus: A One Health approach of awareness, modern diagnostics and multi-disciplinary networking"


2 Pornpan Suntornsut
"Designing an intervention to prevent melioidosis in Northeast Thailand: a focus group study using the behavior change wheel"


3 Andrew G. Silver
"Quality improvement for clinics in remote areas of Myanmar"


4 Hans Overgaard
"Integrating dengue and diarrhea control in rural schools in Colombia: A cluster-randomized controlled trial"

5 Thitima Cherdtrakulkiat
"HIV and sexually transmitted infections among non-Thai men attending Voluntary Counseling and Testing Service, Bangkok, Thailand, 2005–2014"


6 Wipas Wimonsate
"Factors associated with adherence to the Thai national guidelines for annual HIV voluntary counselling and testing, Silom Community Clinic @TropMed,"


7 Aung Naing Cho
"Community based systems for the detection, treatment and reporting of malaria cases in Myanmar: Landscaping exercise with implementing partner organizations"

DISCOVERY OF A NOVEL ZOONOTIC BORNAVIRUS: A ONE HEALTH APPROACH OF AWARENESS, MODERN DIAGNOSTICS AND MULTI-DISCIPLINARY NETWORKING

Jonas Schmidt-Chanasit[1],
Bernd Hoffmann[2],
Dennis Tappe[2], Dirk Höper[2],
Christiane Herden[2],
K. Schlottau[2], A. Boldt[2],
Ch. Mawrin[2], O. Niederstraßer[2],
T. Mueller[2], M. Jenckel[2],
E. van der Grinten[2], Ch. Lutter[2],
B. Abendroth[2], JP. Teifke[2],
K. Tauscher[2], Ch. Fast[2],
S. Herzog[2], Ch. Frank[2], K. Stark[2],
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Background and objectives: Three breeders of variegated squirrels developed a progressive and finally fatal meningoencephalitis within a few months after symptom onset. Lesions with mononuclear infiltration were suggestive for a viral infection, and veterinary and human health institutes and officials worked together to find the causative agent.

Materials and methods: Standard diagnostics, and subsequently a metagenome pipeline using next-generation sequencing (NGS) and the RIEMS analysis workflow, were used for pathogen identification and characterisation. Novel molecular diagnostics and serology tests were developed and evaluated for the newly discovered virus. Public health measures were implemented.

Results: No infectious agent was detected by extensive standard laboratory investigations, but NGS analysis revealed the presence of a novel bornavirus in a contact squirrel. Subsequent intensive analysis including novel RT-qPCR and antigen staining confirmed its presence in samples of the deceased patients and the squirrel. Whole-genome analyses demonstrated that this novel virus forms a separate lineage within the bornavirus species. Additional positive animals could be identified and high bornavirus-specific antibody titers were detected. A test procedure for live animals was established.

Conclusion: This discovery of a bornavirus with zoonotic potential demonstrated the power of novel diagnostic methods and the need of effective awareness systems in a One Health approach.

Keywords: bornavirus, NGS, squirrel, meningoencephalitis

DESIGNING AN INTERVENTION TO PREVENT MELIOIDOSIS IN NORTHEAST THAILAND: A FOCUS GROUP STUDY USING THE BEHAVIOR CHANGE WHEEL

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Background: Melioidosis, an often fatal infectious disease in Northeast Thailand, is caused by skin exposure or ingestion of the causative organism (*Burkholderia pseudomallei*) presenting in soil and environmental water. Recommendations for melioidosis prevention include using protective gear such as rubber boots if direct contact with soil and environmental water is necessary and consuming bottled or boiled water. Here, we use a systematic approach to define barriers and to inform the design of the future intervention to support behavior changes.

Methods: Nine focus group discussions were conducted to evaluate factors influencing preventive behaviors recommended. A total of 76 people at risk from melioidosis (diabetics) in Ubon Ratchathani, northeast Thailand, participated in the focus group sessions. The Theoretical Domains Framework (TDF) was used to define and categorize the barriers. The Capability Opportunity Motivation and Behaviour (COM-B) system and Behavior Change Wheel (BCW) model were used to systematically define the priority of barriers and to choose components of the intervention, respectively.

Results: Knowledge, beliefs about consequences, Intention and goals, environmental context and resources, social/professional role and identity, and social influence were the key domains identified as barriers. Most participants thought that there was no harm in not doing the recommended preventive behaviors, did not intend to follow the recommendation, and found that rubber boots and gloves were hot and uncomfortable while working in muddy rice fields. Participants noted that inputs from physicians, diabetic clinics, friends, family and mass media would be required for them to change these behaviours. Education, persuasion, environmental restructuring, modeling and enablement were identified as important components needed for the intervention.

Conclusion: There are a number of barriers to adopting behaviors recommended for melioidosis prevention. We recommend that a multifaceted intervention would be required to implement the behavioral change in melioidosis prevention effectively.

Keywords: Melioidosis, Focus Group, Prevention, Health Education, Theoretical Domains Framework, Behavior Change Wheel.

QUALITY IMPROVEMENT FOR CLINICS IN REMOTE AREAS OF MYANMAR

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This presentation follows up the presentation on the first year of the project given at JITMM 2013. Results over the following two years afford data for evaluating the effectiveness of the project.

The Karen Department of Health and Welfare (kdhw.org) operates, together with partner community-based organizations, 57 clinics serving a target population exceeding 200,000 villagers in southeastern Burma. At the instigation of the International Rescue Committee, logbook review for randomly selected cases of malaria, diarrhea, and ARI have been conducted annually since 2012. The review checks for lapses such as failure to record signs of dehydration in diarrhea patients or giving antiobiotics to patients with common colds.

A quality improvement (QI) project was initiated June, 2012. Major obstacles are multiple languages, remoteness of clinics, and lack of direct communication with the KDHW office. Flip charts to facilitate remembering targeted procedures were given to participating clinics. Volunteer QI coordinators at the clinics return logbook review forms about every 3 months. The project team returns charts to track improvement month to month. Although QI coordinators receive little or no compensation, 8 clinics with 2 QI coordinators each have joined the project.

The annual logbook review, in which QI staff do not participate, included 4 QI clinics and 2 non-QI clinics in both 2012, the baseline year, and in 2014. Despite the paucity of data, results showed that the QI clinics improved significantly more than non-QI clinics on diarrhea measures from 2012 to 2014. The difference was just short of significance for ARI. For malaria, all clinics improved 100% or more, so no difference could be significant.

Keywords: logbook review, quality improvement, volunteer, health clinics, Karen, malaria, diarrhea, ARI, pneumonia, checklist, remote, Myanmar, Burma, evaluation, effectiveness

INTEGRATING DENGUE AND DIARRHEA CONTROL IN RURAL SCHOOLS IN COLOMBIA: A CLUSTER-RANDOMIZED CONTROLLED TRIAL

Diarrheal disease and dengue fever are major global health problems with mutual risk factors. In many countries, households and institutions need to store water for consumption. Fecal contamination of stored water is a common source of diarrhea. Stored water also provides breeding sites for dengue vector mosquitoes. Integrating control interventions and educational strategies in schools could potentially improve students' health. The main objective of this trial was to investigate whether interventions targeting dengue and diarrhea risk factors in schools could significantly reduce primary outcomes a) absence due to diarrheal disease and b) dengue vector infestations in the schools. A factorial cluster randomized controlled trial was carried out in 34 rural primary schools in Colombia. Schools were randomized to one of four study arms: interventions for diarrhea (DIA), dengue (DEN), diarrhea and dengue (DIADEN), and control (CON; no interventions). The dengue interventions reduced the Breteau indices by an average of 78% (p=0.029) and the diarrhea interventions significantly improved water quality, reducing *E. coli* colony forming units by 78% on average (p=0.008). However, the interventions had no apparent effect on the primary outcomes. This trial presents a new paradigm for the application of control strategies that could potentially affect both dengue and diarrheal illnesses. Interventions were well received, highly appreciated by students and teachers, reduced mosquito breeding and improved water quality. Integrated interventions targeting these diseases in a school context provide a novel strategy to reduce the burden of these two major global public health problems. ⁂

Keywords: Pupil absence, *Aedes aegypti*, mosquito, water storage, water contamination

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HIV AND SEXUALLY TRANSMITTED INFECTIONS AMONG NON-THAI MEN ATTENDING VOLUNTARY COUNSELING AND TESTING SERVICE, BANGKOK, THAILAND, 2005–2014

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Sirirat Lertpruek[1],
Wichuda Sukwicha[1],
Jaray Tongtoyai[1],
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Background: Men who are non-Thai nationals may have unique risks for HIV and sexually transmitted infections (STI) in Bangkok. We describe HIV/STI prevalence and incidence among non-Thai men attending Voluntary Counseling and Testing (VCT) service at the Silom Community Clinic in Bangkok, Thailand.

Methods: We used VCT data from 2005–2014. We assessed client nationality and country of origin based on self-report. HIV testing was provided for free using rapid tests. *Treponema pallidum* (TP) screening was performed using the rapid plasma reagin (RPR) and, if reactive, using a TP-specific antibody test; we considered syphilis as a reactive TP-specific antibody test. Gonococcal testing was performed using a Gram stain for symptomatic men.

Results: Of 9,228 VCT clients, 10.3% (n=954) were non-Thai, and 84.3% (805/954) were men who have sex with men (MSM). The median age was 32 years (Interquartile Range: 26–42) and 370 (38.8%) were Asian, with Myanmar being the country of origin for 27.3% (n=101). Among all 954 non-Thai, the HIV prevalence was 16.1% (n=154); syphilis prevalence was 5.5% (n=52); symptomatic gonococcal prevalence was 2.5% (n=24); and, 517 (54.2%) returned for a repeat visit. Among the 393 HIV-uninfected non-Thai men, HIV incidence was 4.6 per 100 person-years (PY); 9.0 per 100 PY among those aged 18–24 years.

Conclusion: We found a high HIV incidence and HIV and STI prevalence among non-Thai nationals, especially young men. These men may benefit from specific prevention services at the time of the visit as many do not have a follow-up visit.

Keywords: Men who have sex with men, HIV; Sexually Transmitted Infections

FACTORS ASSOCIATED WITH ADHERENCE TO THE THAI NATIONAL GUIDELINES FOR ANNUAL HIV VOLUNTARY COUNSELLING AND TESTING, SILOM COMMUNITY CLINIC @TROPMED, 2010–2015

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Sarika Pattanasin[1],
Pikunchai Luechai[1],
Kanokpan Pancharoen[1],
Sumetha Hengprasert[1],
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Benjamaporn Chaipung[1],
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Background: In October 2010, the Thailand Ministry of Public Health released guidelines recommending men who have sex with men (MSM) access HIV voluntary counseling and testing (VCT) ≥ 2 times per year. We investigated factors associated with adherence to these guidelines among clients of the Silom Community Clinic @TropMed during 2010–2015.

Methods: We included baseline HIV-uninfected MSM who attended our clinic from October 2010 to July 2014 and followed them until July 2015. Using the number of VCT visits divided by the time from first to last test, MSM were placed into two groups: < 2 tests/year (non-adherence) and ≥ 2 tests/year (adherence). We used logistic regression to determine factors associated with adherence, adjusted for interval between tests and demographic characteristics.

Results: From the VCT database we had 4,282 baseline HIV-uninfected MSM: 1,722 (40.2%) repeated VCT with a median of 3 tests (Interquartile Range [IQR] 2–4), and a median interval of 1 year (IQR 0.5–1.9). Among 4,282 men, 1,216 (28.4%) adhered to the guidelines. Having VCT during one's own birth month (Adjusted Odds Ratio [AOR] 2.0, 95% Confidence Interval [CI] 1.7–2.5), having VCT during peak visit months (after major Thai holidays) (AOR 2.3, 95% CI 2.0–2.7), and having any sexually transmitted infection (STIs) (AOR 1.7, 95% CI 1.4–2.0) were independently associated with adherence to the guidelines.

Conclusion: About one-fourth of our MSM clients adhered to the Thai national guidelines for VCT, although some may have been tested elsewhere. Birthday and seasonal holidays, along with STI visits, may serve as repeat visit adherence reminders.

Keywords: MSM, HIV, VCT, guidelines, repeat

COMMUNITY BASED SYSTEMS FOR THE DETECTION, TREATMENT AND REPORTING OF MALARIA CASES IN MYANMAR: LANDSCAPING EXERCISE WITH IMPLEMENTING PARTNER ORGANIZATIONS

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The proportion of malaria cases reported by Village Health Volunteers (VHV) is increasing as attempts to eliminate malaria and drug resistant parasites intensify in Myanmar. However, VHV systems are highly fragmented with management delegated across implementing partners (IPs). A landscaping exercise with IPs delivering community case management of malaria was carried out in 2015 to identify examples of best practice and avenues to harmonize VHV systems. Quantitative and qualitative data was collected from 30 informants representing 20 organizations. The scope of study included the coverage in 2014, overview of the systems, malaria-specific vs. integrated functions, VHV roles and responsibilities- including in case management and Directly Observed Therapy (DOT). Also investigated were recruitment, training and supervision, strategies for retention, supply chain management, systems for monitoring and evaluation, data collection management and reporting systems, feedback mechanism and suggested actions to improve harmonization of VHV systems. Information was synthesized using a matrix table and analyzed by two analysts. Although VHV systems can be successful, a better understanding of coordination mechanisms, ways of tracking and updating VHV coverage and activities and harmonization of incentive systems is needed. The study evaluated the potential role of criteria including active VHVs, patient referrals, targeted active case detection, evaluation methods, and mechanisms to improve quality and completeness of data collection reported to central level. Barriers to DOT implementation from VHV perspective were explored. In order to maximize the effectiveness and efficiency of VHV activities, development of a harmonized guideline through coordination between National Malaria Control Programme, donor organizations and IPs would be recommended.

Keywords: Village Health Volunteers, Malaria

THURSDAY 3rd DECEMBER 2015

16.00 – 17.30
Room E

S38 - TOOLS FOR MALARIA ELIMINATION (Panel Discussion)

Moderators :

Jetsumon Prachumsri

Jeeraphat Sirichaisinthop

An open discussion session moderated by representatives from MOPH and with speakers and experts from the Faculty of Tropical Medicine, Mahidol University.

This session is an opportunity for practitioners to learn more about malaria elimination in Thailand and to get useful updates from researchers and public health professionals. The session is participatory and has ample time for questions.

Please note, this session is in Thai only.

จัดการบรรยายเป็นภาษาไทย ในหัวข้อ “เครื่องมือที่จำเป็นต้องมีในการกำจัดโรคมาลาเรียของประเทศไทย” เพื่อแนะนำเครื่องมือที่มีประสิทธิภาพในการช่วยกำจัดมาลาเรียให้หมดจากประเทศไทยภายในปี พ.ศ. 2567

ซึ่งประกอบด้วยวิทยากรจากคณะเวชศาสตร์เขตร้อน มหาวิทยาลัยมหิดล วิทยากรจากกระทรวงสาธารณสุข และ นักวิจารณ์ผู้เชี่ยวชาญร่วมเสนอประเด็นข้อซักถามอันเป็นประโยชน์ต่อผู้เข้าฟังการบรรยายในหัวข้อเรื่องดังต่อไปนี้

1. ประสิทธิภาพของการเฝ้าระวังทางระบาดวิทยา
2. มาตรการที่กระทรวงสาธารณสุขใช้ในการเฝ้าระวัง และแปลผลข้อมูล
3. วิธีการปฏิบัติเพื่อการกำจัดโรคมาลาเรีย เช่น วิธี MDA วิธี MSAT
4. การสร้างแบบจำลองเพื่อการกำจัดโรคมาลาเรีย

FRIDAY 4th DECEMBER 2015

9.00 – 10.30
Room A

S33 - DRUG AND VACCINE DISCOVERY THROUGH PARASITE GENOMES

Chairperson :

Poom Adisakwattana

Invited Speakers :

1 Aaron R Jex
'Genomic assembly and analysis of highly heterzygotic polyploidal parasites"

2 Aaron R Jex
"Genome-wide functional annotation of parasites through protein structure prediction"

3 Momar Ndao
"Characterization of the immune responses elicited by the immunization of mice with *Schistosoma mansoni* Cathepsin B in the presence of CpG or Montanide ISA 720 VG"

GENOMIC ASSEMBLY AND ANALYSIS OF HIGHLY HETERZYGOTIC POLYPLOIDAL PARASITES

Aaron R Jex[1,2], Staffan Svard[3], Robin B Gasser[2]

1 Walter & Eliza Hall Institute, Parkville, VIC, Australia
2 Veterinary and Agricultural Sciences, University of Melbourne, Parkville, Vic, Australia
3 Uppsala University, Cell and Molecular Biology, Uppsala, Sweden

A high level of genetic heterozygosity is a significant challenge in the de novo assembly and analysis of the genomes of any organismal group or tissue. For research of parasites, high heterozygosity is a major obstacle to generating highly complete assemblies and exploring complex gene families and repetitive sequence regions (e.g., telomeres) where important virulence genes are often found. An inability to culture many parasites in vitro coupled with their often small size is a major contributor to this challenge, as it prevents the generation of clonal lines for sequencing and precludes sequencing from individual parasites, at least in any practical sense. A further major challenge is that many parasitic are polyploidal or exhibit a high level of genetic variation among individuals. Using existing bioinformatic approaches, we present a strategy for assembling non-redundant and highly complete genomes from heterozygotic and polyploidal templates and exploring allelic and haplotypic diversity within sequence datasets representing a complex pool of individual parasites. ✻

GENOME-WIDE FUNCTIONAL ANNOTATION OF PARASITES THROUGH PROTEIN STRUCTURE PREDICTION

Aaron R Jex[1,2], Brendan Ansell[2], Ross S Hall[2], Robin B Gasser[2], Ivo Mueller[1]

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[2] *Veterinary and Agricultural Sciences, University of Melbourne, Parkville, Vic, Australia*

Understanding gene function is critical for target-guided drug discovery and characterizing the molecular biology of any parasite. Although gene knockout, silencing and other functional genomic tools provide the gold standard for determining gene function, these tools are often poorly developed for many parasites and/or impractical at a large-scale. At the genomic level, predicting gene function relies heavily on inferring homology through comparative sequence alignment with known genes. In this process, the large evolutionary distance between many parasites and the genes in functional databases presents a significant challenge. As a consequence, many parasite genes are annotated as 'hypothetical' proteins of unknown function; e.g., 40 and 60% of coding genes for many parasite genomes. However, a protein's function is tightly related to its structure, which is often highly conserved even when the underlying sequence is not. I-TASSER is a leading software package allowing prediction of protein structure and the inference of gene function based on comparisons to solved protein structures in the RCSB protein databank. Through massively parallelized computational biology, we are using this approach to predict structural models for the hypothetical proteomes of a variety of parasites, greatly expanding on their proposed functional annotation. We discuss strategies to benchmark these predictions and the implications of this resource for understanding the molecular biology of human malaria and facilitating target-guided drug discovery.

CHARACTERIZATION OF THE IMMUNE RESPONSES ELICITED BY THE IMMUNIZATION OF MICE WITH *SCHISTOSOMA MANSONI* CATHEPSIN B IN THE PRESENCE OF CPG OR MONTANIDE ISA 720 VG

Alessandra Ricciardi[ab],
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[c] Institute of Parasitology, McGill University, Montreal, Quebec, Canada
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Schistosomiasis is the most important human helminth infection due to its impact on public health. A vaccine could contribute to a long-lasting decrease in disease spectrum and transmission. Our previous vaccine study using *Schistosoma mansoni* Cathepsin B (SmCB) resulted in 59% and 60% worm burden reduction with CpG oligodeoxynucleotides and Montanide ISA720 VG as adjuvants, respectively. Furthermore, antibody production was significantly augmented in the vaccinated mice; both formulations elicited SmCB-specific total IgG endpoint titers > 120,000. In this study, the role of antibody-dependent cell-mediated cytotoxicity in SmCB-mediated protection was evaluated by incubating the parasite in the presence of pre-immune or immune sera with isolated lung CD45$^+$ cells. These cells were obtained from mice immunized with recombinant SmCB adjuvanted with either CpG oligodeoxynucleotides or Montanide ISA 720 VG. Cells and sera from adjuvant and saline control animals were also included. SmCB + Montanide induced the highest killing when immune serum was present; suggesting the contribution of antibodies in cell-mediated parasite killing. In contrast, SmCB + CpG induced constant increased parasite killing which was independent of the addition of immune sera; implying that only cellular effects were elicited. To further investigate the immunological mechanisms, different cell populations were isolated and analyzed. For the SmCB + CpG formulation, the killing was maintained in the absence of CD4$^+$ cells. Differently, for the SmCB + Montanide formulation, the effect is lost in the absence of CD4$^+$ cells. These results shed light on the different immunes responses elicited by the two SmCB formulations.

FRIDAY 4th DECEMBER 2015

9.00 – 10.30
Room B

S34 - MALARIA III: TOOLS FOR SURVEILLANCE AND CONTROL

Chairpersons :

Arjen Dondorp

Pradip Rathod

Invited Speakers :

1 Rupam Tripura
"Application of ultra-sensitive malaria NAAT tool"

2 Sureemas Buates
"LAMP application for surveillance system"
(Abstract not available)

3 Mehul Dhorda
"Quality assurance in malaria parasite detection identification and quantification"
(Abstract not available)

4 Richard Maude
"Genetic reconnaissance in the Greater Mekong Subregion"

APPLICATION OF ULTRA SENSITIVE MALARIA NAAT TOOL

Rupam Tripura

Mahidol-Oxford Tropical Medicine Research Unit, Thailand

The subclinical reservoir of malaria parasitaemias is an important source of transmission and persistence of malaria parasitaemias even in areas of low seasonal transmission. Characterising the epidemiological characteristics over time of asymptomatic malaria parasitaemias is a necessary prerequisite for elimination. Ultrasensitive quantitative PCR methods of malaria detection (uPCR) have been developed recently which can identify the majority of infected individuals. Using uPCR for the detection of parasitaemia, the entire population of three Cambodian villages in Pailin province were followed over a 12 month period.

A cross sectional survey in June 2013 (M0) found 32/1447 (2.2%) asymptomatic residents had *P. falciparum*, 48/1447 (3.3%) had *P. vivax*, 4/1447 (0.3%) had mixed infections, and in 142/1447 (9.8%) a *Plasmodium* species (P. species) was detected but there was insufficient DNA to identify the species. Monthly follow-up without treatment of 24 adult participants with asymptomatic mono or mixed *P. falciparum* infections found that 3/24 (13%) remained parasitaemic for 2 to 4 months, whereas the remaining 21/24 participants had cleared their parasitaemia after one month. In contrast, 12/34 (35%) adult participants with *P. vivax* mono-infection at M0 carried malaria parasites (*P. vivax* or *P. species*) during more than 6 of the following 11 monthly surveys.

This longitudinal survey in the very low transmission setting of Western Cambodia using ultrasensitive detection shows limited duration of *P. falciparum* carriage, but prolonged carriage of *P. vivax* infections. Radical treatment of *P. vivax* infections by 8-aminoquinoline regimens will probably be necessary to eliminate all malaria from Cambodia rapidly.

