JOINT INTERNATIONAL TROPICAL MEDICINE MEETING 2022 (JITMM 2022 Hybrid)

"Leveraging the Pandemic Experience: Our Tropical Medicine Community Rejuvenated"

7-9 December 2022

Montien Surawong Hotel, Bangkok, Thailand

Program and Abstracts Book

Hosted by

Mahidol University
Faculty of Tropical Medicine

Co-Organizers:

Mahidol University

Department of Disease Control

Chula
Chulalongkorn University

MORU
Tropical Health Network

TCEB
THAILAND CONVENTION & EXHIBITION BUREAU

Organizers and Co-Organizers

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

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Wednesday 7 December 2022

K1: Opening Ceremony and Keynote Address

8:30-9:15hr

Room A

Opening Ceremony by Organizers and Co-organizers

Report
Weerapong Phumratanaprapin
Chair, JITMM 2022 Organizing Committee
Dean, Faculty of Tropical Medicine, Mahidol University

Welcome Address

1. **Thares Krasanaiyarawiwong**
   Director-General, Department of Disease Control, Thailand Ministry of Public Health

2. **Nicholas Day**
   Director, Mahidol-Oxford Tropical Medicine Research Unit (MORU)

3. **Suttipong Wacharasindhu**
   Senior Executive Committee, School of Global Health
   (Representing Chanchai Sittipunt
   Dean, Faculty of Medicine, Chulalongkorn University)

4. **Pratap Singhasivanon**
   Secretary General/Coordinator of SEAMEO TROPMED Network

Opening Remarks
Banchong Mahaisavariya
President, Mahidol University

Opening Keynote Address: 27th Chamlong-Tranakchit Harinasuta Lecture

9:15-10.00hr

Chairperson: Weerapong Phumratanaprapin

Keynote Speaker:

PREVENTING THE NEXT PANDEMIC: THE POWER OF A GLOBAL EARLY WARNING SURVEILLANCE SYSTEM

Dennis Carroll

Global Virome Project

Wednesday 7 December 2022

S1: Advanced Information Technology for Tropical Medicine

10:30-12:00hr

Room A

Chairpersons:
1. **Anna Förster**
2. **Saranath Lawpoolsri Niyom**

Invited speakers:

1. **A PIPELINE FOR MOSQUITO DETECTION AND CLASSIFICATION FROM WINGBEAT SOUNDS**
   Myat Su Yin
   Faculty of ICT, Mahidol University

2. **PROGNOSTIC PREDICTION OF DHF IN PEDIATRIC PATIENTS: A MULTI-SITE STUDY**
   Peter Haddawy
   Faculty of ICT, Mahidol University

3. **A MOBILE SYSTEM FOR DENGUE VECTOR MONITORING AND CONTROL**
   Thomas Barkowsky
   University of Bremen

4. **MODELING THE SPREAD OF RABIES IN THAILAND: A BOTTOM-UP APPROACH**
   Anuwat Wiratsudakul
   Faculty of Veterinary Science, Mahidol University

Wednesday 7 December 2022

S2: Management of Severe Dengue

10:30-12:00hr

Room B

Chairpersons:

1. **Usa Thisyakorn**
2. **Weerapong Phumratanaprapin**

Invited speakers:

1. **KIDNEY COMPLICATIONS AND THEIR MANAGEMENT IN DENGUE INFECTION**
   Weerapong Phumratanaprapin
   Faculty of Tropical Medicine, Mahidol University

2. **DENGUE: AN OVERVIEW AND MANAGEMENT**
   Terapong Tantawichien
   Faculty of Medicine, Chulalongkorn University

3. **CARDIOVASCULAR COMPLICATION IN DENGUE**
   Chayasin Mansanguan
   Faculty of Tropical Medicine, Mahidol University

4. **PULMONARY COMPLICATIONS IN DENGUE**
   Chaisith Sivakorn
   Faculty of Tropical Medicine, Mahidol University

5. **DENGUE IN ICU SETTING**
   Nattachai Srisawat
   Faculty of Medicine, Chulalongkorn University

Wednesday 7 December 2022

S3: Virtual Reality in Medical Education

10:30-12:00hr

Room C

Chairpersons:
1. **Aongart Mahittikorn**
2. **Toshio Naito**

Invited speakers:

1. **HOW VR CHANGES MEDICAL EDUCATION IN JAPAN AND THE FUTURE OF VR EDUCATION**
   Yutaro Oikawa
   Jolly Good Inc., Corporate Planning Department

2. **VIRTUAL REALITY IN MEDICAL EDUCATION**
   Hirotake Mori
   Faculty of Medicine, Juntendo University

3. **VR CONTENT DEMONSTRATION (THAILAND TO JAPAN)**
   Rapeepan Prasertbun
   Faculty of Tropical Medicine, Mahidol University

4. **VR CONTENT DEMONSTRATION (JAPAN TO THAILAND)**
   Simon Valenti
   Juntendo University

Wednesday 7 December 2022

S4: Liver Stage Malaria

10:30-12:00hr

Room D

Chairpersons:
1. **Sebastian Mikolajczak**
2. **Wanlapa Roobsoong**

Invited speakers:

1. **STRATEGIES FOR RADICAL CURE: FROM ANTI-HYPNOZOITE TO ANTI-RELAPSE**
   Erika Flannery
   Novartis Institute for Tropical Diseases

2. **DISCOVERY OF NOVEL CHEMOTYPES EFFECTIVE AGAINST RELAPSING MALARIA**
   Alison Roth
   Walter Reed Army Institute of Research

3. **TRANSMISSION ELECTRON MICROSCOPY TECHNIQUES TO CHARACTERIZE THE ULTRASTRUCTURAL FEATURES OF MALARIA LIVER STAGES**
   Gabriel Mitchell
   Novartis Institute for Tropical Diseases

4. **A DUAL LUMINESCENCE ASSAY TO STUDY ANTIMALARIAL COMPOUNDS AND HOST-PATHOGEN INTERACTIONS DURING THE LIVER STAGE OF MALARIA**
   Laura Torres
   Novartis institute for Tropical Diseases

5. **UNDERSTANDING DRUG METABOLIC ACTIVITY AND HEPATOTOXICITY IN LONG-TERM CULTURE OF PRIMARY SIMIAN HEPATOCYTES**
   Eve Vorada Chuenchob
   Novartis Institute of Tropical Diseases

Wednesday 7 December 2022

S5: Way Forward to Leverage Pandemic Prevention

10:30-12:00hr

Room E

Chairpersons:
1. **Opass Putcharoen**
2. **Sudarat Damrongwatanapokin**

Invited speakers:

1. **SURVEILLANCE AND SPILLOVERS MONITORING**
   Supaporn Wacharapluesadee
   Emerging Infectious Disease - Clinical Center, King Chulalongkorn Memorial Hospital

2. **EID INNOVATION**
   Linfa Wang
   Duke-NUS Medical School, Singapore

3. **VACCINE DEVELOPMENT**
   Kiat Ruxrungtham
   Chula Vaccine Research Center, Faculty of Medicine, Chulalongkorn University

4. **BUILDING A GLOBAL EID RESEARCH NETWORK**
   Dennis Carroll
   School of Global Health, Faculty of Medicine, Chulalongkorn University

Wednesday 7 December 2022

[Lunch Symposium] QIAGEN Innovation to Making Improvement in Life Possible

12.00-13.00hr

Room A

Chairpersons:

1. **Phairat Royros**
2. **Tewarit Soongrung**

Invited speakers:

1. **REVOLUTION OF DETECTION IN TROPICAL INFECTIOUS DISEASES WITH NEUDRY TECHNOLOGY**
   Chun Wei Chiam
   Senior Sales Application Specialist, Infectious Diseases, Southeast Asia

2. **FINDING THE NEEDLE IN HAYSTACK IN TROPICAL DISEASES STUDY WITH NANOPLATE BASED DIGITAL PCR TECHNOLOGY**
   Amelia Lum
   Sales Application Specialist Life Science APEC

Wednesday 7 December 2022

S6: MORU-OUCRU Student Showcase

13.00-14.30hr

Room A

Chairpersons:
1. **Wirichada Pan-ngum**
2. **Leigh Jones**

Invited speakers:

1. **ANALYZING HUMAN POPULATION MOVEMENT DATA FOR MALARIA CONTROL AND ELIMINATION**
   Greta Tam
   Mahidol Oxford Tropical Medicine Research Unit (MORU)

2. **RELEVANT INTERVENTIONS TO TACKLE THE GAPS IN HIV PREVENTION AND CARE IN KEY AFFECTED POPULATIONS, MYANMAR**
   Ni Ni Tun
   Mahidol Oxford Tropical Medicine Research Unit (MORU)

3. **BIG DATA AND VACCINATION: EXPLORE THE IMPACTS OF COVID-19 ON CHILDREN ROUTINE MEASLES VACCINATION IN VIETNAM USING VACCINE REGISTRY DATA**
   Ong Phuc Thinh
   Oxford University Clinical Research Unit (OUCRU)

4. **UNDERSTANDING HEPATITIS C TREATMENT COST IN VIETNAM**
   Nguyen Anh Huyen
   Oxford University Clinical Research Unit (OUCRU)

5. **DEVELOPING MOLECULAR MULTIPLEX DIAGNOSTICS FOR TROPICAL PATHOGENS**
   Witchayoot Huangsuranun
   Mahidol Oxford Tropical Medicine Research Unit (MORU)

6. **RISK MAPPING OF ARBOVIRUSES: A SYSTEMATIC REVIEW OF DATA, MODELS, COVARIATES, AND METHODS OF EVALUATION**
   Yalda Jafari
   Mahidol Oxford Tropical Medicine Research Unit (MORU)

7. **ANTIBODY RESPONSE TO DIFFERENT BURKHOLDERIA PSEUDOMALLEI ANTIGENS**
   Apinya Pumpuang
   Mahidol Oxford Tropical Medicine Research Unit (MORU)

8. **DEFINING THE EPIDEMIOLOGY OF ACUTE FEBRILE ILLNESS IN RURAL SOUTH AND SOUTHEAST ASIA**
   Christopher Chew
   Mahidol Oxford Tropical Medicine Research Unit (MORU)

Wednesday 7 December 2022

S7: Addressing Dengue Challenges

13.00-14.30hr

Room B

Chairperson:
1. Pratap Singhasivanon

Invited speakers:

1. WOLBACHIA REPLACEMENT STRATEGY TO COMBAT DENGUE: MALAYSIA EXPERIENCE
Nazni binti Wasi Ahmad
Institute for Medical Research, Kuala Lumpur Malaysia

2. CARICA PAPAYA LEAVES: EVIDENCE BASED THERAPEUTICS FOR DENGUE
Mohd Ridzuan bin Mohd Abd Razak
Institute for Medical Research, Kuala Lumpur Malaysia

3. KNOWLEDGE, ATTITUDES, AND PRACTICES OF PUBLIC ELEMENTARY AND HIGH SCHOOL TEACHERS ON DENGUE IN A PROVINCE OF THE PHILIPPINES
Ernesto R. Gregorio, Jr.
College of Public Health, University of the Philippines Manila

4. DENGUE DIAGNOSIS PREDICTION USING BAYESIAN NETWORK MODEL
Saranath Lawpoolsri Niyom
Faculty of Tropical Medicine, Mahidol University

Wednesday 7 December 2022

S8: Frontier Research in Tropical Diseases for Sustainable Development Goals (SDGs)

13.00-14.30hr

Room C

Chairpersons:
1. Narisara Chantratita
2. Le Van Tan

Invited speakers:

1. STRENGTHENING CAPACITY TO UNDERSTAND IMMUNITY TO SARS-COV-2 AND OTHER EMERGING PATHOGENS
Susanna Dunachie
Oxford University Hospitals NHS Trust, University of Oxford

2. EXPERIENCE ON GENOMIC SURVEILLANCE AND DEVELOPMENT OF INACTIVATED COVID-19 VACCINE IN MYANMAR
Nay Myo Aung
Department of Microbiology, Defense Services Medical Academy, Yangon, Myanmar

3. MATCHING MULTI-LOCUS SEQUENCE TYPES OF SOIL AND CLINICAL ISOLATES OF BURKHOLDERIA PSEUDOMALLEI IN MYANMAR: THE IDENTIFIABLE MISSING LINKS
Chanwit Tribuddharat
Faculty of Medicine Siriraj Hospital, Mahidol University

4. DRUG DISCOVERY FROM NEW RESOURCES FOR FIGHTING AGAINST TROPICAL INFECTIONS
Aunchalee Thanwisai
Department of Microbiology and Parasitology, Faculty of Medical Science, Naresuan University

Wednesday 7 December 2022

S9: Free Paper I: COVID-19 and Other Viral Diseases

13.00-14.30hr

Room D

Chairpersons:
1. Pornsawan Leaungwutiwong
2. Viravarn Luvira

Invited speakers:

1. INCIDENCE OF SAR-CoV-2 INFECTION AMONG FULLY-VACCINATED TRAVELERS TO THE PHUKET SANDBOX PROGRAM 2021, THAILAND
Thunyaporn Sirijantradilok
Other (Institute of Preventive Medicine, Department of Disease Control, Ministry of Public Health, Thailand)

2. SIDE EFFECTS OF COVID-19 VACCINES AMONG KINDERGARTEN AND ELEMENTARY SCHOOLERS—THAILAND CASE
Chutimon Singkiao
Department of Disease Control, Ministry of Public Health, Thailand

3. FEASIBILITY OF NASO/OROPHARYNGEAL SWAB COLLECTION FROM PEDIATRIC RESEARCH PARTICIPANTS IN CEBU, PHILIPPINES
Clarissa De Guzman
Institute of Child Health and Human Development, National Institutes of Health

4. ASSESSMENT OF ADHERENCE TO COVID-19 PREVENTIVE MEASURES AMONG RESIDENTS IN MYANMAR
Nyan Lin Maung
Defence Services Medical Academy, Myanmar

5. DEVELOPMENT OF SEQUENCE-INDEPENDENT, SINGLE-PRIMER-AMPLIFICATION AND OXFORD NANOPORE SEQUENCING IN TRACKING HAND-FOOT-AND-MOUTH DISEASE TRANSMISSION AMONG CASES AND CONTACTS IN KINDERGARTENS, THAILAND
Janjira Thaipadungpanit
Faculty of Tropical Medicine, Mahidol University

Wednesday 7 December 2022

S10: Helminths: Should These Be Neglected Diseases?

13.00-14.30hr

Room E

Chairpersons:

1. Dorn Watthanakulpanich
2. Urusa Thaenkham

Invited speakers:

1. CASE SERIES OF DISSEMINATED STRONGYLOIDIASIS IN MALAYSIAN PATIENTS WITH COVID-19
Azlin Muhammad
Medical Faculty, Universiti Kebangsaan, Malaysia

2. FROM PAST TO PRESENT: OPPORTUNITIES AND TRENDS IN THE MOLECULAR DETECTION AND DIAGNOSIS OF STRONGYLOIDES STERCORALIS
Abigail Hui En Chan
Faculty of Tropical Medicine, Mahidol University

3. INTESTINAL PARASITES IN RURAL COMMUNITIES IN NAN PROVINCE, THAILAND: CHANGES IN BACTERIAL GUT MICROBIOTA ASSOCIATED WITH MINUTE INTESTINAL FLUKE INFECTION
Ajala Prommi
Research Unit of Systems Microbiology, Chulalongkorn University

Wednesday 7 December 2022

S11: Therapeutic Antibodies Against Viral Pathogens

15.00-16.30hr

Room A

Chairpersons:
1. **Pongrama Ramasoota**
2. **Thammanitchpol Denpetkul**

Invited speakers:

1. THERAPEUTIC HUMAN MONOCLONAL ANTIBODY AGAINST DENGUE VIRUS; TOWARD COMMERCIALIZATION

Pongrama Ramasoota
Faculty of Tropical Medicine, Mahidol University

2. POTENTIAL DENGUE THERAPEUTIC CANDIDATES BASED ON DENGUE NS1 PROTEIN

Pannamthip Pitaksajjakul
Faculty of Tropical Medicine, Mahidol University

3. GENERATION OF A SINGLE-CHAIN FRAGMENT VARIABLE (scFv) ANTIBODY AGAINST SARS-COV-2 RBD PROTEIN USING CONVALESCENT PATIENTS-DERIVED PHAGE DISPLAY LIBRARIES

Surachet Benjathummarak
Faculty of Tropical Medicine, Mahidol University

4. ANTIBODY DEPENDENT ENHANCEMENT (ADE) OF SARS-CoV-2 INFECTION

Atsushi Yamanaka
Research Institute for Microbial Diseases (RIMD), Osaka University

Wednesday 7 December 2022

S12: Chikungunya Virus Epidemiology and Vaccine Development

15.00-16.30hr

Room B

Chairperson:
1. **Stefan Fernandez**

Invited speakers:

1. **CHIKUNGUNYA EPIDEMIOLOGY IN SOUTHERN THAILAND**
   Aaron R. Farmer
   Armed Forces Research Institute of Medical Sciences

2. **PHASE 2 STUDY ASSESSING SAFETY AND IMMUNOGENICITY OF A CHIKUNGUNYA VACCINE IN RECIPIENTS OF OTHER ALPHAVIRUS VACCINES VERSUS ALPHAVIRUS NAÏVE CONTROLS**
   Patrick Ajiboye
   Emergent BioSolutions, USA

3. **ADVANCES IN THE DEVELOPMENT OF A SINGLE-SHOT LIVE-ATTENUATED CHIKUNGUNYA VACCINE CANDIDATE**
   Vera Buerger
   Valneva Austria GMBH

Wednesday 7 December 2022

S13: Tropical Medicine Tournament

15.00-16.30hr

Room C

Moderators :

1. Jittima Dhitavat
2. Athit Phetrak
3. Supachai Topanurak
4. Wirongrong Chierakul

Wednesday 7 December 2022

S14: Host Genetics in Falciparum Malaria

15.00-16.30hr

Room D

Chairpersons:
1. **Arjen Dondorp**
2. **Kesinee Chotivanich**

Invited speakers:

1. **HBS ALLELE FREQUENCIES IN AFRICA REVEAL MALARIA ATTRIBUTABLE CHILDHOOD MORTALITY IN THE PRE-TREATMENT AREA**
   Arjen Dondorp
   Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

2. **SAFETY OF SINGLE LOW DOSE PRIMAQUINE IN AFRICAN CHILDREN WITH FALCIPARUM MALARIA**
   Bob Taylor
   Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

3. **G6PD DEFICIENT RED CELLS AND ASEXUAL BLOOD STAGE DEVELOPMENT OF P. FALCIPARUM**
   Tianrat Piteekan
   Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

Wednesday 7 December 2022

S15: Free Paper II: COVID-19: Impact on Other Diseases and Management Policy

15.00-16.30hr

Room E

Chairpersons:
1. Suparat Phuanukoonnon
2. Kraichat Tantrakarnapa

Invited speakers:

1. DEFINING THE SOCIAL DETERMINANTS OF ANTIMICROBIAL CONSUMPTION DURING COVID-19: A REVIEW
Mutiara Shinta Noviar Unicha
Tropical Medicine, Faculty of Medicine, Public Health, and Nursing, Universitas Gadjah Mada, Indonesia

2. THE IMPACT OF COVID-19 PANDEMIC ON DIRECTLY OBSERVED TREATMENT SHORT COURSES(DOTS) PROGRAM FOR TUBERCULOSIS IN NEPAL
Ruby Maka Shrestha
Dhulikhel Hospital Kathmandu University Hospital

3. GLOBAL RESEARCH AGENDA ON PUBLIC HEALTH AND SOCIAL MEASURES: WHO’S EFFORTS IN SCIENCE AND HEALTH DIPLOMACY FOR HEALTH EMERGENCIES
Ryoko Takahashi
World Health Organization

4. DEVELOPMENT OF A MODEL ONE-STOP APPROACH TO POST-COVID 19 AND OTHER REHABILITATION CONDITIONS IN NEPAL
Puspanjali Adhikari
Dhulikhel Hospital Kathmandu University Hospital

Thursday 8 December 2022

Plenary Session (with morning coffee)

08.00-09.00hr

Room A

Chairperson: Prof. Nicholas Day

Plenary speaker :

IMPACT, LEGACY AND LESSONS FROM THE RECOVERY TRIAL

Sir Peter Horby
Professor of Emerging Infections and Global Health, University of Oxford
Director, Pandemic Sciences Institute

Thursday 8 December 2022

S16: Updates on New Vaccines : Tuberculosis, mRNA Influenza and HIV Vaccines

09.00-10.30hr

Room A

Chairperson:
1. **Punnee Pitisuttithum**
2. **Sant Muangnoicharoen**

Invited speakers:

1. **NEW TB VACCINES - SUCCESSES AND CHALLENGES**
   Anh Wartel
   International Vaccine Institute (IVI)

2. **MODERNA INFLUENZA VACCINE PROGRAM**
   Jintanat Ananworanich
   Moderna

3. **UPDATE AND CHALLENGES OF NEW GENERATION VACCINES**
   Punnee Pitisuttithum
   Faculty of Tropical Medicine, Mahidol University

Thursday 8 December 2022

S17: Meet the Experts (Bioethics)

09.00-10.30hr

Room B

Panelists :

1. **Jaranit Kaewkungwal**
   Faculty of Tropical Medicine, Mahidol University

2. **Christine Grady**
   Department of Bioethics, NIH Clinical Center

3. **Reidar Lie**
   University of Bergen

4. **David Wendler**
   Department of Bioethics, NIH Clinical Center

5. **Holly Taylor**
   Department of Bioethics, NIH Clinical Center

6. **Zhai Xiaomei**
   Center for Bioethics, Chinese Academy of Medical Sciences

7. **Calvin Ho**
   The University of Hong Kong

8. **Kenji Matsui**
   Division of Bioethics and Healthcare Law, National Cancer Center Japan

Thursday 8 December 2022

S18: Infection, Prevention, and Control [MOPH]

09.00-10.30hr

Room C

Chairpersons:
1. Weerawat Manosuthi
2. Jurai Wongsawat

Invited speakers:

1. HOT TOPIC IN INFECTION CONTROL 2022
Darunee Chotiprasitsakul
Department of Disease Control, Ministry of Public Health, Thailand

2. COVID-19 PANDEMIC IMPACT ON ANTIMICROBIAL RESISTANCE
Lantharita Charoenpong
Bamrasnaradura Infectious Diseases Institute

3. WHAT'S NEW IN COVID-19: INFECTION CONTROL PERSPECTIVE
Visal Moolasart
Department of Disease Control, Ministry of Public Health, Thailand

4. WHAT’S NEW IN COVID-19: INFECTION CONTROL PERSPECTIVE
Chaisiri Srijareonvijit
Department of Disease Control, Ministry of Public Health, Thailand

5. PREVENTION OF EID FROM ABROAD: PUBLIC HEALTH AND HOSPITAL MANAGEMENT
Jurai Wongsawat
Department of Disease Control, Ministry of Public Health, Thailand

6. PREVENTION OF EID FROM ABROAD: PUBLIC HEALTH AND HOSPITAL MANAGEMENT
Rome Buathong
Department of Disease Control, Ministry of Public Health, Thailand

Thursday 8 December 2022

S19: Free Paper III: Vector Biology and Vector Control

09.00-10.30hr

Room D

Chairpersons:
1. **Patchara Sriwichai**
2. **Leo Braack**

Invited speakers:

1. REPRODUCTIVE CONTROL OF MOSQUITOES: CHALLENGES AND OPPORTUNITIES
Laura Harrington
Cornell University, Ithaca, NY USA

2. LARVICIDAL POTENTIAL OF SILVER NANOPARTICLES SYNTHESIZED FROM SOLANUM XANTHOCARPUM LEAF EXTRACTS: ECO-FRIENDLY TOOLS FOR CONTROLLING MOSQUITO VECTORS
Kumar Vikram
Indian Council of Medical Research (ICMR)

3. DEVELOPMENT AND ASSESSMENT OF A NOVEL COMMUNITY E-LEARNING PLATFORM FOR AEDES-BORNE DISEASES
Rattanaporn Boonmeepom
Burapha University

4. ONLINE PRACTICAL STUDIED OF CHIGGER MITE (TROMBICULIDAE) AS VECTORS OF SCRUB TYPHUS
Rawadee Kumlert
Division of Vector Borne Diseases, Department of Disease control, Ministry of Public Health, Thailand

5. THE POTENTIAL OF ON-LINE CITIZEN SCIENCE APPLICATION FOR COMMUNITY-PARTICIPATORY MONITORING OF MOSQUITOES, DEVELOPED IN THIS STUDY
Mika Saito
Graduate School of Medicine, University of the Ryukyus

6. INCLUDING MOBILITY TO OPTIMIZE MOSQUITO CONTROL INTERVENTION STRATEGIES
Richard Paul
Institut Pasteur, France

Thursday 8 December 2022

S20: Applied Social Science in Tropical Disease Prevention and Control

09.00-10.30hr

Room E

Chairperson:
1. Suparat Phuanukoonon

Invited speakers:

1. A SPATIAL ANALYSIS OF GEOGRAPHIC ACCESS TO PUBLIC HEALTHCARE FACILITIES IN CÔTE D'IVOIRE
Gaëlle T. Sehi
University of California- Irvine

2. CONFLICT AND CHOLERA: QUANTIFYING THE IMPACT OF AIR RAIDS ON YEMEN'S CHOLERA INCIDENCE
Maia Tarnas
University of California, Irvine

3. A CONCEPTUAL FRAMEWORK TO UNDERSTAND EXTRACTIVE SETTLEMENTS AND DISEASE: DEMOGRAPHY,
ENVIRONMENT, AND EPIDEMIOLOGY.
Natasha Glendening
University of California Irvine

4. FACTORS HINDERING COVERAGE OF TARGETED MASS TREATMENT WITH PRIMAQUINE IN A TOWNSHIP IN NORTHERN MYANMAR
Pyae Linn Aung
Faculty of Tropical Medicine, Mahidol University (Mahidol Vivax Research Unit (MVRU)

Thursday 8 December 2022

S21: One Health Approach in Emerging Vector Borne and Zoonotic Diseases

11.00-12.30hr

Room A

Chairpersons:

1. **Padet Siriyasatien**
2. **Sonthaya Tiawsirisup**

Invited speakers:

1. **EID ZOONOTIC**
   Opass Putcharoen
   Faculty of Medicine, Chulalongkorn University

2. **AUTOCHTHONOUS LEISHMANIASIS IN THAILAND: UPDATE IN CLINICAL ASPECTS AND VECTOR BIOLOGY**
   Kanok Preativatanyou
   Faculty of Medicine, Chulalongkorn University

3. **ANIMAL VECTOR BORNE DISEASES**
   Sonthaya Tiawsirisup
   Faculty of Veterinary Science, Chulalongkorn University

4. **IMPLEMENTING ONE HEALTH APPROACHES TO CONFRONT EMERGING AND RE-EMERGING ZOONOTIC DISEASE THREATS**
   Ratanaporn Tangwangvivat
   Department of Diseases Control, Ministry of Public Health

Thursday 8 December 2022

S22: Rejuvenate Medical Entomology: Chance and Challenge

11.00-12.30hr

Room B

Chairpersons:
1. Suchada Sumruayphol
2. Rutcharin Potiwat

Invited speakers:

1. ADVANCES IN VOLATILE PYRETHROID EVALUATION FOR VECTOR CONTROL IN THE GREATER MEKONG SUBREGION
Jeffrey Hii
James Cook University, North Queensland, Australia

2. CHALLENGES OF MOSQUITO SENSOR AND AI APPLICATION FOR VECTOR SURVEILLANCE
Michael Weber
Research & Development of Biogents, Germany

3. DOSE-DEPENDENT BLOOD-FEEDING ACTIVITY AND OVARIAN ALTERATIONS TO PM2.5 IN AEDES AEGYPTI
Thipruethai Phanitchat
Faculty of Tropical Medicine, Mahidol University

Thursday 8 December 2022

S23: Health in Detention: Make Inequity, Equity Make Difficulty, Access Easily [MOPH]

11.00-12.30hr

Room C

Chairpersons:
1. **Anupong Sujariyakul**
2. **Pahurat Kongmuang Taisuwan**

Invited speakers:

1. **PROVIDING MEDICAL AND PUBLIC HEALTH SERVICES IN PRISONS**
   Chutarat Chintakanont
   Department of Corrections, Ministry of Public Health

2. **ACCESS TO TREATMENT RIGHTS AND THE USE OF BUDGETS IN THE MANAGEMENT OF MEDICAL SERVICE**
   Kanitsak Chantrapipat
   Office of Primary Care NHSO

3. **HEALTH IN DETENTION**
   Vivien Lusted
   ICRC

4. **DISEASE PREVENTION AND CONTROL IN PRISONS COMPARE WITH COMMUNITY AT LARGE: LESS OR EQUITY**
   Pahurat Kongmuang Taisuwan
   Department of Disease Control, Ministry of Public Health

Thursday 8 December 2022

S24: Understanding Plasmodium Liver Stage Development for the Design of Novel Vaccine and Drug Interventions

11.00-12.30hr

Room D

Chairpersons:
1. **Noah Sather**
2. **Ashley Vaughan**

Invited speakers:

1. **IN VIVO ASSESSMENT OF PLASMODIUM VIVAX CHESSON STRAIN LIVER STAGE INFECTION: NOVEL STUDIES TO ASSESS HYPNOZOITE FORMATION, PERSISTENCE, ACTIVATION, AND RELAPSE**
   Gigliola Zanghi
   Seattle Children's Research Institute

2. **HOST REGULATION OF PLASMODIUM VIVAX DORMANT AND REPLICATING LIVER FORMS**
   Alexis Kaushansky
   Seattle Children's' Research Institute

3. **USING NON-HUMAN PRIMATES TO UNDERSTAND HOST-PATHOGEN BIOLOGY AND ACCELERATE VACCINE DEVELOPMENT**
   Brandon Wilder
   Seattle Children's Research Institute

4. **CREATION OF A LATE LIVER STAGE-ARRESTING PLASMODIUM FALCIPARUM GENETICALLY ATTENUATED VACCINE**
   Ashley Vaughan
   Seattle Children's Research Institute

Thursday 8 December 2022

S25: Innovative Approaches of COVID-19 Diagnosis and Prevention

11.00-12.30hr

Room E

Chairperson:
1. Uracha Ruktanonchai

Invited speakers:

1. nSPHERE NEGATIVE PRESSURIZED HELMET
Paisan Khanchaitit
National Nanotechnology Center (NANOTEC), National Science and Technology Development Agency (NSTDA), Thailand

2. NANOPARTICLE-BASED LATERAL FLOW ASSAY PLATFORM FOR PLATFORM FOR RAPID DETECTION & SCREENING: FROM RESEARCH TO APPLICATION DURING COVID-19 PANDEMIC
Natpapas Wiriyachaiporn
National Nanotechnology Center (NANOTEC), National Science and Technology Development Agency (NSTDA), Thailand

3. COXY-AMP: A RAPID AND SENSITIVE COLORIMETRIC LAMP FOR COVID-19 DETECTION
Wansika Kiatpathomchai
National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), Thailand

Thursday 8 December 2022

[Lunch Symposium] Communicable Disease-Dengue Fever: The Spread and Detection

12.30-13.30hr

Room A

Chairperson:
1. Tan Kim Kee

Invited speakers:

1. POPULATION MOBILITY AND THE SPREAD OF DENGUE
Sazaly Bin Abu Bakar
Tropical Infectious Diseases Research and Education Centre (TIDREC), University of Malaya, Kuala

2. DEVELOPMENT OF SEMI QUANTITATIVE LATERAL FLOW TEST FOR NS1 DENGUE SELF TEST AND DETECTION OF SEVERE DENGUE
Nurul Shazaline Zainudin
Accobiotech Sdn Bhd

Thursday 8 December 2022

S26: Young Investigator Awards I

13.30-15.00hr

Room A

Chairpersons:
1. **Narisara Chantratita**
2. **Suparat Phuanukoonnon**

Invited speakers:

1. **FEBRILE ILLNESS AMONG ADMITTED PATIENTS OF COVID- 19-ASSOCIATED RHINO-ORBITAL-CEREBRAL MUCORMYCOSIS: A PHYSICIANS' EXPERIENCE FROM A TERTIARY CARE CENTRE IN NORTHERN INDIA**
   Saurabh Pandey
   PMC Hospital

2. **ANTIBODY AVIDITY MATURATION FAVORS SARS-COV-2 CONVALESCENTS OVER VACCINATED INDIVIDUALS GRANTING BREADTH IN NEUTRALIZABILITY AND TOLERANCE AGAINST VARIANTS**
   Yu Nakagama
   Department of Virology & Parasitology, Graduate School of Medicine, Osaka Metropolitan University

3. **STRUCTURAL CHARACTERIZATION AND COMPARISON OF BIFUNCTIONAL HPPK-DHPS ENZYME WITH PATHOGENIC MICROBES**
   Rini Chaturvedi
   ICGEB

4. **DEVELOPMENT OF SELF-TEST KIT FOR DETECTION OF DENGUE FEVER**
   Nurfatihah Zulkifli
   Tropical Infectious Diseases Research and Education Centre (TIDREC), Universiti Malaya

5. **IN-SILICO AND IN-VITRO APPROACH ON ANTI DENGUE ACTIVITY OF MARMELINE (AEGLE MARMELOS) AGAINST DENGUE VECTOR, AEDES AEGYPTI AND DENGUE VIRUS NS5 METHYLTRANSFERASE**
   Kovendan Kalimuthu
   Annamalai University

Thursday 8 December 2022

S27: Emerging Viral Diseases

13.30-15.00hr

Room B

Chairpersons:
1 Supaporn Wacharapluesadee.
2. Pornsawan Leaungwutiwong

Invited speakers:

1. GLOBAL VIROME PROJECT
Dennis Carroll
Global Virome Project

2. EMERGING VIRAL DISEASES: MILITARY CONCERNS
Stefan Fernandez
AFRIMS

3. EYWA - EARLY WARNING SYSTEM FOR MOSQUITO BORNE DISEASES
Jonas Schmidt-Chanasit
University of Hamburg

4. TIME COURSE OF ANTIBODY RESPONSES AND NEUTRALIZATION CAPACITY IN LONGITUDINAL SERUM SAMPLES FROM PCR-CONFIRMED COVID-19 PATIENTS AND COVID-19 VACCINEES
Ronald Von Possel
Bernhard Nocht Institute for Tropical Medicine

Thursday 8 December 2022

S28: Control and Elimination of Tropical Diseases in China

13.30-15.00hr

Room C

Chairpersons:
1. **Jetsumon Prachumsri**
2. **Guojing Yang**

Invited speakers:

1. **SCHISTOSOMIASIS ELIMINATION IN CHINA**
   Xiao-Nong Zhou
   National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention

2. **FROM 30 MILLION CASE TO ZERO: EXPERIENCES FROM MALARIA ELIMINATION IN CHINA**
   Qi Gao
   Jiangsu Institute of Parasitic Diseases, Wuxi, People's Republic of China

3. **HOW TO CONTROL COVID-19 IN THE WORLD?**
   Hong-Zhou Lu
   Department of Infection and Immunology, Shanghai Public Health Clinical Centre, Fudan University, Shanghai, China

4. **TROPICAL MEDICINE DEVELOPMENT AT HAINAN MEDICAL UNIVERSITY**
   Guojing Yang
   School of Tropical Medicine, Hainan Medical University

Thursday 8 December 2022

S29: Epidemiological and Genetic Malaria Risk Factors

13.30-15.00hr

Room D

Chairperson:
1. Mallika Imwong

Invited speakers:
1. PLASMODIUM FALCIPARUM AND PLASMODIUM VIVAX RESISTANCE TO ANTI-MALARIAL DRUGS IN INDONESIA
Farindira Vesti Rahmasari
Faculty of Medicine and Health Sciences Universitas Muhammadiyah Yogyakarta, Indonesia

2. GLUCOSE-6-PHOSEPHATE DEHYDROGENASE DEFICIENCY AND MALARIA AMONG PRIMARY SCHOOL CHILDREN IN BORDER PATROL POLICE SCHOOLS, MAE HONG SON PROVINCE
Nardlada Khantikul
The Office of Disease Prevention and Control No.1 Chiang Mai, Department of Disease Control, Ministry of Public Health

3. THE USE OF GLUCOSE-6-PHOSPHATE DEHYDROGENASE SCREENING TEST FOR MALARIA ELIMINATION IN THAILAND, 2015 – 2022
Aungkana Saejeng
The Office of Disease Prevention and Control No.1 Chiang Mai, Department of Disease Control, Ministry of Public Health

Thursday 8 December 2022

S30: Mathematical Models to Inform Health Policy Decisions in Countries in Asia

13.30-15.00hr

Room E

Chairpersons:
1. **Wirichada Pan-ngum**
2. **Borame Sue Lee Dickens**

Invited speakers:

1. **RING VACCINATION FOR A POTENTIAL YELLOW FEVER OUTBREAK IN AN ASIAN CITY**
   Borame Sue Lee Dickens
   NUS Saw Swee Hock School of Public Health

2. **WORKING TOWARDS HEPATITIS B ELIMINATION BY 2030: MODELING APPROACH TO OPTIMISE STRATEGIES TO REDUCE MOTHER-TO-CHILD TRANSMISSION**
   Myka Harun Sarajan
   Mahidol-Oxford Tropical Medicine Research Unit (MORU)

3. **THE ECONOMIC IMPACT OF ROTAVIRUS VACCINATION: A COMPARATIVE MODELLING STUDY**
   Phetsavanh Chanthavilay
   Unit for Health Evidence and Policy, Institute of Research and Education Development, UHS, Lao PDR

4. **DATA-DRIVEN MATHEMATICAL MODEL FOR CROSS-BORDER CONTROL OF COVID-19 IN REOPENING OF THAILAND'S BORDER**
   Vidhyagorn Mahd-Adam
   Faculty of Tropical Medicine, Mahidol University

Thursday 8 December 2022

S31: Resilience Against Emerging Infectious Disease Threats

15.30-17.00hr

Room A

Chairpersons:
1. **Leo Braack**
2. **Raman Velayudhan**

Invited speakers:

1. **THE GLOBAL ARBOVIRUS INITIATIVE**
   Raman Velayudhan
   World Health Organization Neglected Tropical Diseases

2. **PANDASIA – A PROJECT FOR UNDERSTANDING ZOONOTIC SPILLOVER PATHWAYS FOR PANDEMIC PREVENTION AND PREPAREDNESS**
   Hans Overgaard
   Centres for Disease Control & Prevention, Atlanta, USA

3. **ANOPHELES STEPHENSI: CURRENT ACTIONS AND PLANS**
   Seth Irish
   WHO GMP/Vector Control and Insecticide Resistance Unit, Geneva, Switzerland

Thursday 8 December 2022

S32: Tick-borne Pathogens Detection and Non-Pathogenic Microorganisms

15.30-17.00hr

Room B

Chairpersons:
1. **Pornsawan Leaungwutiwong**
2. **Dorothée Missé**

Invited speakers:

1. **HIGH-THROUGHPUT NANOTECHNOLOGIES FOR TICK-BORNE PATHOGENS DETECTION**
   Sara Moutailler
   UMR BIPAR (ANSES, INRAE, ENVA)

2. **TOWARDS A BETTER SURVEILLANCE AND PREVENTION OF TICK-BORNE ENCEPHALITIS VIRUS ALIMENTARY INFECTIONS**
   Nolwenn Dheilly
   ANSES, Animal Health laboratory, UMR Virology

3. **SEVERE FEVER WITH THROMBOCYTOPENIA SYNDROME VIRUS: THE FIRST CASE REPORT IN THAILAND**
   Supitcha Ongkittikul
   Phyathai3 Hospital

4. **THE TICK MICROBIOME: WHY NON-PATHOGENIC MICROORGANISMS MATTER IN TICK BIOLOGY**
   Olivier Duron
   MIVEGEC Lab

Thursday 8 December 2022

S33: Improving Quantitative Decision Making for Policy in the Asia-Pacific Region

15.30-17.00hr

Room C

Chairpersons:
1. Jodie McVernon
2. Wirichada Pan-ngum

Invited speakers:

1. SPARK INTRODUCTION
Jodie McVernon
The Peter Doherty Institute for Infection and Immunity, The University of Melbourne and Royal Melbourne Hospital

2. MODELLING TO INFORM CONTROL POLICIES FOR SOIL-TRANSMITTED HELMINTH INFECTIONS
Patricia Campbell
Faculty of Medicine, Dentistry and Health Sciences; the Doherty Institute for Infection and Immunity, University of Melbourne, Australia

3. SUPPORTING REMOTE RESEARCH WITH SPARK
Logan Wu
Walter and Eliza Hall Institute of Medical Research, Parkville Victoria, Australia

4. RESEARCH TO IMPROVE QUANTITATIVE DECISION MAKING FOR POLICY
Lauren Smith
Walter and Eliza Hall Institute of Medical Research, Parkville Victoria, Australia

5. UNDERSTANDING THE IMPACT OF POPULATION IMMUNITY ON FUTURE COVID-19 WAVES: AN INDIVIDUAL-BASED MODELLING STUDY
Yasmin McDonough
Walter and Eliza Hall Institute of Medical Research, Parkville Victoria, Australia

6. TRAINING AND CAPACITY BUILDING WITH SPARK
Wirichada Pan-ngum
Faculty of Tropical Medicine, Mahidol University

7. TRAINING AND CAPACITY BUILDING WITH SPARK
Zarni Lynn Kyaw
Faculty of Tropical Medicine, Mahidol University

8. CAPACITY BUILDING AT BIOMEDICAL AND HEALTH INFORMATICS, MAHIDOL UNIVERSITY TROUGH SPARK NETWORK
Karina Lestari
Faculty of Tropical Medicine, Mahidol University

Thursday 8 December 2022

S34: What Makes a Good Randomized Controlled Trial

15.30-17.00hr

Room D

Chairperson:
1. Rachel Hallett
2. Phaik Yeong Cheah

Invited speaker:

1. INTRODUCING THE GOOD CLINICAL TRIALS COLLABORATIVE - GCTC
Sir Martin Landray and Rachel Hallett
GCTC, hosted by Protas

2. PUTTING RESEARCH ETHICS IN CONTEXT: RETHINKING VULNERABILITY AND AGENCY WITHIN CASE STUDIES IN THAILAND, KENYA AND SOUTH AFRICA
Phaik Yeong Cheah
Mahidol Oxford Tropical Medicine Research Unit (MORU)

3. DATA MANAGEMENT FOR CLINICAL TRIALS
Naomi Waithira
Mahidol Oxford Tropical Medicine Research Unit (MORU)

4. LESSONS FROM COVID-19
Sir Peter Horby
Nuffield Department of Medicine, University of Oxford

Thursday 8 December 2022

S35: Nutrition, Gut Microbiome and Immune Response

15.30-17.00hr

Room E

Chairpersons:
1. Amornrat Aroonnual
2. Pattaneeya Prangthip

Invited speakers:

1. IDENTIFICATION OF PROBIOTICS WITH ANTIMICROBIAL ACTIVITY AND IMMUNE MODULATION
Narisara Chantratita
Faculty of Tropical Medicine, Mahidol University

2. FEASIBLE BIOMARKERS FOR CORONARY HEART DISEASE RISK IN THAI HYPERLIPIDEMIA PATIENTS
Piyaorn Chornchoem
Faculty of Tropical Medicine, Mahidol University

3. GUT MICROBIOME AND CANCER IMMUNOTHERAPY RESEARCH
Supachai Topanurak
Faculty of Tropical Medicine, Mahidol University

4. FEASIBLE BIOMARKERS FOR CORONARY HEART DISEASE RISK IN THAI HYPERLIPIDEMIA PATIENTS
Yaowapa Maneerat
Faculty of Tropical Medicine, Mahidol University

Friday 9 December 2022

S36: Young Investigator Awards II

08:30-10:00hr

Room A

Chairpersons:
1. Chawarat Rotejanaprasert
2. Thundon Ngamprasertchai

Invited speakers:

1. DETECTION OF SUBCLINICAL MYCOBACTERIUM LEPRAE INFECTION THROUGH DETECTION OF ANTIBODIES (IGM) IN CHILDREN IN FAMILIES WITH A HISTORY OF LEPROSY
Khariri Khariri
Faculty of Medicine, Universitas Indonesia

2. IMPLEMENTATION AND EFFECTIVENSS OF REACTIVE SURVEILLANE AND RESPONE STRATEGIES FOR MALARIA ELIMINATION: A SYSTEMATIC REVIEW AND META-ANALYSIS
Win Han Oo
Burnet Institute

3. TOWARDS MALARIA ELIMINATION IN MYANMAR: SCALING UP THE REACH AND UPTAKE OF PERSONAL PROTECTIVE MEASURES IN MOBILE AND MIGRANT POPULATIONS
Thae Maung Maung
Department of Medical Research, Myanmar

4. DESIGN AND CHARACTERIZATION OF PLASMOTAC TO INDUCE TARGET DEGRADATION IN PLASMODIUM FALCIPARUM MALARIA PARASITES
Ekkaphot Khongkla
National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA)

5. EXPERIENCE ON 1-3-7 SURVEILLANCE AND RESPONSE APPROACH AT THE PRIMARY HEALTH CARE SETTING IN MYANMAR
Poe Poe Aung
Maastricht University and Malaria Consortium

6. EVALUATION OF THE REACTIVE SURVEILLANCE AND RESPONSE STRATEGY FOR MALARIA ELIMINATION IN VIETNAM: A MIXED-METHODS STUDY
May Chan Oo
Burnet Institute

Friday 9 December 2022

S37: Special Session: Ethics Review of Biobank and Registry Research I

08:30-10:00hr

Room B

Chairpersons:
1. Reidar Lie

Invited speakers:

1. **THE US DATA PROTECTION FRAMEWORK AND RESEARCH**
   Holly Taylor
   Department of Bioethics, NIH Clinical Center

2. **EU AND GDPR RELEVANCE FOR RESEARCH**
   Reidar Lie
   University of Bergen

3. **THE NEW CHINESE DATA PROTECTION LEGISLATION AND RESEARCH**
   Zhai Xiaomei
   Center for Bioethics, Chinese Academy of Medical Sciences

4. **PERSPECTIVE FROM JAPAN**
   Kenji Matsui
   Division of Bioethics and Healthcare Law, National Cancer Center Japan

5. **PERSPECTIVE FROM SINGAPORE**
   Calvin Ho
   The University of Hong Kong

6. **ETHICS REVIEW OF BIOBANK AND REGISTRY RESEARCH: PERSPECTIVE FROM THAILAND**
   Somruedee Chatsirircharoenkul
   Director of Siriraj Biobank

Friday 9 December 2022

S38: Free Paper IV: Tropical Diseases: Surveillance and Treatment

08:30-10:00hr

Room C

Chairpersons:

1. **Kittipong Chaisiri**
2. **Aongart Mahittikorn**

Invited speakers:

1. **CROSS TRANSMISSION OF TRICHURIS TRICHIURA AND TRICHURIS VULPIS BETWEEN HUMANS AND ANIMALS IN CARAGA REGION, PHILIPPINES**
   Angelou Marie Aquino
   University of the Philippines Los Banos

2. **PREVALENCE OF HEAD LICE WITH RESISTANCE GENE AND RISK FACTORS OF HEAD LICE INFESTATION IN THAI RURAL AREA**
   Natthamongkol Sanganate
   Phramongkutklao College of Medicine

3. **PHARMACOKINETIC-PHARMACODYNAMIC ANALYSIS OF BENZNIDAZOLE IN A PRE-CLINICAL ANIMAL MODEL OF CHAGAS DISEASE**
   Frauke Assmus
   Faculty of Tropical Medicine, Mahidol University (Mahidol-Oxford Tropical Research Unit)

4. **BIOLOGICAL EVALUATIONS OF EXTRACT AND FRACTIONS OF COMBRETUM DOLICHOPETALUM LEAF FOR THE MANAGEMENT OF SOME TROPICAL DISEASES (TDS)**
   Thaddeus H Gugu
   University of Nigeria Nsukka

5. **SURFACE-MODIFIED LIPID NANOPARTICLES FORMULATED WITH BIOCOMPATIBLE EXCIPIENTS ENHANCED THE PHARMACODYNAMICS OF ARTEMETHER IN MICE EXPERIMENTALLY INFECTED WITH PLASMODIUM BERGHEI MALARIA**
   Franklin Chimaobi Kenechukwu
   University of Nigeria

Friday 9 December 2022

S39: Recent Advance in Leptospirosis

08:30-10:00hr

Room D

Chairperson:
1. Nattachai Srisawat

Invited speakers:

1. MULTIPLEX QPCR FOR SCREENING LEPTOSPIROSIS AND OTHER TROPICAL INFECTIOUS DISEASES
Janjira Thaipadungpanit
Faculty of Tropical Medicine, Mahidol University

2. PATHOPHYSIOLOGY OF LEPTOSPIROSIS ASSOCIATED AKI
Chih-Wei Yang
Chang Gung University College of Medicine, Taoyuan, Taiwan

3. ZERO DEATH IN LEPTOSPIROSIS
Nattachai Srisawat
Tropical Medicine Cluster, Chulalongkorn University

Friday 9 December 2022

S40: Free Paper V: Bacterial Diseases

08:30-10:00hr

Room E

Chairpersons:
1. Muthita Vanaporn
2. Nathamon Kosoltanapiwat

Invited speakers:
1. GENOTYPIC VIRULENCE PROFILES AND ASSOCIATIONS IN SALMONELLA ISOLATED FROM MEAT SAMPLES IN WET MARKETS AND ABATTOIRS OF METRO MANILA, PHILIPPINES
Rance Derrick Pavon
Pathogen-Host-Environment Interactions Research Laboratory, Institute of Biology (UP Diliman, Quezon City, Philippines

2. FECAL CONTAMINATION AND ANTIMICROBIAL RESISTANCE IN URBAN GARDENS IN METRO MANILA, PHILIPPINES
Pierangeli Vital
Natural Sciences Research Institute, University of the Philippines Diliman

3. MULTI-DRUG RESISTANT BACTERIAL CONTAMINATION ALTERING HEALTHY FRUITS AND VEGETABLES INTO DANGEROUS SOURCE OF INFECTION
Suraj Khatri
Research Institute for Bioscience and Biotechnology (RIBB), Nepal

4. RESISTANCE MECHANISMS AMONG THE NON-CARBAPENEMASE-PRODUCING CARBAPENEM-RESISTANT KLEBSIELLA PNEUMONIAE
Yee Qing Lee
Department of Medical Microbiology, Faculty of Medicine, University of Malaya, Kuala Lumpur, Malaysia

5. MOLECULAR DIAGNOSIS OF BACTERIAL INFECTION IN NEGATIVE BLOOD CULTURE FLUID
Yasithirra Devi Kirishnan
Faculty of Health Science, University Sultan Zainal Abidin (UniSZA), Gong Badak Campus

6. SURVIVAL OF HYPERMUCOVISCOUS CARBAPENEM RESISTANT K. PNEUMONIAE IN A SERUM KILLING ASSAY
Zhi Xian Kong
Department of Medical Microbiology, Faculty of Medicine, University of Malaya

Friday 9 December 2022

S41: Vertical Transmission in the Tropics

10.30-12.00hr

Room A

Chairpersons:
1. **Kriengsak Limkittikul**
2. **Thanyawee Puthanakit**

Invited speakers:

1. **VERTICAL TRANSMISSION IN THE TROPIC**
   Thanyawee Puthanakit
   Faculty of Medicine, Chulalongkorn University

2. **CONGENITAL SYPHILIS: IS IT POSSIBLE TO ELIMINATE?**
   Suvaporn Anugulruengkitt
   Faculty of Medicine, Chulalongkorn University

3. **ELIMINATION OF VERTICAL TRANSMISSION OF HEPATITIS B**
   Suchada Jiamsiri
   Department of Disease Control, Ministry of public health, Thailand

Friday 9 December 2022

S42: Special Session: Ethics Review of Biobank and Registry Research II

10.30-12.00hr

Room B

Chairpersons:
1. Reidar Lie

Invited speakers:

1. **THE US DATA PROTECTION FRAMEWORK AND RESEARCH**
   Holly Taylor
   Department of Bioethics, NIH Clinical Center

2. **EU AND GDPR RELEVANCE FOR RESEARCH**
   Reidar Lie
   University of Bergen

3. **THE NEW CHINESE DATA PROTECTION LEGISLATION AND RESEARCH**
   Zhai Xiaomei
   Center for Bioethics, Chinese Academy of Medical Sciences

4. **PERSPECTIVE FROM JAPAN**
   Kenji Matsui
   Division of Bioethics and Healthcare Law, National Cancer Center Japan

5. **PERSPECTIVE FROM SINGAPORE**
   Calvin Ho
   The University of Hong Kong

6. **ETHICS REVIEW OF BIOBANK AND REGISTRY RESEARCH: PERSPECTIVE FROM THAILAND**
   Somruedee Chatsirircharoenkul
   Director of Siriraj Biobank

Friday 9 December 2022

S43: Plasmodium knowlesi: Situation and Challenges (Thai language) [MOPH]

10.30-12.00hr

Room C

Chairperson:
1. Supawadee Poungsombat

Invited speakers:

1. **MALARIA ELIMINATION AND CHALLENGES (THAI SESSION)**
   Apinya Niramitsantipong
   Bureau of Vector Borne Disease, Department of Disease Control, Ministry of Public Health

2. **MALARIA ELIMINATION AND CHALLENGES (THAI SESSION)**
   Pathomporn Prikchoo
   Office of Diseases and Prevention Control Region 12 Songkhla

3. **MALARIA ELIMINATION AND CHALLENGES (THAI SESSION)**
   Suravadee Kitchakarn
   Bureau of Vector Borne Disease, Department of Disease Control, Ministry of Public Health

Friday 9 December 2022

S44: Free Paper VI: Vector Borne Diseases

10.30-12.00hr

Room D

Chairpersons:
1. **Pornsawan Leaungwutiwong**
2. **Sirasate Bantuchai**

Invited speakers:

1. THE PARASITE GENETIC AND HOST IMMUNOLOGICAL DETERMINANTS OF IMMUNE ESCAPE IN PLASMODIUM FALCIPARUM MALARIA

Myo Naung
WEHI

2. ACCEPTABILITY AND FEASIBILITY OF COMMUNITY-DELIVERED INTEGRATED MALARIA ELIMINATION MODEL FROM PERSPECTIVES OF VOLUNTEERS AND COMMUNITY LEADERS IN YANGON REGION, MYANMAR

Ei Phyu Htwe
Burnet Instiute, Myanmar

3. THE INAPPROPRIATE ANTIMICROBIAL AGENT PRESCRIPTIONS AMONG CONFIRMED DENGUE CASES IN HOSPITAL FOR TROPICAL DISEASES: A RETROSPECTIVE COHORT STUDY

Ashley Siribhadra
Faculty of Tropical Medicine, Mahidol University

4. A PUTATIVE NEW SPECIES OF RICKETTSIA SP. HL-1 IN HAEMAPHYSALIS HYSTRICIS FROM DOMESTIC ANIMALS IN HUALIEN, EASTERN TAIWAN

Jing-Syuan Huang
Institute of Environmental and Occupational Health Sciences, College of Public Health, National Taiwan University, Taipei

5. DYNAMICS OF WNV INFECTION IN CULEX MOSQUITOES

Sylvie Lecollinet
CIRAD

6. GENETIC DETERMINANTS OF THE VIRULENCE OF MEDITERRANEAN WNV ISOLATES

Lise Fiacre
CIRAD

Friday 9 December 2022

S45: Free Paper VII: Diseases Surveillance Tools

10.30-12.00hr

Room E

Chairpersons:
1. Sadudee Chotirat
2. Wang Nguitragool

Invited speakers:

1. A NEW SEROLOGIC APPROACH FOR ESTIMATING THE POPULATION-LEVEL INCIDENCE OF SCRUB TYPHUS
Kristen Aiemjoy
Faculty of Tropical Medicine, Mahidol University

2. NS1-BASED FCγR IGG COMPETITION ELISAS ALLOW DIFFERENTIATION OF FLAVIVIRUS-INDUCED HUMORAL IMMUNE RESPONSES
Christina Deschermeier
Bernhard Nocht Institute for Tropical Medicine

3. SCHISTOSOMA JAPONICUM (KATSURADA, 1904) DETECTION IN HUMANS AND ANIMALS IN SELECTED ENDEMIC AREAS IN CARAGA REGION, MINDANAO, PHILIPPINES USING MICROSCOPY, QPCR, AND MITOCHONDRIAL NAD1 GENE ANALYSIS
Vachel Gay Paller
Institute of Biological Science, University of the Philippines Los Baños

4. DEVELOPMENT OF AN APTAMER-BASED SANDWICH ASSAY FOR THE DETECTION OF LEPTOSPIROSIS
Marjo Mendoza
Institute of Biology, College of Science, University of the Philippines Diliman, Quezon City, Philippines

5. A VGG16 CONVOLUTIONAL NEURAL NETWORK MODEL-BASED WEB APPLICATION TO INTERPRET THE IGM LATERAL FLOW DIAGNOSTIC TEST OF ACUTE LEPTOSPIROSIS DIAGNOSIS
Santi Maneewatchararangsri
Faculty of Tropical Medicine, Mahidol University

Friday 9 December 2022

S46: Small Molecules Drug Discovery for Tropical Diseases

13:00-14:30hr

Room A

Chairpersons:

1. **Sumalee Kamchonwongpaisan**
2. **Marie Hoarau**

Invited speakers:

1. OPPORTUNITIES AND CHALLENGES OF NEXT-GENERATION ANTIFOLATES AGAINST PROTOZOAL INFECTIONS – TARGET-BASED DESIGN TO OVERCOME ANTIFOLATE RESISTANCE

Jarunee Vanichtanankul
National Center for Genetic Engineering and Biotechnology (BIOTEC)

2. TARGETING 'UNDRUGGABLE TARGET' – HIJACKING PLASMODIUM PROTEIN DEGRADATION SYSTEM

Nitipol Srimongkolpithak
National Center for Genetic Engineering and Biotechnology (BIOTEC)

3. ESTABLISHING MODELS FOR ASSESSING PROPHYLAXIS AND TRANSMISSION-BLOCKING ACTIVITIES TO SUPPORT MALARIA ELIMINATION POLICIES

Natapong Jupatanakul
National Center for Genetic Engineering and Biotechnology (BIOTEC)

4. PRIORITIZING PLASMODIUM FALCIPARUM ESSENTIAL GENES FOR ANTIMALARIAL DEVELOPMENT BY ANALYSIS OF CONDITIONAL LOSS-OF-FUNCTION MUTANTS

Philip J. Shaw
National Center for Genetic Engineering and Biotechnology (BIOTEC)

Friday 9 December 2022

S47: Introduction to Scholarly Publishing for Researchers: What are editors, reviewers and publishers looking for?

13:00-14:30hr

Room B

Moderator:
1. Yoottapong Klinthongchai

Invited speakers:

1. INTRODUCTION TO SCHOLARLY PUBLISHING FOR RESEARCHERS: WHAT ARE EDITORS, REVIEWERS AND PUBLISHERS LOOKING FOR?
Dale Seaton
Elsevier Life Sciences Publishing

2. INTRODUCTION TO SCHOLARLY PUBLISHING FOR RESEARCHERS: WHAT ARE EDITORS, REVIEWERS AND PUBLISHERS LOOKING FOR?
Bilge San
Elsevier Life Sciences Publishing

Friday 9 December 2022

S48: Climate Change and Vector Borne Disease [MOPH]

13:00-14:30hr

Room C

Chairperson:

1. Apinya Niramitsantipong

Invited speakers:

1. Surapong Sarapa
Division of Research and Development for Meteorological Information

2. Piti Mongkalangoon
Bureau of Vector Borne Diseases, Department of Disease Control, Ministry of Public Health

Friday 9 December 2022

S49: EDCs (Endocrine Disrupting Chemicals) and Health: A Challenge for Our Society

13:00-14:30hr

Room D

Chairperson:

1. **Kraichat Tantrakarnapa**

Invited speakers:

1. **EDCs AND HEALTH: A CHALLENGE FOR OUR SOCIETY**
   Vichit Supornsilchai
   Faculty of medicine, Chulalongkorn University

2. **THYROID DISRUPTING CHEMICALS AND ENVIRONMENTAL HEALTH IMPLICATIONS IN HUMAN POPULATION**
   Kyungho Choi
   Department of Environmental Health Sciences, School of Public Health, Seoul National University, Korea

3. **THE HOKKAIDO STUDY ON ENVIRONMENT AND CHILDREN’S HEALTH: OVERVIEW AND CHILDREN’S CHEMICAL EXPOSURE LEVELS**
   Atsuko Ikeda-Araki
   Faculty of Health Sciences, Hokkaido University

Friday 9 December 2022

K2 : Closing Ceremony and Keynote Address

14:30-15:30hr

Room A

Chairperson : Jetsumon Prachumsri

Invited speaker :

1. **NUCLEOSIDE-MODIFIED MRNA THERAPEUTICS**
   Drew Weissman
   Perelman School of Medicine, University of Pennsylvania

Poster Sessions

Wednesday 7 December 2022
16:30-20:00hr
and
Thursday 8 December 2022
17.00-20:00hr

Poster presenters (In-person):

Poster 1. THE EPIDEMIOLOGICAL STUDY OF ANTIMICROBIAL RESISTANT ENTEROBACTERALES AMONG INTERNATIONAL TRAVELERS VISITING THAILAND
Kachamard Padungpattanodom
Faculty of Tropical Medicine, Mahidol University

Poster 2. DNA APTAMER SELECTION THROUGH CELL-SELEX FOR THE DETECTION OF LEPTOSPIROSIS
Chembie Almazar
Institute of Biology, University of the Philippines Diliman

Poster 3. INHIBITORY ACTIVITY OF PSIDIUM GUAJAVA L. LEAVES ESSENTIAL OIL AGAINST CLINICAL ISOLATES OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS
Gianne Lariz Magsakay
UP Manila National Institutes of Health

Poster 4. SEROSURVEY OF SCRUB TYPHUS IN INDONESIA: A CROSS-SECTIONAL ANALYSIS OF ARCHIVED FEVER STUDIES SAMPLES
Kartika Saraswati
Eijkman-Oxford Clinical Research Unit

Poster 5. TREND OF COLISTIN RESISTANCE AMONG CARBAPENEM-RESISTANT ACINETOBACTER BAUMANNII (CRAB) ISOLATES IN MALAYSIA
Jia Jie Woon
Department of Medical Microbiology, Faculty of Medicine, University of Malaya

Poster 6. SPATIOTEMPORAL CLUSTERS AND TRENDS OF PNEUMOCYSTIS CARINII PNEUMONIA IN KOREA
Howoo Nam
Dept. of Parasitology, College of Medicine, Catholic University of Korea

Poster 7. MOLECULAR SEROTYPING BY PHYLOGENETIC ANALYSES OF A 1498BP SEGMENT OF THE INVA GENE OF SALMONELLA
Windell Rivera
University of the Philippines

Poster 8. OCCURRENCE OF NON-TYPHOIDAL SALMONELLA FROM RETAIL FOODS MARKETED IN BANGKOK, THAILAND
Thida Kongngoen
Faculty of Tropical Medicine, Mahidol University

Poster 9. COVID-19 VACCINE PERCEPTION AND HESITANCY DURING COVID-19 CRISIS IN THAI PEOPLE
Pahurat Kongmuang Taisuwan
Secretariat Office of the Royal Development Projects Committee, Department of Disease Control, Ministry of Public Health

Poster 10. COVID-19 PANDEMIC EFFECT ON THE TREND OF HEPATITIS A IN JAPAN, FRANCE, AND THAILAND
Kazuteru Murakoshi
Juntendo University School of Medicine

Poster 11. miR-3646 MEDIATED MOLECULAR TARGETING OF NRP1 AS PROMISING THERAPEUTIC REGULATOR IN SARS-COV-2 PATHOGENESIS
Taruneet Kaur
National Dairy Research Institute, Karnal,India

Poster 12. OVERCOMING CHALLENGES IN THE FIELD DURING THE COVID-19 PANDEMIC AND SUPERTYPHOON RAI
Angela Rose Macasero
University of the Philippines National Institutes of Health, Institute of Child Health and Human Development

Poster 13. IMPACT OF SEASON AND EXTREME WEATHER EVENTS ON HOSPITALIZED DENGUE IN CEBU, PHILIPPINES
Kiarah Louise Florendo
UP-National Institutes of Health- Institute of Child Health and Human Development

Poster 14. CLADE REPLACEMENT OF DENGUE VIRUS TYPE 3 (DENV-3) GENOTYPE III IN MALAYSIA
Kim-Kee Tan
University of Malaya

Poster 15. ANTI-DENGUE AND MOSQUITOCIDAL PROPERTIES OF SQUALENE COMPOUND AGAINST DENGUE VIRAL PROTEIN NS2 AND ITS VECTOR, AEDES AEGYPTI
Rajaganesh Rajapandian
Bharathiar University

Poster 16. IDENTIFICATION AND DEVELOPMENT OF A PROMSING PAN-SEROTYPE ANTI-DENGUE VIRUS CLINICAL CANDIDATE
Katherine Chan
Novartis Institutes for Biomedical Research, Inc.