Keywords: subclinical reservoir,Ultrasensitive quantitative PCR

GENETIC RECONNAISSANCE IN THE GREATER MEKONG SUBREGION

Richard J Maude[1,2,3],
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[3] Center for Communicable Disease Dynamics, Harvard TH Chan School of Public Health, Boston, USA
[4] Wellcome Trust Sanger Institute, Hinxton, UK
[5] Medical Research Council (MRC) Centre for Genomics and Global Health, University of Oxford, Oxford, UK

Resistance to antimalarials is the most serious threat to the control and elimination of *P. falciparum* malaria in to the Greater Mekong Subregion (GMS). To maximise the probability of success, elimination strategies must take into account important epidemiological factors, e.g. the prevalence of resistance to current frontline antimalarials, and to alternative drugs; the local levels of transmission; and the contribution of population movement to dissemination of resistance.Here, we present a genetic epidemiological surveillance system (GenRe-Mekong) that will support national malaria control programmes (NMCPs) with extensive and timely information on antimalarial resistance and parasite population structure, derived from high-throughput genotyping of dried blood spot (DBS) samples.

The simple field collection procedures require minimal training and allow the system to integrate with established routine diagnostic and treatment workflows, e.g. through networks of village health workers or health facilities run by governments or NGOs. Samples are assigned unique barcodes, which simplifies metadata collection and allows integration of genotypes with demographic, travel or clinical data. Each sample is genotyped for a detailed set of known genetic markers for resistance to artemisinin, to its partner drugs, and to other classes of antimalarials; for resistance-predisposing genetic backgrounds; and for co-infection with *P. vivax*. The resulting genetic "report cards" are rapidly made available to NMCPs to create reports and maps of markers, and support intervention strategies. Further genetic analyses will be conducted at population level, e.g. to investigate the parasites' geographical origin; identify rapidly-expanding clonal populations; and estimate population diversity and transmission. The application of mathematical modelling using high-resolution genetic data, combined with epidemiological data from other sources, will enable the study of gene flow and resistance spread in the sampled regions.

GenRe-Mekong is currently implementing in pilot projects in Cambodia, Vietnam and Bangladesh, in partnership with the national malaria control programmes. It also collects samples across the GMS, through multi-site research projects such as TRACII.

FRIDAY 4th DECEMBER 2015

9.00 – 10.30
Room C

S35 - MALARIA IV: Health System Readiness and Community Engagement for Malaria Elimination

Chairpersons :

Kamolnetr Okanurak

Suparat Phuanukoonnon

Invited Speakers :

1 Myo Thiha Zaw
"Community engagement in malaria elimination: Myanmar experiences"

2 Rungrawee Tipmontree
"Thailand's way of engaging community for malaria elimination"

3 Suparat Phuanukoonnon
"The health system readiness for Malaria elimination: what it needs for malaria control program in Papua New Guinea"

COMMUNITY PARTICIPATION IN MALARIA PREVENTION AND CONTROL: MYANMAR EXPERIENCES

Myo Thiha Zaw

Health and Disease Control Unit (HDCU), Nay Pyi Taw, Myanmar

Malaria is still one of the public health problems in Myanmar, resulting morbidity rate of 6.44/1000 population and mortality rate of 0.48/100000 population in 2013. As malaria is prevalent in 284 out of 330 townships, nearly two third (62%) of population are living in malaria endemic area. Myanmar has committed to achieve malaria elimination by 2030, and National Malaria Control Program (NMCP) is carrying out malaria control activities as nationwide. With the specific strategy of intensifying community participation, involvement and empowerment, community-based malaria control program has been introduced and implemented since 2006-2007 and expanded in total 182 townships and 3875 volunteers were trained in 2013. Although the community-based malaria programs were conducting, these programs were highly influenced by health authorities, leading passively involvement of community, and getting less chance to involve in initial planning of programs, then resulting lower community participation and higher rate of attritions in these programs. Therefore, community-based intervention study was conducted in malaria endemic villages in Mandalay region of Myanmar. Community participation program was developed and implemented using the steps of community action cycle, while participatory learning and action approaches were used as community mobilization tools to increase participation. Evaluation was done for the community participation program using the process and outcome indicators. To assess the nature of community participation within community participation program, a spidergram analysis with five process indicators was applied. Villagers in the experimental group accepted the program and participated in action plan of program, resulting better understanding of malaria-related knowledge and perception than those in the control group. The use of community volunteers as community development facilitators in community-based malaria prevention and control was feasible and an empowerment approach of community participation was effective for improving the knowledge, perception, preventive behaviours and treatment seeking behaviours of community which leads to an increased community participation in malaria prevention and control. ⁂

Keywords: community-participation malaria prevention control myanmar

THAILAND'S WAY OF ENGAGING COMMUNITY FOR MALARIA ELIMINATION

Rungrawee Tipmontree

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Thailand is gearing up implementation of malaria elimination aiming to reach the goal "Thailand free from malaria by 2025" Community is considered a vital element to accelerate malaria elimination and retain program success. Implementation of the program needs more than just active community participation but also a sustainable engagement to prevent reintroduction of malaria. A phase-specific strategy for community engagement is constructed to pave different interventions to promote participation of the community in prevention, control and surveillance for malaria elimination.

The benefits of malaria elimination will be communicated to community to get their participation. Community assessment will be carried out to obtain information about risk perception, knowledge and behaviors and barriers to participation and eventually to be used as a basis to construct interventions. Advocacy meetings and campaigns will be held to disseminate relevant information and to raise community awareness. Community will be engaged from planning to implementation and evaluation of the program with active involvement from local leaders, NGOs and other community organizations to assure achievement. The engagement emphasizes ownership by community to create a model of networking for malaria elimination within local context. Empowerment activities will be provided to maximize capacity of different population groups e.g. volunteers, schoolchildren and community members. Communication program with tailored IEC/BCC strategies, tools and materials will be developed to promote active participation, to change behavior and to improve provision of. Recognition of community's success in malaria elimination will be performed to sustain the engagement and to scale up the program.

Keywords: malaria elimination, community participation

THE HEALTH SYSTEM READINESS FOR MALARIA ELIMINATION: WHAT IT NEEDS FOR MALARIA CONTROL PROGRAM IN PAPUA NEW GUINEA

Suparat Phuanukoonnon

Papua New Guinea Institute of Medical Research, Goroka, 441, Papua New Guinea

In Papua New Guinea, investment by the Global Fund to Fight AIDS, Tuberculosis and Malaria (the Global Fund) has played an important role in scaling up the response to these three diseases. The malaria control program under the Global Fund has been successfully reduced the malaria rate by 60-80% in PNG. To maintain the low rates of malaria leading to malaria elimination, is possible with an integrated control approach using mass drug administration with effective vector control measures, as well as attentions to strengthen health system. This paper summarizes some qualitative research projects undertaken in 2004 to 2013 in PNG as part of the formative research for health system and health promotion assessment for maternal health, tuberculosis and malaria services. It provides some highlights of the health beliefs and health-seeking behaviours amongst a range of urban and rural populations. The findings showed severely limited and overburdened pool of human resources, both at management and service delivery levels in PNG health system. However, positive synergies of Global Fund support include engagement of civil-society partners, and a reliable supply of high-quality bed-nets, rapid test kits and anti-malaria drugs. Community engagement has been crucial, how members of the community perceive and respond to diseases and health problems are important variables to take into account when planning interventions and priorities in a health system. Participatory planning was a key aspect of the success of this initiative. Using an empowerment approach, opportunities exist to extend the development of language-group networks in the cause of effective health promotion and disease prevention in PNG.

FRIDAY 4th DECEMBER 2015

09.00 - 12.30
Room D

S36 - ASIAN SCHOOL HEALTH SYMPOSIUM: Role of the evidence base in supporting SHN policy and programming

Sponsored by *London Centre for Neglected Tropical Research (LCNTDR)*

Organizers : *Faculty of Tropical Medicine (FTM), Mahidol University; Partnership for Child Development (PCD); and Japan Consortium for Global School Health Research (JC-GSHR)*

Session 1 :
09.00 - 10.00

Opening Remarks & Keynote Address

Chairpersons :

1 Yaowalark Sukthana
2 Kitti Larpsombatsiri

Speaker :

Roy Anderson
LCNTDR, Imperial College London, UK
"Progress in STH control by Mass Drug Administration in SE Asia"

Session 2 :
10.00 - 11.30

Translating Evidence to Programmatic Action

Chairperson:

Laura Appleby

Speakers :

1 Hugo Turner
Imperial College London, UK
"Changing our STH strategies: Cost and cost-effectiveness considerations"

2 Jun Kobayashi
University of the Ryukyus & JC-GSH, Japan
"Disaster prevention education"

3 Lesley Drake
PCD, Imperial College London, UK
"The Evolution of School Health and Nutrition: Looking Forward"

09.00 - 12.30
Room D

S36 - ASIAN SCHOOL HEALTH SYMPOSIUM: Role of the evidence base in supporting SHN policy and programming *(Continued)*

Sponsored by *London Centre for Neglected Tropical Research (LCNTDR)*

Organizers : *Faculty of Tropical Medicine (FTM), Mahidol University; Partnership for Child Development (PCD); and Japan Consortium for Global School Health Research (JC-GSHR)*

Session 3
11.45 - 12.00

Report from WHO technical meeting in 2015

Chairperson :

Jun Kobayashi

Speaker :

Sachi Tomokaw
Shinshu University & JC-GSHR, Japan
"The Future We Want"

Session 4 :
12.00 - 12.30

Discussion, Summary and Wrap-up

Chairperson :

Roy Anderson

Lesley Drake

Ernesto R. Gregorio

"Beyond Bangkok: regional vision moving forward"

FRIDAY 4th DECEMBER 2015

11.00 – 11.45
Watergate Ballroom

S37 - SORNCHAI LOOAREESUWAN MEDAL

Keynote Speaker :

Kevin C. Kain
University of Toronto, Canada; McLaughlin-Rotman Centre for Global Health; Center for Travel and Tropical Medicine, Toronto General Hospital

MECHANISMS OF MALARIA: NEW INSIGHTS TO SAVE LIVES AND SAVE BRAINS

Dr. Kain is a Professor of Medicine at the University of Toronto, the Director of the McLaughlin-Rotman Centre for Global Health, holds a Canada Research Chair in Molecular Parasitology, and is the Director of the Center for Travel and Tropical Medicine at Toronto General Hospital. As these multiple roles show, Dr Kain has a clear passion and commitment to the fields of Tropical Medicine and Global Health.

One of Dr Kain's main research goals has been to attempt to elucidate the molecular basis for adverse outcomes in malaria and to translate this knowledge into novel therapeutic interventions. As part of his research Dr. Kain has worked extensively in the tropics and sub-tropics including New Guinea, Madagascar, Uganda, Laos, Thailand and the Amazon basin.

Alongside his research Dr Kain is a strong advocate for global health equity, knowledge sharing and education, the use of appropriate and sustainable technologies and the training of research scientists in the developing world. This highlights his holistic understanding of his field and his desire to make a difference and empower others to do the same.

Receiving the Sornchai Looareesuwan Medal is of special significance for Dr Kain as Prof. Sornchai acted as a mentor for Dr Kain during his career. To commemorate his receiving of the Sornchai Looareesuwan Medal Dr Kain will deliver a presentation entitled "Mechanisms of Malaria: new insights to save lives and save brains"

11.45 - 12.15 PRESENTATION OF AWARDS/AND CLOSING REMARKS

MERS - COV SCREENING HEALTH MEASURE AT 4 AIRPORTS FOR HAJJ PILGRIM IN THAILAND, 2015

Mayurachat Biaklang,
Aschara Thukrua,
Patikom Vivattananon,
Monjira Thamangraksat,
Dararat Sirimongkol,
Orathai Timpong,
Waraluk Tangkanakul

Bureau of General Communicable Diseases, Department of Disease Control, Ministry of Public Health.

There are around 2 – 3 million Hajj Pilgrims every year. In 2015, 10,400 Thai muslims joined Hajj Pilgrim. Department of Disease Control has implemented Middle East Respiratory Syndrome Corona Virus (MERS-CoV) screening health measure at 4 airports for Hajj pilgrim during 30 September – 26 October, 2015. There were 10,350 out of 10,400 Hajj Pilgrim (99.5%) receiving MERS-CoV screening health measure at 4 airports. The initial diagnosis of Hajj Pilgrim having fever was Upper Respiratory Tract Infection (URI) 1,313 (12.68%). URI cases were found at Suvarnabhumi airport 6.14% (316/5,142), Hat Yai international airport 11.08% (346/ 3,121), Narathiwat airport 56.41 %(651/1,154). Of these URI cases 61 (4.64%) met patient under investigation (PUI) definition. PUI screened at Suvarnabhumi airport 0.15% (8/5142), Hat Yai International airport 0.86 % (27/3121), Narathiwat airport 1.55% (18/1,154) and Phuket international airport 0.88% (8/903) respectively. No confirmed MERS-CoV was found. The screening health measure at 4 airports showed its efficiency for MERS-CoV outbreak's containment.

Keywords: Hajj pilgrims, Middle East Respiratory Syndrome Corona Virus (MERS-CoV), Containment

G6PD PERFORMANCES, CAMBODIA

Sovannaroth Siv

Background: The glucose-6-phosphate dehydrogenase deficiency (G6PDd) prevalence in Cambodia showed in variety range from 8.1% to 37.5% for male and 3.1% to 6.9% for female with the majority of Viangchan variant (>90%). The safety radical cure for *P. vivax* with the recommend primaquine for malaria elimination was urgently needed.

Methods: The CareStart G6PD RDT (Access Bio, New Jersey, USA), a novel rapid diagnostic test and the most commonly used test, the fluorescent spot test (FST) were assessed against the quantitatively measured G6PD enzyme activity for detecting G6PDd. Subjects were healthy males and non-pregnant females aged 18 years or older residing in Pailin Province, western Cambodia.

Findings: Of the 938 subjects recruited for the performances of the CareStart G6PD RDT and the FST, according to different cut-off values used to define G6PDd were very similar. For the detection of severe and moderately severe G6PDd (enzyme activity ,30%, ,3.6 UI/g Hb) in males and females, sensitivity and negative (normal status) predictive value were 100% for both point-of-care tools. When the G6PDd cut-off value increased (from ,40% to ,60%), the sensitivity for both PoCs decreased: 93.3% to 71.7% (CareStart G6PD RDT, p51026) and 95.5% to 73.2% (FST, p51026) while the specificity for both PoCs remained similar: 97.4% to 98.3% (CareStart G6PD RDT, p50.23) and 98.7% to 99.6% (FST, p50.06).

Conclusion: The CareStart G6PD RDT reliably detected moderate and severe G6PD deficient individuals (enzyme activity ,30%), suggesting that this novel point-of-care is a promising tool for tailoring appropriate primaquine treatment for malaria elimination in Cambodia.

Abstracts

POSTER PRESENTATIONS

2-4 December 2015

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Poster No. 1

IDENTIFICATION OF A NOVEL PLASMINOGEN-BINDING SEQUENCE IN THE LOOP REGION OF *PLASMODIUM FALCIPARUM* ENOLASE

Hiroyuki Oku[1], Yudai Kimoto[1], Nana Isomoto[1], Suguru Niwa[1], Kazuo Shinozuka[1],
Kazuhiko Yano[2], Shigeyuki Kano[2]

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[2] *National Center for Global Health and Medicine*

Objective - The interaction of *Plasmodium falciparum* with human plasmin(ogen) represents a mechanism to invade host-cells, such as human erythrocytes and mosquito midgut, by capturing surface-associated proteolytic activity in the infected host. Plasminogen binds to surface displayed *P.f.* enolase (PfEno) and is subsequently activated to the serine protease plasmin by host-derived tissue plasminogen activator or urokinase. In this poster, we will report a novel plasminogen-binding site of PfEno by using synthetic peptide libraries.

Methods - The screening was done for a library of the 35-amino-acids peptide sequence at the loop region of PfEno. It was divided into six overlapping peptides of 10 amino acids each with an offset of five amino acids, and analyzed with plasminogen. Binding analysis of plasminogen was performed using plasminogen in conjunction with peroxidase labelled anti-plasminogen antibodies.

Result - Previously, Lorena *et al* reported that the ^{277}D**K**SLV**K**^{282} sequence of PfEno were proposed as a binding site for the kringle motifs of plasminogen which contain lysine binding sites. In this study, we have identified a yet more plasminogen-binding site of PfEno. The ELISA and Dot-Blot analysis of the synthetic peptide library identified a 10-residue sequence as the stronger binding epitope mediating interaction between plasminogen and PfEno. Interestingly, the 10-residue sequence is located within an exposed surface loop in each of the monomers of the quaternary structure of PfEno, which may be a suitable target for inhibitory antibody for the host to overcome the acute symptomatic stage of falciparum malaria.

Keywords: Synthetic-peptide epitope-mapping, Plasminogen, Enolase, Malaria

Poster No. 2

HIGH GENETIC DIVERSITY OF *PVMSP1*F3 AND *PVCSP* GENES AMONG *PLASMODIUM VIVAX* ISOLATES ALONG THE BORDERS OF THAILAND

Sarunya Maneerattanasak[1], Panita Gosi[2], Srivicha Krudsood[3], Jarinee Tongshoob[1], Charlotte A. Lanteri[2], Georges Snounou[4] and Srisin Khusmith[1,5,#]

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Knowledge of the population genetics and transmission dynamics of *Plasmodium vivax* is crucial in predicting the emergence of drug resistance, relapse pattern and novel parasite phenotypes, all of which are relevant to the control of vivax infections. This study aims to analyse the multiplicity and genetic diversity of *P. vivax* genes under selective pressure from field isolates along the borders of Thailand. Two hundred and sixty seven *P.vivax* isolates collected during two periods 10 years apart along the borders of Thailand were analysed. The parasites were genotyped by nested-PCR followed by PCR-RFLP targeting selected polymorphic loci of *Pvmsp1* and *Pvcsp* genes. The total number of distinguishable allelic variants was 17 and 7 for *Pvcsp* and *Pvmsp1* respectively with high genetic diversity of *Pvcsp* (H_E=0.845) and *Pvmsp1* (H_E=0.707). Of the 267 isolates, 4.9% and 14.6% harboured mixed *Pvmsp1* and *Pvcsp* genotypes with a mean multiplicity of infection (MOI) of 1.06 and 1.15, respectively. The overall frequency of multiple genotypes was 17.6%. The genetic diversity of isolates collected at the Thai-Myanmar border was higher than that of parasites collected at the Thai-Cambodian border. When the frequencies of allelic variants of each gene during the two distinct periods were analysed, significant differences were noted for *Pvmsp1* (P=0.018) and *Pvcsp* (P=0.033) allelic variants. Despite the low malaria transmission levels, the *P. vivax* population in Thailand exhibit a high degree of genetic diversity, in particular for *Pvmsp1* and *Pvcsp*, with indications of geographic and temporal variations in frequencies for some variants. These results are of relevance to monitoring the emergence of drug resistance and to the elaboration of measures to control vivax malaria.

COMMUNITY ENGAGEMENT IN MALARIA PREVENTION AND CONTROL AMONG ETHNIC MINORITY GROUPS IN RATANAKIRI AND MONDOLKIRI PROVINCE

Poster No. 3

Ratana Somrongthong [1], Hoy Vannara [2], Pork Nivitu [3], Chhun Chanvut [4], Kem Sam O [4], Jaran Lumlert [5], Sirinate Pi yaji tpirat [5], Chaluoi Othintarayuth [1]

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Background: The initiative of HE Prime Minister Samdech Hun Sen and HRH Princess Maha Chakri Sirinthorn, the Community-Based Malaria Control Project in Ratanakiri and Mondolkiri has been underway since 2007. The key principle is a respect for local cultures in encouraging healthy behavior for disease control. In October 2014, the Community Life Competence Process (CLCP) was introduced to enhance ownership of malaria issues and response by the community.

Objective: This report aims to share the lessons learned of the CLCP.

Findings: Forty two local facilitators from Mondolkiri and Ratanakiri Provinces were recruited for the CLCP in 6 villages. They were trained on the CLCP including; Ways of Thinking (believing in people capacity), Ways of Working (SALT: Stimulate/Support/Share, Appreciate, Listen/Learn/Link, Transfer/Team), and the Steps of Working (dream building, self-assessment, resource mapping, action planning and self-measurement of progress). They were also introduced to essential facilitation skills. After being equipped, local facilitators teamed up to facilitate the community visioning and action planning activities in their respected communities. The process encouraged them to look first at their existing resources before exploring resources from the outside. In Ratanakiri province, the villagers contributed their labour and construction equipments while an NGO provided necessary materials to build the primary school. For Mondolkiri province, participating families have cleared the space, dig the pits, collected woods while waiting for outside support for other materials. In conclusion, through the CLCP communities now felt ownerships of their dreams and action plans. Communities will need regular coaching and support particularly in the first stages of the engagement.

Keywords: Malaria, Community Life, Competence Process, Ethnic group, Cambodia

Poster No. 4

EPIDEMIOLOGICAL SITUATION OF MALARIA AND ITS CONTROL AND ELIMINATION IN BANGLADESH

Mohammad Jahirul Karim[1,3], Md. Mushfiqur Rashman[2],
Abu Nayeem Md Sohel[3], Anjan Saha[3], Sazid Ibna Zaman[1],
Lisa J White[1,4], Richard J Maude[1,4,5]

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[5] *Harvard School of Public Health Boston, USA*

The Malaria Eradication Program in Bangladesh started in the 1960s and came close to eliminating malaria by widespread use of DDT and active and passive case detection. However, during the liberation war in 1971 the eradication program was discontinued and malaria greatly resurged. The National Malaria Control Program (NMCP) was formed in 1977 with the initial aim of control. Since 2007, NMCP activities have been greatly strengthened and accelerated with funding from the Global Fund and partnership with a BRAC-led 21 Member NGO Consortium and academic and research institutions. This has coincided with a near 3-fold decrease in annual confirmed malaria cases from 84,690 in 2008 to 26,891 in 2013 and there is now a plan for elimination. Widespread use of artemisinin combination therapies, long-lasting insecticide treated bednets and vector control measures were major contributors to this decrease. However the number of confirmed cases has almost doubled to 57,480 in 2014 with this increase continuing into 2015. *P falciparum* is found in 94% of cases and 97% occur in the three Hill Tract Districts in the Southeast. An analysis of historical malaria incidence data and malaria control activities will be presented with the aim of identifying possible causes and contributors to the sudden increase in malaria cases in Bangladesh. Possible contributors that will be discussed area change in climate and timing of the monsoon, relaxation of malaria control activities due to decreasing disease burden, a similar increase in cases in adjacent Tripura State in India and stockouts of ACTs. Challenges to achieving malaria elimination and strategies being considered to reverse the recent increase and ultimately achieve elimination, including increased community level diagnostics, improved drug supply, mass drug administration and mathematical modelling, will be discussed.

Keywords: Malaria, Epidemiological Situation, Elimination, Bangladesh

FIELD BASED *IN VITRO* INVASION INHIBITION ASSAY OF *PLASMODIUM VIVAX*

Poster No. 5

Wanlapa Roobsoong [1], Pattarasuda Puasri[1], John Adams [2], Jetsumon Prachumsri [1]

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[2] Department of Global Health, University of South Florida, USA

Evaluation of blood stage vaccines against *P. vivax* is hindered by the lack continuous culture limiting researchers ability to have reproducible, reliable and standardized protocol. The optimization of *in vitro* invasion inhibition assay (IIA) of *P. vivax* is the aim of this study. Two major factors that directly impact the assay are the parasites and the host red blood cells. Since field isolates of *P. vivax* are always asynchronous and parasitemias are usually low (often <0.05%), parasite enrichment is needed. Furthermore, *P. vivax* preference to invade reticulocytes requires addition of these cells to assays. Every study likely uses a different donor plus different sources of reticulocytes are utilized, including peripheral blood, cord blood and hematopoietic stem cell culture. The source as well as the percentage of reticulocytes that are optimal for IIA have yet to be determined. In this study, these variable factors of the IIA were targeted for optimization to simplify and increase the robustness of the assay. Prior to short term culture an enrichment of schizonts by 45% Percoll gradient was performed to efficiently increase the parasitemia. The Next Optiprep-purified reticulocytes were labeled with DDAO SE before being added as target cells to the IIA. Flow cytometry was used to quantify the signal of SYBR Green staining of parasite nuclear content. In the combination of host labeling and parasite staining, only parasites that invaded the providing reticulocytes were identified. The optimized IIA assay has been validated with anti-DBPII monoclonal antibodies and the details data will be presented and discussed.

Keywords: *Plasmodium vivax*, Invasion-inhibition-assay, anti-DBP, Flow-cytometry

Poster No. 6

THE CONSULTATIVE PROCESS OF DEVELOPING ROLL BACK MALARIA'S NEW "ACTION AND INVESTMENT TO DEFEAT MALARIA 2016-2030"

Helen Prytherch[1], Vanessa N. Racloz[2], Amadou Bah[3], Sally Stansfield[4], Maxine Whittaker[5]

[1] *Swiss Tropical and Public Health Institute, University Basel, Switzerland,*
[2] *Roll Back Malaria Partnership,*
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In July 2015 the Roll Back Malaria Partnership's second generation Global Malaria Action Plan, *Action and Investment to defeat Malaria 2016–2030 (AIM) – for a malaria-free world* was presented to world leaders at the 3rd International Conference on Financing for Development in Addis Ababa. AIM is the companion document to the WHO *Global Technical Strategy for Malaria 2016–2030*, and the process of their development has been strongly coordinated. Both documents share the 2016–2030 timeline of the Sustainable Development Goals, and provide direction towards the new WHO/RBM 2030 malaria goals.

AIM positions malaria in the wider health and development agenda, and calls for a multisectoral, inter-country and people-centered response post 2015. It is the result of a participatory consultative process that involved over 1600 stakeholders from more than 90 countries. Care was taken to involve countries with differing levels of transmission across all malaria-affected regions of the world. Regional and country level consultations were arranged with partners from the malaria community, broader health system and sectors as diverse as agriculture, infrastructure, education and housing. Constituency meetings with representatives of academia, civil society, donors and the private sector were also held, as well as community consultations to learn more about local responses, in particular in remote, fragile and high-burden communities. Social media was used to reach out to a wider audience, and a public online review of the draft document was held in English, French and Spanish.

Keywords: Malaria post-2015

APPLICATION OF ANTI-MALARIA RESCUE PACK AND ACTIVE CASE DETECTION IN MALARIA ACTIVE SURVEILLANCE AMONG MILITARY PERSONNEL DEPLOYED IN THAI-CAMBODIAN BORDERS AREAS OF OPERATION (AOs)

Poster No. 7

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Areas of Operation (AOs) along Thai borders are considered as risk areas of malaria transmissions. Civilians who lived along these areas were suffered from this potentially life-threatening disease including soldiers conducting their missions. Royal Thai Army (RTA) Medical department concerned the welfare to conserve the fighting forces from disease and non-battle injury (DNBI). AFRIMS-RTA innovated the portable detection and treatment set called AFRIMS Anti-Malaria Rescue Pack (which won the Thailand Public Service Awards; TPSA 2015 of Office of the Public Sector Development Commission) for well-trained medical sergeant to early detect and treat malaria patient during operating in the backcountry. In addition, we have conducting a continuous surveillance program, malaria active case detection in base of operations, to obtain the epidemiological information of malaria in AO Thai-Cambodian border. In Fiscal Year 2015, blood examination for malaria detection was performed in 6,851 soldiers and 21 positive cases were founded, 6 of *P. falciparum*, 14 of *P. vivax* and 1 of Mix infections, for a rate of infection of 0.31% (malaria infection rates 0.64% in civilians). Once detected, the infection treated immediately to break the cycle of disease thus control the spread of malaria. The decreased prevalence of malaria infection in this area from Fiscal Year 2014 (0.45%) could implied that application of anti-malaria rescue pack accompanied with active case detection as defensive strategies have been effectively implemented to prevent troops deployed to military operating areas from malaria infection and decreased transmission of disease

Keywords: Malaria, Anti-Malaria rescue pack, Thai-Combodian borders, Areas of Operation

Poster No. 8

RESIDUAL ANTIMALARIAL LEVELS IN *PLASMODIUM FALCIPARUM* MALARIA PATIENTS FROM SELECTED MALARIA-ENDEMIC SITES IN INDIA: AN EMERGING THREAT

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Background: The emergence of drug resistance is one of the major threats in malaria control programme, mainly due to the irrational treatment practices and self-medication of antimalarials in malaria-endemic areas. Such practices may also affect the treatment outcome as well as could promote the spread of drug resistance in the community. The present study quantified the residual antimalarials level in *Plasmodium falciparum* infected patients.

Methods: A total of 139 patients belonging to Bilaspur district (Chattisgarh) and Betul districts (Madhya Pradesh) in India were enrolled in the ongoing surveillance studies for the treatment of antimalarials (artesunate+sulphadoxine-pyrimethamine) as per national treatment policy. Their clinical follow-up was done as per WHO guidelines (2009). Heparinised blood (100µl) was taken on 31ET filter paper for quantifying antimalarials level on day 0 and post-treatment sulphadoxine levels on day 7 using High Performance Liquid Chromatography.

Results: About 27.3% of the patients showed residual antimalarials on day 0. Surprisingly, the residual levels did not correlated well with the information collected on case record forms. A significantly lower parasite density/µl of blood was observed in samples having residual antimalarials ($p<0.05$) than the samples without residual antimalarials.

Conclusions: The residual antimalarials detected in the blood might be due to the previous drug episodes, self medication or irrational treatment practices by the treating physicians. Awareness towards rational treatment practices is the need of hour.

Keyword Drug-resistance, Malaria, Residual drug level

GENETIC DIVERSITY OF *PLASMODIUM FALCIPARUM* POPULATIONS IN MALARIA DECLINING AREAS OF SABAH, NORTHERN BORNEO

Poster No. 9

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Malaysia has a national goal to eliminate malaria by 2020. However, there are still malaria cases remaining at endemic foci in Sabah. In the context of achieving malaria elimination targets, one of the key components is understanding the malaria parasite diversity through genetic population study. Thus, the objective of this study was to determine the genetic diversity level of *P. falciparum* isolates in Kalabakan and Kota Marudu by antigenic and neutral microsatellite markers. Active case detection was performed on selected study sites. All individuals at the sites were screened for malaria with rapid diagnostic kit and individuals positive for *P. falciparum* were selected for blood collection. Fifty microliters of malaria infected blood were spotted on the filter paper prior to parasite DNA extraction. Malaria species confirmation was done by PCR techniques. The *P. falciparum* DNA were subjected to genotyping for antigenic markers; merozoite surface protein-1 (MSP-1), merozoite surface protein-2 (MSP-2) and glutamate rich protein (GLURP) and 10 neutral microsatellite markers. The size of polymorphic alleles, multiplicity of infection (MOI), mean number of alleles, expected heterozygosity (*He*), linkage disequilibrium (LD) and genetic differentiation (F_{ST}) were determined. In Kalabakan, the *P. falciparum* polymorphic alleles of MSP-1 and MSP-2 belongs to family K1 and FC27 respectively. The GLURP genotype VI (751-800 bp) were predominant. The MOI for MSP-1 and MSP-2 were 1.65 and 1.20 respectively. The mean number of alleles per microsatellite locus was 1.70. The *He* level of Kalabakan *P. falciparum* for MSP-1, MSP-2, GLURP and neutral microsatellites were 0.17, 0.37, 0.70 and 0.33, respectively. A significant LD was observed (0.495, $p<0.01$). In Kota Marudu, the polymorphic alleles of MSP-1 and MSP-2 belongs to MAD20 and 3D7 family types respectively. The GLURP genotype IV (651-700 bp) was predominant. The MOI for both MSP-1 and MSP-2 were 1.05. The mean number of alleles per microsatellite locus was 3.60. The *He* level of Kota Marudu *P. falciparum* for MSP-1, MSP-2, GLURP and neutral microsatellites were 0.24, 0.25, 0.69 and 0.30, respectively. A significant LD was observed (0.601, $p<0.01$). Genetic differentiation between Kalabakan and Kota Marudu was high (F_{ST} =0.532). The results showed a high allele frequency (low number of allele per locus) and with low level of diversity (low H_e) for the antigenic and neutral microsatellite markers suggesting the limited genetic diversity of *P. falciparum* parasite populations circulating in Kalabakan and Kota Marudu. In addition, the different allele patterns of *P. falciparum* population indicating a clonal and unique population in each of the sites. Therefore, there are feasibility of eliminating this population and achieving the national malaria elimination targets.

Poster No. 10

CURRENT MALARIA SITUATION IN LAO PDR BASED ON DNA ANALYSIS BY SATREPS PROJECT

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SATREPS (Science and Technology Research Partnership for Sustainable Development) is a Japanese government program in collaboration between the Japan Agency for Medical Research and Development, and the Japan International Cooperation Agency, that promotes joint research targeting global issues, involving partnerships between researchers in Japan and developing countries. One of the important studies in the Lao SATREPS project is genetic epidemiology of malaria. Lao Ministry of Health has set a goal to eliminate malaria in this country by 2030. To achieve this goal, we need to know the real malaria situation in the country. We report the current malaria situation in Attapeu province based on DNA analysis. A total of 381 villagers participated in this survey in May 2015. Three diagnostic methods: microscopy, a rapid diagnostic test (RDT) and Real-Time PCR (RT-PCR) were used to detect malaria parasites. Two *Plasmodium falciparum* (*Pf*) and 3 *P. vivax* (*Pv*) were detected by the RDT, while 5 *Pf* and 37 *Pv* were detected by RT-PCR. All the 37 *Pv* cases were asymptomatic. Thus the sensitivity and specificity of the RDT for *Pf* were 40.0% and 100.0% and those for *Pv* were 8.1% and 100.0%, respectively. *Pv* was shown to be a predominant species in the study area in May 2015 by RT-PCR, while *Pf* was a predominant species in the area in 2013 by the Standard-Methods. These results suggest that RT-PCR can detect lower density of *Pv* (in asymptomatic-carriers), compared to the Standard-Methods, and that the prevalence of *Pv* among the villagers is higher than we have expected.

Keywords : SATREPS project, Lao PDR, Malaria

CHARACTERIZING MALARIA INFECTION AND ARTEMISININ RESISTANCE INFECTION AMONG POPULATIONS CROSSING FORMAL AND INFOMAL BORDER POINTS ON THE CAMBODIA-LAOS BORDER

Poster No. 11

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Cross border population movements done by Mobile Migrant Population (MMP) in particular are a challenge for malaria elimination. MMP can contribute in the spreading and reintroduction of malaria jeopardizing current control efforts. Finding novel ways to target these mobile groups is currently a focus of attention across the Greater Mekong Sub-region. A survey conducted in 2013 in Cambodia-Lao border identified malaria parasites in 11.5% of cross border population and K13 propeller domain gene mutation in 62.5% of *P. falciparum* samples. While this study provided information on cross border malaria prevalence at an official border site, little is known about what is occurring along the porous and non-controlled unofficial Cambodia-Lao border posts.

The aim of this study is to identify and compare the spread of malaria infection and resistance to artemisinin at official and unofficial border points. 4500 symptomatic and asymptomatic migrants will be tested for malaria infection (RDT and PCR) and for artemisinin resistance markers (PCR). Incidence will be described and compared between border points. Risk factors and transmission hotspots will be identified through standardized questionnaires and will be used to support National Centre for Parasitology, Entomology and Malaria Control (CNM) to identify priorities and target interventions in bordering areas.

Keywords: Malaria, Artemisinin Resistence, Cross Border

Poster No. 12

CHILDHOOD MALARIA INFECTION AND SCHOOL PERFORMANCE IN CHILDREN LIVING IN A MALARIA ENDEMIC AREA, WESTERN BORDER OF THAILAND

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Background: Malaria infection is still a major public health problem worldwide. Children are among the high risk group for malaria infection; some of them may have multiple attacks during their childhood. Malaria may affect neurological in children and lead to poor school performance in short-term (within 1-2 years). However, little knowledge has known about long-term impact of malaria infection in children. This study examined the association between childhood malaria infection and school performance among schoolchildren in primary-secondary school of Tanousri subdistrict, Suanphuang district, Ratchaburi province, Thailand.

Methods: A retrospective cohort study was conducted among schoolchildren aged 6 years old and older in a primary-secondary school of Tanousri subdistrict. History of malaria infection was obtained from the medical record of a malaria clinic in the area. School performance was assessed by using score in Thai language and Mathematics.

Results: A total of 457 students aged between 6-17 years was included in the study; 135 of them (30%) had history of uncomplicated malaria infection. The majority of them (83%) had last malaria infection in the past 3 years. Both of mean in mathematics and Thai language score decreased with increasing number of malaria attack. Mean scores were not associated with duration since the last malaria attack. The association between malaria infection and school performance was not significant after adjusting for potential confounders.

Conclusion: Past malaria infection during childhood was not associated with school performance, suggesting that the impact of childhood malaria infection on school performance may not last long.

Keywords: Malaria infection, School performance

CAPACITY BUILDING FOR MALARIA AND VECTOR BORNE DISEASE CONTROL PROGRAMME FOR THE SUB DISTRICT LEVEL SURVEILLANCE AND RAPID RESPONSE TEAM (SRRT) IN THAILAND

Poster No. 13

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Vector borne diseases are illnesses caused by pathogens and parasites in human populations. In Thailand, every year there are more than 50,000 cases and over 50 deaths from vector borne diseases such as dengue, malaria, scrub typhus, chikungunya fever and leishmaniasis. The Bureau of Vector Borne Disease works together with partners and many different government sectors to strengthen and enhance the capacity building in the proactive surveillance system including case detection, case investigation and vector control measures for the sub district health officers called as Surveillance and Rapid Response Team (SRRT) which are including sub district health promoting hospitals, sub district municipality administrative organizations, village health volunteers, village malaria volunteers and NGO workers in the sub district areas. The objective of the surveillance training program is to provide basic knowledge on malaria and vector borne diseases and to enable health personnel at sub district level to do malaria and vector borne disease surveillance, investigation, prevention and control. The capacity building in disease surveillance will be helpful for the malaria elimination and vector borne disease control program and will be useful for the SRRT at sub district level to do case investigation and control diseases effectively. Moreover, SRRT will also transfer the knowledge and educate villagers and others health personnel for effective prevention and control of vector borne diseases.

Keywords: Capacity Building, Vector Borne Disease

Poster No. 14

ACIDS CAUSING METABOLIC ACIDOSIS IN PATIENTS WITH SEVERE MALARIA (ASSESSING BY NOVEL METHOD)

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Acidosis is an important cause of mortality in severe falciparum malaria. A simultaneous bioanalytical method for qualitative and quantitative assessment in plasma of eight small organic acids potentially contributing to acidosis in severe malaria was developed and validated. High-throughput strong anion exchange solid-phase extraction in a 96-well plate format was used for sample preparation. Hydrophilic interaction liquid chromatography (HILIC) coupled to negative mass spectroscopy was utilized for separation, detection and quantification. Eight possible small organic acids; L-lactic acid (LA),α-hydroxybutyric acid (aHBA), β-hydroxybutyric acid (bHBA), p-hydroxyphenyllactic acid (pHPLA), malonic acid (MA), methylmalonic acid (MMA), ethylmalonic acid (EMA) and α-ketoglutaric acid (aKGA) were analyzed simultaneously using a ZIC-HILIC column. This method was validated according to U.S. Food and Drug Administration guidelines with additional validation procedures for endogenous substances. LC-MS acid concentration profiles in relation to clinical parameters of three groups; severe malaria, uncomplicated malaria and healthy were analyzed by pattern recognition analysis to compare, classify and predict unknown samples. The results of principal component analysis (PCA) showed that four acids (LA, aHBA, bHBA and pHPLA) have more significant discriminant power than other four, thus they all considered. In addition, PCA result showed that healthy could be classified from malaria completely with variance of three first PCs (73.11, 15.41 and 7.84%, respectively), however severe could not classify from uncomplicated completely. Linear discriminant analysis (LDA) model indicated excellent sensitivity and specificity for identification of malaria and healthy in cross validated prediction. However, the result indicated fair sensitivity (65%) and good specificity (91%) for identification of severe and uncomplicated in cross validated prediction. This could be useful tool for better understanding the pathogenesis of acidosis in severe malaria patients. Furthermore, this could guide to the development of new therapies.

Keywords: Acidosis, Severe malaria, Unidentified acids, Liquid Chromatography-Mass Spectrometry, Chemometrics

POLYMORPHISM IN *PLASMODIUM FALCIPARUM* K13-PROPELLER FROM THAI-MYANMAR BORDER IN 1996-1997

Poster No. 15

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Artemisinin-based combination therapy (ACT) is recognized as the most effective treatment of *Plasmodium falciparum* malaria and has contributed to the reduction in malaria related mortality and morbidity. However, the emergence and spread of artemisinin resistance is the most important obstacle for malaria control and prevention. Recently, a K13-propeller polymorphism has been found to be a useful molecular marker associated with artemisinin resistance. And to date, at least 60 mutations have been identified. Although the ACT has been used as first-line therapy in Thailand since 1995, all reports have analyzed samples collected after 2002. In this study, we evaluated the polymorphism of K13-propeller in isolates from Thai-Myanmar border area in 1996 and 1997 to provide baseline prevalence of K13-propeller mutations at an early date of artemisinin use. We analyzed 109 samples diagnosed as *P. falciparum* infection by microscopy when collected. All the samples were confirmed by PCR as *P. falciparum* infection, and M579T and A582T polymorphisms were found by sequencing in one sample. Our study suggested that, even in an early date of artemisinin use, polymorphisms in *P. falciparum* K13-propeller existed and had been waiting for their selection in Thai-Myanmar border.

Keywords: *Plasmodium falciparum*, K13-propeller, Artemisinin-based therapy

Poster No. 16

SEROPREVALENCE OF *TOXOPLASMA GONDII* IN FREE RANGE CHICKEN (*GALLUS DOMESTICUS*) FROM KHON KAEN PROVINCE

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Toxoplasmosis is zoonotic diseases which worldwide spread. The oocyst of *Toxoplasma gondii* is resistance in environment and contaminated in soil, fruits and water resources. *Toxoplasma gondii*-infected meat of chicken (*Gallus domesticus*) is consumed widely in many countries including Thailand. This study aims to determine the seroprevalence of *T. gondii* from Khon Kaen province, northeast Thailand using Latex agglutination. Two hundred and fifty five free range chickens from Khon Kaen province were collected serum. Specific IgG antibody to *T. gondii* in chicken sera was determined by Latex agglutination kit (Biomeriuax, France). Seropositive of anti-*T. gondii* antibody at cut off 1:40 were found in 26 of 257 (10.12%) chickens. The antibodies to *T. gondii* were 3 (4.62%) in Muang, 10 (16.95%) in Banphai, 3 (5.45%) in Nongrua, 5 (8.33%) in Banfang and 5 (50.0%) in Chonnabot. The result of this study revealed that infection with *T. gondii* was found in free range chicken from Khon Kaen province. It has been conclude that the undercooked chicken meat could be source of *T. gondii* infection.

Keywords: *Toxoplasma gondii*, chicken, Latex agglutination

SURVEY OF INTESTINAL PROTOZOA IN PIGS AND THEIR IN-CONTACT HUMANS IN NAKHON PATHOM PROVINCE, THAILAND

Poster No. 17

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In spite of long-term global efforts and large investments to decrease the disease burden, enteric protozoan diseases remain a major health issue worldwide, especially in developing countries. *Blastocystis*, *Enterocytozoon* and *Cryptosporidium* 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 *Blastocystis*, *Enterocytozoon* and *Cryptosporidium* was done using nested PCR. In human, 4/142 (2.8%) of *Blastocystis* and 13/142 (9.2%) of *Enterocytozoon* were found while 32/102 (31.4%) of *Blastocystis* and 17/102 (16.7%) of *Enterocytozoon* were found in pigs. No *Cryptosporidium* (0%) was detected in both pig and human samples. Although further studies are required to clarify the species/genotype of these parasites in this region, the significance of the present results highlights that it is crucial to strength surveillance on intestinal pathogens as close contact between humans and pigs may increase the risks of zoonotic transmission, especially from *Blastocystis* and *Enterocytozoon*.

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

Poster No. 18

DETECTION AND MOLECULAR IDENTIFICATION OF *CRYPTOSPORIDIUM* FROM EDIBLE BIVALVES OF MANILA BAY, PHILIPPINES

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Manila Bay is known to be one of the propagation sites of edible bivalves in the Philippines. The harvests in this site target the demands of the Metro Manila markets. While consumption of raw or lightly-cooked bivalves is very common in the Philippines, studies show that bivalves might be contaminated with pathogens which are harmful to humans. This is because of their filter feeding mode of nutrition. One common pathogen is the protozoan parasite of the genus *Cryptosporidium* (Phylum Apicomplexa) that has emerged as one of the major causes of human gastroenteritis in both developed and developing countries. In this study, isolation of*Cryptosporidium* oocysts from edible bivalves was done using combination of both sucrose flotation and immunomagnetic separation (IMS). Based on microscopic investigations, *Cryptosporidium* oocysts were found in 69 out of 144 samples that were collected in six major bivalve harvesting sites around Manila Bay. Since oocysts of different species of *Cryptosporidium* are indistinguishable by microscopic examinations, molecular approaches were carried out to determine the species of the oocysts obtained. The DNA sequence analysis of the 18S rRNA gene was found to detect *C. parvum*, *C. hominis*, and *C. meleagridis* in 47 out of the 69 microscopy positive samples. *C. parvum* and *C. hominis* are known to be the cause of majority of human cryptosporidiosis worldwide while *C. meleagridis* is known to infect avian species. This study showed that humans and other animals ingesting contaminated shellfish are exposed to both host-specific and anthropozoonotic *Cryptosporidium* species of public health significance.