Poster 17. STRUCTURAL ANALYSIS OF DENGUE VIRUS TYPE 2 STRAINS WITH DIFFERENT PROLIFERATIVE CAPACITY
Yoshihiro Samune
Osaka University

Poster 18. THE FORCE OF NATURAL DENGUE INFECTION AMONG DENGUE-NAÏVE CHILDREN RESIDING IN CEBU, PHILIPPINES

MariaVinna Crisostomo
Institute of Child Health and Human Development, National Institutes of Health, University of the Philippines Manila

Poster 19. POPULATION MOBILITY AND THE SPREAD OF DENGUE - HISTORY AND PHYLOGENETIC ANALYSIS OF DENGUE VIRUS TYPE 3 GENOTYPE I IN MALAYSIA
Sazaly Abubakar
University of Malaya

Poster 20. PREVALENCE AND RISK FACTORS FOR OPISTHORCHIS VIVERRINI INFECTION IN A RURAL REGION OF CENTRAL THAILAND
Apiwit Jariyanukroh
Phramongkutklao College of Medicine

Poster 21. WHAT A KAP SURVEY REVEALS ABOUT THE AWARENESS REGARDING THE LEISHMANIASIS AMONG THE COMMUNITY OF AN ENDEMIC AREA IN SRILANKA?
Mayumi Manmperi
Ministry of Health, Nutrition and Indigenous Sciences

Poster 22. TRANSCRIPTOME PROFILING OF MALE AND FEMALE ASCARIS LUMBRICOIDES REPRODUCTIVE TISSUES
Orawan Phuphisut
Faculty of Tropical Medicine, Mahidol University

Poster 23. DEVELOPMENT OF RECOMBINANT PROTEIN-BASED IMMUNODIAGNOSIS FOR DETECTION OF GNATHOSTOMA SPINIGERUM INFECTION
Preeyarat Malaithong
Faculty of Tropical Medicine, Mahidol University

Poster 24. SOCIO-ECONOMIC AND RISK FACTORS OF INTESTINAL HELMINTHIASES IN SELECTED ENDEMIC COMMUNITIES IN MINDANAO, THE PHILIPPINES
Kim Louisse Patagnan
Institute of Biological Sciences, University of the Philippines Los Baños

Poster 25. PREVALENCE AND RISK FACTORS FOR OPISTHORCHIS VIVERRINI INFECTION IN A RURAL REGION OF CENTRAL THAILAND
Natthida Karnsomlarp
Faculty of Tropical Medicine, Mahidol University

Poster 26. TREMATODE INFECTIONS OF GENUS FILOPALUDINA IN THA CHIN RIVER BASIN, NAKHON PATHOM PROVINCE, THAILAND.
Ketsamon Panthong
Department of Biology, Faculty of Science, Silpakorn University

Poster 27. A DIGITAL PLATFORM FOR ANALYSIS AND VISUALIZATION OF MALARIAL EPIDEMIOLOGICAL DATA
Amit Sharma

National Institute of Malaria Research, India and International Centre for Genetic Engineering and Biotechnology, India

Poster 28. KNOWLEDGE, ATTITUDE AND PRACTICE OF FOREST-GOING MOBILE AND MIGRANT POPULATION IN CAMBODIA AND LAO PDR ON MALARIA PREVENTION: A CROSS-SECTIONAL SURVEY

Win Htike
Burnet Institute

Poster 29. GEOGRAPHICAL DISTRIBUTION OF SUBMICROSCOPIC MALARIA IN LOCALITIES WITH HIGH RISK OF MALARIA REINTRODUCTION IN MALAYSIA

Adela Ida Anak Jiram
Institute for Medical Research, Malaysia

Poster 30. PERFORMANCE OF RAPID DIAGNOSTIC TESTS (RDT) AND MICROSCOPY IN ACCURATE DIAGNOSIS OF MALARIA IN TWO NORTH-EAST DISTRICTS OF INDIA

Hari Shankar
Indian Council of Medical Research

Poster 31. INADEQUATE INVOLVEMENT OF PRIVATE HEALTH FACILITIES IN MALARIA CASE REPORTING IN PAPUA PROVINCE, INDONESIA: URGENT NEED FOR ENGAGEMENT TO ACHIEVE ELIMINATION

Ajib Diptyanusa
WHO Indonesia Country Office

Poster 32. ACCEPTABILITY OF A COMMUNITY-DELIVERED INTEGRATED MALARIA ELIMINATION MODEL TO COMMUNITY MEMBERS IN YANGON REGION, MYANMAR

Aung Khine Zaw
University of Medicine, Yangon

Poster 33. EVALUATION OF THE ULTRA-SENSITIVE RAPID DIAGNOSTIC TEST (US-RDT) PERFORMANCE FOR MALARIA DIAGNOSIS

Chorpaka Tangjaroenpoonsuk
Faculty of Tropical Medicine, Mahidol University

Poster 34. ENTOMOLOGICAL SURVEILLANCE OF Plasmodium knowlesi MALARIA

Pathomporn Prikchoo
Office of Diseases and Prevention Control Region 12 Songkhla Province

Poster 35. THE EFFICACY PLANTS EXTRACTS OF DERRIS ELLIPTICA, ACORUS CALAMUS AND ARTOCARPUS ALTILIS FOR AEDES AEGYTI MOSQUITO LARVICIDE AND REPELLENT ACTIVITIES

Rittiporn Benarlee
Office of Diseases and Prevention Control Region 12 Songkhla Province

Poster 36. DEVELOPMENT OF AN OPTIONS ASSESSMENT TOOLKIT FOR NATIONAL MALARIA PROGRAMS TO DETERMINE THEIR OPTIMAL VIVAX RADICAL CURE OPTIONS

Sanjaya Acharya
Menzies School of Health, Darwin Australia

Poster 36. DEVELOPMENT OF AN OPTIONS ASSESSMENT TOOLKIT FOR NATIONAL MALARIA PROGRAMS TO DETERMINE THEIR OPTIMAL VIVAX RADICAL CURE OPTIONS

Sanjaya Acharya

Menzies School of Health, Darwin Australia

Poster 37. PREVALENCE OF METABOLIC SYNDROME AMONG MILITARY POPULATION IN MYANMAR

Ye Nyi Nyi

Defence Services Medical Research Centre, Myanmar

Poster 38. FORMULATION AND DEVELOPMENT OF READY TO EAT EMERGENCY FOOD BARS FOR DISASTER MANAGEMENT IN CRITICAL CONDITIONS

Pyae Phyo Kyaw

Faculty of Tropical Medicine, Mahidol University

Poster 39. SENSITIVITY AND SPECIFICITY OF DPP® FEVER PANEL II ASIA IN THE DIAGNOSIS OF MALARIA, DENGUE AND MELIOIDOSIS

Premjit Amornchai

Mahidol Oxford Tropical Medicine Research Unit

Poster 40. THE QUALITY OF VETERINARY MEDICINES AND THEIR IMPLICATIONS FOR ONE HEALTH

Vayouly Vidhamaly

Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit

Poster 41. UNBIASED METAGENOMIC NEXT-GENERATION SEQUENCING TO DEFINE THE FEBRILE LANDSCAPE IN CAMBODIA

Gechlang Tang

International Center of Excellence in Research, U.S National Institutes of Health, Cambodia

Poster 42. THE STUDY OF MICROBIOLOGICAL AIR QUALITY OF LABORATORY ANIMAL SCIENCE UNIT, FACULTY OF TROPICAL MEDICINE, MAHIDOL UNIVERSITY

Thanyaluk Krasae

Faculty of Tropical Medicine, Mahidol University [Office of Research Services]

Poster 43. BUBBLE AND SEAL FROM DISEASE PREVENTION AND CONTROL POLICY TO LESSONS FOR THE HEALTH SECURITY OF THAILAND

Benjamaporn Pinyopornpanich

Department of Disease Control

Poster 44. CERCARIAL INFECTIONS OF GASTROPODS IN CHAO PHRAYA RIVER BASIN, NONTHABURI PROVINCE AND PATHUM THANI PROVINCE, THAILAND

Wivitchuta Dechruksa

Department of Biology, Faculty of Science, Silpakorn University

Poster 45. EVALUATION OF COVID-19 SCREENING ASSAY USING FULLY AUTOMATED NUCLEIC EXTRACTION AND REAL-TIME PCR, BD MAX OPEN SYSTEM

Panuvit Rienpradub

Mahidol Oxford Tropical Medicine Research Unit

Poster 46. ORIENTIA TSUTSUGAMUSHI STRAINS IN RATS AND CHIGGER MITES IN AN ENDEMIC AREA AND NON-ENDEMIC AREA OF SCRUB TYPHUS

Wasinee Sriplong

Office of Diseases and Prevention Control Region 12 Songkhla Province

Poster 47. COMPARISON OF IMMUNOGENICITY AND SAFETY OUTCOMES OF A MALARIA VACCINE FMP013 / ALFQ IN RHESUS MACAQUES (MACACA MULATTA) OF INDIAN AND CHINESE ORIGIN

Monica Martin

Walter Reed Army Institute of Research

Poster 48. THE ROLE OF BURKHOLDERIA PSEUDOMALLEI CYCLE INHIBITING FACTOR IN HUMAN NEURONAL CELL INFECTION

Amporn Rungruengkitkun

Faculty of Tropical Medicine, Mahidol University

Poster 49. NOVEL DUAL-STAGE ACTIVE ANTIMALARIAL ACRIDONES

Jane Kelly

Portland State University

Poster 50. TAMBJAMINES AS NOVEL MULTIPLE-STATE ANTIMALARIALS

Papireddy Kancharla

Portland State University

Poster 51. ANTIMICROBIAL RESISTANCE AND VIRULENCE CAPACITY OF VIBRIO SPP. AND AEROMONAS SPP. ISOLATED FROM RAW SEAFOOD MARKETED IN BANGKOK, THAILAND

Witawat Tunyong

Faculty of Tropical Medicine, Mahidol University

Poster 52. THE SEROPREVALENCE STUDY OF MEASLES, MUMPS, RUBELLA, AND VARICELLA IMMUNITY AMONG THAI ADOLESCENCE AND YOUNG ADULT

Sajikapon Kludkleeb

Faculty of Tropical Medicine, Mahidol University [Hospital for Tropical Diseases]

Poster 53. TWO CHIKUNGUNYA VIRUS STRAINS OF A MONOPHYLETIC ORIGIN CIRCULATING IN 2021-2022 OUTBREAK IN BALI, INDONESIA

Yora Permata Dewi

Exeins Health Initiative

Poster 54. ACUTE FEBRILE ILLNESS STUDY IN PRIMARY AND SECONDARY REFERENCE HEALTH CARE FACILITY IN MAKASSAR, SOUTH SULAWESI, INDONESIA

Ida Yus Sriyani

Exeins Health Initiative

Poster 55. SEROPREVALENCE OF ARBOVIRUSES IN HUMANS AND CO-LOCATED LONG-TAILED MACAQUES IN CAMBODIA

Somnang Man

National Institute of Health

Poster 56. MULTIPLEX REAL-TIME RT-PCR ASSAY FOR STUDYING EPIDEMIOLOGY OF THE ARBOVIRUS INFECTIONS IN SOUTH AND SOUTHEAST ASIA

Saranya Wongrattanapipat

Mahidol Oxford Tropical Medicine Research Unit

Poster 57. THE SEROPREVALENCE OF HEPATITIS E VIRUS IN URBAN AND PERI-URBAN NEPAL
Nishan Katuwal
Dhulikhel Hospital, Kathmandu University Hospital

Poster 58. ANALYSIS OF ANTIBIOTIC SUSCEPTIBILITY IN HAEMOPHILUS INFLUENZAE FROM TERTIARY CARE HOSPITAL IN KUALA LUMPUR, MALAYSIA
Anis Najwa Muhamad
Universiti Malaya

Poster 59. REAL-TIME CELL ANALYSIS METHOD TO MONITOR THE VASCULAR INTEGRITY OF HUMAN UMBILICAL VEIN ENDOTHELIAL CELLS DURING VIRUS INFECTION.
Jo Ern Wong
Universiti Malaya

Poster 78. DOXYCYLINE RESPONSE IN ACUTE FEBRILE ILLNESS AT UMPHANG HOSPITAL
Carlo Perrone
Mahidol Oxford Tropical Medicine Research Unit

E-Poster presenters (Virtual):

Poster 60. BENCHMARKING CRISPR-CAS12A FOR POINT-OF-CARE MELIOIDOSIS DETECTION IN LOWER MIDDLE-INCOME COUNTRIES: A MOLECULAR DIAGNOSTICS STUDY
Sukritpong Pakdeerat
Mahidol Oxford Tropical Medicine Research Unit

Poster 61. ATYPICAL PRESENTATION OF SCRUB TYPHUS: A CASE REPORT FROM THE MALDIVES
Hisham Imad
Faculty of Tropical Medicine, Mahidol University [Mahidol Vivax Research Unit (MVRU)]

Poster 62. ASSOCIATION OF COMORBIDITIES WITH MORTALITY IN COVID-19 PATIENTS IN NATIONAL LEVEL HOSPITAL IN CENTRAL JAKARTA INDONESIA
Siti Nurhayati Mukti
Gadjah Mada University

Poster 63. THE CAUSAL MODEL COMPONENTS AFFECTING COVID-19 PREVENTION BEHAVIORS IN THE ELDERLY WITH DIABETES
Samran Siriphakhamongkhon
OPDC. 3 Nakhon Sawan CDC. Thailand

Poster 64. COMPARISON OF CYTOKINE LEVELS IN SARS-COV-2 AND ARBOVIRUS INFECTION DURING ACUTE PHASE OF THE DISEASE
Bunya Seeyankem
Prince of Songkla University

Poster 65. EVALUATION OF FIDELITY AMONG COMMUNITY-DELIVERED INTEGRATED MALARIA ELIMINATION VOLUNTEERS IN YANGON REGION, MYANMAR
Kaungmyat Khant
Burnet Institute, Myanmar

Poster 66. SURVEILLANCE OF DENGUE, CHIKUNGUNYA AND ZIKA VIRUSES IN WILD CAUGHT AEDES MOSQUITOES COLLECTED CONCURRENTLY WITH LAB CONFIRMED HUMAN CASES IN PUNJAB, INDIA

Taruna Kaura
PGIMER, Chandigarh

Poster 67. MOLECULAR SERVEY OF HAEMOSPORIDIAN PARASITES IN CULICODES BITING MIDGES (DIPTERA, CERATOPOGONIDAE)

Saowalak Kaewmee
Faculty of Medicine, Chulalongkorn University

Poster 68. PREVALENCE AND MOLECULAR CHARACTERIZATION OF ENTEROCYTOZOON BIENEUSI IN ELD'S DEER (PANOLIA SIAMENSIS) IN CHINA

Yun Zhang
Hainan Medical University-The University of Hong Kong Joint Laboratory of Tropical Infectious Diseases, Hainan Medical University

Poster 69. PREVALENCE AND MOLECULAR CHARACTERIZATION OF GIARDIA DUODENALIS AND ENTEROCYTOZOON BIENEUSI IN IMPORTED LONG-TAILED MACAQUES (MACACA FASCICULARIS)

Guangxu Ren
Department of Pathogenic Biology, Hainan Medical University, Haikou, Hainan, China

Poster 70. PREVALENCE AND GENETIC CHARACTERIZATION OF ENTEROCYTOZOON BIENEUSI FROM THE POPULATION OF CENTRAL MOUNTANINOUS REGION IN HAINAN

Xiuyi Lai
Department of Pathogenic Biology, Hainan Medical University, Haikou, Hainan, China

Poster 71. MOLECULAR EPIDEMIOLOGY OF BLASTOCYSTIS AMONG THE POPULATION OF THE CENTRAL MOUNTAINOUS REGIONS IN HAINAN, CHINA

Yuan Wang
Department of Pathogenic Biology, Hainan Medical University, Haikou, Hainan, China

Poster 72. FACTORS ASSOCIATED WITH COVID-19 PREVENTIVE BEHAVIORS AMONG OLDER ADULTS IN THE CENTRAL REGION UPPER REGION OF THAILAND

Sawanya Siriphakhamongkhon
Office of Disease Prevention and Control 3, Department of Diseases Control, Ministry of Public Health

Poster 73. EVALUATION OF THE EFFECTIVENESS OF PASSENGER SURVEILLANCE SYSTEM INTERNATIONAL DISEASE CONTROL PORT AND QUARANTINE

Kannika Kanchanasuwan
Department of Diseases Control, Ministry of Public Health

Poster 74. DETECTION OF AMEBIC COLITIS AMONG CHILDREN IN TERTIARY HOSPITAL IN JAKARTA

Inawaty
Parasitologist Universitas Indonesia

Poster 75. SERUM PROTEIN IDENTIFICATION AS POTENTIAL BIOMARKERS FOR BRUCELLOSIS INFECTION

Jamaayah Zahidi
Bacteriology Unit, Institute for Medical Research (IMR), National Institute of Health (NIH),Ministry of Health Malaysia

Poster 76. EVALUATING AND INTERPRETING ANTIBIOTIC SUSCEPTIBILITY OF BURKHOLDERIA PSEUDOMALLEI ISOLATES FROM MALAYSIA BY ZONE DIAMETER DISTRIBUTIONS

Shirley Yi Fen Hii

Institute for Medical Research, National Institute of Health Malaysia

Poster 77. REPLICATION KINETICS OF MALAYSIAN SARS-COV-2 IN VERO E6 CELLS

Siti Nur Zawani Rosli
Institute for Medical Research (IMR), National Institutes of Health (NIH), Ministry of Health Malaysia

Abstracts Book

Wednesday 7 December 2022

K1: Opening Ceremony and Keynote Address

9.15-10:00hr

Room A

Abstract No. : ABS0001888

PREVENTING THE NEXT PANDEMIC: THE POWER OF A GLOBAL EARLY WARNING SURVEILLANCE SYSTEM

Dennis Carroll

Authors : Dennis Carroll

Affillation : Chair, Leadership Board, Global Virome Project

Senior Advisor, Global Health Security, URC

Distinguished Professor of Faculty of Medicine, Chulalongkorn University

The ongoing COVID-19 pandemic has laid bare our collective weaknesses in being able to effectively respond to the emergence of a highly contagious and lethal microbial threat. Despite extraordinary advances over the past century in science and in global health standards, we still live in a world where the threat of an infectious agent can emerge anytime and anyplace without warning and spread rapidly to every community and every household without regard to national borders. Over the course of the remainder of this century, the likely frequency of epidemics and pandemics will continue to increase, driven to a large extent by demographic trends, including urbanization, and environmental degradation, climate change, persistent social and economic inequalities, and globalized trade and travel. New efforts are needed to craft global strategies, policies and regulatory frameworks that more directly address the multi-sectoral aspects of disease emergence to improve our collective capacities to prevent, as well as rapidly detect and respond to threats. Key among these new efforts is building an early warning surveillance system spanning wildlife, livestock and human populations This talk will explore how such a multi-sectoral surveillance system will contribute to an enhanced capacity to forecast future threats and enable early intervention before they pose a threat.

Keyword : Surveillance, Early Warning

Wednesday 7 December 2022

S1 : Advanced Information Technology for Tropical Medicine

10:30-12:00hr

Room A

Abstract No. : ABS0001851

A PIPELINE FOR MOSQUITO DETECTION AND CLASSIFICATION FROM WINGBEAT SOUNDS

Myat Su Yin

Authors : Su Yin M.[1], Haddawy P.[1,2], Ziemer T. [2], Wetjen F.[2], Supratak A.[1], Kanrawee C.[1], Siritanakorn W.[1], Chantanalertvilai T.[1], Sriwichai P.[3] and Sa-ngamuang C.[1]

Affillation : [1]Faculty of ICT, Mahidol University, 999 Phuttamonthon 4 Road, Salaya, Nakhon Pathom, Thailand; [2]Bremen Spatial Cognition Center, University of Bremen, Enrique-Schmidt Str. 5, Bremen, Germany; [3]Faculty of Tropical Medicine, Mahidol University, Ratchathewi, Bangkok, Thailand

Introduction: Effective targeting of mosquito-born disease control efforts requires accurate estimates of mosquito vector population density. Current approaches are mainly manual, where specially designed mosquito traps or ovitraps are placed in areas of interest and recovered the next day. The individual mosquitoes are classified into species and counted in an entomological laboratory. This process is costly, slow, and inefficient.

Methods: In this study, we implemented a software pipeline for the detection and classification of mosquito species and sex from wingbeat sounds. We consider four mosquito species present in Thailand: the primary vectors of dengue (Aedes aegypti, Aedes albopictus), the primary vectors of malaria (Anopheles dirus), and the common non-disease-carrying mosquito (Culex quinquefasciatus). First, the mosquito wingbeat portions are detected from the audio stream using a detector component based on autocorrelation. For each of the detected wingbeats portions, the mosquito species and sex are determined using a classifier. We implemented a lightweight deep learning-based classifier which is suitable to be deployed on small IoT sensor devices. Our 1D-CNN convolutional neural network model operates directly on a low-sample-rate raw audio signal, avoiding a costly feature extraction step used by other machine learning approaches.

Results: When a fast binary mosquito detector precedes the classifier, we can reduce the computational demand compared with the use of the classifier alone by a factor of 10.

Conclusion: We conclude that the combination of an efficient mosquito detector with a convolutional neural network provides for an excellent trade-off between accuracy and efficiency to detect, classify and count mosquitoes.

Keyword : mosquitoes, vector-borne disease, deep learning, audio event, detection, classification

Abstract No. : ABS0001850

PROGNOSTIC PREDICTION OF DHF IN PEDIATRIC PATIENTS: A MULTI-SITE STUDY

Peter Haddawy

Authors : Haddawy P.[1,2], Su Yin M.[1], Mairang D.[1], Avirutnan P.[1], Meth P.[1], Srikaew A.[1], Wavemanee C.[1]

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

Introduction: Dengue fever (DF) affects over 20 million people globally each year. Between 2% and 5% of patients infected with the dengue virus progress to dengue hemorrhagic fever (DHF) with associated mortality risk, especially in children. Given the large numbers of dengue infections annually, effective clinical management requires identifying those patients at high risk of developing DHF so they can be most closely monitored.

Methods: In this study, we developed prognostic models to predict DHF among patients with suspected dengue by applying machine learning techniques to clinical data from pediatric patients gathered over a period of 18 years from Khon Kaen Hospital and Songkhla Hospital in Thailand. The models were implemented for primary care units without lab facilities and general hospitals with lab facilities. We investigated the transferability of the models by building them using the data from one hospital and testing on the other.

Results: The models built with the complete dataset provide good predictive accuracy. We find that applying a model built using only data from one hospital to the other can reduce accuracy. This seems due to variation in the importance of attributes among the two hospitals, which can be mitigated by adding attributes relevant to the new setting.

Conclusion: We conclude that effective prognostic prediction of DHF is possible, but care must be taken when transferring a prognostic model built with data from one clinical setting to another. Benefit can be gained by tuning the model to the new setting.

Keyword : Dengue, machine learning, prognostic prediction, model transferability

Abstract No. : ABS0001855

A MOBILE SYSTEM FOR DENGUE VECTOR MONITORING AND CONTROL

Thomas Barkowsky

Authors : Barkowsky T.

Affillation : University of Bremen

When a dengue fever infection case is detected, a fast response in investigating the suspected infection site and in eliminating existing mosquito larvae is required. In this presentation, we will report about the development of a smartphone application to support public healthcare staff in Thailand working in dengue vector control. Based on established procedures, the system helps with organizing and distributing tasks and thus allows for a timely response when dengue fever outbreaks are detected. All necessary information like open and allocated tasks, addresses and locations, and contact data are provided to the personnel in charge through the mobile app. While inspecting potential sites of infection the system supports the surveillance of vector occurrence, the collection of data, as well as the recording of completed and upcoming tasks. The system is realized as a comprehensive client-server IT infrastructure, which is why all data collected are immediately accessible and are archived for future evaluation and assessment.

Keyword : Dengue vector control, mobile applications, mosquito surveillance

Abstract No. : ABS0001858

MODELING THE SPREAD OF RABIES IN THAILAND: A BOTTOM-UP APPROACH

Anuwat Wiratsudakul

Authors : Wiratsudakul A.[1], Kusakunniran W.[2], Thanapongtharm W[3.]

Affillation : [1]Department of Clinical Sciences and Public Health, and the Monitoring and Surveillance Center for Zoonotic Diseases in Wildlife and Exotic Animals, Faculty of Veterinary Science, Mahidol University, Nakhon Pathom, Thailand; [2]Faculty of Information and Communication Technology, Mahidol University, Nakhon Pathom, Thailand [3]Department of Livestock Development (DLD), Bangkok, Thailand

Introduction: Rabies is a deadly viral zoonosis causing almost sixty thousand deaths worldwide every year. Dogs are identified as major reservoirs of the virus, and dog bites cause most human cases. To achieve a global target to stop human deaths from dog-mediated rabies by 2030, controlling rabies in dogs is crucially important. However, a better understanding of how rabies spreads and is controlled locally is essential to develop national and beyond policies. This study thus aimed to explore how rabies spreads in dog populations and estimate the area where dog vaccination should be immediately provided.
Methods: We first modeled how dogs move using a probabilistic model. Then, we modeled the viral propagation in dog populations using a Susceptible-Exposed-Infectious-Removed (SEIR) model.
Results: With our model settings, we primarily found that rabies may spread to a radius of around 2.15 – 3.25 km from the index case. Nonetheless, field validation is needed in the next step.

Conclusion: We estimated the size of the area where control measures should be urgently implemented once a rabies outbreak occurs. This local simulation can guide the national policy as a bottom-up approach.

Keyword : Dog, Modeling, Policy, Rabies, Thailand

Wednesday 7 December 2022

S2 : Management of Severe Dengue

10:30-12:00hr

Room B

Abstract No. : ABS0001915

KIDNEY COMPLICATIONS AND THEIR MANAGEMENT IN DENGUE INFECTION

Weerapong Phumratanaprapin

Authors : Weerapong Phumratanaprapin

Affillation : Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol University

Dengue infection presents with a wide clinical spectrum, ranging from asymptomatic to severe manifestations with organ involvement. Acute kidney injury (AKI) is one of the atypical manifestations of dengue infection. Due to its vast diversity in different populations, the use of heterogeneous criteria to determine the presence of AKI in dengue patients led to difficulties in assessing the true incidence of dengue-associated AKI. The overall incidence of dengue-associated AKI ranged from 0.9% to 69.4%. The main pathophysiology in dengue-infected AKI is acute tubular damage. Many factors are associated with AKI in dengue, including older age, obesity, male sex, severe dengue, diabetes mellitus, and coexisting bacterial infection. The management of AKI in dengue includes fluid and electrolyte management, monitoring of volume status, avoiding nephrotoxic agents, and considering supportive renal replacement therapy (RRT) for patients who meet the criteria for initiating RRT. Clinicians should closely monitor kidney function, especially in high-risk groups, to detect AKI early and implement appropriate management.

Keyword : No keyword available

DENGUE: AN OVERVIEW AND MANAGEMENT

Terapong Tantawichien

Authors : Terapong Tantawichien

Affillation : Faculty of Medicine, Chulalongkorn University

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001881

CARDIOVASCULAR COMPLICATION IN DENGUE

Chayasin Mansanguan

Authors : Chayasin Mansanguan

Affillation : Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol university

Dengue fever is a life-threatening vector-borne tropical disease. Dengue Viral Infection (DVI) is a major health problem in many parts of the world. Cardiac complications are amongst the important consequences of DVI. The manifestations and frequency of cardiac involvement in dengue are difficult to describe and define. Among studies, the incidence of cardiac involvement in DVI varies from 15-40%. Clinical features of cardiac involvement in dengue are often asymptomatic through palpitation, chest pain, hypotension, pulmonary edema and cardiogenic shock. Cardiac manifestations in DVI ranges from transient atrioventricular block, relative bradycardia, and mild elevation of cardiac biomarkers to myocarditis and/or pericarditis, and death.

Keyword : Dengue, cardiovascular, DVI

Abstract No. : ABS0001698

PULMONARY COMPLICATIONS IN DENGUE

Chaisith Sivakorn

Authors : Sivakorn C.[1,2]

Affillation :
[1]Department of Clinical Tropical Medicine, Faculty of Tropical Medicine
[2]Intensive Care Unit, University College London Hospitals, NHS Foundation Trust, London, UK

Dengue lung disease's pathophysiology is yet unclear. Plasma leakage in dengue hemorrhagic fever (DHF) is thought to be caused by endothelium-related functional alterations caused by mediators, and in most cases, recovery is quick with no lasting effects. The plasma leakage syndrome and alveolar damage associated with dengue infection may be significantly influenced by the host immune response and the phenomenon of antibody-dependent enhancement. There have been reports of a variety of respiratory symptoms in dengue patients. When serositis is present in DHF, pleural effusion is the most frequently seen in about 38.6% of cases of severe dengue illness. Non-cardiogenic pulmonary edoema shares the same aetiology as pleural effusion. This type of pulmonary edoema is also influenced by disturbance of colloid oncotic pressure. Fluid replacement therapy may worsen this issue, which is typically encountered during the convalescence phase, as evidenced in pleural effusion. On the other hand, additional dengue systemic issues including dengue myocarditis can also be present along with cardiogenic pulmonary edoema. From previous reports, diffuse alveolar injury, acute respiratory distress syndrome, bronchopneumonia, pneumonitis, and alveolar hemorrhage are all manifested in severe dengue infection.

Keyword : Dengue, lung, complications

Abstract No. : ABS0001920

DENGUE IN ICU SETTING

Nattachai Srisawat

Authors : Nattachai Srisawat

Affillation : Faculty of Medicine, Chulalongkorn University

Dengue is one of the re-emerging infections in the Tropics. There is no specific drug to treat this condition. Supportive treatment including hemodynamic optimization, fever control, and prevention end organ injury is the only available treatment. Therefore, every suspected/confirmed dengue patients should be assessed for fluid status. Lactate and bedside ultrasound has been applied to detect plasma leakage early in severe dengue infection. Currently, dynamic parameters (stroke volume variation, pulse pressure variation, inferior vena cava (IVC) collapsibility index, passive leg raising test, and end expiratory occlusion test) predict the fluid responsiveness better than static parameters (central venous pressure, pulmonary capillary wedge pressure). If the patient shows signs of dehydration, the fluid of choice is still crystalloid rather than colloid. Norepinephrine is still the vasopressor of choice. Finally, the target mean arterial pressure (MAP) should be at least 65 mmHg except in chronic hypertension patients who required a MAP of at least 80 mmHg.