Keywords: *Cryptosporidium*, Manila Bay, bivalves

DISTRIBUTION OF *BLASTOCYSTIS* SUBTYPES IN VILLAGERS LIVING IN CENTRAL PART OF THAILAND

Poster No. 19

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Blastocystis is an intestinal protozoan parasite commonly found in humans and animal hosts. *Blastocystis* infection is transmitted by fecal-oral route. Several methods can be used to examine this parasite such as microscopy, culture and molecular techniques. Based on the characterization of the small-subunit ribosomal RNA (*ssrRNA*) gene, at least 17 subtypes (STs) of *Blastocystis* have been identified. A total of 130 stool samples were collected and extracted DNA. Nested PCR and DNA sequencing were performed. The results showed that the prevalence of *Blastocystis* infection was 3.07% (4/130). ST3 (2.3%; 3/130) was the predominant subtype, followed by ST2 (0.77%; 1/130). Therefore, proper health education in parasitic infection should be performed in this villagers. However, further study is required to increase the sample size and collect the stool samples from the animals.

Keywords: *Blastocystis*, villagers, subtypes

Poster No. 20

MOLECULAR CHARACTERIZATION OF *BLASTOCYSTIS SP*. IN LONG-TAILED MACAQUES (*MACACA FASCICULARIS*) FROM THE PHILIPPINES

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Blastocystis sp. is a common intestinal protozoan parasite that infects humans, domestic animals, and wild animals. In particular, it infects wild animals such as non-human primates and monkeys. Recent studies have classified *Blastocystis sp*. into 17 different subtypes (STs) based on a 600-bp partial segment sequence of its 18S SSU-rRNA. Due to its wide range of hosts, *Blastocystis sp*. STs are being studied to identify possible animal-to-human and human-to-animal transmissions. In the Philippines, *Blastocystis sp*. has been previously detected and subtyped in 4 Philippine long-tailed macaques. The STs present were identified as ST1, ST2, and ST3. In this study, *Blastocystis sp*. STs present in captive Philippine macaques from the Parks and Wildlife Bureau (PAWB) were identified. ST identification can be a helpful tool in determining possible host-specificity of certain *Blastocystis sp*. STs. Thirty-three (33) out of 62 (53.22%) Philippine macaques were positive for *Blastocystis sp*. in culture. Of the 33, 12 isolates were PCR-positive. Sequencing shows that 11 of the 12 isolates are ST1 while the remaining 1 isolate was ST3. Results show that ST1 is more common in this set of captive macaques in the Philippines compared to other STs (e.g., ST2, ST3).

Keywords: *Blastocystis, Macaca fascicularis* subtyping

SUBTYPE ANALYSIS OF *BLASTOCYSTIS* SP. ISOLATES FROM SYMPTOMATIC AND ASYMPTOMATIC INDIVIDUALS IN THE PHILIPPINES

Poster No. 21

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Blastocystis sp. is an intestinal protozoan parasite commonly found in humans and animals. This parasite can also be found in water samples. *Blastocystis* sp. has 17 different subtypes (STs) based on its full 18S SSU-rRNA gene sequence. However, these STs can also be properly determined by sequencing the 600-bp partial segment of the *Blastocystis* sp. 18S SSU-rRNA gene. This barcoding region can be amplified by the primers RD5 and BhRDr. Knowledge on common STs found in symptomatic and asymptomatic patients could help in identifying STs related to symptoms of gastrointestinal disease. So far, only 5 *Blastocystis* sp. human isolates have been subtyped and published in the Philippines using the 18S SSU-rRNA sequence ST classification. This study aims to determine the distribution of *Blastocystis* sp. STs in symptomatic and asymptomatic individuals in the Philippines. A total of 68 sequences were obtained from DNA extracts of *Blastocystis* sp. collected from residents of different areas in the Philippines. These include residents of the cities of Pateros (n=29), Manila (n=11), provinces of Laguna (n=2), Rizal (n=17), and Batangas (n=1). Also included are patients from the Philippine General Hospital (n=4) and Philippine Heart Center (n=2) and zookeepers from Manila Zoo (n=2). ST3 is the most prevalent ST in this dataset (77.27%). The other STs identified were ST1 (24.24%) and ST4 (1.52%). The results are similar to other studies in Asian populations where ST3 is the most common ST.

Keywords: *Blastocystis*, humans, subtypes, Philippines

Poster No. 22

HUMAN GIARDIASIS IN MALAYSIA: ASSOCIATION BETWEEN THE PRESENCE OF CLINICAL MANIFESTATIONS AND THE ASSEMBLAGE

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Objective: The cross-sectional study was conducted to determine any association between *Giardia intestinalis* assemblage and the presence or absence of clinical manifestations in participants less than 15 and ≥15 years of age.

Methods: Stool samples were collected from 611 participants, aged between 2 and 74 years old. Demographic data were collected through a structured questionnaire. All samples were processed with Wheatley's trichrome staining for the primary identification of cysts and/or trophozoites. Molecular characterization was carried out by nested-PCR and sequence analysis of the triosephosphate isomerase (*tpi*) gene.

Results: The *tpi* gene was successfully amplified from 98 (89.1%) of the 110 microscopically positive for *G. intestinalis*. Among these, 62 and 36 were assemblages A and B, respectively. A significant association was found between assemblage A and symptomatic and between assemblage B and asymptomatic in the overall populations studied ($p < 0.05$), and in the participants less than 15 years ($p < 0.01$). Nevertheless, if only participants of ≥15 years of age were considered, no statistically significant relationship between assemblage and symptomatic and asymptomatic giardiasis was found.

Conclusion: It was concluded that giardiasis is still a public health problem in Malaysia, with a predominance of assemblage A. The present findings also provide evidence that host factors may affect the presence of clinical manifestations more than *G. intestinalis* assemblage.

Keyword Giardiasis, assemblage, children, diarrhea, Malaysia

MOLECULAR METHOD OF VISCERAL LEISHMANIASIS DIAGNOSIS IN NEPAL

Poster No. 23

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Introduction: There are, nowadays, global concerns to control, eliminate, if possible, the deadliest tropical diseases mainly through the improvement in early diagnosis, adequate and prompt treatment. *Leishmania donovani* is a protozoan parasite transmitted by phlebotomine sand flies which causes a disease commonly known as visceral leishmaniasis (VL). Microscopy is still considered as a gold standard for diagnosis of VL. However, a great disadvantage of microscopy is the requirements of infrastructures, supplies and to be performed by well-trained personnel. Rapid diagnostic tests (RDTs) are being deployed and used to improve diagnosis.

Methodology: We evaluated *Leishmania* RDT kit as a DNA source for quality control method and/or for further molecular surveillance. One hundred and forty seven samples were obtained from suspected VL patients who visited hospitals for proper diagnosis and treatment. Blood accumulated RDT kits were used for DNA extraction. As a proof-of-principle, we PCR amplified minicircle kinetoplast DNA from RDT kits.

Result: We were able to detect up to one parasite per microliter even from samples stored at room temperature for 3 months. The diagnostic capacity of the RDTs assessed by PCR positivity, showed a sensitivity of 61% and specificity of 71%. We showed that it was possible to detect very low *Leishmania* parasites in RDTs using a PCR-based method. We identified a variety of kinetoplast DNA sequences in Nepalese clinical samples.

Conclusion: DNA can be extracted from used RDTs and may constitute an important, reliable, and affordable tool to assist in future leishmaniasis molecular surveillance methods.

Keyword Visceral Leishmaniasis, RDT, Nepal

Poster No. 24

VISCERAL LEISHMANIASIS INDUCED BY NEWLY EMERGED *LEISHMANIA MARTINIQUENSIS* IN BALB/C MICE USING DIFFERENT ROUTES OF PARASITE INOCULATION

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Leishmania martiniquensis is a newly emerged parasitic protozoan causing autochthonous human infection in Thailand. Since fundamental pathologic research of *L. martiniquensis* infection using murine experimental model is lacking, the aim of this research was to study parasite burden and pathology in BALB/c mice experimentally inoculated with 5x10^6 *L. martiniquensis*promastigotes via subcutaneous (s.c.), intraperitoneal (i.p.) and intravenous route (i.v.). On 7, 14, 28 and 112 days post-infection, dpi, microscopic examination of impression smear and molecular detection of *L. martiniquensis* DNAs of liver and spleen were conducted to evaluate parasite burden. Hematocrit values, weights and histopathology of livers and spleens were comparatively assessed between different routes and time points. From impression smear, levels of parasite burden in liver and spleen on 7, 14 and 28 dpi via i.v. route were found significantly higher than did other groups ($p<0.05$). On 112 dpi via i.v. route, no parasite was detected in liver whereas high level of amastigotes was still persistent in spleen ($p<0.05$). These results were also correlated with molecular detection results in target organs. The weights of liver in i.v. group were significantly higher on 7, 14, 28 dpi while the weights of spleen were significantly higher in all time points ($p<0.05$). The numbers of liver granuloma were significantly greater in all time points ($p<0.05$). This study is the first to demonstrate that *L. martiniquensis* is pathogenic in experimental BALB/c mice via i.v. and i.p. routes hence enabling to serve as a murine model for visceral leishmaniasis.

Keywords: *Leishmania martiniquensis*, BALB/c mouse, experimental infection pathology

PREVALENCE OF CATTLE HAEMOPARASITES IN CHACHOENGSAO PROVINCE, THAILAND

Poster No. 25

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Anaplasma, Babesia, Theileria, and *Trypanosoma* are important pathogenic haemoparasites found in cattle worldwide. Transmission cycle of these parasites involves arthropod vectors including blood sucking flies and/or ticks. All of these haemoparasites affect animal health status and lead to a decrease in animal production. The presence of these parasites contributes to economical impacts of livestock industries. This study investigated the prevalence of haemoparasites and the presence of arthropod vectors in Chachoengsao province, Thailand. One hundred and one blood samples were collected from non-clinical sign cattle between February and March 2015. These samples were examined for haemoparasites by using microscopic examination of thin blood smears. A total of 31.68% (32/101) of cattle were only infected with *Anaplasma marginale*, and 13.85% (14/101) of cattle were only infected with *Theileria* spp. In addition, a total of 4.95% (5/101) of cattle were co-infected with *Anaplasma marginale* and *Theileria* spp. Blood-sucking arthropod vectors found in the study areas included *Culex* spp., *Haematobia* spp., *Rhipicephalus (Boophilus) microplus*, and *Stomoxys calcitrans*. However, further studies need to be performed to indicate roles of these vectors in the ecology and transmission cycle of haemoparasites in Thailand.

Keywords: Haemoparasites, Cattle, Chachoengsao, Microscopy examination

Poster No. 26

MOLECULAR SURVEY OF PARASITIC FILARIA IN DOMESTIC CATS AND POTENTIAL VECTORS FROM SURAT THANI, THAILAND

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Filariasis is an important tropical parasitic disease caused by filarial nematode with different clinical manifestation *eg*, elephantiasis, scrotal hydrocele and lymphedema *etc*. In Thailand, the filarial infections have been reported in human, resovoir host (cat) and vector, especially in Surat Thani province. In this study, 78 individual cat's dried blood spots and 804 potential vectors (*Mansonia* spp. and *Culex* spp.) collected from Surat Thani province in 2014 were detected for filarial infection using Nested-Polymerase Chain Reaction (PCR) and DNA sequencing. The result showed that 11 (14.10%) of cat blood samples were infected with filaria including 5 *Dirofilaria repens* (45.45%), 3 *Brugia pahangi* (27.27%) and 3 *Dirofilaria immitis* (27.27%). Fortunately, *B. malayi* was not been found in this survey. For investigation of filarial infection in mosquitoes, 795 individual *Mansonia* spp. (*M.annulata*, *M.indiana*, *M.uniformis* and *M.bonneae*) and 9 individual *Culex* spp. (*C.tritaeniorhynchus, C.gelidus, C.quinquefasciatus*) were pooled into 5-20 mosquitoes/tube and are being determined by molecular identification as above. In this survey, detection of potential zoonotic filariasis in domestic cats and probably in vectors may consider and concern as a health problem in human and domestic animals in this area.

Keywords: Filaria, domestic cat, Nested PCR

Poster No. 27

SEROPREVALENCE OF CANINE VECTOR-BORNE INFECTIONS IN MAJOR REGIONS OF BANGKOK, THAILAND

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Ehrlichiosis, Anaplasmosis, Lyme borreliosis and heartworm disease are important canine vector-borne diseases and considered as potentially zoonotic agents. The aim of this study was to perform serological survey of their causative pathogens. From monthly mobile public veterinary service between April and December 2014, the retrospective study was conducted from the data of parasitological diagnostic results. Dog blood samples were examined for the presence of blood parasites by using Woo's method and Giemsa-stained buffy coat smear technique. Plasma was isolated and serologically tested with SNAP®4Dx® Plus. From a total of 423 canine blood samples, 4.0% (17/423) were positive to any parasite by conventional microscopic examination. *Hepatozoon canis*, large form of *Babesia*, sheathed microfilaria, unsheathed microfilaria, and *Ehrlichia canis* were found 3.3% (14/423), 0.5% (2/423), 0.5% (2/423) 0.2% (1/423) and 0.2% (1/423), respectively. For the serological test result, 45.7% (122/267) out of 267 samples tested were seropositive to any parasite. Antibodies against *Ehrlichia canis* and/or *E. ewingii* and *Anaplasma phagocytophilum* and/or *A. platys* were detected 26.2% (70/267) and 2.6% (7/267) of tested samples, respectively. Circulating antigens of *Dirofilaria immitis* was found 0.4% of tested samples (1/267). Simultaneous presences of antibodies against *Ehrlichia canis* and/or *E. ewingii* and *Anaplasma phagocytophilum* and/or *A. platys* were detected 16.1% (43/267) whereas antibody against *Ehrlichia canis* and/or *E. ewingii* and *Dirofilaria immitis* antigen were concurrently detected 0.4% (1/267). None of the samples was positive to *Borrelia burgdorferi* antibody detection. The result from this study is the most updated on seroprevalence of canine vector-borne infections in Bangkok, Thailand.

Keywords: dog, vector-borne disease, seroprevalence, Bangkok

Poster No. 28

OXIDATIVE STRESS-MEDIATED MOUSE LIVER LESIONS CAUSED BY *CLONORCHIS SINENSIS* INFESTATION

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Clonorchis sinensis is a high-risk pathogenic helminth that strongly provokes inflammation, epithelial hyperplasia, periductal fibrosis, and even cholangiocarcinoma (CCA) in chronically infected individuals. Chronic inflammation is associated with an increased risk of various cancers due to the disruption of redox homeostasis. Accordingly, the present study was conducted to examine the time course relationship between histopathologic changes and the appearance of oxidative stress markers, including lipid peroxidation (LPO), enzymes involved in LPO, and mutagenic DNA adducts in the livers of mice infected with *C. sinensis*, as well as proinflammatory cytokines in infected mouse sera. Histopathologic phenotypes, such as bile duct epithelial hyperplasia, periductal fibrosis, edema, and inflammatory infiltration, increased in infected livers in a time-dependent manner. Intense immunoreactivities of LPO products (4-hydroxy-2-nonenal [HNE]; malondialdehyde [MDA]), cyclooxygenase-2 (COX-2), 5-lipoxygenase (5-LOX), and 8-oxo-7,8-dihydro-2′-deoxyguanosine (8-oxodG) were concomitantly observed in these injured regions. We also found elevated expressions of COX-2 and 5-LOX in *C. sinensis* excretory-secretory product-treated CCA cells. Moreover, the levels of proinflammatory cytokines such as TNF-α, ILβ-1, and IL-6 were differentially upregulated in infected sera. With regard to oxidative stress-mediated carcinogenesis, our findings suggest that *C. sinensis* infestation may disrupt host redox homeostasis, creating a damaging environment that favors the development of advanced hepatobiliary diseases such as clonorchiasis-associated CCA.

Keywords: *Clonorchis sinensis*; Cholangiocarcinoma; Oxidative stress; Lipid peroxidation; Proinflammatory cytokines

THIRD STAGE *GNATHOSTOMA SPINIGERUM* LARVA EXCRETORY SECRETORY ANTIGENS ALTER FUNCTION OF FC GAMMA RECEPTOR I MEDIATED MONOCYTES IN PERIPHERAL BLOOD MONONUCLEAR CELL CULTURE

Background: Third (infective) stage *Gnathostoma spinigerum* larvae (L3) mainly cause human Gnathostomiasis. *G. spinigerum* L3 migrate throughout subcutaneous tissues, vital organs and the central nervous system, and can cause sudden death. Interestingly, they can survive and evade host cellular immunity for months or years. The effects of *G. spinigerum* ES products involved in larval migration and immune-evasive strategies are unknown. Monocyte is one of innate immune cells that protect against helminthic infections by phagocytosis. Fc gamma receptor I (FcγRI) is a high affinity receptor particularly expressed on monocytes and macrophages. The cross-linking of FcγRI and antigen-antibody complex initiates signal transduction cascades in phagocytosis. This study investigated whether ES antigen (ESA) from *G. spinigerum* L3 affected monocyte functions.

Results: Cultures of normal peripheral blood mononuclear cells (PBMC) separated from healthy buffy coats were used as a human immune cell model. ESA was prepared from *G. spinigerum* L3 culture. Using real-time quantitative reverse transcription-polymerase chain reaction (qRT–PCR) ESA tended to down regulate FcγRI mRNA expression in PBMC during 90 min of observation. Flow cytometry analysis revealed a trend of phenotypic decreased FcγRI expression on monocyte surface at 12 hours (h) of cultivation. Consistently, significant reduced monocyte-mediated phagocytosis capacity was observed after 12 h of ESA pretreatment ($P = 0.001$).

Conclusions: Our results support that *G. spinigerum* ESA modulates monocyte function via transcriptional down-regulation of FcγRI expression. This study provides preliminary information for future in-depth studies to elucidate mechanisms of immune-evasive strategy of *G. spinigerum* larvae.

Keywords: *Gnathostoma spinigerum*, excretory secretory, FcγRI, monocytes, phagocytosis

Poster No. 29

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Poster No. 30

ASSESSMENT OF SCHISTOSOMIASIS ENDEMIC AREAS DECLARED NEARING ELIMINATION USING PARASITOLOGICAL AND SEROLOGICAL TECHNIQUES

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Accurate diagnosis and surveillance of schistosomiasis remain a problem in the Philippines due to the low sensitivity of current diagnostic technique routinely used, Kato-Katz technique. This may pose problem in determining true status of infection in endemic areas, particularly in areas at near-elimination level. This study aimed to determine appropriate diagnostic test for diagnosis and surveillance of *S. japonicum* in areas at near-elimination level. Specifically, this study aimed to determine prevalence of schistosomiasis using Kato-Katz technique, FECT, COPT, and ELISA antibody & antigen detection tests in selected study sites, and to compare sensitivity and specificity of the different diagnostic techniques. The study was conducted in Bohol, Zamboanga del Norte (ZDN), and Agusan del Sur (ADS).

Bohol had zero prevalence using KK and 0.2% using FECT. ZDN had zero prevalence using both parasitological techniques. ADS had a prevalence of 17.6% using KK and 2.5% using FECT. For serological techniques, Bohol had a 10.1%, 15.7%, and 5.1% seroprevalence using COPT, ELISA Ab, and ELISA Ag respectively. ZDN had 12%, 18.3%, and 12.9% using COPT, ELISA Ab, and ELISA Ag respectively. ADS had 27.2%, 58.5%, and 30.5% using COPT, ELISA Ab, and ELISA Ag respectively.

Results highlight that current prevalence data on schistosomiasis being reported, which is based on parasitological techniques, is not likely reflective of the true prevalence of the infection. It also points to the need to include serological tests as one of the surveillance methods to estimate the true prevalence of schistosomiasis in endemic areas. Results showed ELISA Ab and Ag detection as the tests to be strongly considered to fill this particular need.

Keywords: Schistosomiasis, diagnosis, surveillance, prevalence, ELISA

THIRD STAGE *GNATHOSTOMA SPINIGERUM* LARVA EXCRETORY SECRETION INDUCE APOPTOSIS IN HUMAN PERIPHERAL BLOOD MONONUCLEAR CELL CULTURE

Poster No. 31

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Background: Human gnathostomiasis, mainly *Gnathostoma spinigerum (G. spinigerum)*, is an important foodborne zoonosis in endemic areas of Central and South America, and Asia. The pathogenesis is caused by *G. spinigerum* L3 migrate through subcutaneous tissue and internal organs such as brain, spinal cord, auditory, ocular, and produce intermittent, migratory swelling in the skin near or distant from the original site and may last for a week. Interestingly, *G. spinigerum* L3 can survive and evade from host cellular immunity for months or years.

Apoptosis is a structurally distinct mode of cell death that is morphologically characterized by cell shrinkage occurred with transient but violent surface bubbling and blebbing, ultimately resulting in the separation of the cell into a cluster of membrane-bound bodies. Previous studies have been reported the modulation of host immunity, and the occurrence of apoptosis of immune cells associated with excretory secretion (ES) released from various helminthes. This study aimed to determine whether ES could induce apoptosis in human immune cells. Cultures of normal peripheral blood mononuclear cells (PBMC) separated from healthy buffy coats were used as a human immune cell model. ES was prepared from *G. spinigerum* L3 culture. PBMC treated with ES (0.1-1.0 µg /ml) were investigate morphology changes, amount of apoptotic cells by flow cytometry (FACS) using annexin V/propidium iodide method.

Results: FACS analysis revealed ES at the dose of 0.5-1 microgram /ml was markedly induced apoptosis in PBMC culture during 18-48 hours of incubation. While PBMC cultured in medium alone or plus interleukin-2 were mostly intact.

Conclusion: The findings may contribute the understanding in one of immune evasion strategies of *G. spinigerum* L3 in the infected patients.

Keywords: *Gnathostoma spinigerum*, excretory secretory, apoptosis

Poster No. 32

THE EFFECTIVITY OF PERSONAL THERAPY BEFORE THE IMPLEMENTATION OF MASS TREATMENT IN LYMPHATIC FILARIASIS IN SOUTH BORNEO, INDONESIA

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Background Lymphatic filariasis (LF) still endemic in Indonesia. *Brugia malayi* is the main species that cause of LF in Indonesia with prevalence more than 70%. Mass treatment will be implemented if the mf rate is more than 1%. Personal treatment in LF caused by *Brugia malayi* is DEC 5 mg/body weight/day for 10 days. The aim of this study is to see the effectivity of personal therapy compared to mass treatment.

Method The study was conducted in Gullinggang Village, one of 3 villages with microfilaria positive, from March 2014 until March 2015. Total 15 subjects with microfilaria positive were given DEC for 10 days in March 2014. Six months and 1 year post therapy, finger blood was taken from all of the subjects. Measured blood samples of 60 mm^3 made on slides and divided into 3 lines (20 mm^3/line) then stained with giemsa. The identification and counting of microfilaria was carried out.

Results Most of the Gullingang village inhabitants are rubber plantation farmer who engaged at the plantation site from 6 am to 12 pm and exposed to mosquitoes. From 15 subjects, only 6 subjects (40%) completed the therapy, the rest either did not complete the therapy or did not take the therapy at all. Six months post therapy, 1 of the 6 subjects became mf positive again (2 mf/60 mm^3 blood). One year post therapy, total of 2 subjects from 6 subjects became mf positive again (1-2 mf/60 mm^3 blood).

Conclusion The transmission of LF in Gullingang Village happened as soon as 6 months post therapy. If the personal therapy implemented to treat the patients just not effective, how about the mass therapy?

Keywords: *Brugia malayi*, personal therapy

HIGH PREVALENCE AND INTENSITY OF STH INFECTIONS IN MASBATE PROVINCE: TEN YEARS AFTER IMPLEMENTATION OF INTEGRATED HELMINTH CONTROL PROGRAM IN THE PHILIPPINES

Poster No. 33

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Soil-transmitted helminth (STH) infections remain a public health concern in the Philippines, particularly in preschool-age children (PSAC). This study was conducted to provide baseline parasitological and hemoglobin data in PSAC in selected municipalities in Masbate, a province with the third lowest human development index in the Philippines. The cross sectional study, which included 1,224 PSAC, utilized Kato-Katz technique and HemoCue 201+ analyzer to assess the parasitological and hemoglobin status, respectively.

Results showed a prevalence of STH infections of 72% and moderate-heavy intensity infections of 41%. Co-infection rate was high with *Ascaris-Trichuris* co-infection being most common in 40% of those surveyed. These parameters were high even in barangays declared as open defecation free by Action Contre La Faim and local government units. Prevalence of anemia is also high at 50%.

The high burden of STH infections, similar to the burden ten years ago prior to the implementation of the Integrated Helminth Control Program, reflects gaps in helminth control in the country. This could be attributed to low deworming coverage, confounding challenges in water, sanitation, and hygiene (WASH), challenges in health promotion and high poverty incidence, among others.

Recommended strategies to improve STH control include increasing access to preventive chemotherapy through program integration and strategies such as Day Care Center-based deworming, improving WASH, and addressing the social determinants of health (SDH). The War on Worms Campaign, which improved helminth control outcomes in various sites in the country, may also be adopted.

Recent developments in global health such as inclusion of neglected tropical diseases in the sustainable development goals and interests on universal health care and SDH also provide opportunities in addressing STH infection more effectively. ✻

Keywords: STH infection, anemia, preschool, Philippines

DETECTION OF VIABLE HOOKWORM OVA FROM WASTE WATER

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Poster No. 34

A method for a detection of viable hookworm ova from wastewater and environmental samples is fundamental to identify the source of infection in hookworm endemic regions. In this study, we have evaluated efficacy of the Propidium Monoazide (PMA) to discriminate the non-viable hookworm ova from viable ones. The method was further validated using raw wastewater, human fecal and environmental soil samples. Results of this study confirmed that PMA-qPCR has resulted 80 % - 100% reduction in gene copy numbers for 50% viable + 50% non-viable and 100% non-viable *Ancylostoma caninum* ova. Similar results were also observed for viable and non-viable ova seeded wastewater. The percentage of reduction was statistical significant ($P < 0.05$). For the human fecal samples, average gene copy numbers obtained from qPCR and PMA-qPCR was found to be similar ($1.2 \in 102$ to $2.1 \in 105$) and ($2.5 \in 103$ to $2.9 \in 105$), respectively indicating present of viable *Necator americanus* ova in them. Conversely, *Ascaris lumbricoides* gene copy numbers in the environmental soil sample determined by qPCR was significantly ($P > 0.05$) higher than the gene copy numbers determined by PMA-qPCR. However, the ova recovery rate of flotation method and DNA extraction efficiency of Mo Bio Power Soil DNA extraction kit was variable within and between the samples that could have the variation in gene copy numbers determined by PMA-qPCR from ova seeded wastewater samples. Variation in the gene copy numbers in different stages of helminth ova need to be further investigated to adopt the PMA-qPCR for monitoring health risk associated with wastewater 46 reuse as well as identifying the source of infection in a community.

Keywords: Hookworm, Health Risk

PRIORITIZING NEGLECTED TROPICAL DISEASES IN THE PHILIPPINES AS PART OF THE POST-2015 AGENDA: LESSONS FROM FOUR VILLAGES IN LEYTE PROVINCE

Poster No. 35

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The post-2015 agenda will require prioritizing neglected tropical diseases (NTDs) that continue to affect poor communities.

In March 2015, using the Kato-Katz technique we examined stool specimens of adults and children from 209 randomly-selected families in Leyte, Philippines. The wealth index of each family was calculated based on the asset-based approach. Adults were interviewed about past treatment and access to the national social health insurance (PhilHealth) and conditional cash transfer (CCT) programs. Data analysis was done using the Generalized Linear Mixed Model.

Prevalence of schistosomiasis (SCH), soil-transmitted helminthiasis (STH), and coinfection, respectively, was 13.7%, 64.0%, and 10.5% in adults (n=408) and 11.6%, 65.1%, and 9.1% in children (n=519). An adult with SCH was 2.8 times likely to have a child with SCH; conversely, a child with SCH was 13.8 and 5.8 times likely to have a parent and sibling, respectively, with SCH. An adult with STH was 3.9 times likely to have a child with STH; a child with STH was 4.6 times likely to have a parent with STH. Wealth index was inversely associated with SCH (OR=0.8) and coinfection (OR=0.8) in adults and STH (OR=0.8) in children. An adult with PhilHealth was 2.5 times likely to have coinfection, while a child in a CCT family was 2.9 and 2.8 times likely to have SCH and coinfection, respectively.

Results suggest the need for a creative control strategy that targets families at-risk, which should set the stage for better control of NTDs in support of the post-2015 agenda.

Keywords: Schistosomiasis, helminthiasis, neglected tropical diseases

Poster No. 36

CHANGE ON MRNA EXPRESSION IN GROWTH PROCESS OF ADULT FEMALE *AEDES ALBOPICTUS*

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Objective Mosquito-borne diseases are transmitted to human hosts via blood feeding of adult female mosquito. Blood feeding is initiated by host seeking behavior. Recently we reported that host seeking behavior of adult female mosquito on day 6 post emergence was increased compared with that on day 0. However host seeking behavior relating proteins are unknown. In this study, we compared mRNA expression in adult female *Aedes albopictus* between day 0 and day 6 post emergence using GS Junior system (Roche) for inference of host seeking behavior relating proteins.

Methods Each adult female mosquito on day 0 and day 6 post emergence were homogenated. Total RNA was extracted from these homogenates using ISOGEN and RNeasy Plus Mini Kit. Subsequently mRNA was extracted using Oligotex^{TM}–dT30mRNA Purification Kit. Reverse transcription was carried out using cDNA Synthesis Kit. This product was applied to GS Junior system. Sequences were analyzed by CLC Genomics Workbench software.

Results Sequences on day 0 and day 6 was 56851 reads and 151351 reads, respectively. As the result on assembly to these reads, 2924 contigs on day0 and 16674 contigs on day 6 were induced. This result suggested that variation of expression of mRNA increases in adult female mosquito on day 6 post emergence compare with day 0. Moreover, comparison of mRNA expression between day 0 and day 6 showed that 10 proteins, which do not expressed on day 0, highly expressed on day 6 and digestive enzyme Proteins such as tryposin and endopeptidase were included in these proteins.

Keywords: mosquito, host seeking behavior, mRNA

AEDES AEGYPTI (L.) AND *AEDES ALBOPICTUS* (SKUSE) LARVAL SURVEY FOR DENGUE VECTOR SURVEILLANCE IN REMOTE VILLAGES OF RATTANAKIRI AND MONDULKIRI, CAMBODIA

Poster No. 37

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Dengue fever, a serious illness with epidemiological, social, and economic impact, is a growing public health problem globally and in Southeast Asia including Cambodia. *Aedes aegypti* L. and *Aedes albopictus* (Skuse) are vectors of dengue fever transmission. Larval surveys were conducted during September 2014 – September 2015. Two villages in each province were selected for the survey. Young mosquito stages were randomly collected to distinguish the predominant species in the study areas. Our purpose was to determine larval indicies and the key containers of *Aedes* species, in remote rural areas of Rattanakiri and Mondulkiri provinces, Cambodia.

Aedes albopictus was the predominant species found in Rattanakiri and Mondulkiri provinces. Key positive containers differed among each province, with 4 and 5 types in Mondulkiri and Rattanakiri respectively. *Aedes* larval indicies were locality- and also seasonal-specific which will be further discussed. Health education and community-based vector control were recommended for dengue disease surveillance and control.

Keywords: Larval indicies, key container, *Aedes* mosquitoes, Cambodia

Poster No. 38

ABUNDANCE AND DISTRIBUTION OF ANOPHELES MOSQUITOES IN UBON RATCHATHANI PROVINCE, NORTHEASTERN THAILAND

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Malaria is still of public health concern in Thailand, especially along the national borders. In 2014, Ubon Ratchathani province in northeastern Thailand had the highest number of malaria cases of all Thai provinces. We conducted a survey of adult anopheline mosquitoes in six sites along the border to Laos in the province. Adult female mosquitoes were collected by human (indoors and outdoors) and cattle bait from (March 2013 to March 2015). Mosquitoes were morphologically identified in the field. Of the 10,021 *Anopheles* mosquitoes collected, 9,306 (93.1%) and 695 (6.9%) were from the rainy and dry seasons, respectively. Further, 9,485 (94.6%) were collected on cattle and 536 (5.4%) on human bait. The most abundant species was *An. hyrcanus* group; 72.5% of all mosquitoes collected. Only 199 specimens (1.9%) of primary malaria vectors were collected, belonging to the *Dirus* complex, *Minimus* complex and *Maculatus* group. The secondary vectors, *An. barbirostris, An. philippinensis* and *An. annularis*, constituted 1,547 (15.1%) of all collected mosquitoes. Most primary vectors were collected in the Khong Chiam district. The most abundant species on humans were *An. hyrcanus* group (n=91), *An. barbirostris* (n=77) and *An. philippinensis* (n=42). Although, many malaria cases occur in the province there is a low density of important malaria vectors in these study villages. Therefore, malaria most likely occurs in forest areas. Further studies on malaria vector distribution, as well as human behaviors, are necessary to understand malaria dynamics in the province. This information will contribute to improved vector control in the province.

Keywords: Malaria, vector, human and cow bait, ecology, Lao PDR border

PROTEOMIC ANALYSIS OF IMMUNOGENIC PROTEINS FROM SALIVARY GLANDS OF FEMALE *ANOPHELES SUNDAICUS*

Poster No. 39

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The salivary gland of female *Anopheles mosquito* has important role in parasite transmission. The salivary gland-derived components can enhance the infection of *Plasmodium* because they consist of anticoagulant, anti-inflammatory and immunosuppressive factors that are needed in blood feeding and inhibiting host response like hemostasis and immune response. As immunomodulatory factors, salivary proteins also induce host immune response involving immunoglobulin E (allergic reaction), immunoglobulin G (IgG) and T-lymphocyte-mediated hypersensitivity response, thus these proteins are antigenic and immunogenic for human. Salivary proteins that induce the production of IgG anti-salivary proteins have been developed as biomarker of mosquito bite's exposure or malaria risk. The salivary gland proteomes of *Anopheles sundaicus* as major malaria vector in Indonesia have not been extensively studied yet. The objective of this study was to identify immunogenic proteins from the salivary glands of female *Anopheles sundaicus* using a proteomic approach (one-dimensional gel electrophoresis followed by LC-MS/MS). Previous study has revealed that the most immunogenic proteins of salivary glands from female *An.sundaicus* had molecular weights of 46, 41, 33, and 31kDa. Computational bioinformatic analysis by MASCOT server identified all of these immunogenic proteins are novel proteins, therefore transcriptomic or genomic approach is needed to determine their biological functions in blood feeding and malaria transmission.

Keywords: *Anopheles sundaicus*, saliva,immunogenic, protein, proteomic

Poster No. 40

INSECTICIDE SUSCEPTIBILITY AND *PLASMODIUM* DETECTION IN *ANOPHELES* MOSQUITOES IN UBON RATCHATHANI PROVINCE, THAILAND

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Malaria is common in hilly forested areas along national borders in Southeast Asia. Insecticide resistance in malaria vectors is a major threat to vector control and prevention of vector-borne diseases. Insecticide resistance in malaria vectors has been detected in Vietnam, Cambodia, and to some extent Thailand; however, it has not been clearly described along the Thai-Lao border areas. This study aims to determine insecticide resistance status of *Anopheles* species and *Plasmodium* infection in primary and secondary vectors in Ubon Ratchathani province. Mosquitoes were collected by human landing and cattle bait in six sites during the rainy and dry seasons of 2013-2015. Mosquitoes were morphologically identified and susceptibility to deltamethrin, permethrin and DDT estimated following WHO protocols. The effect of pre-exposure to the synergists PBO and DEF was assessed in resistant mosquitoes. Complete bioassays (n≥100 mosquitoes) were only achieved for *An. hyrcanus* group, which was resistant to all insecticides tested (mortality ranged from 48-94%). An indication of resistance to DDT in *An. barbirostris* group was found, but was susceptible to deltamethrin and permethrin. *An. maculatus* group were susceptible to deltamethrin, and *An. nivipes* and *An. philippinensis* were susceptible to all three insecticides. PBO increased mortality rates to deltamethrin and permethrin in *An. hyrcanus* group. Screening for *Plasmodium* infection in primary and secondary vectors was performed by real-time PCR. There were no positive samples out of 955 mosquitoes tested. This study provides information that may be useful for the implementation of effective malaria vector control strategies.

Keywords: Malaria, vectors, *Anopheles*, pyrethroids, insecticide resistance, *Plasmodium* detection

Poster No. 41

IVERMECTIN INHIBITS THE DEVELOPMENT OF *PLASMODIUM VIVAX* IN *ANOPHELES DIRUS* AND *ANOPHELES MINIMUS*

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Novel vector control interventions are urgently needed to assist malaria elimination efforts in the Greater Mekong Subregion (GMS). Previous laboratory work demonstrated that ivermectin inhibits the development of *Plasmodium falciparum* in *Anopheles gambiae* (*i.e.*sporontocidal). Ivermectin is lethal to numerous important GMS malaria vectors including: *An. dirus*, *An. minimus*, *An. campestris*, and *An. sawadwongporni*. Here we present that ivermectin is sporontocidal to *Plasmodium vivax* in *An. dirus* and *An. minimus*when ivermectin is co-ingested with gametocytes at the lethal concentration that kills 25 and 5 percent of mosquitoes (*i.e.* LC_{25} and LC_5). Briefly, gametocytemic blood was drawn from *P. vivax*-infected persons reporting to malaria clinics in Thailand, the blood was mixed with dilutions of ivermectin, and then fed to *An. dirus* and *An. minimus* in membrane feeders. Oocyst prevalence in *An. dirus* was reduced at the ivermectin LC_{25} by 44% ($X^2=29.52$, $P<0.0001$) and LC_5 by 34% ($X^2=17.9$, $P<0.0001$) and oocyst intensity was reduced at the ivermectin LC_{25} by 51% ($P=0.0022$) and LC_5 by 25% ($P=0.0389$). Oocyst prevalence in *An. minimus* was reduced at the ivermectin LC_{25} by 59% ($X^2=21.72$, $P<0.0001$) and LC_5 by 31% ($X^2=12.93$, $P=0.0003$) and oocyst intensity was reduced at the ivermectin LC_{25} by 28% ($P=0.1018$) and LC_5 by 35% ($P<0.0001$). In addition to the mosquito-lethal effects of ivermectin, ivermectin has substantial transmission blocking potential, therefore, ivermectin mass drug administrations to humans could be a powerful new tool to aid malaria elimination efforts in the GMS.

Keywords: Ivermectin, *Anopheles*, *Plasmodium vivax* sporontocidal

Poster No. 42

NEW INSIGHTS ON THE OVIPOSITION CONTAINER TYPE SELECTION OF *AEDES* MOSQUITO SPECIES IN DENGUE TRANSMISSION FOCI OF BANGKOK, THAILAND

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To help to planning community-based vector control initiatives for the prevention and control of dengue updated information on the vector species populations is required. With the arching aim to ascertain the oviposition container type selection by *Aedes* mosquito in Bangkok the immature stage, (larva 4th instar-L4 and pupa) was monitored bi-weekly, by using two kinds of ovitraps (earthenware jars and black color plastic). Two kinds of human made artificial containers were set up in two dengue transmission foci at Bang-Khae and Taling-Chan, selected base on the history of dengue incidence. The immature stage, (larva 4th instar-L4 and pupa) was monitored bi-weekly, by using two kinds of ovitraps (earthenware jars and black color plastic). All stage of mosquitoes was reared to adult at laboratory before identification by morphology. The abundance of immature stage in black plastic container was higher than earthenware jar in Bang-Khae whereas in Taling-Chan, the abundance of immature stage in earthenware jar was higher than black plastic container. In Bang-Khae *Aedes aegypti* was dominant while in Taling-Chan, *Aedes aegypti* and Aedes scutellaris equally co-exist. In Taling-Chan, houses surrounding with bush shown higher abundance of *Aedes scutellaris* than that *Aedes aegypti*. The co-existence of *Aedes aegypti* and *Aedes scutellaris* was more commonly observe in ovitrap located near the houses surrounding with bush whereas in ovitrap that place more outside the house was found only *Aedes scutellaris*.

Keywords: *Aedes*, Dengue, Vector, Bangkok

VECTOR BIONOMICS AND INSECTICIDE RESISTANCE IN MALARIA VECTORS IN LAO PDR: AN UPDATE

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Poster No. 43

In Lao PDR, a recent national survey on malaria incidence showed that 65% of the population is still living in transmission areas. It is, therefore, important to carry out entomological collections to study distributional and behavioral patterns of malaria mosquito vectors to plan effective vector control strategies. In 2014, we conducted a survey in 10 provinces during the rainy (June-October) and dry (January-June) seasons to better understand the distribution and bionomics of malaria vectors and investigate their susceptibility status to public health insecticides. Mosquito collections were carried out using human landing catches (indoors and outdoors) and cow bait collection for four consecutive nights at each location and season. The susceptibility of vectors to insecticides was evaluated using WHO cylinder kits. A total of 7,438 *Anopheles* mosquitoes belonging to 26 different species were collected (n=3,385, 46%, 19 species, dry season and n=4,053, 54%, 22 species, rainy season). Primary and secondary malaria vectors were found in all provinces. The human biting rates of the most abundant primary vectors, *Anopheles minimus* s.l. and *An. maculatus* s.l., ranged from 0.03 to 4 and 0.03 to 2 during the dry season and from 0.03 to 2 and 0.03 to 0.71 during the rainy season, respectively. The results showed that the biting pattern of malaria vectors was all along the night both indoors and outdoors. This emphasizes that bed-nets are still appropriate for protecting people during the night but additional tools are needed to target outdoor transmission. Resistance to the formerly used DDT was found in a population of *An. maculatus* s.l. but no resistance to insecticides used for malaria control in Lao PDR was found in the vectors, indicating that vector control by the use of conventional insecticides (pyrethroids) is still effective but continued monitoring of insecticide susceptibility is necessary to early detect potential occurrence/migration of insecticide resistance in malaria vectors in Lao PDR.

Keywords: malaria, *Anopheles* bionomics, insecticide-susceptibility, human-biting-rate

Poster No. 44

COMMUNITY-BASED PROGRAM OF LARVIVOROUS FISH IN DOMESTIC WATER CONTAINERS AND COMMUNITY MOBILIZATION FOR CONTROL OF THE DENGUE MOSQUITO VECTOR IN CAMBODIA AND LAO PEOPLE'S DEMOCRATIC REPUBLIC: THE COMBATING DENGUE IN ASEAN STUDY

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An integrated vector control program was implemented in rural districts in Cambodia and Lao People's Democratic Republic (total of 39 villages, population 33,867) during 2010-2011. The program included community education, mobilization and participation aimed at increased dengue awareness, effective environmental management and efficient and sustained use of the guppy fish *Poecilia reticulata* in key domestic water containers for vector control. Routine dengue control and awareness activities were implemented over one transmission season in control districts (total of 21 villages, population 23,362). Outcomes were assessed by repeated cross-sectional surveys of randomly selected households.

At 6, 9, 12 and 15 months after program initiation in Cambodia, the intervention was associated with a statistically significant reduction in the mean number of pupae per person detected in entomological surveys. Regression coefficients were -1.55, $p=0.003$; -4.36, $p<0.001$; -4.24, $p<0.001$; -2.17, $p<0.001$ respectively. Marked and sustained reductions occurred in container (CI), house (HI) and Breteau (BI) indices in the intervention district but not in control. In Lao PDR the intervention effect was significant at 5 months (-1.54; $p=0.025$) and 9 months (-1.3; $p=0.042$) but not at 12 month. Generally more marked reductions in CI, HI, BI occurred in the intervention district and all indices were zero at final 16 months.

Integrated community-based interventions that include the introduction of small numbers of *Poecilia reticulata* to key domestic water storage containers and strategies to promote awareness of dengue and community participation can reduce vector breeding and therefore the risk of dengue.

Keywords: community-based, larvivorous fish, dengue vectors

HUMAN ANTIBODY RESPONSE TO *ANOPHELES* SALIVARY PEPTIDE AS A BIOMARKER TO ASSESS THE RISK OF MALARIA TRANSMISSION IN THE THAI-MYANMAR BORDER

Poster No. 45

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Malaria along the Thai-Myanmar border malaria displays geographical heterogeneity and is characterized by high prevalence of submicroscopic carriage and the emergence of artemisinin-resistant strains of *Plasmodium falciparum*. The aim of this study was to assess the risk of malaria transmission in this area by the use of specific *Anopheles* salivary peptide (gSG6-P1) as an epidemiological tool for evaluating human exposure to *Anopheles* bites. Epidemiological and entomological surveys were conducted from April 2013 to March 2014 in four sentinel villages characterized by high submicroscopic carriage. Dried blood spots were collected in filter papers among all inhabitants during epidemiological surveys at baseline (Month 0) and then every three months up to 12 months (M3, M6, M9 and M12). "Heatmaps" for human IgG responses for each village and survey time point were created using QGIS 2.4 and the "heatmap" plugin (http://www.qgis.org/). Multivariate mixed models showed that the levels of IgG response of people significantly varied according to village and survey and were positively correlated with the abundance of total *Anopheles* spp. as well as primary malaria vectors (P<0.0001). The higher the abundance of malaria vectors (as measured by the human biting rates) the greater was the probability to being high immune responder (P=0.002). Other factors related significantly to the human response to malaria vector bites were age and season. However, the frequent use of long lasting insecticidal nets was not associated with low IgG responses to *Anopheles* saliva. Spatial clusters (hotspots) of high IgG responders were identified within the villages hence indicating that some area/people are at higher risk to malaria vector bites. Based on these results, the gSG6-P1 biomarker proves to have great potential for malaria epidemiology studies in the Thai-Myanmar border. ⁂

Keywords: Malaria transmission, *Anopheles*, Human antibody response, Biomarker gSG6-P1

Poster No. 46

BITING FLY FAUNA COMPOSITION IN DIFFERENT FARMING PRACTICES AREAS IN CENTRAL REGION OF THAILAND

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The ecological origin and emergence of novel human pathogens is often driven by ecological changes, especially with how human populations interact with animal reservoirs. Therefore, the biting fly taxonomic diversity has been ascertained among different farming practices in the sub-urban area of Bangkok

Adults were collected using CDC type miniature light trap baited with dry ice as a source of CO_2 operating between 1800-0700 Hrs, and *BG(BIOGENT)-Sentinel* traps operating for 24 Hrs. The taxon richness of biting flies were observed in the different farming practices the sub-urban areas of Bangkok, namely, Agriculture, Bird, the livestock of Goat and Sheep and the cow.