Keyword : No keyword available

Wednesday 7 December 2022

S3 : Virtual Reality in Medical Education

10:30-12:00hr

Room C

HOW VR CHANGES MEDICAL EDUCATION IN JAPAN AND THE FUTURE OF VR EDUCATION

Yutaro Oikawa

Authors : Yutaro Oikawa

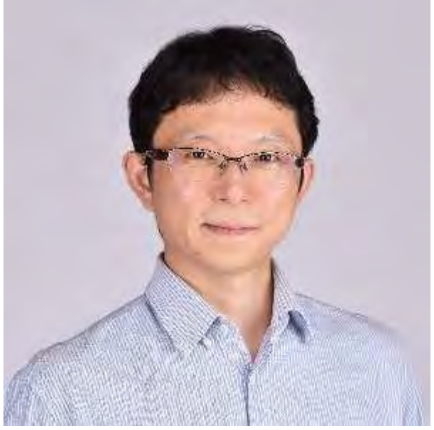
Affillation : Jolly Good Inc., Corporate Planning Department

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001897

VIRTUAL REALITY IN MEDICAL EDUCATION



Hirotake Mori

Authors : Hirotake Mori[1,2], Yutaro Oikawa[3], Simon Valenti[1], Rapeepun Prasertbun[1,2], Aongart Mahittikorn[2], Toshio Naito[1]

Affillation : [1]Department of General Medicine, Juntendo University Faculty of Medicine, Japan; [2]Department of Protozoology, Faculty of Tropical Medicine, Mahidol University, Thailand; [3]JOLLY GOOD Inc. Japan

Virtual Reality (VR) is an innovative tool in medical education. High-quality multi-person education is possible without concern about time and location. Here, we will introduce the status and prospect of VR in medical education. We will bring the VR sets and connect between Thailand and Japan, letting audiences experience the realistic sensation.

Keyword : Virtual Reality, Medical Education

VR CONTENT DEMONSTRATION (THAILAND TO JAPAN)

Rapeepan Prasertbun

Authors : Rapeepan Prasertbun

Affillation : Faculty of Tropical Medicine, Mahidol University

No abstract available

Keyword : No keyword available

VR CONTENT DEMONSTRATION (JAPAN TO THAILAND)

Simon Valenti

Authors : Simon Valenti

Affillation : Juntendo University

No abstract available

Keyword : No keyword available

Wednesday 7 December 2022

S4 : Liver Stage Malaria

10:30-12:00hr

Room D

Abstract No. : ABS0001833

STRATEGIES FOR RADICAL CURE: FROM ANTI-HYPNOZOITE TO ANTI-RELAPSE

Erika Flannery

Authors : Erika L. Flannery[1], Vorada (Eve) Chuenchob[1], Reginara Souza De Assis[1], Matthew Fishbaugher[1], Hanna Schulz[1], Alex Chao[1], Pamela Orjuela-Sanchez[1], Thierry T. Diagana[1], Sebastian A. Mikolajczak[1]

Affillation : [1]Novartis Institute for Tropical Disease

Introduction: Approximately 80% of Plasmodium vivax blood stage infections are due to re-activation of the dormant form of the parasite that resides in the liver. Current treatment options are limited and have practical challenges due to restrictions on use in target populations.

Methods: We use a phenotypic screen to test anti-hypnozoite efficacy of 50,000 compounds with diverse chemical properties. We have also developed several target-based programs to leverage high-thoughput biochemical screening methods. Additionally, to identify functional activity and anti-relapse compounds we use an in vivo humanized mouse model.

Results: Phenotypic screening and target-based screening identify several compounds with anti-hypnozoite activity. Further profiling of hit compounds reveal important considerations for intracellular parasitic screens. In vivo results combined with in vitro observations suggest hypnozoites are not immediately cleared from cells for all mechanisms of anti-hypnozoite activity.

Conclusion: A concerted effort of phenotypic and target-based drug discovery to identify novel compounds is needed to eliminate the hypnozoite reservoir.

Keyword : Plasmodium vivax, relapse, latentcy, dormancy, hypnozoite, drug discovery

Abstract No. : ABS0001799

DISCOVERY OF NOVEL CHEMOTYPES EFFECTIVE AGAINST RELAPSING MALARIA

Alison Roth

Authors : Karl Kudyba[1], Rich Eastman[2], Daniel Talley[2], Samantha Aylor[1], Sharon Mcenearney[1], Susan Leed[1], Ubalee Ratawan[3], Zaira Rizopoulos[4], Brice Campo[4], Charlotte Lanteri[1], **Alison Roth[1]**

Affillation : [1]Experimental Therapeutics, Walter Reed Army Institute of Research, 503 Robert Grant Ave, Silver Spring, MD 20910, USA; [2]National Center for Advancing Translational Sciences, National Institute of Health, 9800 Medical Center Drive, Rockville, MD 20850, USA; [3]Department of Entomology, Armed Forces Research Institute of Medical Sciences, 315/6 Rajvithi Rd, Bangkok 10400, Thailand; [4]Medicines for Malaria Ventures, Rte de Pré-Bois 20, 1215 Meyrin, Switzerland

Efforts to eradicate Malaria from the global human population require drugs that target hypnozoites, the latent liver stage form of Plasmodium vivax. To date, 8-Aminoquinolines (8AQs) are the only compound class approved by world health regulators for combating the dormant liver form and preventing relapse. Unfortunately, these compounds have been demonstrated to be hemolytic to individuals with glucose-6-phosphate dehydrogenase deficiency. Furthermore, 8AQs require cytochrome P450 metabolism to form active intermediates, thus gene polymorphisms can alter drug efficacy. The need to expand our anti-hypnozoite drug repertoire is clear. To model dormant infections, our in vitro assay utilizes Plasmodium cynomolgi infected Rhesus hepatocytes and evaluates compounds for prophylactic or radically curative activity against relapsing malaria. With this approach, we have been able to develop a high-throughput platform to screen for novel liver stage antimalarial drugs. To date, we have tested over 250,000 small molecules, identifying over 600 active hits that represent diverse chemotypes. A select subset of these hits have demonstrated multi-stage activity and are moving forward into WRAIR's malaria pre-clinical testing paradigm. In hopes of further expanding our screening capabilities we have established a collaborative network to produce AI models, incorporate cell phenotype-based approaches, generate new synthetic molecules and explore mechanism of action.

Keyword : Hypnozoite, liver stage, high-throughput, drug discovery, malaria.

Abstract No. : ABS0001707

TRANSMISSION ELECTRON MICROSCOPY TECHNIQUES TO CHARACTERIZE THE ULTRASTRUCTURAL FEATURES OF MALARIA LIVER STAGES

Gabriel Mitchell

Authors : Mitchell G.[1], Harupa-Chung A.[2], Zalpuri R.[3], Chuenchob V.[2], Torres L.[1], Flannery E.L.[2], Jorgens D.M.[3] and Mikolajczak S.A.[2]

Affillation : [1]Open Innovation at Novartis Institute for Tropical Diseases, Novartis Institutes for BioMedical Research, Emeryville, California, USA; [2]Novartis Institute for Tropical Diseases, Novartis Institutes for BioMedical Research, Emeryville, California, USA; [3]Electron Microscope Laboratory, University of California, Berkeley, California, USA

Introduction: The infection of the liver is an obligatory step leading to malaria. Following hepatocyte invasion, malaria parasites differentiate into replicative or dormant forms, the latter known to reactivate and cause clinical relapses. The liver stages of malaria remain elusive because of challenges hindering access to well-established technologies, including electron microscopy.
Methods: Correlative Light - Electron Microscopy (CLEM) was used to characterize the liver stages of Plasmodium berghei (non-relapsing rodent parasite) and Plasmodium cynomolgi (relapsing simian parasite). Human hepatoma Huh7 cells or primary monkey hepatocytes were infected with GFP-expressing P. berghei or wild-type P. cynomolgi for 2 and 7 days, respectively. The position of liver stages and host cells was first mapped using light and fluorescence microscopy, and samples were further processed and imaged using transmission electron microscopy (TEM). Liver stages were detected using endogenous fluorescence or with a low-detergent immunofluorescence analysis (LD-IFA) protocol recognizing the parasite protein UIS4.
Results: CLEM images were acquired for the liver stage of P. berghei using endogenous fluorescence and the LD-IFA protocol. Host and parasite organelles were identified and imaged at high resolution using both approaches, and LD-IFA induced only minimal damages to samples. A first collection of TEM images was acquired for the replicative and dormant liver stages of P. cynomolgi using LD-IFA.
Conclusion: This study developed a CLEM protocol allowing the imaging of malaria liver stages from species that lack reliable tractable genetic systems. It also revealed the ultrastructural features of malaria liver stages.

Keyword : Plasmodium berghei, Plasmodium cynomolgi, CLEM, schizonts, hypnozoites

Abstract No. : ABS0001708

A DUAL LUMINESCENCE ASSAY TO STUDY ANTIMALARIAL COMPOUNDS AND HOST-PATHOGEN INTERACTIONS DURING THE LIVER STAGE OF MALARIA

Laura Torres

Authors : Torres L.[1], Harupa-Chung A.[2], Fishbaugher M.E.[2], Mendiola A.[3], Chao A.[2], Marelli A.[3], Orth A.P.[3], Gable J.E.[2], Flannery E.L.[2], Mikolajczak S.A.[2], Mitchell G.[1]

Affillation : [1]Open Innovation at Novartis Institute for Tropical Diseases, Novartis Institutes for BioMedical Research, Emeryville, California, USA; [2]Novartis Institute for Tropical Diseases, Novartis Institutes for BioMedical Research, Emeryville, California, USA; [3]Novartis Institutes for Biomedical Research, San Diego, California, USA

Introduction: Our arsenal of antimalarials constantly needs to be renewed because of the emergence of resistance. Innovating therapeutics targeting parasite or host determinants of the malaria liver stage (LS) will contribute to combat malaria. Here, a dual luminescence assay evaluating LS formation and host viability was generated as a tool to study antimalarial compounds and host-pathogen interactions.
Methods: Cas9 and Renilla luciferase genes were integrated in the HuH7 hepatoma cell line. Host cells were infected with Plasmodium berghei expressing the firefly luciferase and treated with compounds at 2 hours post-infection. LS formation and host cell viability were evaluated at 2 days post-infection using luminescence assays and immunofluorescence high-content microscopy (HCM). Cas9-expressing cells were transduced with a small set of lentiviruses carrying scramble or host gene-targeting sgRNAs, and infected with P. berghei 7 days later.
Results: The luminescence of the Renilla and firefly luciferases was linear over a range of cell seeding concentrations and multiplicity of infections. The dual luminescence assay was successful at simultaneously determining the anti-liver stage activity and the cytotoxicity of known compounds and required 2.5-fold less sporozoites than HCM to achieve robustness. Using CRISPR-Cas9 technology, the role of the host protein SR-BI for the formation of P. berghei LS was confirmed by both the dual luminescence assay and HCM.
Conclusion: The dual luminescence assay is adding to our toolbox and provides a fast and reliable approach to study compounds and the role of host factors during the LS of malaria.

Keyword : Plasmodium berghei, schizonts, high-content microscopy, CRISPR-Cas9

Abstract No. : ABS0001803

UNDERSTANDING DRUG METABOLIC ACTIVITY AND HEPATOTOXICITY IN LONG-TERM CULTURE OF PRIMARY SIMIAN HEPATOCYTES

Eve Vorada Chuenchob

Authors : Vorada (Eve) Chuenchob[1], Linda Xiao[1], Erika L. Flannery[1], Suresh B. Lakshminarayana[1], Sebastian Mikolajczak[1], Thierry T. Diagana[1]

Affillation : [1]Novartis Institute For Tropical Diseases

To discover a radical cure drug for plasmodium vivax (pv), the human malaria-causing relapsing parasite, we used p. Cynomolgi (pc), the monkey relapsing parasite which is phylogenetically similar and more abundant in resources. Differences in compound efficacy between primary simian hepatocytes (psh) were anticipated, therefore we characterized metabolic activity and hepatotoxicity in several psh lots. We developed an in vitro radical cure assay that uses pc sporozoites to infect psh in a 384-well format. Compounds are added to media 4 days post-infection (dpi) and refreshed 5 ,6, and 7 dpi. The cells are fixed 8 dpi and parasites and host cell nuclei are counted using high content imaging. In addition, host cell viability is measured based on the quantitation of the adenosine triphosphate (atp) present as well as the release of adenylate kinase (ak) from damaged cells. To understand drug metabolic stability, samples were collected at several timepoints after dosing and enzymatic activity was assessed. Cytotoxicity measurements using nuclei count and atp were very similar while the viability measured using ak was 2-3 times more sensitive in certain compound classes. In addition, compounds were metabolized at different rates between psh lots and in some cases this metabolic activity could be correlated with compound efficacy. Depending on the criteria of interest, different measurement targets to assess toxicity, such as atp, ak, and nuclei count can be more sensitive in distinct compound classes. Furthermore, characterization of enzymatic activity in psh lots provides insight into efficacy of compound classes in different psh lots.

Keyword : Malaria, Plasmodium Vivax, Relapse, Latency, Hypnozoite, Metabolism, Cytotoxicity

Wednesday 7 December 2022

S5 : Way Forward to Leverage Pandemic Prevention

10:30-12:00hr

Room E

SURVEILLANCE AND SPILLOVERS MONITORING

Supaporn Wacharapluesadee

Authors : Supaporn Wacharapluesadee

Affillation : Emerging Infectious Disease - Clinical Center, King Chulalongkorn Memorial Hospital

No abstract available

Keyword : No keyword available

EID INNOVATION

Linfa Wang

Authors : Linfa Wang

Affillation : Duke-NUS Medical School, Singapore

No abstract available

Keyword : No keyword available

VACCINE DEVELOPMENT

Kiat Ruxrungtham

Authors : Kiat Ruxrungtham

Affillation : Chula Vaccine Research Center, Faculty of Medicine, Chulalongkorn University

No abstract available

Keyword : No keyword available

BUILDING A GLOBAL EID RESEARCH NETWORK

Dennis Carroll

Authors : Dennis Carroll

Affillation : School of Global Health, Faculty of Medicine, Chulalongkorn University

No abstract available

Keyword : No keyword available

Wednesday 7 December 2022

[Lunch Symposium] QIAGEN Innovation to Making Improvement in Life Possible

12.00-13.00hr

Room A

Abstract No. : ABS0001876

REVOLUTION OF DETECTION IN TROPICAL INFECTIOUS DISEASES WITH NEUDRY TECHNOLOGY

Chun Wei Chiam

Authors : Chiam C.W.

Affillation : QIAGEN (Senior Sales Application Specialist, Infectious Diseases, Southeast Asia)

Critical decisions for patient care are dependent on accurate and timely clinical laboratory results. To meet this demand, your lab needs full automation, faster turnaround times, scalability and streamlined IVD workflows. In addition, you might also have Laboratory Developed Tests (LDTs) that you wish to implement in parallel with IVD workflows.
NeuMoDx™ Molecular Systems address these needs – and more. With intuitive 3-step workflow, it is industry's first true continuous random-access solution and is scalable to meet the needs of the modern clinical laboratory. It is fully automated analyzers that use proprietary NeuDry™ technology that enabling room temperature storage, no needs for reagent reconstitution and long onboard stability after loading into system. Universal extraction chemistry uses paramagnetic beads with a patented affinity coating to extract nucleic acid, and real-time PCR chemistry in a multi-sample microfluidic cartridge. This unique integration of robotics with advanced microfluidics delivers industry-leading usability, enhanced performance, increased efficiency, and rapid turnaround.

Keyword : NeuMoDx™ Molecular Systems, IVD, LDT, NeuDry, true random access, microfluidic

Abstract No. : ABS0001877

FINDING THE NEEDLE IN HAYSTACK IN TROPICAL DISEASES STUDY WITH NANOPLATE BASED DIGITAL PCR TECHNOLOGY

Amelia Lum Yun Leng

Authors : Amelia Lum Yun Leng

Affillation : QIAGEN Pte., Ltd.

Bacteria, fungi, viruses and parasitic metazoans are present in the environment and are part of all aspects of human life, from human health to food production. Each individual microbe can cause various harmful effect causing diseases to human body. Therefore, specific detection and monitoring of microbes are important.

Digital Polymerase Chain Reaction(dPCR) technology is a novel method for absolute quantification of target nucleic acids, where molecules are randomly distributed into many partitions following Poisson Distribution. QIAGEN dPCR Nanoplate based technology would enable rapid profiling and identification of microbes from various samples including Wastewater, infectious diseases, human microbiome and many more.

Keyword : dPCR, Digitial PCR, Nanoplate, Partition, QIAcuity

Wednesday 7 December 2022

S6 : MORU-OUCRU Student Showcase

13.00-14.30hr

Room A

ANALYZING HUMAN POPULATION MOVEMENT DATA FOR MALARIA CONTROL AND ELIMINATION

Greta Tam

Authors : Greta Tam

Affillation : MORU

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001875

RELEVANT INTERVENTIONS TO TACKLE THE GAPS IN HIV PREVENTION AND CARE IN KEY AFFECTED POPULATIONS, MYANMAR

Ni Ni Tun

Authors : Ni Ni Tun[1,2] ,Frank Smithuis[1,2] ,Christopher P. Conlon[3], Tinne Gils[4], Lutgarde Lynen[4], Josefien van Olmen[5]

Affillation : [1] Medical Action Myanmar; [2]Myanmar Oxford Clinical Research Unit; [3]University of Oxford
[4]Institute of Tropical Medicine, Antwerp; [5]University of Antwerp.

Myanmar is a low-resource country with highly concentrated HIV prevalence in key affected populations (KAP): female sex workers (FSW) with 5.6%, men who have sex with men (MSM) with 6.4% and people who inject drugs (PWID) with 19%. There were an estimated 240 000 people living with HIV, 10 000 new HIV infections and 7700 AIDS-related deaths in 2019. To control HIV, research for strategies in KAP care is urgently needed. Medical Action Myanmar (MAM) is a medical organization, working in Myanmar for KAP's HIV/HCV care. MAM introduced a number of innovative strategies for KAP's HIV/HCV care. With my thesis, I analyzed MAM's innovative HIV programs aim to improve KAP's HIV care in Myanmar. First, I analyzed the uptake and utilization of HIV viral-load testing among KAP and vulnerable population on treatment after introduction of near-point-of-care HIV viral-load testing in slum areas, Yangon. Since MSM has a particular high HIV prevalence in Yangon (28.4%), I investigated uptake and retention of MAM's pre-exposure prophylaxis of HIV infection (PrEP) program among MSM in Yangon. As PWID shared the highest HIV prevalence, I explored HIV cascade-of-care in MAM's innovation harm reduction program, networked harm reduction outreach team with integrated community malaria volunteers. Lastly but not least, the HCV cure rate and 1-year re-infection rate among PWID will be examined on MAM's tele-mentoring program of integrated HCV-HIV-harm reduction services in remote area.

Keyword : Key affected population, near-point-of-care HIV viral load testing, Pre-exposure prophylasis of HIV infection, integrated harm reduction, tele-mentoring

Abstract No. : ABS0001872

BIG DATA AND VACCINATION: EXPLORE THE IMPACTS OF COVID-19 ON CHILDREN ROUTINE MEASLES VACCINATION IN VIETNAM USING VACCINE REGISTRY DATA

Ong Phuc Thinh[1]

Authors : Ong Phuc Thinh[1,2], Marc Choisy[1,2]

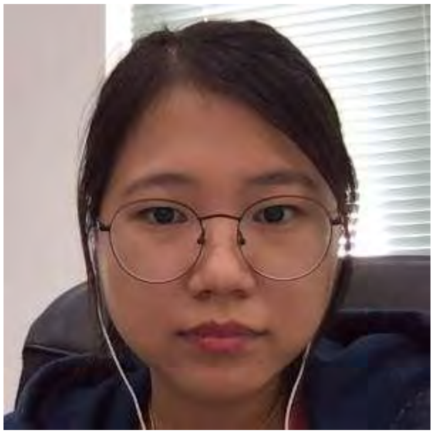
Affillation : [1]OUCRU; [2]University of Oxford

COVID-19 epidemic and its control measures potentially led to delays or missed measles vaccination of children in Vietnam. We used the National Vaccine Registry containing data on routine vaccination of children born after 2017 to evaluate the impacts of a 3-weeks national lockdown imposed in April 2020 and several city-wide lockdowns in Hai Duong province. Nearly no delayed vaccination was observed in provinces with high economic activity (e.g. Ha Noi, Bac Giang) before COVID-19 period but a fraction of children scheduled in March 2020 had a delayed vaccination of 2 months and almost all children scheduled in April 2020 experienced a 1-month delay. Meanwhile, in remote and mountainous areas (e.g. Lai Chau, Yen Bai), the delay pattern was only observed in March but not in April 2020. In Hai Duong, beside the national lockdown in April 2020, there were two more lockdowns, one in August 2020 and one in February 2021. Vaccine coverage at 6 months after the scheduled date of the first shot from May 2020 to April 2021 decreased by an average of 9.8 (6.5 – 12.6) ompared to the same period a year before. The percentage of children who were scheduled to be vaccinated during the lockdown periods that switched from public to private clinics were 42.4% (33.8 – 51.3) in August 2020 and 47.1% (34.8 – 59.6) in February 2021, twice as much as the average of 20.4% (15.6 – 25.3) during the rest of 2020 and 2021.

Keyword : vaccine registry; big data; COVID-19; measles; vaccination

Abstract No. : ABS0001873

UNDERSTANDING HEPATITIS C TREATMENT COST IN VIETNAM



Huyen Anh Nguyen

Authors : Huyen Anh Nguyen

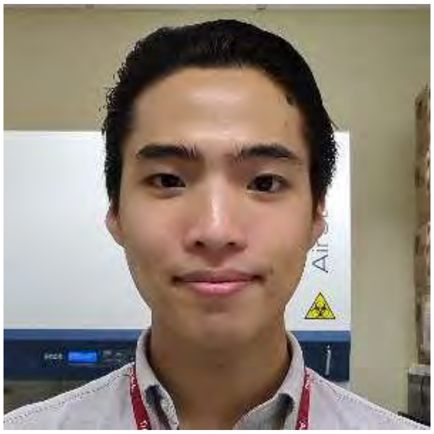
Affillation : Oxford University Clinical Unit, Ho Chi Minh City, Vietnam; 2MRC Centre for Global Infectious Disease Analysis, School of Public Health, Imperial College London, Norfolk Place, London, W2 1PG, UK.

In Vietnam, chronic hepatitis C (HCV) prevalence has been estimated to up to 4.7% (of 95 million people) in 2017, which is higher than in other countries in the region. Direct-Acting Antiviral (DAAs) have revolutionized HCV treatment and can achieve a very high cure rate (>90%). However, the high cost of DAAs creates barriers to treatment, leading to challenges for the Vietnam healthcare system. Our study aims to investigate the cost of DAA treatment, which can suggest improving DAAs treatments assessment in the population. To estimate the cost incurred by outpatients undergoing DAA treatment, we investigated costs from 102 HCV outpatients recruited between August 2020 to August 2021, at the Hospital for Tropical Diseases in Vietnam. Our results revealed that the average DAAs treatment total cost per outpatient ranges from US$1300 to US$1725 without health insurance. Even for those with health insurance, the patients out-of-pocket payment is still considerable, taking from 43% to 100% of the total DAAs treatment cost. DAA treatment was found to be significantly cost-saving (five-time reduction) compared to the old treatment (peg-interferon). In addition, we also found a big gap in the patients direct non-medical costs (including food, traveling, accommodation costs), with patients living in rural areas having to pay four times higher than those from urban areas, raising the concern of geographic inequity. Therefore, DAAs should be recommended in a broad population, instead of Peg-Interferon treatment. The healthcare system should consider providing the DAAs treatment at the primary healthcare level to bridge the inequity gap.

Keyword : health economics, cost analyses, low-middle incomes countries, hepatitis C

Abstract No. : ABS0001874

DEVELOPING MOLECULAR MULTIPLEX DIAGNOSTICS FOR TROPICAL PATHOGENS



Witchayoot Huangsuranun

Authors : Huangsuranun W.[1,2], Thaipadungpanit J.[1,3], Lubell Y[1,2], Batty E.[1,2]

Affillation : [1]Mahidol-Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [2]Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, UK; [3]Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

Introduction: Definitive diagnostics of many pathogens are done in laboratories with real-time PCR being the gold standard. However, in rural Southeast Asia, testing requires sample collection and transportation to a reference laboratory which is costs time and money. Most undifferentiated fevers are given treatment before diagnosis, leading to overuse of antibiotics. To address this problem, many point-of-care tests (POCTs) are developed to be used outside of laboratories. An emerging method for POCTs is isothermal amplification such as loop-mediated isothermal amplification (LAMP) and recombinase aided amplification (RAA). These methods allow for amplification of a target sequence at a constant temperature, eliminating the need of a thermal cycler.

Methods: Whole blood was spiked with dengue virus and extracted with Lucigen's QuickExtract DNA solution using a protocol recommended by the manufacturer. The extracted product was detected with real-time PCR. LAMP was performed with dengue genomic RNA according to manufacturer's protocol.

Results: Dengue genomic RNA was successfully extracted with the QuickExtract solution as detected by real-time PCR. Separately, LAMP was able to amplify dengue RNA as detected by agarose gel electrophoresis. Both methods only require a hotplate to perform. To set up the reaction for SHERLOCK, the template must be in the form of RNA. As LAMP produces DNA products, a transcription stage was also performed, and the RNA product was detected with Qubit 3.0 fluorometer.

Conclusion: Rapid extraction and isothermal amplification has been separately performed successfully for dengue virus.

Keyword : Molecular diagnostics, Isothermal amplification

Abstract No. : ABS0001861

RISK MAPPING OF ARBOVIRUSES: A SYSTEMATIC REVIEW OF DATA, MODELS, COVARIATES, AND METHODS OF EVALUATION

Yalda Jafari

Authors : Lim A.[1], **Jafari Y.[2]**, Rotejanaprasert C.[2], Maude R.[2], Brady O.[1]

Affillation : [1]Mahidol-Oxford Tropical Medicine Research Unit (MORU); [2]London School of Hygiene and Tropical Medicine

Introduction: There is a lack of global risk maps and consensus in methods for mapping risk of arboviruses. The purpose of this review is to provide an overview of the methods and covariates used to map risk of arboviruses, namely Dengue, Zika, Chikungunya, and Yellow Fever.

Methods: A literature search for studies mapping risk of Dengue, Zika, Chikungunya or Yellow Fever was conducted in Embase, Medline, Global Health and Web of Science from inception to 6 July 2022. Information on study characteristics, methodology, covariates, spatial resolution, validation, and prediction criteria amongst other details are extracted by two authors (AL, YJ) and summarized. Quality review of the included studies will be completed.

Results: After removing duplicates, we screened 7,742 records, 113 of which were included in the systematic review. About 75% of articles were focused on Dengue, followed by Zika, Chikungunya, Yellow Fever, and a combination of these diseases. Top three covariates included in the studies were temperature, rainfall, and population density with Bayesian framework and machine learning often the preferred approach to risk mapping. Only 16% of studies examined collinearity among covariates, while 39% used structured random effects to account for spatial autocorrelation.

Discussion: Our review summarizes the methodology and covariates used to inform risk maps of arboviruses. The results of this review will help inform future work on spatial predictions of arboviruses and will help inform public health response.

Keyword : risk mapping, arboviruses, prediction

Abstract No. : ABS0001889

ANTIBODY RESPONSE TO DIFFERENT BURKHOLDERIA PSEUDOMALLEI ANTIGENS

Apinya Pumpuang

Authors : Apinya Pumpuang[1,2], Suporn Paksanont[1], Rungnapa Phunpang[3], Peeraya Ekchariyawat[4], Adul Dulsuk[3], Siriorn Loupha[3], Kochnipa Kwawong[3], Yaowaree Charoensawat[1], EkkachaiThiansukhon[5], Nicholas P. J. Day[3,6], T. Eoin West[8], Mary N. Burtnick[1,7], Paul J. Brett[1,7], Narisara Chantratita[1,3]

Affillation : [1]Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [2]Department of Clinical Pathology, Faculty of Medicine, Vajira Hospital, Navamindradhiraj University, Bangkok, Thailand; [3]Mahidol-Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [4]Department of Microbiology, Faculty of Public health, Mahidol University, Bangkok, Thailand; [5]Department of Medicine, Udon Thani Hospital, Udon Thani, Thailand; [6]Center for Tropical Medicine and Global Health, University of Oxford, Oxford, United Kingdom; [7]Department of Microbiology and Immunology, University of Nevada, Reno School of Medicine, Reno, Nevada, USA; [8]Division of Pulmonary and Critical Care Medicine, Harborview Medical Center, and International Respiratory and Severe Illness Center, University of Washington, Seattle, WA, USA.

Burkholderia pseudomallei is a causative agent of melioidosis, which is endemic in tropical regions. Melioidosis treatment is often failure and no vaccines for melioidosis available. In this study, we 1) characterized the classes and subclasses characteristics of B. pseudomallei-specific antibodies present in human plasma samples of melioidosis patients by ELISAs, 2) determined how antibody differently responses to B. pseudomallei infection between groups of subjects in association with disease characteristics, and 3) characterized the potential function(s) of specific antibodies from melioidosis patients. Five B. pseudomallei antigens including O-polysaccharaide (O-PS), hemolysin co-regulated protein (Hcp1), alkyl hydroperoxide reductase (AhpC), and two outer membrane proteins (OMP) were used. In addition, the function of antibody in antibody-mediated cellular phagocytosis (ADCP) and antibody-mediated complement deposition (ADCD) were investigated. IgG-OPS and IgG-Hcp1 were purified from pooled serum obtained from melioidosis patients. Serum from melioidosis patients significantly enhanced B. pseudomallei uptake into THP-1 cells compared with pooled serum from healthy donors. In melioidosis patients, Hcp1 induced high IgG levels while OPS induced high IgG and IgA levels. OMPs and AhpC induced low antibody levels. The area under receiver operating characteristic curve (AUROCC) to discriminate melioidosis cases from healthy donors was highest for anti-Hcp1 IgG (0.92) and anti-OPS for IgG (0.91) and IgA (0.92). Anti-Hcp1 IgG1 and anti-OPS IgG2 had the greatest AUROCCs (0.87 and 0.95, respectively) compared to other IgG subclasses for each antigen. Enhanced opsonization and C3b deposition were observed with IgG-OPS and IgG-Hcp1. This study provides insight into the antibody levels and functions in human melioidosis.

Keyword : Burkholderia Pseudomallei / O-Polysaccharide / Hcp1 / Antibody / Adcp / Adcd / Antibody Function / Vaccine / Melioidosis / Antigen

Abstract No. : ABS0001878

DEFINING THE EPIDEMIOLOGY OF ACUTE FEBRILE ILLNESS IN RURAL SOUTH AND SOUTHEAST ASIA

Christopher Rusheng Chew

Authors : Chew R.[1, 2, 3]

Affillation : [1]Mahidol Oxford Tropical Medicine Research Unit, Bangkok, Thailand; [2]Centre for Tropical Medicine and Global Health, University of Oxford, Oxford, UK; [3]Faculty of Medicine, University of Queensland, Brisbane, Australia

Background: Fever is common but non-specific symptom of infection. Malaria, previously the leading cause of acute febrile illness (AFI) in the region has declined markedly, but the primary care management of non-malarial AFI in rural South and Southeast Asia (SSEA) is hampered by the poor laboratory diagnostic capacity, low healthcare staff skill levels, and the lack of knowledge of disease epidemiology.

Aims: To define the epidemiology of AFI in SSEA syndromically and microbiologically.

Methods: Demographic, symptom, epidemiological, and vital sign data will be collected over 12-18 months from 100,000 consecutive patients of all ages presenting with AFI to primary care providers at sites in Thailand, Laos, Cambodia, Bangladesh, and the Thai-Myanmar border which are part of the South and Southeast Asian Community-based Trials Network. Patients will have dried blood spots collected at the time of presentation and at follow-up 28 days later. Approximately 10% of these will be assayed for malaria, murine typhus, scrub typhus, other rickettsioses, dengue, chikungunya, non-dengue flaviviral infection, and non-chikungunya alphaviral infection by means of a combination of molecular and serological diagnostics. Syndromic and microbiological diagnoses will be formulated based on the above data. In parallel, a household survey assessing health-seeking behavior for AFI will be conducted at all sites. For each site and overall, the relative incidences and outcomes of AFI by syndrome and disease, accounting for seasonality, can, thus, be calculated.