The *Culicinae* family was the most abundant in the every farming practices type, being the *Culex* the most predominant genus; followed by the Ceratopogonidae, *Culicoides spp*.; and the less abundant family was *Phlebotomine* sandflies.

Keywords: Culicidae, Ceratopogonidae,Psychodidae, Farming, Bangkok

PEDICULOSIS CAPITIS AMONG STUDENTS AT THE AR-RHAUDATUL HASANAH ISLAMIC BOARDING SCHOOL IN MEDAN, NORTH SUMATERA - INDONESIA

Poster No. 47

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Pediculosis capitis is a common parasitic disease, found especilly in overcrowded communities, but data on its epidemiology and morbidity is scanty.

This is a descriptive study conducted on 2012 at Ar-Rhaudatul Hasanah islamic boarding school in Medan, North Sumatera - Indonesia. 180 samples were chosen by random sampling. Participants were living in the dormitory area of the school. They were examined for the presence of the head louse (*Pediculus humanus capitis*). Additionally, questionnaires by guided interview were also used to assess participants\' level of knowledge and attitude towards hygiene related to the disease. 64 participants (36 %) were found positive for pediculosis capitis. The age group of 11-15 years and females were most frequently affected. Lack of knowledge showed linear connection to increased cases of infestation, while good knowledge and attitude towards hygiene might not significantly implicate less chances of infection if the other infected patients as source of infection were nearby in a crowded residential community, for example in a dormitory setting.

Keywords: pediculosis capitis, knowledge

Poster No. 48

PREVALENCE OF THE HEAD LICE INFESTATION AMONG THE CHILDREN IN WELFARE CENTRES IN KUALA LUMPUR, MALAYSIA: HIGHLIGHTING THE KNOWLEDGE, ATTITUDE AND PRACTICE

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Introduction: The aim of the study was to determine the prevalence of head lice infestation in relation to knowledge, attitude and practice among the children in the welfare centres in Kuala Lumpur. There has been no report of KAP published on this topic in Malaysia.

Methods: A total of 294 children with mean age of 13.52 ± 2.78 years old were given the questionnaire which comprised of social demographic data, environmental and personal hygiene, and also knowledge of head lice. They were interviewed face to face. General inspection of their head and neck area and examination for head lice were done.

Results: The prevalence of head lice infestation among the children in welfare centres in Kuala Lumpur was 35.71%. The infestation rates were highest among girls with 51.45% and among the age group of 7-9 years old with 53.33%. There was significant association between head lice infestation with gender and age. Knowledge showed no association with head lice infestation. In term of attitude and practice, several factors showed significant association with head lice infestation which include number of children per room, frequency of cleaning room, sharing clothesand length of hair.

Conclusion: The attitude and practice has relation with head lice infestation. These factors are modifiable and easily included in daily hygienic practices. Caregivers of these centres need to prioritised room cleanliness reduce number of children per room and cut hair short where applicable.

Keywords: Headlice, Welfare, Prevalence, KAP Malaysia

STICKY PUPARIUM: A SPECIAL CHARACTERISTIC OF MUSCID FLY *SYNTHESIOMYIA NUDISETA* (WULP) (DIPTERA: MUSCIDAE) IMMATURE STAGE

Poster No. 49

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Synthesiomyia nudiseta (Wulp) (Diptera: Muscidae) is a forensically important fly in many tropical countries, and is normally associated with corpses found indoors. Based on a forensic case, the presence of an adhesive substance produced during prepupal development was reported and described. Numerous prepupae and puparia of this species were found adhered side by side on a mattress, where a decomposed body was recovered inside an apartment in Kuala Lumpur, Malaysia. The immature stage, in particular the pupa, displays a special characteristic which may assist early species identification for forensic investigation. The surface ultrastructure of the adhesive layer analysed by scanning electron microscopy showed a sponge-like appearance. We suggest this adhesive substance may be secreted by this species as a protective mechanism to prevent it from being predated by other insects such as parasitoids. Based on the specimens analysed, the post-mortem interval for this case was estimated to be between 12 to 16 days. ⁂

Keywords: *Synthesiomyia nudiseta*, puparium, forensic entomology

Poster No. 50

VECTOR COMPETENCE OF *AEDES ALBOPICTUS* (SKUSE) AND *AEDES AEGYPTI* (LINNAEUS) FOR *PLASMODIUM GALLINACEUM*

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Plasmodium gallinaceum is an intracellular protozoa parasite that caused avian malaria disease. It is transmitted by various mosquito species such as *Aedes, Culex*, and Mansonia. However, vector competence of each mosquito species for this parasite might be different. This study was conducted to compare vector competence of *Ae. albopictus* and *Ae. aegypti* for *Plasmodium gallinaceum*. The study was divided into 15 experiments, each of which consisted of three mosquito groups including 60 *Ae. albopictus* (>F10), 60 *Ae. aegypti* (>F10). The mosquitoes of each experiment were allowed to feed on infected chicken at different levels of parasitemia (1.1-52.7%) and gametocytemia (0.1-5.2%). Blood-fed mosquitoes were kept and observed for mortality rate daily. On day five post blood feeding, 30 *Ae. albopictus* (>F10), 30 *Ae. aegypti* (>F10) from each experiment were dissected, counted for oocysts on the midgut wall, and observed for the sporozoites in the salivary glands. All of the three mosquito groups could support the development of this parasite which was indicated by oocyst and sporozoite formation. However, levels of parasite in the blood meal were not related to the oocyst count in both mosquito species. Comparison of the oocyst count among the three mosquito groups was different ($p<0.05$). *Ae. aegypti* ($p<0.05$). This study suggested that both *Ae. albopictus* and *Ae. aegypti* are competent vector for *Plasmodium gallinaceum*. Mosquito species and generation also affected the parasite development.

Keywords: Vector competence *Aedes albopictus Aedes aegypti*

OBSERVATIONS ON THE CONSUMPTION AND KILLING DURATION OF *TOXORHYNCHITES SPLENDENS* (WIEDEMANN) LARVAE ON *AEDES AEGYPTI* (L.) PREY

Poster No. 51

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Observations were made on the consumption and killing behavior of third and fourth larval instars of *Toxorhynchites splendens* feeding on *Aedes aegypti* larvae. All experiments were performed under laboratory conditions at 25+2ºC, 80+10% relative humidity, and 12 hour light-dark photophase. The different methods used by *T. splendens* to consume or kill their prey were categorized into 7 major types. Types 1 to 5 involved complete consumption of prey and were frequently observed among both 3rd and 4th-instars. The most common method was Type 1 which involved grasping the prey with the mouth brushes and quickly consuming the struggling larva within 1.50 minutes. Types 6 and 7 were used to describe behavior where prey are killed but not consumed. Forth instar *T. splendens* larvae were monitored at two hour intervals to observe their killing behavior. The most common method was Type 7 which involved grasping prey and holding tightly with the mouthparts for at least one minute until the struggling larva ceased moving. Consumption and killing behavior of the mosquito *T. splendens* provide baseline data for using the predatory larvae of this species in biological control programs.

Keywords: *T. splendens, Ae. aegypti*, consumed, killing

Poster No. 52

EFFECT OF DAY AND NIGHT ON FEEDING RATE AND TOTAL PREY CONSUMPTION DURING LARVAL DEVELOPMENT OF *TOXORHYNCHITES SPLENDENS* (WIEDEMANN)

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The effect of day and night on predatory behavior of *Toxorhynchites splendens* was studied in the laboratory. *T. splendens* were reared at 25° C with a relative humidity of 80+10% and a photoperiod of 12 hour light followed by 12 hour dark (0600-1800 light and 1800-0600 dark). Each instar of *T. splendens* was provided *Aedes aegypti* larvae of the same developmental instar as a source of prey. The numbers of prey consumed and killed were recorded at 6 hour intervals (0000-0600, 0600-1200, 1200-1800, and 1800-2400). The duration of each *T. splendens* larval instar and effect on predation of *Aedes aegypti* larvae were recorded. The results showed that *T. splendens* larvae consumed the most prey at night from 0000-0600 (8.4 prey/1st instar, 16.1 prey/2nd instar, 28.2 prey/3rd instar and 31.5 prey/ 4th instar). At each time interval the 4th instar larvae consumed more prey than the other instars. The predators killed the most prey from 0600 -1200 (14.4 prey/3rd instar and 65.0 prey/4th instar). Killing behavior was not observed among 1st and 2nd instars. Killing rates for 3rd and 4th instars were 28.6 and 219.6 per day, respectively. The average immature duration of the first, second, third and fourth instar larvae were 1.1, 2.2, 3.3 and 6.3 days. These findings are useful for understanding biological controls programs using *T. splendens*.

Keywords: *T. splendens*, *A.aegypti*, consumption, killing,

MORPHOLOGICAL AND MOLECULAR IDENTIFICATION OF IXODID TICK SPECIES IN CHAO CHI-ON NON HUNTING AREA AND BANGLAMUNG WILDLIFE BREEDING CENTER, CHONBURI PROVINCE, THAILAND

Poster No. 53

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Ixodid ticks are important vectors in the transmission cycle of various diseases in both humans and animals most of which are zoonotic diseases. W*ildlife animals are considered reservoirs of tick-borne diseases.* Because of a relationship between ixodid tick species and pathogens, the information about tick diversity and distribution will be valuable for predicting their possibility to play an important role in disease transmission cycle in a specific area. Recently, molecular identification was defined more accurately than morphological identification due to the variation of tick species and small-sized structures of immature stage of ticks which is difficult to identify by using only morphological characteristics. This study investigated the ixodid tick diversity and distribution in wildlife habitats. Ixodid ticks were collected from Chao Chi-on non hunting area and Banglamung wildlife breeding center, Chonburi province, Thailand by dragging and searching methods. All of the samples were examined under microscope to recognize genus and/or species using morphological identification keys. Representatives of larvae, nymphs, and adults were examined by using polymerase chain reaction and mitochondrial 16s rRNA sequencing for species confirmation. The finding from this study indicated a diversity of ixodid tick species including *Haemaphysalis lagrangei*, *Haemaphysalis wellingtoni*, and *Rhipicephalus* (*Boophilus*) *microplus*. This study provided the information of tick species in wildlife habitats which yields a better understanding of tick ecology. However, further studies need to be performed to indicate the association of tick and important zoonotic diseases.

Keywords: Morphology, Molecular, Identification, Tick, Thailand

Poster No. 54

DISTRIBUTION AND ECOLOGICAL ASPECTS OF PHLEBOTOMINE SANDFLIES AROUND PIKUN THONG ROYAL DEVELOPMENT STUDY CENTER IN NARATHIWAT PROVINCE SOUTHERN OF THAILAND

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According to the distribution ecology aspects of *Phlebotomus* sand flies, the operation research was conducted within 5 kilometers radian area of Pikun Thong Royal Development Study Center in Maung district, Narathiwat province. Sand flies were collected by using light trap and performed in 12 difference physical areas namely 1) Cattle enclosure 2) Goat enclosure 3) Duck enclosure 4) Chicken enclosure 5) Rabbit enclosure 6) Rubber plantation 7) Fruit garden 8) Palm plantation 9) Swap forest 10) Foothill forest far from sea 11) Foothill forest near sea and 12) 50 meter above sea. Light traps were laid from 06.00 pm - 06.00 am. Every study areas were conducted under quite difference climate. The average of minimum and maximum temperature range were 27.4° ± 0.32° C and 30.38° ± 0.73°C and the average of minimum and maximum percentages of humidity in the air range were 73 ± 1 and 81.8 ± 0.89. The results revealed that total number of collected sand flies were 349, belonging to *Phlebotomus* spp. (46.37%, 5 species) and *Sergentomyia* spp. (53.63%, 7 species). The result showed that the different species and density of sand flies according to area types. *P.argentipes* has been known to be the vector of *L.donovani* responsible for visceral leishmaniasis in India and cutaneous leishmaniasis in Sri Lanka. *P.argentipes* was probably a possible vector of human leishmaniasis in Thailand which was almost found in the study area types with highest proportion (53.34%) in cattle enclosure. There were many vectors of leishmaniasis in ecology, the gaps need to be filled and was crucial for leishmaniasis prevention and control at their livestock, agriculture and sylvatic habitats area.

Keywords: distribution, ecology, sand fly

PNEUMOCOCCAL COLONISATION IN YOUNG CAMBODIAN CHILDREN SHORTLY AFTER INTRODUCTION OF PNEUMOCOCCAL CONJUGATE VACCINE (PCV13)

Poster No. 55

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Background: Cambodia introduced the thirteen valent pneumococcal conjugate vaccine (PCV13) into the routine childhood immunisation schedule in January 2015. The aim of the current study was to determine the characteristics of colonising pneumococci in children

Methods: In August 2015, we enrolled children attending the Angkor Hospital for Children out-patient department with minor illnesses. A brief symptom questionnaire, including PCV13 immunisation status, was completed and a nasopharyngeal (NP) swab was collected. NP swabs were processed according to standard World Health Organization protocols and pneumococci were serotyped by latex agglutination and Quellung methods.

Interim results: Four hundred and fifty children were recruited into the study. To date, 162 NP swabs have been processed and pneumococci have been cultured from 93 (57.4%). PCV13 serotypes were identified in 53 culture positive swabs (56.3%). Five children (3.1%) were colonised by >1 pneumococcal serotype. Results from all 450 NP swabs will be presented on the poster.

Keywords: *Streptococcus pneumoniae*, colonisation, vaccine, children

Poster No. 56

ACCURACY AND ACCEPTABILITY OF RESPIRATORY RATE AND PULSE OXIMETER DEVICES IN DETECTING PNEUMONIA SYMPTOMS BY COMMUNITY HEALTH WORKERS AND FIRST-LEVEL HEALTH FACILITY WORKERS IN RATANAKIRI PROVINCE, CAMBODIA

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Pneumonia is responsible for an estimated 17% of deaths in children under five years in Cambodia. Community health workers (CHWs), locally known as extended village malaria workers (VMWs), and first-level health facility workers (FLHFWs) currently diagnose pneumonia by counting respiratory rate using an acute respiratory infection (ARI) timer, which can be challenging and lead to disease misclassification and inappropriate treatment. Malaria Consortium's multi-country Pneumonia Diagnostics Project aims to identify the most accurate and acceptable respiratory rate (RR) timers and pulse oximeters (POx) to support VMWs and FLHFWs in the detection of pneumonia symptoms in children under age five. Five POx devices and two RR counters were selected for evaluation in Cambodia based on literature reviews, formative research, and laboratory testing. VMWs in Cambodia expressed a 'felt' need during the formative research for new pneumonia diagnostic devices, with automation highlighted as a preferred device characteristic. Health-facility based accuracy evaluations were conducted to assess the accuracy of each device when used by VMWs/FLHFWs against reference standards. During this phase, nearly 400 children aged 0-59 months were enrolled in the research study. Preliminary results show health workers are able to successfully use all devices being trialled. Finally, the acceptability of these devices as perceived by VMWs, FLHFWs, and caregivers will be assessed during routine health practice from October-December 2015 using semi-structured interviews, focus group discussions, and an expert panel review of video-recorded assessments. Overall the project findings have the potential to inform how pneumonia diagnostic devices will perform and be perceived in Cambodia.

Keywords: pneumonia, diagnostic devices, under-5, Cambodia

SCRUB TYPHUS INFECTION IN PREGNANCY, REVIEW OF THE LITERATURE AND A CASE STUDY OF A CHLORAMPHENICOL AVERTED MATERNAL MORTALITY IN 3RD TRIMESTER

Poster No. 57

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Scrub typhus caused by *Orientia tsutsugamushi*, is endemic in rural South-East Asia and remains a leading cause of non-malaria, acute undifferentiated fever (AUF). Contracted during pregnancy it may lead to adverse maternal and newborn outcomes including an unknown burden of maternal and newborn mortality.

As Scrub typhus field based diagnostic tests are poor and only a few antibiotics are considered effective and safe in pregnancy, AUF is clinically challenging in endemic areas. In this case costly intensive care avoided a 3rd trimester near miss maternal mortality but not foetal loss at 31^{+4} weeks gestation, after late initial presentation, misdiagnosis, and inappropriate first line antimicrobials. Intravenous chloramphenicol, the antimicrobial most likely responsible for the acute recovery from infection, was correctly administered to save the mother's life with secondary concerns for gray baby syndrome. The cause of death in the neonate could not be established but maternal multi-organ failure and/or *O.tsutsugamushi* vasculitis-associated pathology of the placenta, possibly associated with thrombotic occlusions and/or coagulopathy cannot be excluded.

AUF in pregnant women is potentially life threatening and sepsis protocols are required for scrub typhus endemic settings, at least providing oral azithromycin (and doxycycline if azithromycin is unavailable) to prevent progress to severe disease. Intravenous chloramphenicol should be included in protocols for severe AUF in pregnancy where scrub typhus is endemic. Evidenced based guidelines for AUF in pregnant women in settings where vector borne disease burden is high are required. There is also an urgent need for reliable field based RDTs for scrub typhus.

Keywords: scrub typhus, maternal mortality, stillbirth

Poster No. 58

OPTIMIZING RNA EXTRACTION FROM FRESH CULTURE OF *ORIENTIA TSUTSUGAMUSHI*

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Orientia tsutsugamushi is a gram negative obligate intracellular bacterium that causes serious febrile illness in humans known as scrub typhus. It is an important public health concern, with an estimated one million new cases per year in endemic areas such as South East Asia, South Asia, Australia and the Pacific. Expression profiling studies, RNA-seq and microarray experiments are important to understand bacterial infection mechanisms and causes of pathogenicity. Here, we aimed to develop an RNA extraction method that would yield bacterial RNA of a quality and quantity suitable for RNA sequencing and subsequent gene expression analysis. Freshly propagated *O. tsutsugamushi* in mouse fibroblast L929 cells were harvested and processed to get RNA using a QIAGEN (RNeasy® Plus Mini) kit. The optical density (OD), 260/280 ratio and RNA concentration were used to assess the quality of the sample preparation. We were able to purify high quality bacterial RNA samples, and these were prepared for subsequent analysis using reverse transcription to cDNA followed by qPCR. Samples prepared in this way were used to study the relative expression levels of cell wall biosynthesis genes *MurA*, *MurD*, *MurF*, *pal*, *ddl* and *pbpA2*. We compared gene expression levels at different stages of the infection cycle, and found that expression of most observed genes were increased at early stages of infection. The optimized RNA extraction method in this study provides high quality RNA from freshly cultured obligate intracellular bacteria. This technique will be used in further studies in gene expression profiling including microarray and transcriptomic analysis.

Keywords: *O. tsutsugamushi*, ribonucleic acid (RNA), optical density (OD), cell wall targeted gene, cDNA synthesis, RT-PCR, transcriptomic.

LIVE IMAGING OF THE GENETICALLY INTRACTABLE INTRACELLULAR HUMAN PATHOGEN *ORIENTIA TSUTSUGAMUSHI* USING THE FLUORESCENT DYE CARBOXYFLUORESCEIN SUCCINIMIDYL ESTER

Poster No. 59

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Scrub typhus is a severe febrile illness caused by the gram negative obligate intracellular bacterium *Orientia tsutsugamushi*. This organism is from the family Rickettsiaceae and is transmitted to humans through the bite of trombiculoid mites. The disease is endemic in the Asia-Pacific region but is frequently misdiagnosed due to clinical symptoms that closely resemble other tropical infections. Our understanding of the fundamental mechanisms by which *Orientia* enters and propagates within human cells is less advanced than for other equivalent pathogens. As an obligate intracellular organism, *Orientia* is difficult to culture, and a lack of standardization has hampered studies on its infection cycle.

Fluorescent light microscopy is an important tool in understanding the infection cycle of intracellular pathogens. This can be performed on fixed samples, but this approach cannot give us the full picture of how *Orientia* enters cells and specifically cannot measure its motility over time. Since no tools exist for genetic manipulation *of Orientia,*we have developed an alternative method for live imaging using the small fluorescent dye carboxyfluorescein succinimidyl ester (CFSE) to label live *Orientia*. This dye enters into bacteria where it covalently reacts with amine groups on proteins. One advantage of this dye, which has been used extensivey for labeling mammalian cells such as lymphocytes, is that it can be retained in the bacteria over long periods of time and can therefore be used to follow bacterial division based on the dilution of fluorescence intensity. With this ability to perform live imaging, we are able to better understand the behaviour of *Orientia* and their infection cycle. ⁂

Keywords: *Orientia tsutsugamushi*, scrub typhus, CFSE, live imaging

Poster No. 60

EFFECT OF TEMPERATURE ON FIMBRIAL GENE EXPRESSION AND ADHERENCE OF ENTEROAGGREGATIVE *ESCHERICHIA COLI*

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The influence of temperature on bacterial virulence has been studied worldwide from the viewpoint of climate change and global warming. The bacterium enteroaggregative *Escherichia coli* (EAEC) is the causative agent of watery diarrhea and shows an increasing incidence worldwide. Its pathogenicity is associated with the virulence factors aggregative adherence fimbria type I and II (AAFI and AAFII), encoded by *aggA* and *aafA* in EAEC strains 17-2 and 042, respectively. This study focused on the effect of temperature increases from 29°C to 40°C on fimbrial gene expression using real-time PCR, and on its virulence using an aggregative adherence assay and biofilm formation assay. Incubation at 32°C caused an up-regulation in both EAEC strains 17-2 and strain 042 virulence gene expression. EAEC strain 042 cultured at temperature above 32°C showed down-regulation of *aafA* expression except at 38°C. Interestingly, EAEC cultured at a high temperature showed a reduced adherence to cells and an uneven biofilm formation. These results provide evidence that increases in temperature potentially affect the virulence of pathogenic EAEC, although the response varies in each strain.

Keywords: EAEC, temperature, adherence, gene expression

MOLECULAR DETECTION OF *SALMONELLA ENTERICA* SEROTYPES WELTEVREDEN AND ENTERITIDIS IN MEAT SAMPLES COLLECTED FROM SELECTED WET MARKETS IN METRO MANILA, PHILIPPINES

Poster No. 61

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Salmonella enterica is one of the most significant pathogens that cause food-borne diseases in the world. Majority of *S. enterica* infections in humans are associated with the consumption of contaminated meat products. More than 2,500 *Salmonella* serotypes have been identified and *Salmonella* serotypes Typhimurium and Enteritidis are reported as the most common cause of human salmonellosis in many developed countries. This study aimed to determine the incidence of common *Salmonella* serogroups and *Salmonella* serotypes Weltevreden and Enteritidis in meat samples. Among the 137 *S. enterica* contaminated meat samples, *Salmonella* serogroup O:3,10 (56.93%) was observed to have the highest incidence, followed by serogroups O:4 (49.64%), O:7 (44.53%), O:6,8 (41.61%), undetermined (13.87%), O:9 (9.49%), and O:2 (0%). In serotyping, higher incidence of *S.* Weltevreden (11.68%) was observed compared to *S.* Enteritidis (2.19%) in meat samples, which supported the result of a previous study that detected higher incidence of *S.* Weltevreden compared to *S.* Enteritidis in human clinical samples in the Philippines. High incidence of *S.* Weltevreden and serogroup O:3,10 in meat samples is perhaps indicative of their predominance in human clinical samples in the country. This is the first study in the Philippines that detected *Salmonella* serotypes in meat samples using polymerase chain reaction. It is recommended to detect other *Salmonella* serotypes to determine their incidence, diversity and distribution.

Keywords: Enteritidis, meat, Philippines, *Salmonella*, Weltevreden

Poster No. 62

PREVALENCE OF CONTAGIOUS PATHOGENS IN SUBCLINICAL BOVINE MASTITIS IN SMALLHOLDER DAIRY FARMS, KAENG KHOI, SARABURI PROVINCE, THAILAND

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Staphylococcal and Streptococcal infections are a major problem of subclinical bovine mastitis in worldwide including Thailand. This study aims to investigate the prevalence of the contagious bacterial pathogens causing subclinical bovine mastitis. Forty-six milk samples were collected by aseptic technique from milking cows of twenty dairy farms in Hin son, Kaeng khoi district, Saraburi province, the center of Thailand during September, 2015. The milk samples were collected individually from each milking cows and subjected to Fossomatic™ FC flow cytometry for analyzing and measurement of Somatic Cell Counts (SCC). Setting the cut-off point of SCC = 500,000 cells/ml, the cows were prognosis as intramammary infection and subclinical mastitis. Milk samples were also investigated the prevalence of bacterial pathogens by achieved to conventional assay; gram staining, catalase test, blood hemolysis, coagulase test, and mannitol fermentation test. The results showed the prevalence of contagious bacterial bovine mastitis caused by *Streptococcus agalactiae* 17/46 (36.96%) and *Stapylococcus aureus* 15/46 (32.61%), respectively. An occurrence of subclinical bovine mastitis from these pathogens was significantly associated with the level of somatic cell counts. In conclusion, this study indicated that these areas of the smallholder dairy farms were having a prevalence of subclinical bovine mastitis from the contagious bacterial pathogens; *Streptococcus agalactiae*and *Staphylococcus aureus*. This information could be used for planning the bovine mastitis control program, treatment, and culling in the dairy herds.

Keywords: contagious pathogen, subclinical mastitis, Saraburi, Thailand

EVALUATION OF SURVEILLANCE FOR *STREPTOCOCCUS SUIS* INFECTION IN 5 HOSPITALS IN 5 PROVINCES IN NORTH REGION, THAILAND 2013

Poster No. 63

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Streptococcus suis infection was acquired through consumption of uncooked pork or pork products or pig's blood. A case fatality rate ranged from 5 to 20%. The *Streptococcus suis* infection had been determined to report under national disease surveillance system since 2011. Evaluation of surveillance for *Streptococcus suis* infection was to conduct as a cross sectional quantitative study in 5 hospitals in 5 provinces in North region of Thailand. The objectives were to examine reporting processes of *Streptococcus suis* infection in the general hospitals. Data from medical records that met a case definition were retrieved from January 1 to December 31, 2013. Descriptive analyses were performed by Epi Info. There were 460 cases which were enrolled into the study. Of those 460 cases, 67 cases were compatible with the case definition that were defined as 19 suspected cases, 28 probable cases and 20 confirmed cases. Sensitivity of reporting into the national disease surveillance system was 29.89% while predictive positive value showing result for 44.45%. Representativeness of age distribution was similar between cases from medical records and cases from the national disease surveillance. An average for timeliness of reporting was 4.9 days. Nurses at screening stations could be the focal person to detect any suspected cases of *Streptococcus suis* infection when the cases with exposure history admitted to the hospitals. Training course for nurses to gain knowledge about a natural history of *Streptococcus suis* infection and epidemiology of the disease could be important process to scale up *Streptococcus suis* infection surveillance.

Keywords: *Streptococcus suis*, Surveillance System, Evaluation

Poster No. 64

MOLECULAR TYPING OF METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS* ISOLATED FROM THAMMASAT UNIVERSITY HOSPITAL BY PULSE-FIELD GEL ELECTROPHORESIS

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Methicillin-resistant *Staphylococcus aureus* (MRSA) is one of the main causes of hospital-acquired infections, which are rapidly increasing globally. The most common sites of MRSA infection are bloodstream, ventilator-associated pneumonia, urinary tract, and post-surgical site. Vancomycin is the drug of choice for treatment of most infections caused by MRSA. For the past 10 years, many reports demonstrated that the clinical strains of MRSA with reduced susceptibility to vancomycin (vancomycin MIC creep) were detected. Moreover, high mortality caused by MRSA has been reported worldwide. It is crucial for medical professionals to realize the importance of the variant strains for surveillance and control of the spread. Pulse field gel electrophoresis (PFGE) is one of the most discriminative typing techniques for epidemiological study. The MRSA strains isolated from Thammasat University Hospital has not yet been intensively investigated for genetic characterization. Hence, total of sixty isolates were characterized by using PFGE. The results revealed that ten different PFGE types designated type A, B, C, D, E, F, G, H, I and J were exhibited. The majority of tested MRSA strains were type A (25%) and type G (20%). The strains belonging to PFGE type A had vancomycin MIC creep except one strain while most of non-vancomycin MIC creep MRSA strains belonged to PFGE type G except three strains. The obtained results of epidemiologic characteristics of MRSA will be useful for implementation in clinical practice including monitoring and prevention of the multiple drug-resistant of MRSA infection.

Keywords: Pulse field gel electrophoresis (PFGE), Methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin MIC creep

ISOLATION AND CHARACTERIZATION OF *ENTEROCOCCUS* SPP. FROM IRRIGATION WATERS IN METRO MANILA, PHILIPPINES

Poster No. 65

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The presence of *Enterococcus* spp. in irrigation waters in Metro Manila was evaluated by isolating *Enterococcus* spp. from water bodies that serve as sources used to irrigate fresh produce and characterizing them by culture and molecular methods as well as determining their antibiotic susceptibility through broth microdilution method. *Enterococcus* is a fecal indicator bacterium, commonly associated with a variety of human illnesses and potential human health risks including bacteremia, endocarditis and other infections. Enterococcal antimicrobial resistance has been observed in different studies and poses a problem in the treatment of infections as well as threat of spread of resistance into the environment via the transfer of genes and some virulence factors from enterococci to other pathogenic bacteria. Resistant enterococci may find a way of going inside the body, directly by drinking water or recreational contact or indirectly, by eating fish, meat and agricultural produce. Thus, its presence in food and water draws a great public concern. From a total of 105 water samples, 70 (67%) isolates were observed and confirmed to be *Enterococcus* through PCR. Antibiotic susceptibility testing showed low prevalence of antibiotic-resistant *Enterococcus* spp. in the irrigation waters sampled. Out of 18 randomly selected isolates, none was resistant to tetracycline, ampicillin and chloramphenicol while 6 isolates have intermediate resistance and only 1 has full resistance to ciprofloxacin. This is the first study in the Philippines to assess the presence of *Enterococcus* spp. in irrigation waters used for agricultural produce.

Keywords: *Enterococcus*, irrigation water, antimicrobial resistance

Poster No. 66

ESCHERICHIA COLI CONTAMINATION IN HOUSEHOLD DRINKING WATER IN A SUBURBAN AND A RURAL VILLAGE IN SOUTHERN LAOS

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Drinking water (DW) can serve as a disease transmission source if not properly managed. Our objective was to assess the effect of DW sources, household water management, socio-demographic characteristics, hygiene and sanitation on household DW quality in suburban and rural villages, southern Laos.

A cross-sectional survey was conducted in 2011 in 121 suburban and 114 rural households. Semi-structured interviews and observations obtained household information. DW was collected from 139 suburban and 145 rural water containers and analysed for *E. coli*. Zero-inflated negative binomial regression models were used to assess risk factors of *E. coli* contamination in DW.

E. coli was present in 36.7% of the suburban and 45.5% of the rural containers. The average *E. coli* concentration was higher in rural (73.5 cfu/100 ml) than suburban villages (59.2 cfu/100 ml) ($p>0.05$). In the rural village, DW containers with lids (IRR 5.6, $p=0.023$), and households with no toilets (IRR 15.8, $p<0.001$) were more likely to be contaminated with *E. coli*. Rain-fed water was less likely to be contaminated (IRR 0.2, $p=0.045$). In the suburban village, DW from jars (IRR 27.1, $p=0.001$), bottles (IRR 26.9, $p<0.001$), borehole water (IRR 5.4, $p=0.042$), and households with no toilets (IRR 5.4, $p=0.042$) were more likely to be contaminated with *E. coli*.

Storing DW in jars and bottles, DW from boreholes, and households with no toilets were significant factors of DW contamination. Socio-demographic and hygiene factors had little influence on *E. coli* contamination.

Keywords: Faecal, contamination, drinking water, sanitation.

MOLECULAR DETECTION OF MICROSPORIDIA IN BACKYARD FARM ANIMALS IN LAGUNA, PHILIPPINES

Poster No. 67

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Microsporidia are opportunistic, obligate intracellular parasites that use their unique infection apparatus polar filament to infect a wide range of vertebrate and invertebrate hosts. At least 15 microsporidian species are known to infect humans. Although zoonosis is under question, recent studies have shown that some domestic and wild animals may be natural carriers of some human-infecting microsporidia like *Enterocytozoon bieneusi* and *Encephalitozoon* species, which are commonly associated with diarrhea and genitourinary tract infection. In the Philippines, many families living in rural areas rely on backyard farming for income generation. Backyard farming plays an important role in the total animal production of the country and provides an opportunity for possible pathogen transmission between animals and humans. This study reports the molecular detection and identification of microsporidia present in backyard farm animals in Laguna. Four (2.7%) of the 146 fecal samples collected were positive for microsporidia. Two *Sus scrofa* and one *Anas platyrynchos* were infected with *E. bieneusi*, the most prevalent human-infecting microsporidia. *Vairimorpha* sp. that was previously reported to infect insects was identified in another *S. scrofa.* Additional molecular analysis on *E. bieneusi* genotype is warranted and a wider surveillance of human-infecting microsporidia is needed to prevent possible transmission and spread of microsporidia.

Keywords: microsporidia, backyard farm, Philippines

Poster No. 68

DETECTION OF BACTERIAL CONTAMINATION OF READY-TO-EAT FOODS AT THAMMASAT UNIVERSITY CAFETERIA, RANGSIT CAMPUS

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The objective of this study is detection of bacterial contamination of the ready to eat foods at Thammasat University Rangsit Campus. The samplings were collected from 4 categories of food stuff as the following : food using hight heat of 18 sample, food usings low heat of 9 samples, food using no heat of 9 samples and beverages of 4 samples. All sampling were taken from cafeteria in Rangsit Campus. Study was conducted between October 2014 to November 2014.The food were collected one time in each day (in the afternoon between 11.00 to 12.00). The microbiological quality was determined as total coliform, fecal coliform and *Escherichia coli* by MPN method (Most Probalble Number). The method was confirmed to the standard method produce of the Department of Medical Sciences, Ministry of Public Health, Thailand. The results of study found that ready to eat foods had contaminate bacterial in food using low heat did not standard equal 17.5% of food hight heat 15% and food no heat 2.5% .The samples were tested for coliform bacterial and *Escherichia coli* found that all group of ready to eat food considered under standard based on total bacterial count, coliform bacterial and *Escherichia coli* indicated 35%, 50% and 52% respectively.

Keywords: Quality, Microbiology, Bacterial Contamination, Ready-to-Eat Foods, Food poisoning bacterial

SYSTEMATIC REVIEW OF ANTIMICROBIAL EFFECT OF COCONUT OIL

Poster No. 69

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Coconut oil is the extract from endosperm of coconut (*Cocos nucifera* L.) and it's used for food, medicine and cosmetic in worldwide. Coconut oil has been used for treatment in both conventional medicine and traditional medicine but the clinical evidence base isn't enough for support these regimens. Therefore, this project aim to collect articles which deal with coconut oil by focus on antimicrobial effect included antibacterial, antiviral, antifungal and antiprotozoal activity. Researcher searched articles that concern in activity as above from local and international database for 17 sources such as National Library of Medicine (PubMed), Science citation index expanded (ISI), Cochrane database and Thai Library Integrated System (ThaiLIS) for the keywords was coconut oil, *Cocos nucifera* oil and copra oil. The criteria for selected article was about antimicrobial effect and study designs was unlimited. For the outcome, we divided from standard in each antimicrobial such as using minimum inhibitory concentration; MIC or overall symptom score if that research was clinical studies. The result found 4,507 articles from databases. Thirteen articles were included in our criteria but only 5 articles have found in full texts. Two articles (40%) were clinical studies which have randomized and divided groups, study in HIV patients one and the study in neonate < 34 weeks other. Three of these (60%) were *in vitro* studies. All articles assigned volume and concentration of coconut oil and has two articles have other comparators which not placebo. For evaluation of quality of article, we using Jadad's score for clinical studies and research methodology evaluation for *in vitro* studies but we have less articles that make the conclusion in antimicrobial effect was inadequated. However, we found many studies of chemical compound from coconut oil that might be precious in the future study soon.

Keywords: Coconut oil, antimicrobial, Systematic review

Poster No. 70

MIDGUT MICROBIOTA DIVERSITY OF *AEDES AEGYPTI* (LINNAEUS) AND *CULEX QUINQUEFASCIATUS* (SAY)

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Aedes aegypti and *Culex quinquefasciatus* are important mosquito vectors for many infectious diseases. A number of factors affect vector competence of these mosquitoes for a specific pathogen. The bacteria harbored in the midgut are known to influence the mosquito physiology and can alter the response to various pathogens. Bacteria from midgut of *Ae. aegypti* and *Cx. quinquefasciatus* were cultured and identified by using bacteriological and molecular techniques in this study in which two groups of mosquitoes were examined. The first group was field collected mosquitoes from two areas of Bangkok: Suanluang and Laksi district. The second group was laboratory rearing mosquitoes. Three bacterial genera (*Bacillus, Micrococcus*, and *Staphylococcus*) were identified from field collected *Ae. aegypti* in Suanluang district. Seven bacterial genera (*Cellulomonas*, *Microbacterium*, *Micrococcus, Moraxella, Neisseria, Staphylococcus*, and *Streptococcus*) were identified from field collected *Ae. aegypti* in Laksi district. Twelve bacterial genera (*Acinetobacter, Agrobacterium, Bacillus, Cellulomonas, Chryseomicrobium, Dietzia, Enterobacter, Klebsiella, Microbacterium, Pantoea, Pseudomonas*, and *Staphylococcus*) were identified from laboratory rearing *Ae. aegypti*. Six bacterial genera (*Chryseobacterium, Microbacterium, Micrococcus, Pantoea, Providencia*, and *Staphylococcus*) were identified from field collected *Cx. quinquefasciatus* in Suanluang district. Eleven bacterial genera (*Acinetobacter, Actinomyces, Bacillus, Kocuria, Microbacterium, Micrococcus, Novosphingobium, Pantoea, Pseudomonas, Rhodococcus*, and *Staphylococcus*) were identified from field collected *Cx. quinquefasciatus* in Laksi district. Five bacterial genera (*Microbacterium, Micrococcus, Paenibacillus, Pseudomonas*, and *Staphylococcus*) were identified from laboratory rearing *Cx. quinquefasciatus*. The variation of these midgut microbiota may influence mosquito vector competence for a specific pathogen. However, further studies need to be performed to indicate this relationship.

Keywords: bacteria, *Aedes aegypti*, *Culex quinquefasciatus*

MOLECULAR PHYLOGENETIC ANALYSES OF MOSQUITO FLAVIVIRUS IN THAILAND

Poster No. 71

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Thailand harbour a rich mosquito and ticks biodiversity, and eminent threat for human and animal health, particularly in rural, poor and marginalized populations. Furthermore, 18 isolates of Tembusu virus (TMUV), three un-typed flaviviruses, three alphaviruses, and four unidentified viruses have already been reported from mosquitoes; and more recently, Phasi Charoen virus, Bunyaviridae family have already been identified. Yet, arboviral diseases surveillance programs has have only reported arboviruses such as Dengue, Japanese Encephalitis viruses (Flaviviridae: Flavivirus), Chinkungunya virus (Togaviridae: Alphavirus). Therefore, with the aim of ascertain the flavivirus population infecting the most common mosquitoes inhabiting near human dwellings an entomological surveillance for flavivirus have been carried out in the North, Central and South regions of Thailand.

By combining direct sequencing and virus cell culture from individually homogenized *Aedes* and *Culex* mosquitoes, respectively; and using molecular phylogenetic analyses, we have detected tree different clades, namely *Aedes*, *Culex* and mosquito borne flavivirus. Among the detected flaviviruse, the *Aedes* flavivirus cladded together with the Kamiti River virus (98% similarity) while the *Culex* flavivirus fall in the same clade with the Cx.FV-Surabaya 2 strains (100% similarity), whereas the mosquito borne flavivirus was identified as DENV-2. It is noteworthy, that in the mosquito infected with DENV-2 we also detected *Aedes* flavivirus from the homogenize cultured using Vero cells.

Keywords: Mosquito, Flavivirus, Survey, Thailand

Poster No. 72

PREPAREDNESS FOR THE INVADER MOSQUITO *AEDES (FINLAYA) JAPONICUS*: ITS WINTER BIOLOGY AND BACTERIAL MICROBIOTA DIVERSITY

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Being native to East Asia, the bush or rock pool mosquito *Aedes japonicus japonicus*, has become one of the world most expansive culicid specie. Detected for the first time out of its natural range in the early 1990s in New Zealand, and now a days been detected and established in Canada, USA and several countries in Europe. To date, although no establishment of the specie in Thailand has become public we have studied its winter biology (field and laboratory residual) and its microbiota diversity to contribute the fill up the gap of knowledge of this mosquito in its natural habitat. Mosquito immature stages (larva 4th instar and pupae) abundance was monitored in Shioya, Hokkaido Japan from October 2014 to May 2015. At the laboratory room temperature (15-20°C), on one hand the relative winter biology was ascertained, pupation and adult emergence (including sex ratio) rate; and on the other hand their microbiota diversity at its development stage (larva, pupa and adult) was determined. A decrease on larva and pupa abundance on temperature decreasing manner, from 19.5°C to 7.0°C, was observed in the field. Interestingly, a decrease on the sex ratio (♀ : ♂) from 10:1 to 0:1 were observed accordingly to a temperature decreasing. A molecular based analysis of the cultivable bacteria shows differences on the diversity and bacteria families carrying each development stage, being higher in larvae than that in adults.

Keywords: Invasive, Mosquito, Microbiota

PERFORMANCE OF LIPL32 RECOMBINANT PROTEIN ANTIGEN AS A DIAGNOSTIC INTERMEDIATE FOR LEPTOSPIROSIS

Poster No. 73

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Introduction: Leptospirosis is an important disease with explosive outbreaks occurring in Sri Lanka. Confirmation of disease outbreaks is important for clinicians for proper management of patients. Laboratory diagnosis of leptospirosis in Sri Lanka

Introduction:Leptospirosis is an important disease with explosive outbreaks occurring in Sri Lanka. Confirmation of disease outbreaks is important for clinicians for proper management of patients. Laboratory diagnosis of leptospirosis in Sri Lanka is hindered by the high cost of commercial diagnostic kits and inaccessibility of reagents. Laboratory diagnosis depends on Enzyme-Linked Immunosorbent Assay (ELISA) based on whole bacterial antigens which cause biohazard risk, high production cost and cross reactivity with other organisms of the same genus/family. A diagnostic intermediate using a single recombinant protein antigen to detect both IgM and IgG antibodies of the disease is important to overcome problems associated with whole bacterial antigen/lysate is important.

Objective: Overall objective of this project was to assist confirmation of leptospirosis outbreaks through developing rapid laboratory diagnostic assays.

Methodology: A novel synthetic gene for leptospirosis was designed and expressed in a bacteria vector system. Resulted protein (Lipl32) was purified and an indirect ELISAs was developed with this protein as as a capture antigen. Then, potential use of the protein as a diagnostic tool for the detection of both IgM and IgG antibodies produced against the disease organism was evaluated using a large panel of well characterized serum samples.

Results: Lipl32 protein gave better sensitivity for detection of anti-leptospirosis IgM (93%) and IgG (100%) antibodies when compared with standard methods. There is no significant difference between IgM ELISA with MAT/IgM rapid ELISA ($P=0.00, c^2=14$) and IgG ELISA with MAT ($P=0.004, c^2=8$).

Conclusion: Lipl32 protein has a significant effect for confirmation of leptospirosis outbreaks.

Keywords: leptospirosis, diagnosis, antigens, recombinant proteins

Poster No. 74

HOW CRP RAPID TESTING COULD IMPACT ANTIBIOTICS' PRESCRIPTIONS IN DEVELOPING COUNTRIES?

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The vast majority of febrile episodes in many parts of the malaria endemic world are caused by other causes, yet other than malaria rapid tests no diagnostic tests are readily available for use in remote settings.

While in some areas antibiotics are over-prescribed, contributing to the development of antimicrobial resistance, in others many patients are under-treated. Better targeting of antibiotics in these settings could improve immediate health outcomes while reducing drug pressure and mitigate the emergence of resistance.

Successful malaria elimination is also reliant on maintaining patients' confidence in public health care providers; this could be eroded in the absence of effective management of non-malarial fevers.

Biomarkers such as C-reactive protein (CRP) are used routinely in high-income countries to guide the use of antibiotics in respiratory symptoms and fever without a localized source. CRP has also been found to be a highly sensitive marker of bacterial infection in undifferentiated fever in the Southeast Asia.

In developing countries, the most recent studies on CRP point-of-care (POC) have shown that antibiotic's prescription rates could decrease by 20% in patients with Acute respiratory Infections (ARI). This demonstrates that such biomarkers represent a major component against antimicrobials' resistance; and allow cost-effective solution for targeting antibiotics in low-income settings.

A key objective is now to extend the CRP POC testing to any febrile illnesses; especially in the context of limited health care services.

This evaluation would also need to include optimal threshold(s) identification for CRP levels to guide antibiotic, as well as societal costs and benefits associated with antimicrobial resistance.

Overall, it is crucial to evaluate to what extent point-of-care biomarker testing could improve febrile patient management algorithms.

Keywords: CRP Point-of-care, Antimicrobial resistance, Fever

WARNING SIGNS TO PREDICT DENGUE SEVERITY IN ADULT PATIENTS AT THE HOSPITAL FOR TROPICAL DISEASES, THAILAND

Poster No. 75

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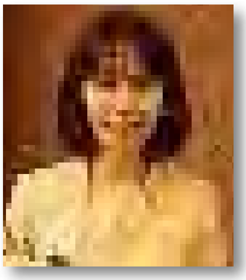
Dengue infection is a major vector-borne disease. It may present as an asymptomatic or a symptomatic infection which leading to multiple complications or fatal outcome. In 2009, the World Health Organization published a revised dengue classification composing of non-severe dengue with or without warning signs and severe dengue (SD). The aim of this study was to assess the warning signs to predict dengue severity in adult hospitalized patients. We conducted a retrospective study of dengue-infected adult patients who admitted to the Bangkok Hospital for Tropical Diseases during (2013 to 2014). A total of 406 patients who fulfilled the eligible criteria were enrolled. The common warning signs were abdominal pain/tenderness, mucosal bleeding and an increase in hematocrit level with a rapid decrease in platelet count. The abdominal pain/tenderness, mucosal bleeding, liver enlargement (>2cm), and an increase in hematocrit with a rapid decrease in platelet count were significantly associated with dengue hemorrhagic fever (DHF). Whereas, abdominal pain/tenderness, persistent vomiting and clinical fluid accumulation were significantly associated with SD. Furthermore, mucosal bleeding and abdominal pain/tenderness had high sensitivity to predict DHF (53.3% and 46.7%, respectively) and SD (52.9% and 64.7%, respectively). The liver enlargement (> 2cm) and clinical fluid accumulation had high specificity to predict DHF (97.0% and 100.0%, respectively) and SD (94.9% and 98.5%, respectively). The clinical fluid accumulation had high PPV (100.0% in DHF and 33.3% in SD) and NPV (80% in DHF and 90% in SD) to predict dengue severity. We concluded that warning signs were associated with dengue severity (DHF/SD). The clinical fluid accumulation was associated with high PPV and NPV to predict dengue severity (DHF/SD). The more warning signs, the more dengue severity encountered.