Implications: This large-scale study will form the foundation upon which further work to improve primary care AFI management in this region can build.

Keyword : Fever; Southeast Asia; South Asia; epidemiology

Wednesday 7 December 2022

S7 : Addressing Dengue Challenges

13.00-14.30hr

Room B

Abstract No. : ABS0001865

WOLBACHIA REPLACEMENT STRATEGY TO COMBAT DENGUE: MALAYSIA EXPERIENCE

Nazni Wasi Ahmad

Authors : Nazni W.A.[1], Noor Afizah A.[1], Cheong Y.L.[1], Wolbachia Team[1], Hasnor H.A.[2], Abu Bakar R.[2], Hapsah M.D.[2], Lee H.L.[1] , Hoffmann A.A.[3], and Sinkins S.P.[4].

Affillation :
[1]Medical Entomology Unit, Infectious Disease Research Centre, Institute For Medical Research, National Institutes of Health, Ministry of Health, Malaysia; [2]Institute for Health Behavioural Research, Ministry Of Health, Bangsar, Kuala Lumpur; [3]Departments of Zoology and Genetics. The University of Melbourne. Melbourne Vic 3010. Australia; [4]MRC-University of Glasgow Centre for Virus Research, Henry Wellcome Building, 464 Bearsden Road, Glasgow, Scotland, UK

No abstract available

Keyword : Aedes aegypti, dengue, Wolbachia, Replacement Strategy, Community engagement

Abstract No. : ABS0001867

CARICA PAPAYA LEAVES: EVIDENCE BASED THERAPEUTICS FOR DENGUE

Mohd Ridzuan Mohd Abd Razak

Authors : Mohd Abd Razak M.R., Afzan A., Mohmad Misnan N., Norahmad N.A., Zainol M., Syed Mohamed A.F.

Affillation : Herbal Medicine Research Centre, Institute for Medical Research, National Institutes of Health, Ministry of Health, 40170 Shah Alam, Selangor, Malaysia

Introduction: Carica papaya leaf juice is commonly used to ease the symptoms of dengue as a complementary therapy. The efficacy of the juice has been proven by a randomised controlled trial conducted in a Malaysian Hospital whereby the orally treated patients showed a rapid increase in the platelet recovery and shortened hospital stay. Therefore, additional preclinical safety and efficacy studies were conducted to evaluate the anti-dengue properties of a standardized freeze-dried C. papaya leaf juice to support further development of a capsule form.
Methods: Preclinical safety studies using standardized freeze-dried C. papaya leaf juice were conducted on Sprague Dawley rats in accordance to OECD guidelines while efficacy studies were conducted in AG129 mice infected with dengue virus. For efficacy assessment, oral treatment of freeze-dried C. papaya leaf juice was performed at 24 hours post infection daily for 3 consecutive days. Blood and tissue samples were used to determine viremia, platelet, and cytokine levels.
Results: Preclinical safety studies showed that the oral treatment of freeze-dried C. papaya leaf juice was safe up to 2000 mg/kg body weight. Also, the treatment significantly decreased proinflammatory cytokines and improved platelet levels of infected AG129 mice. However, there were no marked reduction in viremia in infected AG129 mice receiving the treatment.
Conclusion: Our data suggest that the freeze-dried C. papaya leaf juice could modulate the immune dysregulation caused by dengue viral infection with acceptable safety in preclinical models. This supports C. papaya leaf juice as a potential candidate to be developed as dengue adjunctive therapy.

Keyword : Dengue, Carica papaya, leaf, AG129, cytokine, mouse, adjunctive therapy

Abstract No. : ABS0001869

KNOWLEDGE, ATTITUDES, AND PRACTICES OF PUBLIC ELEMENTARY AND HIGH SCHOOL TEACHERS ON DENGUE IN A PROVINCE OF THE PHILIPPINES

Ernesto Gregorio Jr.

Authors : Gregorio ER Jr.[1] , Salanguit M.B.[1], Santillan M.C.[1], Hernandez P.M.[1], de Los Reyes C.S.[2], Takeuchi R.[2], Medina J.R.[3], Saito M.[4], Kawamura S.[4], Agapito L.G.[5], Morales L.[5], Garcia FB Jr.[1], Kobayashi J.[2]

Affillation : [1]College of Public Health, University of the Philippines Manila/SEAMEO TROPMED Philippines; [2]University of the Ryukyus, Okinawa, Japan; [3]National Institutes of Health, University of the Philippines Manila [4]Chubu Institute for Advanced Studies; [5]City of San Fernando, Schools Division Office, Department of Education

Introduction: Dengue fever is considered an important public health problem in the Philippines. This study measured the health literacy of Filipino teachers who is an important source of school-based health information about dengue.
Methods: We used cross-sectional study to assess the dengue-related knowledge, attitudes, and practices of public elementary and high school teachers from 19 purposively selected schools in one Philippine province. An online pretested survey tool was used to collect the data. Data were analyzed using descriptive statistics.
Results: There were a total of 413 teachers who participated in the survey, The mean age was 38.4, (51.1%) belonging to the 35 to 54 age group and 83.3% are females. 84.7% self-reported to have not experienced dengue while 56.7% knew someone who had dengue previously. The primary and most trusted source of information about dengue was the Department of Health officials (83.7%, 89.3%), and the top media platform used was television (86.2%), followed by Facebook (80.1%). Most participants were knowledgeable about dengue transmission and prevention/control. Most of the frequently missed questions were on the diagnosis and common symptoms of dengue. Most expressed positive health beliefs about dengue. The most commonly practiced activity for dengue prevention was the disposal of garbage and the draining of water containers. The use of videos was the most frequently-mentioned strategy that teachers deemed appropriate for teaching dengue prevention.
Conclusion: Respondents had good knowledge, favorable attitudes, and correct practices on dengue. Knowledge of the diagnosis and symptoms of dengue was low. Video materials were recommended to be an effective teaching method.

Keyword : Dengue, Knowledge, Attitude, Practices, Health Literacy, Public school teachers, Philippines

Abstract No. : ABS0001885

DENGUE DIAGNOSIS PREDICTION USING BAYESIAN NETWORK MODEL

Saranath Lawpoolsri

Authors : Lawpoolsri S.

Affillation : Mahidol University

Diagnosis of dengue infection is a main challenge for dengue case management. Although there are molecular and serology testing to confirm the infection, clinical diagnosis is still the most common diagnosis method due to the limitations of the confirmatory methods. In limited resource settings, the clinical diagnosis mostly relies on clinical manifestations and basic laboratory tests such as complete blood count, mainly fever, tourniquet test, hemoconcentration, and platelet count. However, these clinical and laboratory test results do not directly correlate with the diagnosis outcome. The prediction of dengue outcome generally depends on conditional probability between different predictors. For example, hemoconcentration can be observed after certain days of fever. This clinical diagnosis may be a challenge for unexperienced physicians. In addition, the complex correlation between predictors can be difficult to model using conventional statistical models. Bayesian networks is a type of machine learning; the models represent joint probability distribution among random variables in the model (representing causal relationship between variables). In this presentation, we will demonstrate the use of Bayesian network model as a decision support model for dengue diagnosis.

Keyword : Dengue Diagnosis, Bayesian Networks, Machine learning

Wednesday 7 December 2022

S8 : Frontier Research in Tropical Diseases for Sustainable Development Goals (SDGs)

13.00-14.30hr

Room C

Abstract No. : ABS0001912

STRENGTHENING CAPACITY TO UNDERSTAND IMMUNITY TO SARS-COV-2 AND OTHER EMERGING PATHOGENS

Susanna Dunachie

Authors : Susanna Dunachie[1,2], Narisara Chantratita[3], Barbara Kronsteiner[2], Juthathip Mongkolsapaya[4,5], Raph Hammers[6], Tan le Van[7]

Affillation : [1]Mahidol-Oxford Tropical Medicine Research Unit , Bangkok, Thailand; [2]Nuffield Dept of Medicine Centre for Global Health Research, University of Oxford, Oxford, UK; [3]Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [4]Wellcome Centre for Human Genetics, Nuffield Department of Medicine, University of Oxford, Oxford, UK; [5]Chinese Academy of Medical Science (CAMS) Oxford Institute (COI), University of Oxford, Oxford, UK; [6]Oxford University Clinical Research Unit Indonesia, Jakarta, Indonesia; [7]Oxford University Clinical Research Unit Vietnam, Ho Chi Minh City, Vietnam

COVID-19 has demonstrated how one pathogen can result in mass disease, death and economic disruption worldwide. We need to understand the risks of emerging variants of concern (VoC) in order to inform policies for vaccination and control measures. Much of the world's SARS-CoV-2 immunology research has been conducted in high income countries (HIC), yet new VoC can arise anywhere. It is therefore crucial that LMICs have capacity to study the antibody and T cell responses to SARS-CoV-2 infection and vaccination. The UK PITCH study has monitored the antibody and T cell response to SARS-CoV-2 in healthcare workers over time, providing an evidence base for UK policy decisions on vaccine strategy. Building on this, we have established the Wellcome-funded SEACOVARIANTS (Southeast Asia Initiative to Combat SARS-CoV-2 Variants) consortium led by Tan le Van at OUCRU Vietnam.
SEACOVARIANTS brings together researchers from Vietnam, Thailand, Indonesia, Singapore, UK and USA to expand existing capability to undertake immunology research in Southeast Asia. The work packages include:

1. Establishing a new research platform for assays including N and S protein binding antibody, multiplex sVNT, live FRNT, pseudovirus, interferon-gamma ELISpot, intracellular staining, and CTV proliferation.
2. Rapid prediction of the ability of new variants to evade host immunity and therapeutics, using structural biology
3. Measuring the impact of current VOCs on antibody responses in SEA populations
4. Defining the Impact of current VOCs on T-cell responses in SEA populations
5. Policymaker and public engagement

This talk will outline the key steps and pilot data to date.

Keyword : COVID-19, emerging variants of concern (VoC)

Abstract No. : ABS0001870

EXPERIENCE ON GENOMIC SURVEILLANCE AND DEVELOPMENT OF INACTIVATED COVID-19 VACCINE IN MYANMAR

Nay Myo

Authors : [1]Khine Zaw Oo, [1,3]Ye Win Aung, **[1,2]Nay Myo Aung**, [1,4]Han Tin Aung, [1]Htet Wai Moe, [1]Htin Lin Naung Soe, [1]Zaw Win Htun, Aung, [1]Sis Hmu, [1]Maung Maung Aye, [1]Kyee Myint

Affillation : [1]Defense Services Medical Research Centre; [2]Mahidol University; [3]Khon Kean University, [4]No(8) Medical Battalion

Coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is an ongoing global health emergency. From the beginning of the pandemic in early 2020 in Myanmar, a period during which the Wuhan and Alpha virus variants dominated, the development of molecular techniques was crucial. Various waves of COVID-19 infection occurred. Genomic surveillance was also done six times from January 2021 to March 2022 with Illumina MiSeq FGx platform. Sequences of eighty-three isolates were deposited at GISAID. Omicron variant started in Myanmar since January 2021 and became the sole variant since March. At the time of pandemic, countries struggled for getting vaccine and the producers struggled for scaling up of vaccine production. Therefore, we developed research scale vaccine production pipeline by developing Vero E6 cell culture, and inoculation of widely spreading omicron virus. The real time PCR, and tissue culture infective dose (TCID) results showed promising with effective propagation of virus and inactivation. We clarified the viral infected cells by centrifugation and inactivated with heat. Inoculation on Vero E6 again showed no cytopathic effect showing effective purification. The resultant inactivated vaccine candidate was purified by MicroKros tangential flow system, and sterile filtration with 0.22 μm membrane filter. The concentration and purity of inactivated vaccine candidate were checked with spectrometric and fluorescent method and showed effective purification and antigenicity was maintained. To our facilities, it was needed to prove purified inactivated virion and experts with collaboration in future of Myanmar.

Keyword : COVID-19, SARS-CoV-2, Variant, Vero E6, MicroKros

Abstract No. : ABS0001903

MATCHING MULTI-LOCUS SEQUENCE TYPES OF SOIL AND CLINICAL ISOLATES OF BURKHOLDERIA PSEUDOMALLEI IN MYANMAR: THE IDENTIFIABLE MISSING LINKS

Chanwit Tribuddharat

Authors : Aung N.M., **Tribuddharat C.**

Affillation : Department of Microbiology, Faculty of Medicine Siriraj Hospital, Mahidol University, Thailand

Introduction: The correlation of Burkholderia pseudomallei clinical and soil isolates has never been studied in Myanmar. We have studied spatial relation of B. pseudomallei from patients and soil in Myanmar during 2018-2020.
Methods: There were 21 B. pseudomallei isolates: 5 isolates from soil (out of 1,000 soil samples from 10 townships) and 16 clinical isolates. Phenotypic and genotypic tests (16S rRNA, recA, and TTS1 genes) including Multi-locus sequence typing (MLST) method were used for species identification and clonal analyses.
Results: There was relationship of sequence types in Myanmar and global 5,905 isolates from the B. pseudomallei MLST database. There were 8 novel STs (38%; ST1722-ST1729) and 6 previously identified STs indicating high strain diversity. All STs were classified into 6 groups. Groups 1 (ST56) was clustered with isolates from Bangladesh, Thailand, Cambodia, and Vietnam. Group 2 (ST300) was with Thailand, Bangladesh, and India. Groups 3 (ST354) was with China. Group 4 (ST416) was with Thailand. Group 5 (ST90) was with Australia, Belgium, China, Madagascar, UK, and USA. Group 6 (ST42) was with Bangladesh and India. Matched ST90 were found in 3 clinical and 3 soil isolates in central part of Myanmar, which has previously been identified in many countries.
Conclusions: We found matched ST90 isolates in patients and soil that may indicate the clonal relation and route of transmission. However, the comparison using MLST results may have some limitations for B. pseudomallei in epidemiology study. Whole genome sequencing and SNP analyses are needed to exclude homoplasy from true clonal outbreaks.

Keyword : Burkholderia pseudomallei, MLST, clonal spread, Homoplasy

Abstract No. : ABS0001763

DRUG DISCOVERY FROM NEW RESOURCES FOR FIGHTING AGAINST TROPICAL INFECTIONS

Aunchalee Thanwisai

Authors : Paramaporn Muangpat[1], Wipanee Meesi[l1], Jatuporn Ngoenkam[1], Yothin Teethaisong[2,3], Rapee Thummeepak[1], Sutthirat Sitthisak[1], Sarunporn Tandhavanant[4], Narisara Chantratita[4], Helge B. Bode[5,6], Apichat Vitta[1,7,8], **Aunchalee Thanwisai[1,7,8*]**

Affillation : [1]Department of Microbiology and Parasitology, Faculty of Medical Science, Naresuan University, Phitsanulok, Thailand, 65000; [2]Department of Biomedical Sciences, Faculty of Allied Health Sciences, Burapha University, Chonburi, Thailand, 20131; [3]Research Unit for Sensor Inovation (RUSI), Burapha University, Chon Buri 20131, Thailand; [4]Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand, 10400; [5]Molekulare Biotechnologie, Goethe Universität Frankfurt, Max-von-Laue-Str. 9, Frankfurt am Main 60438, Germany; [6]Max Planck Institute for Terrestrial Microbiology, Department of Natural Products in Organismic Interactions, Marburg 35043, Germany; [7]Center of Excellence for Biodiversity, Faculty of Sciences, Naresuan University, Phitsanulok, Thailand, 65000; [8]Centre of Excellence in Medical Biotechnology (CEMB), Faculty of Medical Science, Naresuan University, Phitsanulok, Thailand

Introduction: Xenorhabdus and Photorhabdus are Gram-negative bacilli belonging to the family Morganellaceae. They are mutualistically associated with the infective juveniles (IJs) of entomopathogenic nematodes of the genus Steinernema and Heterorhabditis, respectively. These bacteria can produce a variety of natural products (secondary metabolites) with broad spectrum bioactivity against bacteria, fungi, protozoa and insect.
Method: We investigated the antibacterial activities of Xenorhabdus and Photorhabdus against 15 strains of antibiotic-resistant bacteria. Further, the study on the morphology of Methicillin-resistant Staphylococcus aureus (MRSA) and cell line toxicity after treating the bacterial extract were studied. In addition, the whole genome of P. akhurstiis subsp. akhurstii was analyzed to identify the secondary metabolite gene cluster.
Result: Photorhabdus extracts had strong inhibitory the growth of S. aureus (MRSA). The interaction between either P. akhurstii subsp. akhurstii extract in combination with oxacillin determined by checkerboard assay exhibited partially synergistic interaction with fractional inhibitory concentration index (FICI) of 0.53. Transmission electron microscopic investigation elucidated that the P. akhurstii subsp. akhurstii extract caused treated S. aureus (MRSA) cell membrane damage. The biosynthetic gene clusters of this bacteria contained non-ribosomal peptide synthetase cluster (NRPS), hybrid NRPS-type I polyketide synthase (PKS) and siderophore, which identified potentially interesting bioactive products: xenematide, luminmide, xenortide A-D, luminmycin A, putrebactin/avaroferrin and rhizomide A-C.
Conclusion: This study demonstrates that P. akhurstiis subsp. akhurstii showed antibacterial activity by disrupting bacterial cytoplasmic membrane and the draft genome provided insights into the classes of bioactive products. This also provides a potential approach in developing a novel antibacterial agent.

Keyword : Xenorhabdus, Photorhabdus, antibacterial activity, methicillin-resistant Staphylococcus aureus, biosynthetic gene cluster, whole genome

Wednesday 7 December 2022

S9 : Free Paper I: COVID-19 and Other Viral Diseases

13.00-14.30hr

Room D

Abstract No. : ABS0001813

INCIDENCE OF SAR-CoV-2 INFECTION AMONG FULLY-VACCINATED TRAVELERS TO THE PHUKET SANDBOX PROGRAM 2021, THAILAND

Thunyaporn Sirijantradilok

Authors : Sirijantradilok T.[1], Rojanaworrarit C.[2], Photisan N.[3]

Affillation : [1] Institute of Preventive Medicine, Department of Disease Control, Ministry of Public Health, Thailand; [2]Department of Population Health, School of Health Professions and Human Services, Hofstra University, New York, USA; [3] Independent Scholar, Khun Han, Sisaket, Thailand

Background and rationale: Thailand's Phuket Sandbox Program was the pioneering COVID-19 quarantine program that allowed travelers who have received a full course of COVID-19 vaccination to travel within the permitted area (Phuket). To assure the wellness of travelers and prevent potential transmission to residents, an evaluation of the SAR-CoV-2 infection rate and its association with different types of vaccines was essential information for re-establishing safe international travel to the tourist attraction.
Methods: Data of all travelers (n=63052) were collected from July 1 to October 31, 2021. The incidence of SAR-CoV-2 was determined. Poisson regression with robust standard error was applied to assess the association between different types of vaccines and infection rate. Kaplan-Meier method and log-rank test were used to describe and compare infection rates among infected travelers with and without symptoms.
Result: Infection rate for SAR-CoV-2 among travelers was 3 per 1,000 populations. The average age among infected individuals was 35.2. Those receiving Gam-COVID-Vac had the highest infection rate (1.7%). The median infection time among the infected was 5 days. High proportions of infection among the infected were observed on the first (29.9%) and the fifth (21.2%) day. The majority of the infected travelers were asymptomatic (82.5%). Infection rates among those with and without symptoms were not significantly different (log-rank test, p= 0.389).
Conclusions: SAR-CoV-2 infection among fully vaccinated travelers could still occur at a rate of 3 per 1,000 populations. The infection rates varied according to the types of vaccine.

Keyword : COVID-19, SAR-CoV-2, Travelers, Travel Medicine, Epidemiology

Abstract No. : ABS0001682

SIDE EFFECTS OF COVID-19 VACCINES AMONG KINDERGARTEN AND ELEMENTARY SCHOOLERS—THAILAND CASE

Chutimon Singkiao

Authors : Singkiao C.[1]

Affillation : The Office of Disease Prevention and Control 9th, Nakhon Ratchasima[1]

Background: Coronavirus 2019 (COVID-19) vaccine administration among schoolchildren is one of the most effective strategies to avoid catastrophe from the pandemic. The aim of the study was to evaluate the incidence of adverse outcomes from getting vaccines against COVID-19 among students aged between 5 and 11 years studying in Thailand.
Methods: This is a retrospective, cross-sectional study whereby Google-form survey on COVID-19 side effects was answered between April and May 2022 by 1,232 participants. Descriptive statistics were used to analyze basic characteristics, and binary logistic regression to compare the incidence of the adverse effects between two age groups: 5- to 8-year-old and 9- to 11-year-old.
Results: The older group had side-effect more than the younger group; 71.99% and 61.11% respectively. The third dose showed the most severe outcome (46.16%). A significant difference in specific symptoms between two-group was shown in myalgia (adjusted OR 1.26, 95%CI 0.96-1.64), fatigue (adjusted OR 1.26, 95%CI 0.96-1.64), and rash (adjusted OR 0.14, 95%CI 0.03-0.70). There was one hospitalized patient with the diagnosis of myocarditis. No fatal cases were reported.
Conclusion: The side-effect following the COVID-19 vaccine in this study had a bit higher incidence than in previous reports; however, there were more adverse outcomes in the older group than in the younger one unidirectionally. Since the children group is now the gap in vaccine administration, encouraging them to accelerate vaccine coverage is the key to bringing us a normal life again; nevertheless, children receiving the third dose should be carefully monitored.

Keyword : Coronavirus 2019 vaccine, Adverse effects, Students

Abstract No. : ABS0001781

FEASIBILITY OF NASO/OROPHARYNGEAL SWAB COLLECTION FROM PEDIATRIC RESEARCH PARTICIPANTS IN CEBU, PHILIPPINES

Clarissa De Guzman

Authors : Clarissa De Guzman[1], Ma. Gladys Nicole Daque[1], March Helena Jane Lopez[1], Anna Maureen Cuachin[1], Maria Vinna Crisostomo[1], Michelle Ylade[1], Jacqueline Deen[1]

Affillation : [1]Institute of Child Health and Human Development, National Institutes of Health - University of the Philippines Manila

During the height of the COVID-19 pandemic in the Philippines, all patients consulting at the hospital emergency department due to fever and other COVID-19 symptoms were required to undergo COVID-19 screening. In this report, we describe the reasons for refusal of parents/guardians to join a pediatric observational study where a nasopharyngeal/oropharyngeal swab was part of the study procedures.

This is a descriptive study of previously collected data from two pediatric observational studies that we conducted in Cebu, Philippines. The studies involved recruitment of pediatric participants with fever and respiratory symptoms and collection of a nasopharyngeal swab (NPS) and/or oropharyngeal swab (OPS) used to test for respiratory pathogens, including SARS-CoV-2, influenza A, influenza B and respiratory syncytial virus.

From July 2021 to June 2022, we screened 149 children who presented at our study sites in Bogo and Balamban, Cebu. The participants' ages ranged from 1 month old to 18 years old and 71 (47.7%) were female. 123/149 (82.6%) did not agree to undergo NPS and/or OPS collection. 41/123 (33.3%) refused collection of NPS/OPS because they did not agree to a repeat swab procedure since the hospital staff already did an initial swab prior to admission, 21/123 (17.1%) did not want to be quarantined in the event the swab was positive for SARS-CoV-2 and 20/123 (16.3) refused due to perceived pain or discomfort during the procedure.

We were able to show that nasopharyngeal and/or oropharyngeal swabbing was not easily acceptable in the community because of various factors associated with the procedure.

Keyword : NPS, OPS, Refusal, Covid-19, Pandemic, Pediatric, Cebu, Philippines

Abstract No. : ABS0001739

ASSESSMENT OF ADHERENCE TO COVID-19 PREVENTIVE MEASURES AMONG RESIDENTS IN MYANMAR

Nyan Lin Maung

Authors : Maung N.L.[1], Htun Y.M.[2], Ko D.K.[1], Htut H.M.[1], Phyoe M.K.[1], Aung W.L.[1], Zaw H.K.[1], Min A.K.[1], Kyaw A.P.[1], Swe T.[1], Sint N.H.[1], Aung Z.[2], Win Z.T.[2], Thu K.S.[2], Shan N.H.[3], Htun N.S.[1], Aung T.H.[1], Pyae L.[1], Tun T.M.[1], Thway A.M.[1], Win T.T.[1]

Affillation : [1]Department of Preventive and Social Medicine, Defence Services Medical Academy, Yangon, Myanmar; [2]Department of Prevention and Research Development of Hepatitis, AIDS and Other Viral Diseases, Health and Disease Control Unit, Nay Pyi Taw, Myanmar; [3]Outpatient Department, No. 1 Military Hospital (500 bedded), Meiktila, Mandalay, Myanmar

Introduction: The adherence to COVID-19 preventive measures is the only option to stop the disease spread and minimize its disastrous impact. Hence, this study aims to assess the level of adherence to COVID-19 preventive measures and associated factors among residents in Myanmar.

Methods: A community based cross-sectional study was conducted among 636 participants in three highest case detected districts of Yangon Region from October to December, 2021. A convenient sampling technique was applied to select the participants and data were collected by the interviews with pre-tested structural questionnaires. Bloom's cut-off point was used to categorize the level of adherence: good, moderate and poor. Binary logistic regression analysis was used to identify the factors associated with poor adherence.

Results: Of all participants, 23.1% were with poor adherence to COVID-19 preventive measures whereas 37.6% and 39.3% with moderate and good adherence respectively. The participants who were 30 years and younger ($p < 0.001$), 31-40 years ($p = 0.001$), below 500,000 kyats of family income ($p = 0.050$), Burmese ethnicity ($p = 0.001$), own business ($p = 0.026$), high school education and below ($p = 0.050$), and low knowledge ($p = 0.002$) were associated with poor adherence to COVID-19 preventive measures.

Conclusion: In this study area, approximately one-fourth of the participants had poor adherence to COVID-19 preventive measures. Addressing the residents with young age, low education level, and previously no infected, enhancement of behavioral change communications, and law enforcement are imperative to strengthen the adherence to COVID-19 preventive measures.

Keyword : adherence, coronavirus, COVID-19 pandemic, knowledge, Myanmar, preventive measures

Abstract No. : ABS0001761

Development of Sequence-Independent, Single-Primer-Amplification and Oxford Nanopore Sequencing in Tracking Hand-foot-and-mouth Disease Transmission among Cases and Contacts in Kindergartens, Thailand

Janjira Thaipadungpanit

Authors : Sittikul P.[1], Yodsawat P.[2,3], Nuanpirom J.[3,4], Kosoltanapiwat N.[5], Batty E.M.[2,6], Sangket U.[3,8], Chatchen S.[1], Day N.P.J. [2,6], **Thaipadungpanit J.[2,7]**

Affillation : [1]Department of Tropical Pediatrics; [2]Mahidol-Oxford Tropical Medicine Research Unit; [5]Department of Microbiology and Immunology; [7]Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [3]Division of Biological Science; [8]Center for Genomics and Bioinformatics Research Faculty of Science Prince of Songkla University, Songkla, Thailand; [4]Integrative Computational Bioscience Center, Mahidol University, Nakhon Pathom, Thailand; [6]Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, UK

Introduction: Hand-foot-and-mouth disease (HFMD) is caused by positive-sense single-stranded RNA viruses in the Enteroviruses genus. It is highly transmissible among children less than five years old. The outbreaks are seasonally reported in kindergartens worldwide, including in Thailand. Their genomes are highly diverse. The Sequence-Independent, Single-Primer Amplification (SISPA) is a random priming method allowing viral genome enrichment with a short process. This method has been used in several viruses (influenza, chikungunya, dengue, and SAR-CoV-2) and uncommon enterovirus isolates to obtain complete genome sequences. The portable Oxford Nanopore Sequencing Technology is helpful for any resource-limited laboratory. We aim to optimise and simplify the whole genome sequencing (WGS) protocol of enterovirus for clinical specimens to investigate HFMD transmission among kindergarten students in Thailand.

Methods: The reported 3-steps SISPA was modified in the starting RNA volume, amount of primers and annealing temperature to increase the final amplicon yield. Additional steps were performed: human cell depletion before RNA extractions from clinical specimens and amplicon purification and size selection after SISPA. We used the ligation, PCR-free, multiplexing native barcode kit and MinION in WGS. Finally, WGS data were analysed using long-read bioinformatics tools. The protocol was validated using throat swabs spiked with virus culture.

Results and Conclusion: The protocol obtained sequences covering over 54-96% of the viral genome depending on the viral starting numbers. Of the total reads, there were 4.89-25.79% of human reads. We show that the SISPA combined with the portable sequencer could be used in virus identification and outbreak investigation when virus isolation is

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

Wednesday 7 December 2022

S10 : Helminths: Should These Be Neglected Diseases?

13.00-14.30hr

Room E

Abstract No. : ABS0001804

CASE SERIES OF DISSEMINATED STRONGYLOIDIASIS IN MALAYSIAN PATIENTS WITH COVID-19

Azlin Muhammad

Authors : Azlin M.Y.[1], Nur Affini G.[1]

Affillation : [1]Universiti Kebangsaan Malaysia

Introduction: The COVID-19 pandemic in Malaysia is part of the ongoing worldwide pandemic of coronavirus disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). As of 20 March 2022, the country is currently ranked third in the number of COVID-19 cases in Southeast Asia and fourth in the number of COVID-19 deaths in the same region. Treatment of the novel Coronavirus Disease 2019 (COVID-19) remains a complicated challenge, especially among patients with severe disease. In recent studies, immunosuppressive therapy has shown promising results for control of the cytokine storm syndrome (CSS) in severe cases of COVID-19. However, it is well documented that immunosuppressive agents (e.g., corticosteroids and cytokine blockers) increase the risk of opportunistic infections. On the other hand, several opportunistic infections were reported in COVID-19 patients. Bacterial and fungal coinfections have been associated with COVID-19 but little is known about parasitic infection. Method: We report a case series of COVID-19 patients who developed disseminated strongyloidiasis following treatment with high-dose corticosteroids and tocilizumab. Results: This case series describes the epidemiology, clinical features and prognosis of disseminated strongyloidiasis infections and polymicrobial bacteraemia in three patients who received immunosuppressive treatment for COVID-19. The laboratory investigations and images of the said parasites are also included. Conclusion: Further research is needed to investigate the relationship between COVID-19 and parasitic coinfection, particularly given the fact that patients with COVID-19 could receive immunosuppressive treatment, a potential risk factor for severe parasitic infection.

Keyword : Disseminated strongyloidiasis, case series, COVID 19, Malaysia

Abstract No. : ABS0001871

FROM PAST TO PRESENT: OPPORTUNITIES AND TRENDS IN THE MOLECULAR DETECTION AND DIAGNOSIS OF STRONGYLOIDES STERCORALIS

Abigail Hui En Chan

Authors : Chan A.H.E.[1], Thaenkham U.[1]

Affillation : [1]Department of Helminthology, Faculty of Tropical Medicine, Mahidol University

Strongyloides stercoralis, a soil-transmitted helminth, approximately affects 30 to 100 million people globally. Mainly found in the tropical and subtropical regions, including Thailand, strongyloidiasis have been reported in the South and Northeast of Thailand. The medical importance of strongyloidiasis lies in the capacity to remain asymptomatic and chronically unnoticed until the host is immunocompromised, causing larva dissemination to various organs resulting in hyperinfection. True prevalence rates of strongyloidiasis may be underestimated, with challenges in diagnosis due to intermittent larva output in stool and lack of sensitive methods. The emphasis of this study is to present an up-to-date review on the current and novel techniques for the diagnosis of S. stercoralis, focusing on the strengths and limitations of each. Parasitological techniques like Baermann-Moraes and agar plate culture to detect larva in stool samples are the current gold standard. However, sensitivity might be inadequate, especially with reduced worm burden. Complementing parasitological techniques, immunological techniques including immunoblot and immunosorbent assays are employed, with higher sensitivity. However, cross-reactivity to other parasites may occur, hampering the assay's specificity. Recently, advances in molecular techniques such as polymerase chain reaction and next-generation sequencing technology provides the opportunity to detect parasite's DNA in stool, blood, and environment samples. Molecular techniques, with their high sensitivity and specificity have the potential to circumvent some of the challenges associated to chronicity and intermittent larva output for increased detection. Improved and novel detection methods can aid in making informed choices, especially in this era where infectious and non-infectious diseases are commonplace.