Keywords: dengue severity, warning signs, adults



Poster No. 76

THE QUALITY OF DENGUE SURVEILLANCE SYSTEM IN HIGH, MEDIUM, LOW ENDEMIC AREAS OF THE OFFICE OF DISEASE PREVENTION AND CONTROL 7th UBON RATCHATHANI PROVINCE

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The Office of Disease Prevention and Control 7th Ubonratchathani Province

This cross-sectional study was to provide quality of dengue surveillance, prevention and control system in high medium and low epidemic areas. The data samples were collected from ICD-10; A90, A91, R50.9 and B34.9 for evaluate dengue classification following by criteria of BOE surveillance and medical diagnostic and then compare with R506 report, household data survey and test mortality rate of *Aedes aegypti* larval. An F-test is statistics for analysis. The study found that overall quality level of BOE surveillance was fair level 69.02%; sensitivity of fair level 56.03%, specificity and negative predictive value was excellent but positive predictive value required improving. By comparison, show that only sensitivity in high and medium epidemic areas of provinces were significant different from low epidemic areas ($p<0.05$). For medical diagnostic criteria showed mostly not used Tourniquet test, overall quality is excellent level 81.70%. Comparative study the provincial in 3 epidemic areas no difference statistically significant ($p>0.05$). Another evaluation household survey, people of 54.57% had knowledge, attitudes and practically was moderate level 69.34%, *House Index* larval was between 8.89–37.78 at all areas. Overall dengue prevention in each area were no statistically significant difference ($p>0.05$). Finally, mortality rate of *Aedes aegypti* larvae to 17 samples of larvicide sand granules 1 ppm within 24hrs.was 100%.

Suggestion for increase quality of system, Bureau of Epidemiology should review definition criteria and diagnostic report to tighten rules and easy to understand by major criteria plus one minor such as tourniquet test positive or petechiae or thrombocytopenia is recommend. ⁂

Keywords: dengue surveillance, prevention and control system, endemic areas

ACUTE HEPATITIS IN THE SETTING OF CHRONIC *SCHISTOSOMA MANSONI* INFECTION AND POST-PRAZIQUANTEL THERAPY

Poster No. 77

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We describe the case of a young Tanzanian man with an acute hepatitis, prior to and following treatment with praziquantel, for biopsy proven chronic *Schistosoma mansoni* liver infection. The patient's clinical and biochemical course improved after prolonged corticosteroid therapy in the setting of effective antihelminth therapy and no other clear aetiology. It is postulated that the hepatitis was due to an immune response to the presence of schistosomal antigen in the liver and immunomodulation prior to and following therapy. Acute hepatitis related to a case of chronic schistosomiasis has not previously been documented in an adult and this case serves as an addition to the literature in regards to diagnosis and management of acute hepatitis in *S mansoni* infection.

Keywords: Schistosomiasis, hepatitis, immunity , diagnosis, treatment

Poster No. 78

TREATMENT COVERAGE AND ALLOCATION PREDICT FUTURE BURDEN OF CHRONIC HEPATITIS C IN NOVEL ANTIVIRAL AGENT ERA, THAILAND

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Aims: This study aims to estimate the future burden of chronic hepatitis C (CHC) and impact of public health policies using novel antiviral agents in Thailand.

Methods: We analyzed data on the hepatitis C virus (HCV) from national epidemiologic surveys and available published literature including prevalence, susceptible populations, transmission, genotypic distributions of HCV, and degree of liver fibrosis, progression of CHC, efficacy of treatments, costs of treatments, and treatment coverage. We compared and evaluated the current standard treatment (pegylated-interferon and ribavirin) against new treatments using novel antiviral agents (sofosbuvir-based treatments) in various treatment policies. A mathematical model of CHC transmission dynamics was constructed to explore the burden of disease using different treatment policies over the next 20 years.

Results: Over the next 20 years, the prevalence of CHC in Thailand is estimated to decrease from 1.09% in 2015 to 0.16%. Expanding treatment coverage is estimated to result in decreasing cumulative deaths from both decompensated cirrhosis (70.1% reduction) and hepatocellular carcinoma (HCC) related to CHC (3.7% reduction). Yearly incidence of HCC associated HCV is estimated to decrease from 5,053 to 2,314 cases per year (54.2% reduction) with expanding treatment coverage. A generalized treatment scenario (proportionally allocated treatment to all stages of disease) is predicted to significantly decrease death from HCC and overall deaths compared to a prioritizing treatment scenario (allocating treatment to significant fibrotic stage first). Apart from a reduced number of deaths from HCC, the incidence of HCC will significantly decrease from 2,314 to 1,133 cases per year at the next 20 years. Based on the extensive coverage scenario and the generalizing treatment scenario, we estimate near-zero incidences of death from decompensated cirrhosis and HCC-related CHC to occur in the next 15 and 23 years, respectively.

Conclusions: Morbidity and mortality related to chronic hepatitis C in Thailand is estimated to significantly decrease over the next 20 years. Treatment coverage and allocation strategies are significant factors impacting the future burden of chronic hepatitis C in a country with limited resources such as Thailand.

Keywords: Hepatitis C, Future burden, Estimation

DETECTION OF ARBOVIRAL GENOMES IN VECTOR MOSQUITOES USING NOVEL DRIED RT-LAMP

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Poster No. 79

Dengue and chikungunya viruses are members of arboviruses, and they cause harmful illness to human health in tropical and even temperate zones. As no effective vaccine and medicine for the diseases is available, immunological and viral genomic diagnoses have been developed as essential detection tools, Immune-chromatography Assay Kit for arboviral-antibody and –antigen, and RT-PCR, respectively.

RT-PCR is well known as one of standard methods for detection of arboviral genome in vectors as well as human patients. However, it takes a half-day depending on sample size to obtain certain result because of necessity of RNA purification of crude samples, RT-PCR reaction time, gel loading process of amplified product, and also of expensive PCR machine. Instead of this method, original RT-LAMP was developed by EIKEN Chemical Co., Ltd. This method can lead a result in a short time than RT-PCR. However this original method needs freezer for keeping regents. Here, we developed dried RT-LAMP method. This totally modified RT-LAMP can be applicable for field study, because of lower cost and no necessity of freezer.

Our data using dengue and chikungunya viral RNA, revealed that newly developed mobile dry RT-LAMP method showed faster result, more sensitive, cost effective and applicable for field study as a screening tool than a standard method, RT-PCR.

Keywords: RT-LAMP, RT-PCR, arbovirus, dengue, chikungunya, vector, viral genome

Poster No. 80

ASSOCIATION OF LOW DENSITY LIPOPROTEIN RECEPTOR RELATED PROTEIN 5 GENETIC VARIATIONS AND BMD IN THAI MENOPAUSE WOMEN

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Postmenopausal osteoporosis and low bone mass are influenced by multiple factors including genetic factors. Low density lipoprotein receptor related protein 5 (LRP5), a co-receptor of Wnt signaling, is an important regulator of bone development and maintenance. The presence of LRP5 single nucleotide polymorphism (SNP), Q89R and N740N was determined by PCR-RFLP method in 275 Thai menopause women. Genotype distribution of Q89R and N740N do not deviate from Hardy Weinberg Equilibrium. In N740N, subjects carrying CC genotype had lower radial 33 BMD (p-value = 0.015). However, there is no association found in Q89R. In conclusion, LRP5 N740N SNP may contribute to osteoporosis susceptibility in Thai menopause women.

Keywords: Osteoporosis, LRP5, Menopause, BMD

ACCEPTABILITY OF ORAL PRE-EXPOSURE PROPHYLAXIS (PREP) FOR HIV PREVENTION AMONG YOUNG MEN WHO HAVE SEX WITH MEN IN BANGKOK, THAILAND

Poster No. 81

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Background: Pre-exposure prophylaxis (PrEP) can reduce HIV incidence. Young men who have sex with men (YMSM) are a population for PrEP, with incidence of 9 per 100 person-years in some studies. Country-specific factors may affect PrEP uptake and adherence. We examined acceptability and factors associated with intention to take daily PrEP among YMSM.

Methods: Thai MSM ages 18–24 years from Bangkok participated in a survey in 2015. Rainbow Sky Association, a NGO working with the MSM community, coordinated the data collection using snowball sampling. Eligibility included self-report of oral/anal intercourse with a man in the past 3 months and consent for participation. Participants completed a self-administered questionnaire about sexual behaviors in the past three months, history of HIV testing, PrEP knowledge and attitude, and intention to take daily PrEP based on the Theory of Planned Behavior using a Likert scale. We evaluated acceptability and factors using Logistic regression.

Results: Of 350 MSM surveyed, 310 (88%) participated. Of 310, 12% were transgender. Fifty-six (18%) of all participants had heard about PrEP, and 20 (36%) correctly identified that PrEP is used for prevention. After receiving information about efficacy and safety, 95 (31%) intended to take daily PrEP. Factors significantly associated with intention to take daily PrEP were history of HIV testing (Adjusted Odd Ratio (AOR), 2.3) and high self-perceived adherence (AOR 3.0).

Conclusion: Acceptability and knowledge of daily PrEP in this population was low. More education about PrEP should be provided, as well as MSM-friendly Voluntary Counseling and Testing services, to facilitate PrEP implementation.

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Keywords: HIV, MSM, PrEP

Poster No. 82

ETIOLOGY OF NON-MALARIA ACUTE UNDIFFERENTIATED FEBRILE ILLNESS: EXPERIENCE OF THE HOSPITAL FOR TROPICAL DISEASES

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Diagnosis of acute undifferentiated febrile illness (AUFI), acute fever without specific-organ symptoms and signs of infection, has still been a common problem in tropical area. Unfortunately, apart from blood smear in malaria, other diseases do not have accurate point of care tests. Thus, we conducted a study to determine etiology and outcome of AUFI. A prospective cross-sectional hospital based study was conducted at the Bangkok Hospital for Tropical Diseases during 2013 to 2015. All enrolled adult AUFI cases, after excluding malaria by blood smear, were tested by rapid diagnostic tests and confirmation tests for tropical infections such as dengue infection (PCR and serology), bacteremia (hemoculture), rickettsiosis (PCR and immunofluorescence) and leptospirosis (PCR and micro agglutination test) on admission and follow up serology with convalescent sera. Of 397 cases enrolled, both IPD and OPD, we could get convalescent sera in only 318 cases. The etiologies could be identified in 227 cases (57.18%). Dengue was the most common cause, 139 cases (35%) followed by murine typhus, leptospirosis, bacteremia/bacterial infection, and scrub typhus. (Figure 1) High dengue prevalence could be explained by dengue outbreak in 2013 and referral of dengue cases from nearby hospitals. Interestingly, co-infection was identified in 11 cases (3%). Among co-infection, there were 7 cases of dual infection of dengue and leptospirosis proved by PCR. High rate of loss follow up for convalescent sera (19.9%) contributed to many undetermined etiology in this study. In conclusion, dengue was the most common etiology of non-malaria AUFI in urban setting of Thailand. Rickettsiosis and leptospirosis were not uncommon while bacterial infection was less common. Thus, empirical antibiotic treatment such as cephalosporin might have limited role. Also, strategies to improve diagnosis is indeed in need.

Keywords: Acute undifferentiated febrile illness

QUANTIFICATION OF CHLOROQUINE AND ITS METABOLITE IN DIFFERENT BIOLOGICAL MATRICES BY LIQUID CHROMATOGRAPHY TANDEM MASS SPECTROMETRY (LC-MS/MS)

Poster No. 83

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For decades, Chloroquine (CQ) has been the drug of choice for the treatment of malaria. It is safe, cheap and widely available, making it ideal for mass drug administration. Its extensive use resulted in rapid and widespread development of resistant parasites and it has been rendered useless for the treatment of *P. falciparum* malaria. However, it remains highly effective against *P. vivax* malaria in most areas and it is currently the frontline drug for the treatment of blood stage *P. vivax* infections. *P. vivax* accounts for 65% of all malaria cases in Asia and South America. Therefore, it is crucial to have sensitive and accurate tools to measure the drug in biological fluids in order to study its pharmacokinetic and pharmacodynamic properties. Here we present a novel set of methods to quantify CQ and its metabolite, desethyl-CQ, in various patient sample matrices. Different high-throughput extraction techniques were used to recover the drug from whole blood (50 µL), plasma (100 µL) and whole blood (50 µL) applied on filter paper followed by quantification with LC-MS/MS. The within-day and between-day accuracy and precision at all quality control levels were well below 15% for all biological fluids. The highly sensitive approach presented here allows quantification of CQ and desetyl-CQ in patient samples in concentrations as low as 1.41 ng/mL. In conclusion, the presented methods are fast, sensitive, accurate and require small volumes of biological fluids which enable pharmacokinetic studies in children and other vulnerable study populations. Whole blood applied on filter paper (dried blood spot) is also a field adapted sampling strategy that enables pharmacokinetic studies in rural areas where centrifugation and cold-chain transport are difficult.

Keywords: chloroquine, method quantification, malaria

Poster No. 84

LARGE SCALE PRODUCTION OF MONOCLONAL ANTIBODIES AGAINST DENGUE VIRUS USING STABLE MAMMALIAN CELL EXPRESSION

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Monoclonal antibody (MAb) can be used as therapeutic and diagnostic reagents for several infectious including viral diseases. To express antibody molecule as recombinant IgG, mammalian cells is the most suitable host, even from transient or stable expression. However, for further application and characterization, large scale recombinant IgG (rIgG) stably produced in Chinese Hamster Ovary (CHO) cells is required. This work reports the production of stable CHO cells expression of rIgG of 2 HuMAbs (1B3B9 and 1G7C2) for large scale production of therapeutic human IgG MAbs against Dengue virus (DENV). Immunoglobulin (IgG) stably expressed CHO cells were produced by transfection of plasmids carrying immunoglobulin genes. Two plasmids containing heavy and light chains of anti-DENV IgG were co-transfected into CHO cells using lipofectamine 2000 (Invitrogen). Two antibiotics, hygromycin and puromycin, were used to select for the CHO stable cells containing light and heavy chain plasmid, respectively. Optimal concentrations of the antibiotics were determined by kill curve analysis for effective selection of stable clones. The single CHO stable cells secreting MAbs were cloned by limiting dilution from the pool of transfected cells. Six to eight stable cells candidates secreting anti-dengue antibodies from each MAb were tested for its stability by passaging the individual candidates for 20 passages. The production yield of each individual clones from each passage were tested using IgG quantitation ELISA. The clones that showed stable expression after several passage without antibiotics were selected for further adaptation to suspension cells grown in serum-free culture medium.

Keywords: Stable expression, Dengue virus, Monoclonal antibody.

POST EARTHQUAKE COMMUNICABLE DISEASE EPIDEMIC PREVENTION APPROACHES IN NEPAL: A REVIEW

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Poster No. 85

Introduction: The aftermath of the Nepal earthquake 2015 brought substantial population displacements and change in environmental situation exposing the vulnerability to the existing pathogens for the transmission. The main causes of communicable diseases aftermath the disaster include: presence of pathogens, displacement of population, change in environment, disruption of basic public utilities, lack of basic health services and food shortage etc. Aftermath of earthquake resulted complete destruction of 392 health facilities and 531 were partially damaged. The disruption of the health programs (diseases prevention and control activities , immunization, vector control) further pose the threats towards increase risk of infectious diseases transmission and outbreaks following the earthquake. The risk of the disease outbreak was associated with the prolonged after effect of the disaster. These after effect included displaced populations, environmental changes, increasing the breeding sites of the vectors, high exposure to and proliferations of disease vectors (rodents, mosquitoes and flies), unplanned and overcrowded temporary shelters, polluted water and poor sanitation, poor nutritional status and poor personal hygiene, low level of immunity to vaccine preventable diseases.

Approach: The protocol was devised to prevent the outbreak of disease after the recent earthquake and assessment of the health risk and diseases was done. The following preventive and control measures were taken on an immediate basis to avoid the spread of communicable diseases following the recent earthquake: water safety, medical services, early warning system, vector control and health promotion measures.

Impact: There was no report of increased incidence of communicable diseases followed by the earthquake in Nepal. ⁂

Keywords: Earthquake, Nepal, epidemic, prevention

Poster No. 86

CLINICAL MANIFESTATIONS AND TREATMENT OUTCOMES OF SCRUB TYPHUS IN UMPHANG HOSPITAL, THAILAND

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Background: Scrub typhus is an acute febrile illness that affects a large population in rural Asia. The district of Umphang in northwestern Thailand is a prototype environment for this disease. This study aimed to identify and describe the clinical manifestations and the outcomes of patients infected with *Orientia tsutsugamushi* in this area.

Methods: Patients presenting with scrub typhus between January 2011 and December 2014 were analysed in this retrospective study. Diagnosis was based on clinical symptoms in conjunction with a positive rapid test, or a pathognomonic eschar lesion.

Results: Eight hundred and fifty seven patients were included in the study, of which 488 were adults and 369 were children. The majority (728; 85%) was included with positive serology on rapid test, 86 patients (10%) had eschar only, and 43 patients (5%) had both positive serology and presence of eschar. The most common symptom was fever (94%) followed by headache (48%) and cough (33%). Eschars were reported in 129 patients with a significantly higher percentage in children than adults ($p < 0.001$), and a different anatomical distribution was found between adults and children. Common complications were elevated transaminases, acute kidney injury and pneumonia. Most of the patients recovered from the disease, with around 1% mortality.

Conclusion: Umphang district has a high incidence of scrub typhus. Clinicians have to be vigilant as patients can present with a variety of clinical symptoms, regardless of the presence of fever. If diagnosed early, the treatment is effective and a favourable outcome can be expected.

ANTI-INFLAMMATORY ACTIVITIES OF DIOSGENIN AGAINST *NAEGLERIA FOWLERI* LYSATE INDUCED-HUMAN MONOCYTES U-937 CELLS

Poster No. 87

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Free living *Naegleria fowleri* amoeba causes fatal primary ameobic meningoencephalitis in humans. Additionally, *N. fowleri* lysate induced strong cytopathic effects and pro-inflammatory cytokines in microglial cell. Our previous study revealed anti-amoebic activity of diosgenin against *N. fowleri* trophozoites. This study investigated effect of diosgenin against pro-inflammatory cytokine genes from human monocytes U-937 cells after stimulation with *N. fowleri* lysate compared to lipopolysaccharides (LPS). The MNTD values of diosgenin and *N. fowleri* lysate on U-937 cells were 250 and 1000 ug/ml. The *N. fowleri* lysate- induced pro-inflammatory TNF-alpha cytokine gene was increased at 3, 6, and 12 hours. LPS–induced pro-inflammatory TNF-alpha cytokine genes were also increased at the same time. Diosgenin decreased TNF-alpha cytokine gene from LPS-induced cells at 3, 6 and 12 hours. TNF-alpha cytokine gene was not changed by diosgenin in *N. fowleri* lysate-induced cells at 12 hours. No significant difference pro-inflammatory IL-1 beta and IL-6 from untreated or diosgenin- treated cell after stimulation with *N. fowleri* lysate or LPS were observed at 3, 6 and 12 hours. It was concluded that diosgenin had anti-inflammatory activity against human monocyte cells by blocking TNF- alpha synthesis.

Keywords: Diosgenin, *Naegleria fowleri* lysate, Anti-inflammatory activities

Poster No. 88

SAFETY OF A RECOMBINANT LIVE ATTENUATED TETRAVALENT DENGUE VACCINE: POOLED ANALYSIS OF 20,667 INDIVIDUALS AGED 9 THROUGH 60 YEARS OF AGE

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Published pooled evaluation of 2 Phase III efficacy trials[1] of the tetravalent dengue vaccine showed vaccine efficacy in individuals 9-16 years against dengue of any severity of 65.5%. Efficacy against severe and hospitalized dengue was 93.2 and 80.8% respectively.

A pooled analysis of safety was conducted across 13 clinical trials (final formulation and 3 dose schedule). This analysis allowed the detection of adverse events with a frequency of ≥ 0.1%. A total of 20,667 individuals aged 9-60 years after at least 1 injection of the vaccine and 9833 controls were included. The data cut-off date was 28th November 2014.

Solicited injection site and solicited systemic reactions were similar between individuals 9-17 and those 18-60 years of age, with no increase in reactogenicity with subsequent injections.

There were no identified safety concerns with unsolicited AEs. The clinical safety profile was similar in subjects who were dengue seropositive and dengue seronegative at baseline.

In this safety database, there were no anaphylactic reactions and serious allergic reactions were rare. No excess of hospitalized or severe dengue cases in vaccinees compared to controls was observed in the 25 months after the first injection. The overall Serious Adverse Event (SAE) reporting rate was comparable in both groups. Few SAEs were considered as related to vaccination. No related deaths have been reported.

In conclusion, the pooled analysis based on 13 clinical trials shows that CYD-TDV has an acceptable safety profile, comparable with control, in individuals 9 through 60 years of age.

Keywords: Tetravalent Dengue vaccine, pool analysis, CYD-TDV, Dengue, safety

TELEMEDICINE: IS THERE A PLACE IN TROPICAL MEDICINE FOR THIS NOVEL APPROACH TO BRING CARE CLOSER TO THE PATIENT

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Country Health SA LHN

Poster No. 89

In many countries, the tyranny of distance affects outcomes of patient care. An innovative model of care can improve these through provision of more cost effective and timely care, easier access to facilities for patients and regional health workers, and minimise the travel and thus improve family support for patients.

This system has been utilised in South Australia to deliver oncological care to rural areas. A retrospective clinical review was performed in 2013-2014, which showed 380 patatients reviewed in such clinics in 2 hospitals. Clinics included pre-therapy reviews 285, restaging visits 39, and 6 new patient consultations. Since then, we are now utilising these clinics to see patients in 4 rural hospitals, with more patients seen each month.

Our health provision model has changed to allow more work satisfaction to health workers, and patient and their families accepting this as an equal quality consultation option. The model of care being innovative, has been readily accepted, saving patients time of travel, and decreasing the burden on metropolitan clinic appointments and budget.

While our clinic is mainly an oncology specialist clinic, this could readily be adopted for any specialist clinic model, including that of tropical medicine. Indeed, there are many similarities including the issues of distance for many patients to travel, centralised care in metropolitan hospitals, and overburdened clinics. Most countries now have basic IT systems that can be adapted to suit this purpose, and further improve the cost effectiveness.

Keywords: Telemedicine, remote, rural, tropical, oncology