Keyword : Strongyloides stercoralis, Molecular detection, Diagnosis, Thailand, Strongyloidiasis

Abstract No. : ABS0001828

INTESTINAL PARASITES IN RURAL COMMUNITIES IN NAN PROVINCE, THAILAND: CHANGES IN BACTERIAL GUT MICROBIOTA ASSOCIATED WITH MINUTE INTESTINAL FLUKE INFECTION

Ajala Prommi

Authors : Ajala Prommi[1] , Kittipong Chaisiri[2]

Affillation : [1]Program in Bioinformatics and Computational Biology, Graduate School, Chulalongkorn University, Bangkok 10330, Thailand; [2]Research Unit of Systems Microbiology, Chulalongkorn University, Bangkok 10330, Thailand; [3]Department of Helminthology, Faculty of Tropical Medicine, Mahidol Bangkok School of Tropical Medicine, Mahidol University Bangkok, Thailand

Gastrointestinal helminth infection likely affects the gut microbiome, in turn affecting host health. To investigate the effect of intestinal parasite status on the gut microbiome, parasitic infection surveys were conducted in communities in Nan Province, Thailand. In total, 1047 participants submitted stool samples for intestinal parasite examination, and 391 parasite-positive cases were identified, equating to an infection prevalence of 37.3%. Intestinal protozoan species were less prevalent (4.6%) than helminth species. The most prevalent parasite was the minute intestinal fluke Haplorchis taichui (35.9%). Amplicon sequencing of 16S rRNA was conducted to investigate the gut microbiome profiles of H. taichui-infected participants compared with those of parasite-free participants. Prevotella copri was the dominant bacterial operational taxonomic unit (OTU) in the study population. The relative abundance of three bacterial taxa, Ruminococcus, Roseburia faecis and Veillonella parvula, was significantly increased in the H. taichui-infected group. Parasite-negative group had higher bacterial diversity (α diversity) than the H. taichui-positive group. In addition, a significant difference in bacterial community composition (β diversity) was found between the two groups. The results suggest that H. taichui infection impacts the gut microbiome profile by reducing bacterial diversity and altering bacterial community structure in the gastrointestinal tract.

Keyword : Gut microbiome; Haplorchis taichui; helminth; minute intestinal fluke; Thailand

Wednesday 7 December 2022

S11 : Therapeutic Antibodies Against Viral Pathogens

15.00-16.30hr

Room A

Abstract No. : ABS0001902

THERAPEUTIC HUMAN MONOCLONAL ANTIBODY AGAINST DENGUE VIRUS; TOWARD COMMERCIALIZATION

Pongrama Ramasoota

Authors : Pitaksajjakul P.[1, 2], Benchathummarak S.[1], Puangmanee W.[1,2], Shioda T.[3], **Ramasoota P.[1, 2]**

Affillation : [1]Center of Excellence for Antibody Research, Faculty of Tropical Medicine, Mahidol University; [2]Department of Social and Environmental Medicine, Faculty of Tropical Medicine, Mahidol University; [3]Research Institute for Microbial Disease (RIMD), Osaka University, Osaka, Japan

Dengue disease caused by the Dengue virus (DENV) has become a world health problem. Each year, 100 million cases require hospitalization. Until present, there is no specific drug for Dengue treatment. Using SPYMEG myeloma cell fused with peripheral blood mononuclear cells obtained from Dengue patients, the hybridoma cell producing neutralizing human monoclonal antibodies (NhuMAbs) anti envelope protein against 4 serotypes of DENV has been established at CEAR. Two candidates NhuMAb (clones 19 and 54) were successfully pre-clinically tested in vitro by 95-100 % neutralized all 4 serotypes of 20 clinical isolates DENV and in vivo tested by significantly decreased mortality of prior DENV intra-cranially mice and eliminated DENV (from 1010 to be 0) in the DENV challenged Marmoset monkeys within 2 days. To make NhuMAb without causing ADE, FC-modified at the LALA position of both NhuMAb clones was established. Industrial scale production of NhuMAbs using the Food and drug administration (FDA) accepted method of Stable expressed Chinese Hamster Ovary (CHO) cells produced at GMP facility was prepared at the licensing company. AG129 mice that 24 hr. prior subcutaneously injected with 105 FFU DENV followed by treated with Fc-modified NhuMAb clone 54 showed almost 100 % survival. The dose-finding was also performed in AG129 mice and it found that the dose for the first in the human trial was 4-6 mg/Kg. The licensing company is ongoing testing this Fc-modified NhuMab clone54 for further PK, PD, and viral clearance in nonhuman primates in 2023, followed by a Phase 1 clinical trial in 2024.

Keyword : Neutralizing, human monoclonal antibodies, Dengue virus, 4 serotypes, envelope protein, Commercialization

Abstract No. : ABS0001901

POTENTIAL DENGUE THERAPEUTIC CANDIDATES BASED ON DENGUE NS1 PROTEIN

Pannamthip Pitaksajjakul

Authors : Rochanawan Sootichote[1], Wilarat Puangmanee[1], Surachet Benjathummarak[2], Pongrama Ramasoota[1,2], **Pannamthip Pitaksajjakul[1,2]**

Affillation : [1]Department of Social and Environmental Medicine, Faculty of Tropical Medicine, Mahidol University, Thailand; [2]Center of Excellence for Antibody Research, Faculty of Tropical Medicine, Mahidol University, Thailand

Introduction: In accordance with no effective therapeutic treatment to flavivirus, dengue virus (DENV) nonstructural protein 1 (NS1) has been considered to develop the vaccine because of no role in antibody-dependent enhancement (ADE). However, both NS1 and its antibody has showed the cross-reactive to host molecules and stimulated anti-DENV NS1 antibody-mediated endothelial damage and platelet dysfunction. For this reason, to apply anti-NS1 antibody as dengue therapeutic candidates, both protective and pathogenic role have to be studied.
Methods: To overcome the pathogenic events and reactogenicity, human monoclonal antibodies (HuMAbs) against DENV NS1 were generated from DENV-infected patients. Dengue neutralization as well as viral replication inhibition were studied. In vitro pathogenic assay to determine its potential roles in inducing or inhibition in cell cytolysis and cell leakage were evaluated.
Results: DENV NS1-specific HuMAbs reveal the therapeutic effects in viral neutralization, reduction of viral replication and enhancement of cell cytolysis of DENV via complement manner. We also demonstrate that DENV NS1 trigger endothelial dysfunction leading to vascular permeability in vitro was impeded by HuMAbs clone M20 and clone 8, and also protect the massive cytokines stimulation (IL-1b, IL-1ra, IL-2, IL-4, IL-5, IL-6, IL-8, IL-9, IL-13, IL-17, Exotoxin, G-CSF, GM-CSF, IP-10, MCP-1, MIP-1α, MIP-1β, TNF-α, PDGF and RANTES).
Conclusion: Collectively, our findings suggest the novel protective NS1 monoclonal antibodies generated from human as therapeutic benefits against DENV infection.

Keyword : Dengue virus, Dengue non-structural protein 1, Human monoclonal antibody, Neutralization, Vascular leakage, Therapeutic antibody

Abstract No. : ABS0001906

GENERATION OF A SINGLE-CHAIN FRAGMENT VARIABLE (scFv) ANTIBODY AGAINST SARS-COV-2 RBD PROTEIN USING CONVALESCENT PATIENTS-DERIVED PHAGE DISPLAY LIBRARIES

Surachet Benjathummarak

Authors : Benjathummarak S.

Affillation : Center of Excellence for Antibody Research (CEAR), Faculty of tropical medicine, Mahidol University

Severe acute respiratory syndrome coronavirus 2 or SARS-CoV-2 is the causative agent of coronavirus disease 2019 (COVID-19), which has become a severe threat to global public health and local economies. Monoclonal antibodies against the spike protein of SARS-CoV-2 have been shown to be effective as prophylaxis and therapy against COVID-19. However, the emergence of variants of concern (VOCs) challenges the efficacy of antibody therapies. The antibody phage display technology is one alternative approach that produces therapeutic antibodies. In this presentation, we aim to describe the generation of human monoclonal antibodies which are specific to RBD of the SARS-CoV-2 by using phage display technology. The single chain variable fragment (scFv) antibody fragments were constructed from the pooled PBMCs of 15 COVID-19 convalescent patients. Antibody genes consisting of variable heavy chains (VH) and light chain (VL) were amplified by PCR with human antibody gene specific primers and prepared for human scFv-phage display libraries. The practical size of the scFv antibody gene library was estimated to be 1.84×107 . Then, four rounds of bio-panning were performed with RBD of the SARS-CoV-2 wild type. Ninety-six colonies were randomly picked for PCR and screened for scFv expressing clone by ELISA. Finally, only eight positives clones were obtained with high reactivity to RBD-WT protein. Further experiments are required, including Neutralization test against SARS-CoV-2, antibody reformatting from scFv to IgG and the neutralizing activity test in vivo. This study will be another one to establish a novel antibody against SARS-CoV-2 by using phage display technology.

Keyword : COVID-19, SARS-CoV-2, RBD protein, scFv, phage display

Abstract No. : ABS0001896

ANTIBODY DEPENDENT ENHANCEMENT (ADE) OF SARS-CoV-2 INFECTION

Atsushi Yamanaka

Authors : Atsushi Yamanaka

Affillation : Research Institute for Microbial Diseases (RIMD), Osaka University

Introduction: Serological survey on human specimens provides valuable biological information about the previous infection history and the current acquired-immune status etc. A part of COVID-19 patients sometimes experiences re-infection and deterioration. Antibody dependent enhancement (ADE), which has been reported from several virus infections such as flavivirus, coronavirus, HIV and Ebola virus, is one of the pathogenic mechanisms relating to the disease severity. Extrinsic ADE mechanism increases uptake of virus into Fc gamma receptor (R)-bearing cells. In the present study, we have established Fc gamma R-expressing VeroE6-TMPRSS2 (FcVero) cells and developed an assay system to detect ADE activity in COVID-19 patient samples.

Methods: A plasmid expressing Fc gamma R was transfected into VeroE6-TMPRSS2 cells, which were selectively incubated in the presence of puromycin and G418. Live SARS-CoV-2 (Wuhan-prototype or European-D614G strain) was inoculated to FcVero cells in the presence of serially-diluted commercial monoclonal antibodies against SARS-CoV-2 or human antibody specimens. Culture supernatants were harvested from the infected FcVero cells, whose infective titers were determined by plaque assay using VeroE6-TMPRSS2.

Results: Monoclonal antibodies showed two-peaks of enhancing activity against both Wuhan and European strains. Human specimens (polyclonal) showed multiple peaks (three or more) of enhancing activity. Antibody dilutions displaying the peaks of enhancing activity were different between Wuhan and European strains. In contrast, no ADE activity was detected on the normal VeroE6-TMPRSS2 cells.

Conclusion: The present study revealed that SARS-CoV-2 might display enhancing activity with multiple-peaks in an Fc gamma R-dependent manner.

Keyword : Antibody dependent enhancement (ADE), Fc gamma receptor, Serology

Wednesday 7 December 2022

S12 : Chikungunya Virus Epidemiology and Vaccine Development

15.00-16.30hr

Room B

Abstract No. : ABS0001784

CHIKUNGUNYA EPIDEMIOLOGY IN SOUTHERN THAILAND

Aaron Farmer

Authors : Kathryn B. Anderson[2], **Aaron Farmer**[1], Darunee Buddhari[1], Thanaporn Hortiwakul[3], Boonsri Charernmak[3], Butsaya Thaisomboonsuk[1], Tippa Wongstitwilairoong[1], Taweewun Hunsawong[1], Chonticha Klungthong[1], Piyawan Chinnawirotpisan[1], Sarunyou Chusri[3] and Stefan Fernandez[1]

Affillation : [1]Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand; [2]SUNY Upstate Medical University, New York, USA; [3]Prince Songkla University, Songkhla, Thailand

Introduction: Chikungunya virus (CHIKV) infections are distributed across the globe, causing significant and, often, lasting morbidity. CHIKV vaccines are in development, but their evaluation is limited by the unpredictability of CHIKV transmission, which classically manifests as explosive epidemics separated by variable interepidemic periods.

Methods: A passive surveillance study for undifferentiated febrile illness was established in Songkla province, southern Thailand, in 2012 and remains ongoing. For this analysis, Individuals of all ages presenting from June 2012 to December 2019 to participating clinical centers with undifferentiated fever or history of fever within 7 days were eligible for enrollment. Those meeting eligibility criteria underwent testing of blood at acute and convalescent timepoints for RT-PCR testing of DENV, CHIKV and ZIKV followed by serological testing for the same pathogens.

Results: From 2012 to 2019, 2127 individuals presented for evaluation. Among 1473 febrile individuals with sufficient volume for acute and convalescent specimens, 391 (26.5%) had molecular or serological evidence of acute CHIKV infection. The proportions of participants confirmed to have CHIKV infection differed by year, being highest during epidemic periods, 39.2% in 2018-2019 (corresponding to a large regional CHIKV outbreak), compared to 18.9% in 2012-2017.

Conclusion: These data indicate possible stable endemicity of CHIKV in the study area, though additional studies are needed to confirm these findings and to discern whether this persistence reflects widespread, low-level transmission or migrating bursts of focal epidemic activity. If confirmed through this and other studies, this could provide a valuable site for future CHIKV research.

Keyword : Chikungunya virus, southern Thailand

Abstract No. : ABS0001840

PHASE 2 STUDY ASSESSING SAFETY AND IMMUNOGENICITY OF A CHIKUNGUNYA VACCINE IN RECIPIENTS OF OTHER ALPHAVIRUS VACCINES VERSUS ALPHAVIRUS NAÏVE CONTROLS

Patrick Ajiboye

Authors : Melinda J. Hamer[1,2,3], Benjamin C. Pierson[4], Jeannine Haller[4], Christine Lee[1], Jack N. Hutter[1], Karen Martins[4], Pamela Glass[4], Dani Liggett[4], Aaron Sanborn[1], James E. Moon[1], Melissa Gregory[4], Crystal Burke[4], Christina Gardner[4], Neha Ghosh[5], Lisa Bedell[5], David Saunders[2,4], Jason Regules[1,4], James M McCarty[6]

Affillation :
[1]Walter Reed Army Institute of Research (WRAIR), Silver Spring, MD; [2]Uniformed Services University (USU) F. Edward Hebert School of Medicine, Bethesda, MD; [3]George Washington University School of Medicine, Washington, DC; [4]United States Army Medical Research Institute of Infectious Diseases (USAMRIID), Fort Detrick, MD; [5]Emergent BioSolutions Inc., Gaithersburg, MD; [6]Stanford University, Stanford, CA

Disclosures: M. Hamer, B. Pierson, J. Haller, C. Lee, J. Hutter, K. Martins, P. Glass, D. Liggett, A. Sanborn, J. Moon, M. Gregory, C. Burke, C. Gardner, D. Saunders, J. Regules: none.
N. Ghosh, L. Bedell: Salary; Emergent BioSolutions, Inc.; J.M. McCarty: Consultant; Emergent BioSolutions, Inc

Immune responses to alphavirus vaccines may be impaired when heterologous alphavirus vaccines are administered sequentially. This Phase 2 open-label study evaluated the safety and immunogenicity of CHIKV VLP vaccine in prior recipients of heterologous alphavirus vaccines.

Adults 18-65 years with prior receipt of an investigational alphavirus vaccine (N=30) and gender/age matched alphavirus vaccine-naïve controls (N=30) were administered 1 dose of 40 μg alum-adjuvanted CHIKV VLP vaccine. The primary immunogenicity endpoint was the CHIKV SNA seroconversion rate (defined as 4-fold rise over baseline) at Day 22. Immunogenicity was assessed by luciferase-based serum neutralizing antibodies (SNA) and safety was assessed by solicited/unsolicited adverse events (AE) and serious adverse events (SAE).

The majority of solicited AEs were of mild/moderate severity. Two alphavirus vaccine-naïve subjects experienced grade 3 solicited events (2/30). The most common systemic solicited AEs were headache, occurring in 7/30 and 4/30 subjects, and myalgia occurring in 4/30 and 7/30 subjects in the prior alphavirus vaccine and alphavirus vaccine-naïve groups, respectively. Injection site pain was reported by 13/30 prior alphavirus vaccine recipients and by 9/30 subjects in the alphavirus vaccine-naïve group. There were no vaccine-related SAEs. The anti-CHIKV SNA seroconversion rate at Day 22 was 100% in both groups. The GMTs peaked in both groups at Day 22.

This alum-adjuvanted CHIKV VLP vaccine was well tolerated and immunogenic in both alphavirus vaccine-naïve and prior recipients of a heterologous alphavirus vaccine; there was no significant difference in the incidence of AEs between the groups.

Keyword : Disclaimer: Material has been reviewed by the Walter Reed Army Institute of Research. There is no objection to its presentation and/or publication. The opinions or assertions contained herein are the private views of the author, and are not to be construed as official, or as reflecting true views of the Department of the Army or the Department of Defense. The investigators have adhered to the policies for protection of human subjects as prescribed in AR 70–25.

Abstract No. : ABS0001802

ADVANCES IN THE DEVELOPMENT OF A SINGLE-SHOT LIVE-ATTENUATED CHIKUNGUNYA VACCINE CANDIDATE

Vera Buerger

Authors : V. Buerger, M. Schneider, S. Hadl, M. Narciso, R. McMahon, S. Toepfer, U. Fuchs, R. Hochreiter, A. Bitzer, K. Kosulin, R. Mader, O. Zoihsl, K. Dubischar, N. Wressnigg, S. Eder-Lingelbach, J.C. Jaramillo

Affillation : Valneva Austria GmbH, Vienna, Austria

Introduction: VLA1553 is a live-attenuated chikungunya virus (CHIKV) vaccine candidate designed for active immunization as a prophylactic measure. Due to the sporadic epidemic occurrence of chikungunya, an immunological surrogate to assess clinical efficacy was accepted by regulators.

Methods: A double-blinded, multicenter, pivotal phase 3 study enrolling 4115 healthy adult volunteers, aged ≥18 years, randomized in a 3:1 ratio to receive VLA1553 or placebo was performed across 43 study sites in the United States (NCT04546724). The primary objective of the study was to evaluate immunogenicity and safety of VLA1553 28 days after immunization and as secondary objective participants were followed up to 180 days. Immunogenicity evaluations were analyzed in a pre-selected subset of 501 participants at 13 study sites.

Results: The pivotal trial met its primary endpoint with 98.9% of subjects achieving seroprotection (263 of 266 participants in the per-protocol immunogenicity subgroup). The immunogenicity profile was maintained over time. Geometric mean titers peaked at day 29, then decreased subsequently, however stayed well above the seroprotective level of antibodies in 96.3% of participants until day 180 (233 of 242 participants in the per-protocol subset tested for immunogenicity). The vaccine was also confirmed to be highly immunogenic in older adults (≥65 years), who achieved equally high seroprotection rates and neutralizing antibody titers as younger adults (<65 years). VLA1553 was also well tolerated with a favourable safety profile.

Conclusion: The generation of protective titers in nearly 100% of vaccinated participants analyzed indicates VLA1553 is an effective candidate for the prevention of disease caused by the CHIKV.

Keyword : Viruses (includes Alphaviruses, Flaviviruses, Other), Chikungunya, Phase 3, Clinical

Wednesday 7 December 2022

S13 : Tropical Medicine Tournament

15.00-16.30hr

Room C

S13 : Tropical Medicine Tournament

Moderators :

1. **Jittima Dhitavat**
   Faculty of Tropical Medicine, Mahidol University

2. **Athit Phetrak**
   Faculty of Tropical Medicine, Mahidol University

3. **Supachai Topanurak**
   Faculty of Tropical Medicine, Mahidol University

4. **Wirongrong Chierakul**
   Faculty of Tropical Medicine, Mahidol University

No abstract available

Keyword : No keyword available

Wednesday 7 December 2022

S14 : Host Genetics in Falciparum Malaria

15.00-16.30hr

Room D

Abstract No. : ABS0001789

HBS ALLELE FREQUENCIES IN AFRICA REVEAL MALARIA ATTRIBUTABLE CHILDHOOD MORTALITY IN THE PRE-TREATMENT AREA

Arjen Dondorp

Authors : Arjen M. Dondorp[1]

Affillation : [1]Mahidol Oxford Tropical Research Unit, Bangkok, Thailand.

Falciparum malaria has been a scourge for humanity since antiquity. This deadly disease has shaped the human genome, selecting for gene mutations protective against severe malaria. The most prominent example is the sickle cell (HbS) allele, for which the malaria-protective effect of sickle-cell trait versus the high mortality of sickle cell disease have driven balancing selection, resulting in hemoglobin S equilibrium allele frequencies of between 15% and 20% in areas of high Plasmodium falciparum transmission in sub-Saharan Africa. From this we estimate that the malaria-attributable childhood mortality in the pretreatment era was between 15% and 24%.

Keyword : Falciparum malaria

Abstract No. : ABS0001913

SAFETY OF SIGLE LOW DOSE RPIMAQUINE IN AFRICAN CHILDREN WITH FALCIPARUM MALARIA

Bob Taylor

Authors : Taylor W.R.[1,2], Olupot-Olupot P.[3,4], Onyamboko M.A.[5], Peerawaranun P.[1], Were W.[3], Namayanja C.[3], Onyas P.[3], Titin H.[3], Baseke J.[4], Muhindo R.[3], Kayembe D.[5], Ndjowo P.O.[5], Basara B.B.[5], Bongo G.S.[5], Okalebo C.B.[3], Abongo G.[3], Uyoga S.[6], Williams T.N.[6,7], Taya C.[1], Dhorda M.[1,2], Tarning J.[1,2], Dondorp A.M.[1,2], Waithira N.[1,2], Fanello C.[1,2], Maitland K.[6,7], Mukaka M.[1,2], Day N.J.[1,2]

Affillation : [1]Mahidol Oxford Tropical Medicine Clinical Research unit, Mahidol University, Bangkok, Thailand; [2]Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, United Kingdom; [3]Mbale Clinical Research Institute, P.O. Box 1966, Mbale, Uganda; [4]Busitema University, P.O. Box 1460, Mbale, Uganda; [5]Kinshasa School of Public Health, University of Kinshasa, Democratic Republic of Congo; [6]KEMRI-Wellcome Trust Research Programme, Kilifi, Kenya; [7]Institute of Global Health Innovation, Imperial College London, London, UK

Introduction: The WHO recommends single low-dose primaquine (SLDPQ) for blocking the transmission of Plasmodium falciparum; however, concerns over its toxicity have hampered its deployment in sub-Saharan Africa.
Methods: We conducted this randomised, double-blind, placebo-controlled, non-inferiority trial in Ugandan and Congolese children aged 6m-11y with acute uncomplicated P falciparum infection and haemoglobin ≥6 g/dL. G6PD status was defined by genotyping the G6PD c.202T allele (A− variant).
Participants were randomly assigned (1:1) to SLDPQ combined with artemether lumefantrine or dihydroartemisinin piperaquine. Primary endpoint was the development of profound (haemoglobin <4 g/dL) or severe (haemoglobin <5 g/dL) anaemia with severity features, within 21 days of treatment. The sample size assumed an incidence of 1·5% in the placebo group and a 3% non-inferiority margin.
Results: Of 4620 patients assessed, 3483 were excluded (2982 were malaria negative). 1137 children, median age 5y, received: 286 AL+SLDPQ, 286 AL+placebo, 283 DHAPP+SLDPQ, and 282 to DHAPP+placebo. Genotyping identified 239 G6PD deficient (d) males and 45 homozygous females (G6PD-deficient group), 119 heterozygous females, 418 normal males and 299 normal females; 17 were of unknown status.
Only three developed severe anaemia: G6PDd-group: 0/133 (placebo) vs. 1/151 (0·66%) ∆= −0·66% (95% CI −1·96 to 0·63; p=0·35); nonG6PDd-group: 1/430 (0·23%, placebo) vs. 1/407 (0·25%) ∆= −0·014% (−0·68 to 0·65; p=0·97). There were 11 transfusions: 2 G6PDd on placebo, 2 G6PDd on SLDPQ.
Conclusion: Gametocytocidal, age-dosed, single low-dose primaquine was well tolerated with a similar safety profile as placebo. These data support the wider implementation of SLDPQ in Africa.

Keyword : Malaria, primaquine, transmission blocking, G6PD deficiency

Abstract No. : ABS0001751

G6PD DEFICIENT RED CELLS AND ASEXUAL BLOOD STAGE DEVELOPMENT OF P. FALCIPARUM

Tianrat Piteekan

Authors : Tianrat Piteekan[1], Amornrat Promsongsil[1], Nicholas PJ Day[1,2], Sasithon Pukrittayakamee[1,3], Arjen M. Dondorp[1,3], Nicholas. J. White[1,2], Kesinee Chotivanich[1,3]

Affillation : [1]Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand, 10400; [2]Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, United Kingdom; [3]Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand, 10400.

Plasmodium falciparum is an intraerythrocytic parasite. Red blood cell (RBC) hemoglobin is the main nutrition source of erythrocytic stage Plasmodium falciparum. Hemoglobinopathy causes parasite growth retardation. This study presented the invasion and growth dynamics of P. falciparum in G6PD deficient RBCs. P. falciparum (TM267) culture was enriched with 60% Percoll in order to get a high synchronized schizont stage, then co-cultured with G6PD deficient-RBCs variants including Canton, Viangchan, and Mahidol. The final parasitemia was 0.5-1% schizont-infected RBCs. Parasite invasion rate was assessed by thin blood film examination and calculated the ratio of parasitemia post-invasion (Day-1) and pre-invasion (Day-0). The median (IQR) invasion rate in G6PD deficient-RBCs was (2.10 (2.00-2.50), compared to in normal RBCs (4.33 (4.00-6.00) (n=9; P= 0.001). The mean (SD) number of merozoites per schizont of G6PD deficient RBCs (13 (1.79)) was significantly lower than those of normal RBCs (14 (1.71), P P. falciparum-infected G6PD deficient RBCs to artesunate and quinine is presented as the 50%-inhibition concentration (IC50). The mean (SD) IC50 of artesunate for G6PD-deficient RBCs and normal RBCs was 1.92 (0.58) and 1.73 (0.62), respectively (P=0.51). The mean (SD) IC50 of quinine for G6PD deficient-RBCs and normal RBCs was 57.63 (27.78) and 68.33 (31.61), respectively (P=0.46). The invasion rate of P. falciparum to the G6PD deficient RBCs was significantly decreased. and that parasite growth was retarded. The susceptibility to artesunate and quinine of P. falciparum-infected G6PD deficient RBCs was not significantly different from P. falciparum-infected the normal RBCs.

Keyword : Plasmodium falciparum, Malaria, glucose-6-phosphate dehydrogenase (G6PD) deficiency

Wednesday 7 December 2022

S15 : Free Paper II: COVID-19: Impact on Other Diseases and Management Policy

15.00-16.30hr

Room E

Abstract No. : ABS0001647

DEFINING THE SOCIAL DETERMINANTS OF ANTIMICROBIAL CONSUMPTION DURING COVID-19: A REVIEW

Mutiara Shinta Noviar Unicha

Authors : Mutiara S.N. Unicha[1], Intan P. Yuliyani[2], Dwi Murdiati[3], Grace FPH Mahu[4], Intan W. Tukiyo[5]

Affillation : [1,4,5]Tropical Medicine, Faculty of Medicine, Public Health, and Nursing, Gadjah Mada University, Yogyakarta, Indonesia; [2]Clinical Pathology, Faculty of Medicine, Public Health, and Nursing, Gadjah Mada University, Yogyakarta, Indonesia; [3]Faculty of Law, Jakarta University, Jakarta, Indonesia

Background: COVID-19 potentially increases antimicrobial resistance by influencing people to consume unnecessary antimicrobials regardless of the clinical justification of severity of illness, particularly home-based COVID-19 patients.
Objective: This review aims to identify the social determinant reasoning associated with COVID-19 which impacted antimicrobial consumption in the community.
Methods: PRISMA flow diagram guidelines for scoping review compiled for this study. The studies from the COVID-19 pandemic timeline from 2020 to 2022 were considered from electronic databases in EBSCO Host, Science Direct, Sage Journals, Scopus, and ProQuest. The CASP checklists were used for the quality appraisal.
Results: The search process found a total of 2.297 relevant studies including 8 potential studies which meet the inclusion criteria from the selection process. Antimicrobial consumption in the community was driven by the requirement of standard healthcare for COVID-19, disruptions of essential healthcare services, inappropriate prescribing, increased unregulated antibiotic use, informal sources of health advice, overcome anxiety, stigmatization of isolation procedures, low-cost medication perception, exaggerated assumption of antimicrobial use which triggered to self-medication, and educational background. Instead, the role of social information is known to impact the behavioral motivation to reduce antibiotic overuse or potentially misleading at the same time.
Conclusions: The social determinants played a critical role in antimicrobial utilization during COVID-19 which drives the community to overuse or reduce consumption. In line, the social community–based approaches were recommended to solve and evaluate the effect of those determinants on the paradigm of antimicrobial consumption as one of the public health challenges.

Keyword : Antimicrobial consumption, Antimicrobial resistance, COVID-19, Public health, Social determinant.

Abstract No. : ABS0001812

THE IMPACT OF COVID-19 PANDEMIC ON DIRECTLY OBSERVED TREATMENT SHORT COURSES(DOTS) PROGRAM FOR TUBERCULOSIS IN NEPAL

Ruby Maka Shrestha

Authors : Ruby Maka Shrestha[1], Biraj Karmacharya[2], Ranju Kharel[2], Sanjeeta Sitaula[3], Anadi KC[3], Virendra Salhotra[4], Vithal Prasad Myneedu[4], Prajwal Pyakurel[4]

Affillation : Dhulikhel Hospital Kathmandu University Hospital[1,2], Institution of Medicine, Nepal[2,3], Birat Eye Hospital[3], SAARC TB and HIV/AIDS Center[4]

Background: Tuberculosis remains a major public health program in Nepal and requires surveillance, clinical assessment, confirmation of diagnosis and supervised treatment regimens for effective management. The COVID-19 pandemic has led to change in prioritization, affecting the functioning of tuberculosis control programs.
Objective: The study aimed to assess the challenges due to COVID- 19 pandemic mainly on national DOTS (Directly Observed Treatment Short-Course) program from health provider's perspectives.
Methods: Semi-structure qualitative interviews were conducted with the health providers to understand the facilitators and barriers of the DOTS program during COVID-19 pandemic. Total 35 interviews were conducted at DOTS centers. Similarly, at local level we interviewed health coordinators from corresponding municipalities (n=21) and TB focal officers from corresponding district (n=37). At provincial level, provincial TB focal officers were interviewed (n=6), whereas at the federal level, two interviews were conducted (n=2) with TB focal chiefs at the Ministry of Health and Population. A thematic analysis approach was used for data analysis utilizing inductive and deductive coding.
Results: Health providers admitted of constant fear, insufficient time for preparation, confusion and insufficient coordination within three tier of health system. Although, majority of the DOTS centers reported to have managed to provide timely TB medicine to the TB patients, occasionally, lab services were interrupted due to transfer of laboratory staff for the COVID duty.
Conclusion: Clinical care for diseases like tuberculosis, that require daily care are impacted hard by scenarios like COVID-19. The preparedness for such circumstances needs to be done in future.

Keyword : Directly Observed Treatment Short course, Tuberculosis, Covid-19, Compliance, Adherence, Anti-tuberculosis treatment, Impact, Effect, Nepal, Low- and Middle-income countries

Abstract No. : ABS0001674

GLOBAL RESEARCH AGENDA ON PUBLIC HEALTH AND SOCIAL MEASURES: WHO'S EFFORTS IN SCIENCE AND HEALTH DIPLOMACY FOR HEALTH EMERGENCIES

Ryoko Takahashi

Authors : Takahashi R.[1], Ludolph R.[1], Nguyen T.[1]

Affillation : [1]World Health Organization

Introduction: The COVID-19 pandemic changed how we respond to a health emergency and protect communities. Public health and social measures (PHSM) such as physical distancing, mask wearing and ventilation have proven critical throughout the pandemic to reduce transmission-relevant contacts and/or make them safer, especially when vaccines and therapeutics are not yet available; vaccine availability and vaccination coverage are limited, and variants of concerns shed uncertainties in the effectiveness of vaccines. However, robust evidence on PHSM effectiveness and health, social and economic impact on communities and societies is limited. Hence, WHO is developing a global PHSM research agenda 2021-2030.

Methods: Towards multidisciplinary, multisectoral, context-specific and comparable research on PHSM, the global research agenda is being developed through a multi-stage survey and consultation process with a wide range of stakeholders and sectors to reflect global diversity.

Results: Urgent research priorities to guide the ongoing and emerging research on PHSM during the COVID-19 pandemic will be established in 2022, which will be followed by the expansion of research priorities to other respiratory pathogens beyond COVID-19 that are pertinent to strengthening research methods, measurements and implementation to prepare for the future pandemics. This research will be indispensable to support health and non-health decision-makers to make PHSM decisions that are based on evidence and relevant to their context.

Conclusion: WHO calls for collaborations across disciplines and sectors on a global PHSM research agenda 2021-2030 to increase science and health diplomacy and strengthen how PHSM ensure community protection as part of the global architecture for

Keyword : non-pharmaceutical intervention, public health and social measures, viral diseases, health emergency, preparedness, response, resilience

Abstract No. : ABS0001721

DEVELOPMENT OF A MODEL ONE-STOP APPROACH TO POST-COVID 19 AND OTHER REHABILITATION CONDITIONS IN NEPAL

Puspanjali Adhikari

Authors : Adhikari P.[1], Shakya R.[2], Vaidya N.[2], Acharya R.[2], Byanju I.[1], Hada M.[1]

Affillation : [1]Dhulikhel Hospital Kathmandu University Hospital; [2]Kathmandu University School of Medical Sciences

People who have been ill with COVID-19 can experience persistent symptoms. WHO has recognized the seriousness of “the Post-COVID-19 condition” calling for more research and rehabilitation with “3Rs”—recognition, research, and rehabilitation. Recognition of the Post COVID-19 condition has increased, but not enough research is being carried out. Dhulikhel Hospital Kathmandu University Hospital (DHKUH) with the technical support from The World Health Organization initiated a APW entitled “Development of a Model One Stop Approach to Post COVID 19 and other Rehabilitation Conditions” for the period of September 1st2021 to December 31st 2022. The Objective of the study was to ascertain case load of Post COVID 19 conditions and develop a multidisciplinary line of care for COVID 19 care pathway. Methods: Post COVID cases were contacted through phone calls and a questionnaire on Post COVID condition was administered. Results: Out of 555 respondents 51.7% were male and 48.3% female. Post COVID conditions were reported as (26.9%: cardiac problems,20.9%: respiratory problems,17.2 %: musculoskeletal problems,15.4%: neurological or vascular,5.4%: psychological health problems,15.9%: irregularities in digestive system,18. 3.4%: dermatological health issues and 1.2 %: of the women had menstrual irregularities). Following the development of post COVID rehabilitation training package and training health workforce at all levels of hospital, DHKUH established a model of pulmonary rehabilitation set-up to cater to the identified post COVID 19 needs of the patients. Conclusion: It is imperative and crucial to establish a set up to manage and rehabilitate the post COVID cases in every levels (primary, secondary, tertiary) of hospitals.

Keyword : POST-COVID CONDITIONS, POST-COVID

Thursday 8 December 2022

Plenary Session (with morning coffee)

08.00-09.00hr

Room A

Abstract No. : ABS0001918

IMPACT, LEGACY AND LESSONS FROM THE RECOVERY TRIAL

Sir Peter Horby

Authors : Sir Peter Horby

Affillation : Pandemic Sciences Institute, Nuffield Department of Medicine, University of Oxford, United Kingdom.

The RECOVERY trial is the world's largest clinical trial into treatments for COVID-19, with more than 48,000 participants across 200 trial sites. The trial was up and enrolling patients in the United Kingdom within six weeks of funding and found one of the world's first COVID-19 treatments, dexamethasone, in June 2020. The trial expanded internationally in 2021 and is now open in Indonesia, Vietnam Nepal, India, South Africa, The Gambia and Ghana. The RECOVERY trial has so far completed evaluation of 11 drugs and continues to assess five others. Professor Sir Peter Horby will reflect on the journey of RECOVERY so far: the lessons learnt, the legacy, and what might be done to improve the efficiency, cost, and impact of randomised controlled trials.

Keyword : infectious diseases randomised controlled clinical trial covid-19

Thursday 8 December 2022

S16 : Updates on New Vaccines : Tuberculosis, mRNA Influenza and HIV Vaccines

09.00-10.30hr

Room A

Abstract No. : ABS0001894

NEW TB VACCINES - SUCCESSES AND CHALLENGES

Anh Wartel

Authors : T. Anh Wartel

Affillation : International Vaccine Institute

The presentation will include a review of the TB global burden that appears to be worsened by the COVID-19 pandemic and the progress of knowledge on the TB pathogenesis that may explain the failure to control the incidence of disease in endemic countries. There is a critical need to understand the roles and involvement of multiple cell types, their differential gene expression, and cytokines in TB infection that may impact the TB vaccine development space. The development of a genetic system in mycobacteria has enabled new molecular diagnostics, chemotherapeutic approaches, and recombinant vaccine candidates, but there are remarkably few clinical trials of new vaccine candidates against TB. However, several promising vaccine candidates' results emphasize the importance of adjuvants in inducing protection from TB infection. Thus, some biomarkers of protection against TB may help shed the light so that more vaccine candidates and smaller clinical trials can be designed. An update on New TB vaccines will be part of the presentation.

Keyword : Vaccines, TB, clinical trials

Abstract No. : ABS0001856

MODERNA INFLUENZA VACCINE PROGRAM

Jintanat Ananworanich

Authors : Ananworanich J.

Affillation : Moderna, Inc., Cambridge, MA, USA

Influenza is associated with substantial disease burden worldwide, continuously circulating and causing seasonal epidemics of variable severity. Vaccines for prevention of influenza using traditional technology are available but often provide limited efficacy; messenger RNA (mRNA) technology has the potential to address the current limitations of traditional platforms by offering more expeditious and flexible vaccine development.
Moderna is pursuing development of several seasonal influenza vaccine candidates. The lead candidate mRNA-1010 is an investigational mRNA-based quadrivalent seasonal influenza vaccine that encodes the hemagglutinin surface glycoproteins of the strains recommended by the World Health Organization: A/H1N1, A/H3N2, B/Victoria, and B/Yamagata. Other vaccines include additional hemaglutinin antigens to expand immunologic coverage or additional neuraminidase antigens to improve immunologic breadth. This presentation will give an overview of the Moderna influenza vaccine portfolio.

Keyword : Influenza, influenza vaccine, mRNA vaccine, Moderna

UPDATE AND CHALLENGES OF NEW GENERATION VACCINES

Punnee Pitisuttithum

Authors : Punnee Pitisuttithum

Affillation : Faculty of Tropical Medicine, Mahidol University

No abstract available

Keyword : No keyword available

Thursday 8 December 2022

S17 : Meet the Experts (Bioethics)

09.00-10.30hr

Room B

S17 : Meet the Experts (Bioethics)

Panelists :

1. Jaranit Kaewkungwal
Faculty of Tropical Medicine, Mahidol University

2. Christine Grady
Department of Bioethics, NIH Clinical Center

3. Reidar Lie
University of Bergen

4. David Wendler
Department of Bioethics, NIH Clinical Center

5. Holly Taylor
Department of Bioethics, NIH Clinical Center

6. Zhai Xiaomei
Center for Bioethics, Chinese Academy of Medical Sciences

7. Calvin Ho
The University of Hong Kong

8. Kenji Matsui
Division of Bioethics and Healthcare Law, National Cancer Center Japan

No abstract available

Keyword : No keyword available

Thursday 8 December 2022

S18 : Infection Prevention and Control [MOPH]

09.00-10.30hr

Room C

Abstract No. : ABS0001830

HOT TOPIC IN INFECTION CONTROL 2022

Darunee Chotiprasitsakul

Authors : Chotiprasitsakul D.

Affillation : Faculty of Medicine Ramathibodi Hospital, Mahidol University

COVID-19 transmission is complex. Classification as airborne or droplet transmission on the basis of the size of particles is insufficient. Multiple factors influence the risk of transmission including viral load in sources, initial droplet size, humidity, ventilation, exposure time, and activities generating aerosols. Surgical masks and filters effectively reduce particles containing viruses. Key determinants of suitable personal protective equipment (PPE) when caring for patients with suspected/confirmed COVID-19 are resources and time of exposure. No one intervention is effective. Layers of multiple interventions are required to control the spreading.

Keyword : COVID-19, transmission, airborne, droplet, personal protective equipment

Abstract No. : ABS0001826

COVID-19 PANDEMIC IMPACT ON ANTIMICROBIAL RESISTANCE

Lantharita Charoenpong

Authors : Lantharita Charoenpong

Affillation : Bamrasnaradura Infectious Diseases Institute, Department of Disease Control, Ministry of Public Health, Nonthaburi, Thailand

The COVID-19 pandemic still has a devastating personal, societal, and economic impact. Up to one-fourth of COVID-19 patients require intensive care unit (ICU) admission, primarily due to severe pneumonia and acute respiratory distress syndrome. Pneumonia from SARS-CoV-2 is difficult to distinguish from other viral and bacterial etiologies. Broad spectrum antimicrobials are frequently prescribed to patients hospitalized with COVID-19 which potentially acts as a catalyst for developing antimicrobial resistance (AMR). Patients with COVID-19 may acquire secondary co-infections which require antimicrobial treatment. Multiple courses of broad-spectrum antibiotics, having mechanical ventilation, receiving invasive devices and organ support increase the risk of hospital-associated infection (HAI), often highly resistant organisms such as Pseudomonas aeruginosa, Acinetobacter baumannii, methicillin-resistant Staphylococcus aureus, Candida auris. COVID-19 also have affected antimicrobial stewardship activities. The pandemic has placed enormous pressure on healthcare systems and diverted resources, personnel, and attention from the diagnosis and management of antimicrobial resistance to COVID-19 diagnosis and contact tracking and tracing.

Keyword : COVID-19 pandemic, antimicrobial resistance

Abstract No. : ABS0001825

WHAT’S NEW IN COVID-19: INFECTION CONTROL PERSPECTIVE

Visal Moolasart

Authors : Visal Moolasart

Affillation : Bamrasnaradura Infectious Diseases Institute, Ministry of Public Health, Tiwanon Road, Nonthaburi, 11000, Thailand. Tel: +66 (0) 2590 3408; Fax: +66 (0) 2590 3411

The COVID-19 pandemic has led to the significant loss of human life worldwide and presents a threatening challenge to public health, logistics, food systems, and work. On the other hand, hospitals received many things for infection control, such as technology, new equipment, more infection prevention control (IPC) staff, planning, and new cooperation between countries. At present, there is just-in-time adoption of technology; new equipment qualifies smooth and efficient processes for management and treatment. Open and ready for innovation are important issues. For example, robots, outdoor swab rooms, modular screening units and modular swab units, mobile negative pressure isolation rooms, and negative/positive pressure isolation chambers.

Lessen learn from COVID-19 in children and adult. In infection control perspective. We have the new issue in COVID-19: infection control perspective. Current guidelines or information in infection control perspectives worldwide strive for optimal and feasible rather than maximal precautions.

The previous study demonstrated that humans can be infected more than once. There have been several cases of reinfection over the past few months. Although the numbers are small compared to those who are infected, it is possible that additional cases of reinfection are not being counted. Finally, the COVID-19 vaccine is the best strategy for infection control of disease.

Keyword : COVID-19, Infection Control Perspective, Vaccine

Abstract No. : ABS0001860

WHAT'S NEW IN COVID-19: INFECTION CONTROL PERSPECTIVE

Chaisiri Srijareonvijit

Authors : Chaisiri Srijareonvijit

Affillation : Bamrasnaradura Infectious Diseases Institute, Department of Disease Control, Ministry of Public Health, Thailand.

Technology in healthcare has been utilized to assist with daily clinical practices and clinical processes, allowing hospitals to develop efficient clinical workflows and facilitate decision-making. The COVID-19 pandemic has accelerated the technological advancements and innovations in infection prevention and control (IPC) practices over the past two years.

SARS-CoV-2 transmission in healthcare settings has been associated to limited isolation capacity, suboptimal IPC practices, physical distancing absenteeism, environmental ventilation, and infected fomites. The following are the implications of IPC technologies in the prevention and control of COVID-19 in healthcare facilities: 1) Ensure triage, early recognition, and source management by analyzing big data for prediction, autoclassification, autofeedback, early detection, and decision support with artificial intelligence and machine learning in order to prevention and control hospital-onset COVID-19. 2) Administrative control interventions that directly interfere with COVID-19 transmission, such as robots, smart personal protective equipment, telehealth and telemedicine, the internet of medical things (IoMT), and wireless sensors. 3) Engineering control interventions, specifically the airborne infection isolation room. 4) Environmental control interventions consisting of ultraviolet C light technology, hydrogen peroxide misting devices, and continuously active disinfection chemicals. 5) Digital health technology and electronic medical record for COVID-19 IPC by combining decision-support tools and predictive modeling through machine learning. 6) IPC education, E-learning, and simulations.

In conclusion, innovative technologies in COVID-19 IPC enhance patient and healthcare worker safety, healthcare system quality, and medical expenses. Future research should investigate, test, and validate the integration of IPC technologies into standard clinical practice, with a particular emphasis on patient-centered outcomes.

Keyword : COVID-19, infection prevention and control, IPC, technology, innovation

PREVENTION OF EID FROM ABROAD: PUBLIC HEALTH AND HOSPITAL MANAGEMENT

Jurai Wongsawat

Authors : Jurai Wongsawat

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

No abstract available

Keyword : No keyword available

ABSTRACT NO. : ABS0001908

PREVENTION OF EMERGING INFECTIOUS DISEASES FROM ABROAD; PUBLIC HEALTH RESPONSE IN THAILAND

Rome Buathong

Authors : Buathong R.

Affillation : Department Of Disease Control, Ministry Of Public Health

Background: The prevention of introduction of emerging infectious disease (EID) into the country is a vital gold for health security in all countries. The surveillance system included proper response for EID is well established in Thailand.
Methods: Thailand has the surveillance system for early case detections in 3 different layers. The first layer is point of entry (POE) surveillance and screening of ill passengers and vehicles. The second layer is hospital detection. This layer is well established by the standard case definition and protocol in both known pathogen and disease X. The third layer is community detection by the event-base surveillance system.
Results: In the past 10 years, Thailand detected EIDs including Severe EV71 in 2008, Zika virus in 2013, MERS cases in 2015, and Severe Fever Thrombocytopenia Syndrome in 2018. The detection of EID in the country was relied on the surveillance system in the hospital and event-base surveillance. The POE is less capability to detect the EID. Until SARS-COV-2 was existing in early 2020 in China. The POE screening was revised by individually two step temperature screening and carefully physical examination. The changing in protocol resulted to successfully identify the confirmed first case of SARS-COV-2 infection among travelers outside China at airport. Furthermore, other airports were also capable to detection the confirmed case of SARS-COV-2 in early 2020.
Conclusions: The strong 3 different layers of early detection for EID from abroad play a major role for success the early containment in Thailand. POE surveillance and response is increasing role.

Keyword : Emerging Infectious Disease, Prevention, International Spreading

Thursday 8 December 2022

S19 : Free Paper III: Vector Biology and Vector Control

09.00-10.30hr

Room D

Abstract No. : ABS0001729

REPRODUCTIVE CONTROL OF MOSQUITOES: CHALLENGES AND OPPORTUNITIES

Laura Harrington

Authors : Laura Harrington

Affillation : Cornell University, Ithaca, NY USA

Mosquito control strategies which rely on manipulating or exploiting mating are rapidly becoming a key tool in the management of mosquito populations. Successful control approaches will need to rely on understanding male and female pre- and post- copulatory behavior, mate choice and reproductive physiology in the context of trait variation under sexual selection. Employing an array of new and existing behavior, acoustic, molecular and biochemical methods, we investigated post mating responses, acoustic behavior and sperm biology of the arbovirus vector Aedes aegypti. Our results highlight the complexity of mosquito mating systems as well as potential for variation under natural conditions. Factors that may influence female behavioral resistance in reproductive control programs will be presented.

Keyword : mosquito mating, Aedes aegypti, control, behavior, acoustics

Abstract No. : ABS0001732

LARVICIDAL POTENTIAL OF SILVER NANOPARTICLES SYNTHESIZED FROM SOLANUM XANTHOCARPUM LEAF EXTRACTS: ECO-FRIENDLY TOOLS FOR CONTROLLING MOSQUITO VECTORS

Kumar Vikram

Authors : Kumar Vikram[1], Pawan Kumar[2], Dinesh Kumar[2], RPS Chauhan[3], Himmat Singh[2]

Affillation : [1]Indian Council of Medical Research, Ansari Nagar, New Delhi-110029, India; [2] ICMR-National Institute of Malaria Research, Dwarka, New Delhi-110077, India; [3] Department of Biochemistry, Magadh University, Bodh Gaya Bihar -824234, India

Introduction: Worldwide, vector-borne diseases like dengue, malaria, filariasis and yellow fever transmitted by mosquitoes are of public health importance. Vector control methods employing synthetic insecticides have developed resistance in mosquitoes and adverse effects on environment and non-target organisms including humans. Nano-based botanical insecticides can be considered as the promising alternative due to several advantages like simple, nontoxic, biodegradable and safe to environment. The present study reported the larvicidal potential of AgNPs derived from Solanum xanthocarpum leaf extract against the third instar larvae of Anopheles stephensi, Aedes aegypti, and Culex quinquefasciatus.

Methods: The synthesis of AgNPs was done by adding leaf extract into silver nitrate solution. The characterization of AgNPs was done by UV-Vis, SEM, TEM, XRD, DLS and SAED. FT-IR analysis was done to support the biosynthesis of silver nanoparticles. Larvicidal activity of AgNPs was investigated against An. stephensi, Ae. aegypti, and Cx. quinquefasciatus according to WHO standard protocol and toxicity was also evaluated against Poecilia reticulate.

Results: Colour change indicated AgNPs synthesis which was further confirmed by a strong surface plasmon resonance. AgNPs were very effective against An.stephensi, Ae. aegypti, and Cx. quinquefasciatus with LC50 and LC90 values of 1.90, 2.36, 2.93, 3.82, 4.31 and 7.63ppm, respectively as compared to aqueous leaf extract after 72h of exposure and were non-toxic against non-targeted organism P. reticulata.

Conclusion: These results suggest that fabricated AgNPs from leaves extract have high larvicidal potential and can be promising eco-friendly tools for controlling mosquito vectors.

Keyword : Vector-borne Diseases, Vector Control, Silver Nanoparticles, Larvicidal Potential

Abstract No. : ABS0001800

DEVELOPMENT AND ASSESSMENT OF A NOVEL COMMUNITY E-LEARNING PLATFORM FOR AEDES-BORNE DISEASES

Rattanaporn Boonmeepom

Authors : Boonmeepom R.[1], Kumlert R.[1], Poungsombut S.[1], Wiroj L[1], Plibai T.[1], Meetham P.[1], Wongpraserta P.[1]

Affillation : [1]Division of Vector Borne Disease, Department of Disease Control, Ministry of Public Health, Thailand

Introduction: In the post-COVID-19 pandemic era of 2022, Thailand faces an increasing trend of Aedes-borne diseases, including dengue hemorrhagic fever, Zika, and Chikungunya. Community health literacy becomes a crucial aspect in reducing the transmission, morbidity, and mortality of these infections. Therefore, the Department of Disease Control (DDC) felt the need to improve the strategies during this crisis, especially risk communication. In this study, we aimed to develop an online course on Aedes-borne disease. This e-Learning platform aimed to raise awareness on the diseases, symptoms, transmission, and prevention. We also set out to evaluate the outcomes and user satisfactions.
Methods: The e-learning course was implemented to student, community, medical personnel and healthcare workers by the web application, including video and online evaluation form. The knowledge improvement was assessed as pre- and posttests, with a cut-off passing grade of 80%. The user satisfaction and feedbacks were collected using a Likert's scale online questionnaire.
Results: We enrolled 1657 participants, 24.86% males and 75.14% females, with ages ranging 25-55 years. There was a [99 %] increase of Aedes-borne disease-related knowledge, understanding, and application. Most respondents had a high level of satisfaction [98%] and found this method useful in distributing information to the community, with appropriate content and training format.
Conclusion: This online e-learning course showed a promising performance to effectively distribute health-related knowledge to the target population. It provided easy access to information with low cost at a flexible timing. In the future, similar platforms might be used to disseminate awareness of other diseases and public

Keyword : e-learning platform, mosquito-borne disease, online course, user satisfaction, risk communication

Abstract No. : ABS0001819

ONLINE PRACTICAL STUDIED OF CHIGGER MITE (TROMBICULIDAE) AS VECTORS OF SCRUB TYPHUS

Rawadee Kumlert

Authors : Kumlert R.[1], Padungtod C.[1], Prasartvit A.[1], Pawestri A.R.[2]

Affillation : [1]Department of Disease Control, Ministry of Public Health, Nonthaburi 11000, Thailand; [2]Department of Parasitology, Faculty of Medicine, Universitas Brawijaya, Malang 65145, Indonesia

Background: Scrub typhus is a neglected vector-borne disease caused by Orientia tsutsugamushi. It is transmitted by the larva of Trombiculid mites (chiggers). If left undetected and untreated, scrub typhus could lead to dire consequences, including death. Thus, the knowledge and awareness toward this disease and its vector it is crucial, particularly for healthcare workers.
Objectives: We aimed to develop and evaluate a practical online course of chigger mite identification and biology to strengthen the basic knowledge of the vector related to prevention and control measures.
Methods: This online course was directed for healthcare officers or related sectors and conducted via online lectures and meetings. An adaptation dichotomous identification key was developed using Mind Maple program. Google classroom was utilized to post course syllabus, modules, worksheets, and evaluations. Course certificates will automatically be sent to participants who excelled the passing grade of 80%.
Results: Eighty participants enrolled in this program. Seventy percent of participants lacked prior knowledge of scrub typhus and 69% showed low skills of basic vector identification. After the course, the average score increased significantly from the baseline ($p < 0.05$). Most participants showed high interest in the topic and learning methods.
Conclusion: Our results suggested that the practical onsite training is effective and well-accepted to distribute infectious disease-related knowledge. The ease of access, low cost, and practicality of this platform makes it suitable for busy professionals keen to update their knowledge and skills. In the future, this method could be applied for other diseases and target participants.

Keyword : chigger mite; scrub typhus; morphological identification; dichotomous key; online course

Abstract No. : ABS0001749

THE POTENTIAL OF ON-LINE CITIZEN SCIENCE APPLICATION FOR COMMUNITY-PARTICIPATORY MONITORING OF MOSQUITOES, DEVELOPED IN THIS STUDY

Mika Saito

Authors : Saito M.[1], Ota T.[2], Oikawa K.[2], Kaneko M.[2], Sekine K.[1], Shimabukuro M.[1]

Affillation : [1]University of the Ryukyus; [2]Rakuno Gakuen University

Introduction: “Citizen science” was defined as the participation of the community in scientific work, through collaboration between scientists and citizens. This Citizen Science approach became a new academic stream world-widely. Since 2018, we have implement citizen science practices at Primary School in Okinawa to develop a model for community-participatory monitoring of mosquitoes for infectious disease control. In this study, we developed on-line application, and will discuss the potentials of citizen science on mosquito borne disease control.
Methods: An application for monitoring mosquitoes was developed based on Esri's ArcGIS Online to enable online collection, sharing, and analysis of data from the results of previous surveys conducted using paper maps. The data was collected using QuickCapture, an app for mobile devices that allows simultaneous input of survey results, date, time, location, and puddle image data. The results of the survey could be shared on a map in real time using Esri's Dashboards.
Results: The application for data collection was simple to be accepted and used by primary school students. And they enjoyed operating devices and monitoring. The survey results can be stored online, and analyzed for the relation between mosquito (Ae. albopictus) breeding site. Heat Map of mosquito and distance between breeding site and bushes were visualized digitally.
Conclusion: Online citizen science has potential to raise curiosity and participation. Participation of a larger number of citizens, could lead more precise analyze such as Seasonal Changes, Identification of hotspots, etc. these may reveal local characteristics and new discoveries through free thinking.

Keyword : On-line citizen science, mosquito-borne infectious disease, community participatory monitoring

Abstract No. : ABS0001719

INCLUDING MOBILITY TO OPTIMIZE MOSQUITO CONTROL INTERVENTION STRATEGIES

Richard Paul

Authors : Telle O.[1], Lefebvre B.[2], Ligsay A.[3], Salazar F.[4], **Paul R.[5]**

Affillation : [1]CNRS, France; [2]EHESP, France; [3]University of Santo Tomas, The Philippines; [4]Research Institut for Tropical Medicine, The Philippines; [5]Institut Pasteur, France

Dengue is one of these major diseases spreading in cities today, with its principal mosquito vector superbly adapted to the urban environment. Current mosquito control strategies are proving inadequate, especially in the face of such urbanisation and novel, evidence-based targeted approaches are needed. Hotspots of dengue have often been associated with socio-economic inequality and offer potential sites for focussing mosquito control, but their role in disseminating virus across the city will be influenced by intra-urban mobility. Auto-dissemination (AD) of insecticide offers a potential approach to exploit the oviposition behaviour of mosquitoes so as to use them to spread the insecticide locally within the identified hotspots. However, although AD has been shown to impact mosquito population density, actual impact on dengue risk remains scarce. Here we present initial studies of the entomological and epidemiological efficacy studies of using AD in urban settings of the Philippines and (ii) on how measures of intra-urban mobility influences the socio-economic determinants of dengue hotspots. AD approaches were found to have an impact on both mosquito densities and human sero-conversion rates at a local scale. Measures of intra-urban mobility had a significant impact on risk factors associated with dengue hotspots. In conclusion, whilst AD approaches offer an alternative to current mosquito control methods, intra-urban mobility needs to be taken into account to assess what impact mosquito control in hotspots might have on dengue spread across the city.

Keyword : Dengue, Hotspots, Mobility, Mosquito control

Thursday 8 December 2022

S20 : Applied Social Science in Tropical Disease Prevention and Control

09.00-10.30hr

Room E

Abstract No. : ABS0001692

A SPATIAL ANALYSIS OF GEOGRAPHIC ACCESS TO PUBLIC HEALTHCARE FACILITIES IN CÔTE D'IVOIRE

Gaëlle T. Sehi

Authors : Gaëlle T. Sehi [1], Peter M. Macharia [2,3], Clarisse A. Houngbedji [4,5], Daniel M. Parker[1]

Affillation : [1]Population Health and Disease Prevention, Public Health, University of California, Irvine, United States; [2]Centre for Health Informatics, Computing and Statistics, Lancaster Medical School, Lancaster University, Lancaster, United Kingdom; [3]Population Health Unit, Kenya Medical Research Institute-Wellcome Trust Research Programme, Nairobi, Kenya; [4]Centre d'Entomologie Médical et Vétérinaire (CEMV), Université Alassane Ouattara, Bouaké, Côte d'Ivoire; [5]Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Abidjan, 01 BP 1003 Abidjan 01, Côte d'Ivoire

Introduction: Worldwide 1.3 billion people lack access to effective and affordable health care, leading to a wide array of negative health outcomes. In Côte d'Ivoire the health system is centralized and some communities lack good access to healthcare facilities. The landscape is complex geographically and travel capacity can vary seasonally - impacting access to health care. Our goal in this research was to map spatial accessibility to public healthcare facilities across the nation, and subsequently to quantify and analyze the proportion of the population that have poor access to timely health care.

Methods: We draw on several sources of open-source data including the locations of healthcare facilities, population distribution, road network, water bodies, elevation, and land cover. We then used these data along with plausible travel scenarios within a cost-distance algorithm in AccessMod (version 5) to generate gridded layers of travel times to the nearest facility, in increasing complexity.

Results: We estimate that 67% of the population is within 1 hour of the nearest public healthcare facility. Conversely, 6% of the total population is located greater than 4 hours from the nearest healthcare facility. There was extreme heterogeneity in access across the landscape; in the Northern region (Bafing) over 23,6% of the population is estimated to live farther than 4 hours travel time to the nearest healthcare facility, compare to 1% of the population in the Southern region (Lacs).

Conclusion: Our findings will be useful for decision makers in improving access to healthcare in marginalized areas. More work should be done to assess nation-wide accessibility and to ensure that all individuals have ready access

Keyword : Spatial Epidemiology; Health care; Côte d'Ivoire

Abstract No. : ABS0001688

CONFLICT AND CHOLERA: QUANTIFYING THE IMPACT OF AIR RAIDS ON YEMEN'S CHOLERA INCIDENCE

Maia Tarnas

Authors : Tarnas M.C.[1], Al Dheeb N.[2], Zaman M.H.[3], Parker D.M.[1]

Affillation : [1]Department of Population Health and Disease Prevention, University of California, Irvine, CA, USA.; [2]Public Health Network, YEMPHNET, Yemen; [3]Department of Biomedical Engineering, Boston University, Boston, MA, USA

Background: Yemen continues to endure widespread cholera outbreaks during ongoing conflict and destructive environmental events. Air raids have been used throughout the conflict to target military and civilian infrastructure. This study aims to quantify the impact of these air raids on cholera incidence.

Methods: We utilized data between 2016 – 2019 on air raids from the Yemen Data Project, NDVI and flooding indices from MODIS satellite imagery, elevation from Shuttle Radar Topography Mission, precipitation from the Climate Knowledge Exchange Portal, and cholera case and population from published work. These data were transformed into weekly intervals and governorates were assigned an annual air raid severity level, ranging from Low (≤ 3 annual air raids) to Severe (173+). We measured the impact of air raid severity via a negative binomial generalized additive model with random intercepts and a smoothed spatial interaction for governorate location while controlling for environmental, temporal, and demographic variables.

Results: After controlling for relevant environmental factors, air raids had a significant impact on cholera incidence across all severity levels, with a maximum of 5.65 (95% CI: 3.75 – 8.51) greater risk in governorates with severe annual air raid levels, compared to governorates with low air raid severity. Surface water was also a strong predictor of increased numbers of cholera cases.

Discussion: Air raids significantly contribute to the widespread burden of cholera in Yemen, even when controlling for relevant environmental factors. Quantifying their impact on cholera incidence further illustrates the man-made nature of the country's cholera outbreak and conflict's devastating effects on health.

Keyword : cholera; Yemen; conflict

Abstract No. : ABS0001796

A CONCEPTUAL FRAMEWORK TO UNDERSTAND EXTRACTIVE SETTLEMENTS AND DISEASE: DEMOGRAPHY, ENVIRONMENT, AND EPIDEMIOLOGY

Natasha Glendening

Authors : Glendening N.[1], Haileselassie W.[2], Parker D.M.[1],
Affillation : [1]Department of Population Health and Disease Prevention, University of California, Irvine, U.S.A.; [2]School of Public Health, Addis Ababa University, Ethiopia

Introduction: Addressing the health needs of atypical communities, especially newly established ones–including short and long-term migrant communities, refugee camps and new settlements–can be complicated for a variety of reasons. As a result, these communities' health needs are often ignored or under-addressed. The aim of this research is to describe a planetary health framework for understanding the environmental, demographic and epidemiologic dynamics, and the resulting health needs, of new settlements that form around small scale extractive industries.
Methods: We used secondary literature analyses to formulate the conceptual model. We then used a primary case study of migrants moving to a newly formed, informal gold mining settlement in a malarious region of Western Ethiopia to highlight the conceptual model.
Results: There are five elements to this conceptual model: A) people start at their place of origin; B) people move to establish a new settlement; C) movement to the settlement induces changes to the local environment, whilst simultaneously; D) movement to the settlement also induces changes to the demography of the place over time; E) both B and C then induce changes to the settlement's epidemiology.
Conclusions: The elements of the conceptual model all alter the health needs and health service demands of the population over time. Overall, for such atypical communities who may fall out of the normal healthcare system, consideration must be made to ensure these populations have steady access to health services and their health needs are met. This conceptual model can help to understand and address the needs of such atypical communities.

Keyword : conceptual model; planetary health; gold mining; malaria; demography; epidemiology; Ethiopia

Abstract No. : ABS0001687

FACTORS HINDERING COVERAGE OF TARGETED MASS TREATMENT WITH PRIMAQUINE IN A TOWNSHIP IN NORTHERN MYANMAR

Pyae Linn Aung

Authors : Pyae Linn Aung[1,2], Myat Thu Soe[1], Than Naing Soe[3], Thit Lwin Oo[1], Kyawt Mon Win[3], Liwang Cui[4], Myat Phone Kyaw[1], Jetsumon Sattabongkot[2], Kamolnetr Okanurak[5] and Daniel M. Parker[6]

Affillation : [1]Myanmar Health Network Organization, Yangon, Myanmar; [2]Mahidol Vivax Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [3]Department of Public Health, Ministry of Health, NayPyiTaw, Myanmar; [4]Division of Infectious Diseases and International Medicine, Department of Internal Medicine, Morsani College of Medicine, University of South Florida, 3720 Spectrum Boulevard, Suite 304, Tampa, FL 33612, USA; [5]Department of Social and Environmental Health, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [6]Department of Population Health and Disease Prevention, Department of Epidemiology, University of California, Irvine, USA

Introduction: Mass treatment with primaquine might be one of the effective interventions to eradicate latent stage hypnozoites in Plasmodium vivax malaria. This study aimed to explore the factors hindering coverage of a 14-day targeted mass treatment with primaquine (TPT) conducted in a malarious township of northern Myanmar.
Methods: During September 2019, a cross-sectional exploratory design including quantitative and qualitative data was conducted following a TPT campaign. Population census, mass blood survey (MBS), follow-up forms and in-depth interviews with community persons were used to collect the data in five villages with high P. vivax prevalence.
Results: Among 2,322 total population, 1,973 (85.0%) involved in initial MBS and 1,208 completed the whole TPT. G6PD deficiency was found among 13.5% of total MBS participants. The risk of G6PD deficiency was high among males and variated by ethnic groups and places of residence. A total of 435 were absent from villages during TPT due to staying in farms or goldmies for their incomes. Of 1,315 eligible samples, farmers and goldminers males aged 15 to 45 years presented higher percentages of non-participation. Qualitative findings showed that most of the non-participation groups were outside the villages during TPT due to time-sensitive agricultural and other occupational or education-related purposes.
Conclusion: Despite overall people willingness to participate being high, only half of the total targeted population completed the TPT. To facilitate high participation, alternative approaches such as giving a short regime, implementing activity around the work sites, or mitigating some inclusion criteria should be considered.

Keyword : G6PD, Malaria, Myanmar, Plasmodium vivax, Primaquine, Social participation

Thursday 8 December 2022

S21 : One Health Approach in Emerging Vector Borne and Zoonotic Diseases

11.00-12.30hr

Room A

EID ZOONOTIC

Opass Putcharoen

Authors : Opass Putcharoen

Affillation : Faculty of Medicine, Chulalongkorn University

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001910

AUTOCHTHONOUS LEISHMANIASIS IN THAILAND: UPDATE IN CLINICAL ASPECTS AND VECTOR BIOLOGY

Kanok Preativatanyou

Authors : Kanok Preativatanyou[1], Chulaluk Promrangsee[1,2], Nopporn Songumpai[3], Glenn Bellis[4], Padet Siriyasatien[1,2]

Affillation : [1]Center of Excellence in Vector Biology and Vector-Borne Disease, Department of Parasitology, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand; [2]Interdisciplinary program of Biomedical Sciences, Graduate School, Chulalongkorn University, Bangkok, Thailand; [3]Division of Infectious Diseases, Department of Internal Medicine, Hatyai Hospital, Songkhla, Thailand; [4]Research Institute for the Environment and Livelihoods, Charles Darwin University, Darwin, Australia.

Leishmaniasis is a neglected vector-borne disease caused by Leishmania parasites and is found commonly in tropical and subtropical countries worldwide. This multispectral disease can manifest cutaneous, mucocutaneous, and visceral involvement, depending on the infecting species and the host immune status. Approximately 53 Leishmania species have been documented and categorized into four subgenera, i.e., Viannia, Leishmania, Sauroleishmania, and recently classified Mundinia (formerly known as 'L. enriettii complex'). Phlebotomine sand flies have been proven as vectors of this parasite group in several endemic areas worldwide. Before 1996, Thailand had only imported cases who returned from the endemic countries. Since then, autochthonous cases without a history of going abroad have continuously been reported, especially in the northern and southern provinces of Thailand. Most of these cases were diagnosed with Leishmania (Mundinia) martiniquensis and Leishmania (Mundinia) orientalis. Besides sand flies, non-phlebotomine vectors, namelyCulicoides biting midges, have recently been identified as the new putative vectors for autochthonous transmission of these two Mundinia species. Therefore, this presentation will focus on a recent update of clinical case reports, entomological investigation, and evidence of emerging parasite co-circulation in a high-transmission setting in the country. Essentially, this novel knowledge would greatly facilitate the establishment of strategies for effective prevention and control of this emerging parasitic disease in Thailand.

Keyword : autochthonous leishmaniasis, Mundinia, Leishmania martiniquensis, Leishmania orientalis, phlebotomine sand flies, Culicoides biting midges, Thailand

Abstract No. : ABS0001816

ANIMAL VECTOR BORNE DISEASES

Sonthaya Tiawsirisup

Authors : Sonthaya Tiawsirisup

Affillation : Animal Vector-Borne Disease Research Group, Parasitology Unit, Department of Veterinary Pathology, Faculty of Veterinary Science, Chulalongkorn University, Bangkok, Thailand

Vector borne diseases (VBDs) are important infectious diseases in humans and animals. Some of them are also emerging infectious in Thailand. Duck Tembusu virus (DTMUV), an emerging infectious disease in ducks, belongs to the Flavivirus genus. Field and laboratory findings indicated the potential role of Culex tritaeniorhynchus in the DTMUV transmission cycle in duck farms in Thailand. Haemoplasma is a trivial name for haemotropic Mycoplasma spp., which can attach to the surface of red blood cells leading to deformity and anemia in pigs. We examined the molecular occurrence and genetic diversity of porcine haemoplasmas in Thai domestic pigs. The frequency of haemoplasma infection was 37.1% in all pigs. Sequencing analysis indicated that at least four species (Mycoplasma suis, Mycoplasma parvum, Candidatus Mycoplasma haemosuis, and a putative novel species) of porcine haemoplasmas were identified. Lumpy skin disease (LSD) is an emerging infectious disease of cattle and water buffalo caused by the lumpy skin disease virus (LSDV). LSDV is believed to be transmitted through direct and indirect contact and mechanical vector. Previous studies show Stomoxys, Rhipicephalus, and Aedes aegypti could transmit LSDV under controlled conditions. African horse sickness (AHS) is a viral disease affecting equids, with mortality rates reaching 90% in naïve populations of horses. African horse sickness virus is transmitted between hosts by Culicoides. AHS was confirmed in horses in Thailand in March 2020. The virus was determined to belong to serotype 1 and is phylogenetically closely related to isolates from South Africa.

Keyword : Animal, Vector, Vector borne disease, Thailand

IMPLEMENTING ONE HEALTH APPROACHES TO CONFRONT EMERGING AND RE-EMERGING ZOONOTIC DISEASE THREATS

Ratanaporn Tangwangvivat

Authors : Ratanaporn Tangwangvivat

Affillation : Department of Diseases Control, Ministry of Public Health

No abstract available

Keyword : No keyword available

Thursday 8 December 2022

S22 : Rejuvenate Medical Entomology: Chance and Challenge

11.00-12.30hr

Room B

Abstract No. : ABS0001862

ADVANCES IN VOLATILE PYRETHROID EVALUATION FOR VECTOR CONTROL IN THE GREATER MEKONG SUBREGION

Jeffrey Hii

Authors : Hii J[1], Kim D.[2], Yan C.[2], Ahebwa A.[2], Chareonviriyaphap T.[2]

Affillation : [1]College of Public Health, Medical and Veterinary Sciences, James Cook University, Australia;
[2]Department of Entomology, Faculty of Agriculture, Kasetsart University, Thailand

Volatile pyrethroids (VPs) provide a promising additional product class for vector control in areas where vectors bite outdoors or during waking hours as well as settings where standard indoor interventions are not adequate or inaccessible.

A total of thirteen laboratory, semifield system (SFS), experimental hut (EH) and open field trials (OFT) of metofluthrin (MFT), transfluthrin (TFT) treated materials or mosquito coils were evaluated for mosquito repellent activity.

Excito-repellency assays and high-throughput screening system showed moderate to high avoidance and mortality to sub-lethal and discriminating concentrations of VP-treated natural and synthetic fabrics among four vector mosquitoes. Short-lived impacts on BGS trap catches were observed in an EH following exposure to TFT and MFT with no change in recapture densities using DDT compared to matched controls (Thailand). Two SFS studies showed that MFT-impregnated nets and TFT-PET vests provided partial protection against Ae. aegypti and An. minimus (Vietnam) and An. harrisoni (Thailand), respectively. Four OFTs showed: a) no significant difference between the protective efficacies of TFT mosquito coils compared to LLINs and coil-LLIN combination (China); (b) no difference in mosquito abundance between control and MFT collections (Cambodia); (c) no observable effect on malaria prevalence of MFT emanators in a low transmission area (Cambodia); (d) low to high protective efficacy of different TFT-treated fabrics. A novel passive VP (TFT) product was the most protective single-intervention preventing 94% of Anopheles landing on collectors in an OFT (Cambodia). Well designed studies are needed to generate evidence based conclusions regarding spatial repellents for prevention of vector-borne diseases.

Keyword : Volatile pyrethroids, evaluation, transflutrin, metofluthrin, laboratory, semifield system, experimental hut, open field trials

Abstract No. : ABS0001839

CHALLENGES OF MOSQUITO SENSOR AND AI APPLICATION FOR VECTOR SURVEILLANCE

Michael Weber

Authors : Michael Weber[1], Martin Geier[1], Andreas Lugauer[1], Armin Kordus[1], Maximilian Epple[1]

Affillation : [1]Biogents AG, Weißenburgstraße 22, 93055 Regensburg, Germany

With global mobility, trade, and climate change, both mosquito vectors and pathogens are increasingly invading new areas. Insecticide-coated bed nets and indoor residual spraying (IRS) have had tremendous success reducing malaria death rates, but their impact now appears to be stagnating. Reasons include insecticide resistance and shifts in vector species and behaviors, for example, outdoor biting.Therefore, "passive" protective methods need to be augmented with "active" methods of mosquito control for reduction of vector populations. Surveillance is a key part of mosquito control and integrated pest management (IPM).Yet, technology and methods for mosquito surveillance have not changed much in 60 years: large amounts of specialist labor (and carbon-based fuel) still result in low temporal and spatial resolution. The simpler method of human landing counts has highly variable results, not to mention being ethically questionable where disease is endemic. "Smart traps" have the potential to address this surveillance bottleneck.We will outline the technical and economic challenges for developing and deploying networks of smart traps. Mosquito sensor technology must be integrated with mosquito traps capable of attracting and capturing hard-to-catch vectors. Often, vector species overlap with other local species in measurable physiological parameters such as wingbeat, requiring new approaches to machine learning and AI model development. Finally, as has been recently reported, science-based mosquito traps by themselves can be an effective, sustainable vector control method.

Keyword : smart trap; mosquito trap; mosquito sensor; mosquito classification; species determination

Abstract No. : ABS0001811

DOSE-DEPENDENT BLOOD-FEEDING ACTIVITY AND OVARIAN ALTERATIONS TO PM2.5 IN AEDES AEGYPTI

Thipruethai Phanitchat

Authors : Thipruethai Phanitchat[1],Sumate Ampawong[2],Artit Yawootti[3],Thammanitchpol Denpetkul[4],Napid Wadmanee[5],Mongkhon Sompornrattanaphan[6] and Chaisith Sivakorn[7]

Affillation : [1]Department of Medical Entomology, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand; [2]Department of Tropical Pathology, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand; [3]Faculty of Engineering, Rajamangala University of Technology LANNA, Chiang Mai 50300, Thailand; [4]Department of Social and Environmental Medicine, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand; [5]Hospital for Tropical Disease, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand; [6]Division of Allergy and Clinical Immunology, Department of Medicine, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok 10700, Thailand; [7]Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand

High levels of fine particulate matter (PM2.5) air pollution are a concern for human health. Several studies have examined the effects of air pollution on human and animal health. However, there is a lack of knowledge about its effects on arbovirus vectors. Thus, we investigated whether PM2.5 concentration alters the blood-feeding activity of Ae. aegypti mosquitoes. We investigated the effect on the females' propensity to blood feed at eight concentrations of PM2.5 ranging from 100 to 1000 μg/m3. Correlation analysis showed blood-feeding activity had a significant strong negative correlation with concentration of PM2.5 ($r_p = -0.85$; $p \le 0.00001$). Exploratory linear and non-linear models showed an exponential decay relationship was the best fitting model (corrected Akaike's information criterion, 193.0; Akaike's weight, 0.766; adjusted R2, 0.780). Ultrastructural study demonstrated PM2.5 did not obstruct the respiratory system, but some fine particles were present on the antenna and abdominal body parts. Ovaries showed a dose–response relationship between PM2.5 level and vacuolated degeneration. In conclusion, the blood-feeding behavior of Ae. aegypti females may have an exponential decay relationship with PM2.5 level, and their ovaries may demonstrate dose-dependent degeneration. These findings may be important in understanding the vector's biology and disease transmission in settings with high PM2.5 levels. These results are important to understand blood-feeding and feeding pattern of mosquitoes during PM2.5 pollution, which is important for disease transmission and vector control.

Keyword : Aedes aegypti, PM2.5, blood-feeding, pollution, arbovirus

Thursday 8 December 2022

S23 : Health in Detention: Make Inequity, Equity Make Difficullty, Access Easily [MOPH]

11.00-12.30hr

Room C

PROVIDING MEDICAL AND PUBLIC HEALTH SERVICES IN PRISONS

Chutarat Chintakanont

Authors : Chutarat Chintakanont

Affillation : Department of Corrections, Ministry of Public Health

No abstract available

Keyword : No keyword available

ACCESS TO TREATMENT RIGHTS AND THE USE OF BUDGETS IN THE MANAGEMENT OF MEDICAL SERVICE

Kanitsak Chantrapipat

Authors : Kanitsak Chantrapipat

Affillation : Office of Primary Care NHSO

No abstract available

Keyword : No keyword available

HEALTH IN DETENTION

Vivien Lusted

Authors : Vivien Lusted

Affillation : ICRC

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001838

DISEASE PREVENTION AND CONTROL IN PRISONS COMPARE WITH COMMUNITY AT LARGE: LESS OR EQUITY

Pahurat Kongmuang Taisuwan

Authors : TAISUWAN P.K.

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

Globally and Thailand, infectious diseases and non-communicable diseases are remaining a major effect to health and healthcare system both in society and in prison. For prisoner's diseases screening in Thailand, we used multi-measurement at an upon arrival, he or she will be tested tuberculosis, HIV-AIDS, syphilis, hepatitis C as well. Meanwhile, people in community at large may avoided because these diseases are perceived as stigma diseases. Moreover, during inmates, first screening will be handed by prison healthcare volunteer-PHV whom well trained and local in all prisons. They would identify high risk of diseases. In case of found high risk, they will inform health care worker then confirm measurement regarding diseases. Confirmed disease cases are referring to cure at the local reference hospital until recovery or release. However, all steps of prisoner seeking health care services depend on prison putting and arranging. For people living in community at large, they can seek health care service themselves. In case of population more concern about health, they may seek health care service for their health and curing diseases. However, diseases occurred in prisons may affect to community at large especially in prison system, infectious diseases are challenges to control, because of prisoners are particularly vulnerable to infected, considered reservoirs facilitating infectious diseases transmission within their enclosed populations. Transmission also occurs through movable prison staff, visitors, and release inmates. Moreover, non-communicable diseases also be burden of health care service in detention and community at large as well.

Keyword : inmate, corrective healthcare, disease prevention and control, health in detention

Thursday 8 December 2022

S24 : Understanding Plasmodium Liver Stage Development for the Design of Novel Vaccine and Drug Interventions

11.00-12.30hr

Room D

Abstract No. : ABS0001701

IN VIVO ASSESSMENT OF PLASMODIUM VIVAX CHESSON STRAIN LIVER STAGE INFECTION: NOVEL STUDIES TO ASSESS HYPNOZOITE FORMATION, PERSISTENCE, ACTIVATION, AND RELAPSE

Gigliola Zanghi

Authors : Gigliola Zanghi[1*], Sumana Chakravarty[2*], Hardik Patel1, Stephen L. Hoffman[2], B. Kim Lee Sim[2], Stefan H.I. Kappe[1,3,4] & Ashley M. Vaughan[1,3] .

Affillation : [1]Center for Global Infectious Disease Research, Seattle Children\'s Research Institute, 307 Westlake Ave N, Seattle, WA 98109, USA; [2]Sanaria Inc., Rockville, Maryland 20850, USA; [3]Department of Pediatrics, University of Washington, Seattle, Washington 98105, USA; [4]Department of Global Health, University of Washington, Seattle, Washington 98195, USA

*These authors contributed equally to this work

A primary goal of Plasmodium vivax liver stage research is understanding the formation, persistence and activation of the hypnozoite, the source of relapses. Hypnozoite research is hampered by the limited access to P. vivax sporozoites. P. vivax sporozoites are primarily obtained from mosquitoes infected with blood from human volunteers harboring gametocytes. Access to volunteers is limited and there is strain-to-strain variability in hypnozoite formation.To overcome these obstacles, we revisited the Chesson strain of P. vivax. To this end, P. vivax Chesson blood stages were propagated in Saimiri monkeys, transmitted to mosquitoes to generate P. vivax Chesson sporozoites which were purified and cryopreserved. We then used these sporozoites to infect human liver-chimeric FRG NOD huHep mice, which are receptive to P. vivax hypnozoite formation and activation. We observed robust liver stage infection in the FRG NOD huHep mice with liver stage schizonts maturing over nine days, releasing exo-erythrocytic merozoites from the liver and into the blood. The hypnozoite:schizont ratio in the liver was consistently 40%:60%, the first quantitative determination of Chesson strain hypnozoite frequency. Hypnozoites persisted and activated after three weeks, causing the first relapses. We performed single cell RNA-seq analysis of sporozoites to address the hypothesis that hypnozoite fate is predetermined. Furthermore, we performed spatial transcriptomics to evaluate how liver stage schizonts and hypnozoites interact with their host hepatocyte. Our P. vivax Chesson model will allow us to gain a better understanding of hypnozoite biology and could aid in the discovery of novel interventions to prevent relapses.

Keyword : P.vivax, Hypnozoite, FRG NOD huHep mice, Single Cell RNAseq, Spatial Transcriptomics

Abstract No. : ABS0001848

HOST REGULATION OF PLASMODIUM VIVAX DORMANT AND REPLICATING LIVER FORMS

Alexis Kaushansky

Authors : Elizabeth K.K. Glennon[1], Wanlapa Roobsoong[2], Ling Wei[1], Jetsumon Sattabongkot[2], **Alexis Kaushansky[1, 3]**

Affillation : [1]Seattle Children's Research University; [2]Mahidol Vivax Research Unit, Faculty of Tropical Medicine, Mahidol University; [3]University of Washington, Departments of Pediatrics and Global Health

Introduction: One of the major hurdles to malaria eradication originates from the ability of Plasmodium vivax to form liver-resident dormant stages called hypnozoites. Upon transmission to the human host by the bite of an infectious mosquito, Plasmodium sporozoites exit the skin, are taken up by the bloodstream and travel to the liver, infecting hepatocytes. For most Plasmodium species, these parasites rapidly develop into schizonts and replicate before progressing to symptomatic blood stage infection. However, in P. vivax infections, some sporozoites do not initially replicate their DNA and instead form hypnozoites, which remain in the liver. These parasite forms can be reactivated weeks to months after initial infection, are resistant to most antimalarials, and are difficult to culture in the lab. Although epidemiological studies are consistent with host regulators of the dormancy and reactivation processes, virtually none of the molecular details about the host determinants of these processes are known.

Methods: We have taken advantage of recent advances in long-term in vitro models and human liver-chimeric mice to investigate the role of host signaling in regulating P. vivax dormant and replicating forms.

Results: Our preliminary data suggest schizonts are more susceptible to modulation of hepatocyte kinase signaling than hypnozoites and that the two forms rely on both overlapping and unique host kinases for their maintenance.

Conclusion: Understanding the mechanisms by which dormant and replicating parasite forms are regulated by host cell processes will allow us to better design effective therapeutics and to understand which individuals are at highest risk of relapse.

Keyword : Plasmodium vivax, liver-stage, hypnozoite, schizont, kinase, host regulation

Abstract No. : ABS0001911

USING NON-HUMAN PRIMATES TO UNDERSTAND HOST-PATHOGEN BIOLOGY AND ACCELERATE VACCINE DEVELOPMENT

Brandon Wilder

Authors : Maya Aleshnick[1], Payton Kirtley[1], Thomas Martinson[1], David Morrow[1], Scott Hansen[1], Luna de Lacerda[2,3,4], Camila R. R. Barbosa[2], Biley Abatiyow[5], Charlie Jennison[5], Ashley Vaughan[5], Caroline Junqueira[2,3,4], **Brandon Wilder[1]**

Affillation : [1]Oregon Health and Science University, Vaccine and Gene Therapy Institute; [2]Instituto René Rachou, Fundação Oswaldo Cruz; [3]Boston Children’s Hospital; [4]Harvard Medical School; [5]Seattle Children\'s Research Institute

The study of interventions against malaria have been buoyed by the diversity of hosts infected by the Plasmodium parasite which allows robust models of infection from mice to humans. Yet rodent models, and even much of the CHMI data, have failed to predict vaccine performance in the field. In contrast, non-human primates (NHPs) infected with primate Plasmodium species have proven to be stringent and more accurately reflect the difficulty in achieving high levels of protection in the field. Non-human primates also more closely mirror human immunological responses. Still, the human malaria parasites only infect new world monkeys imperfectly, and the primate parasites used in more commonly used old world monkeys often differ from their human counterparts in terms of physiology and common vaccine targets. This leaves NHPs with a unique if not imperfect niche within malaria research. Here, we present findings from our with with NHP models of P. knowlesi and P. cynomolgi where we capitalize on the ability to perform experimental infections, longitudinal tissue sampling and parasite transgenesis. This has enabled us to: 1) Validate that P. cynomolgi replicates major aspects of CD8 T cell-mediated immunity to P. vivax; 2) identify a role for non-classical MHC-E-restricted CD8 T cells following blood stage infection; and 3) create a transgenic P. cynomolgi parasite carrying a chimeric 210/247 P. vivax CSP to study the impact of PvCSP-directed interventions on primary and relapse in vivo. With these tools and insights, we hope to fill critical gaps in our knowledge of immunoparasitology in

Keyword : malaria, vivax, knowlesi, cynomolgi, primate, vaccine

Abstract No. : ABS0001866

CREATION OF A LATE LIVER STAGE-ARRESTING PLASMODIUM FALCIPARUM GENETICALLY ATTENUATED VACCINE

Ashley Vaughan

Authors : Debashree Goswami[1], William Betz[1], Janna Armstrong[1], Hardik Patel[1], B. Kim Lee Sim[2], Tao Li[2], Sean C. Murphy[3], **Ashley M. Vaughan[1]**, Stephen L. Hoffman[2], Stefan H.I. Kappe[1]

Affillation : [1]Center for Global Infectious Disease Research, Seattle Children\'s Research Institute, Seattle, WA, United States; [2]Sanaria Inc., Rockville, MD, United States; [3]Department of Laboratory Medicine and Pathology , University of Washington, Seattle, WA, United States

Vaccination with-live-attenuated pre-erythrocytic Plasmodium parasites confers durable, sterilizing immunity against infection. Studies using rodent malaria models conclusively showed that genetically attenuated parasites (GAP), which arrest late in liver stage development engender superior protective immunity compared to early liver stage-arresting RAS or GAPs. Such replication-competent attenuated parasites however have been difficult to establish in Plasmodium falciparum. In recent years, we have identified two gene knockouts in P. yoelii and P. falciparum, which create similar late liver stage arresting replication-competent GAP (LARC GAP) phenotypes. These are, Plasmei2, a cytoplasm-localized RNA-binding protein and an uncharacterized protein expressed in liver stage nuclei which we have termed LINUP. To optimize attenuation, we generated plasmei2-/linup- double knockout parasites (LARC2) in both P. yoelii and P. falciparum. Infection of highly susceptible BALB/cByJ mice with a high dose of 250,000 P. yoelii LARC2 sporozoites did not result in any breakthrough infections, demonstrating that we have successfully generated a fully attenuated LARC GAP. Immunization with P. yoelii LARC2 sporozoites conferred sterilizing immunity against sporozoite challenge. The P. falciparum LARC2 strain was used to generate cryopreserved LARC2 sporozoites and was tested for full attenuation in a liver-humanized mouse model. P. falciparum LARC2 sporozoites have entered GMP manufacturing and are currently slated to be assessed for safety, tolerability, immunogenicity and efficacy in clinical trials in 2022/2023 using an injectable formulation. Vaccine efficacy of P. falciparum LARC2 sporozoites will be evaluated using a controlled human malaria infection with the intravenous administration of heterologous P. falciparum 7G8 sporozoites.

Keyword : Malaria vaccine

Thursday 8 December 2022

S25 : Innovative Approaches of COVID-19 Diagnosis and Prevention

11.00-12.30hr

Room E

nSPHERE NEGATIVE PRESSURIZED HELMET

Paisan Khanchaitit

Authors : Paisan Khanchaitit

Affillation : National Nanotechnology Center (NANOTEC), National Science and Technology Development Agency (NSTDA), Thailand

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001868

NANOPARTICLE-BASED LATERAL FLOW ASSAY PLATFORM FOR RAPID DETECTION & SCREENING

Natpapas Wiriyachaiporn

Authors : Wiriyachaiporn N., Bamrungsap S., Maneeprakorn W., Japrung D.

Affillation : National Nanotechnology Center (NANOTEC), National Science and Technology Development Agency (NSTDA)

Point-of-care test (POCT) is known as a tool/device, which is commonly used in a rapid detection and screening of the target analyte. This is especially prevalent in clinical fields or settings, where centralized laboratory/full automation services are limited. Of those technology platforms, which can be used as a rapid diagnostic test, lateral flow assay (LFA) has gained much interest for either a simple POCT or integrated with other technologies. The platform is considered to be one of the most commercially feasible analytical tools for a rapid and simple on-site qualitative detection with affordable cost. Within this session, the development and trend of a simple lateral flow based biosensor for potential biomedical and diagnostic applications are discussed. The principle, design and available formats, with the integration of the use of nanoparticles as reporters are also included. Subsequently, with the current COVID-19 pandemic situation, further applications on LFA platform as a screening platform during the demand in home used LFA is also discussed.

Keyword : Rapid Testing Platform, Lateral Flow Assay, Nanoparticles

COXY-AMP: A RAPID AND SENSITIVE COLORIMETRIC LAMP FOR COVID-19 DETECTION

Wansika Kiatpathomchai

Authors : Wansika Kiatpathomchai

Affillation : National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), Thailand

No abstract available

Keyword : No keyword available

Thursday 8 December 2022

[Lunch Symposium] Communicable Disease-Dengue Fever: The Spread and Detection

12.30-13.30hr

Room A

Abstract No. : ABS0001852

POPULATION MOBILITY AND THE SPREAD OF DENGUE

Sazaly Abubakar

Authors : Sazaly AbuBakar[1], Nurfatihah Zulkifli[1], Kim-Kee Tan[1] and Nurhafiza Zainal[2]

Affillation : [1]Tropical Infectious Diseases Research and Education Centre (TIDREC), Higher Institution Centre of Excellence (HICoE), Universiti Malaya, 50603 Kuala Lumpur, Malaysia; [2]Department of Medical Microbiology, Faculty of Medicine, Universiti Malaya, 50603 Kuala Lumpur, Malaysia

Introduction: A draconian population mobility restriction known in different countries as population lockdown and home quarantine was introduced after the emergence of the COVID-19 pandemic in 2020. Here, we sought to examine the impact of population mobility restrictions on dengue transmission.
Methodology: Data were gathered from MEDLINE®, WHO Country reports, respective countries\' Ministry of Health websites, and press releases. Data from peer-reviewed publications were used and supplemented with those captured from reference lists and other grey literature sources including news reporting. Reports on dengue including outbreaks, number of cases and deaths, and the possible factors affecting transmission were searched.
Results: Malaysia recorded a 27% drop in dengue cases in 2020, during the period when population mobility restriction was first introduced. Vietnam, Sri Lanka, and China which instituted various forms of population mobility restriction measures also reported a reduced dengue rate of 55-65%, 74%, and 95%, respectively. Earlier, reports and epidemiological statistical models suggested the importance of population mobility in the spread of dengue. In addition, asymptomatic DENV infections with a high level of viremia and human mobility for onward DENV transmission were also highlighted. A resurgence of dengue cases is being reported in Malaysia and other endemic countries in 2022 where population mobility restriction measures have been eased.
Conclusion: The remarkable dropped in dengue cases and dengue-associated deaths during the COVID-19 pandemic lockdown measures supports the assertion that population mobility is pivotal in the spread and transmission of dengue.

Keyword : Asymptomatic, COVID-19, Dengue, Pandemic, Population, Virus

Abstract No. : ABS0001857

DEVELOPMENT OF SEMI QUANTITATIVE LATERAL FLOW TEST FOR NS1 DENGUE SELF TEST AND DETECTION OF SEVERE DENGUE

Nurul Shazalina Zainudin

Authors : Nurul Shazalina Zainudin[1], Sivalingam Rajagopal[1], Murni Noor Al-Amin[1], Ummu Hafizah A Rahman[1], Sazaly AbuBakar[2], Pooi Fong Wong[3]

Affillation : [1]Accobiotech, Jalan Bukit 27, Masai Industrial Park, Bandar Seri Alam, 81750, Masai, Johor, Malaysia; [2]Tropical Infectious Diseases Research and Education Centre (TIDREC), Higher Institution Centre of Excellence (HICoE), Universiti Malaya, 50603, Kuala Lumpur, Malaysia; [3]Department of Pharmacology, Faculty of Medicine, Universiti Malaya, 50603, Kuala Lumpur, Malaysia

Introduction: Dengue is one of the most important mosquito-borne viral diseases in the world. It may present as an asymptomatic infection, mild fever or severe disease. Early diagnosis can help in improving patient care, and providing appropriate and prompt treatment that can prevent complications and mortality. Here, we present a method to detect the dengue virus non-structural protein 1 (NS1) using a semi-quantitative lateral flow test via a smartphone imaging system and another semi-quantitative method for the detection of severe dengue using a gradient ladder bar lateral flow test.

Methodology: Two prototypes were fabricated in the dipstick test format that utilizes host-specific capture and detection antibodies for the detection of dengue virus NS1 antigen in the mild dengue fever patients' sera, and detection of biomarker X in severe dengue sera. An imaging and reporting system was developed to differentiate the positive and negative results for NS1 using a smartphone. While a gradient ladder bar lateral flow optimization was performed for the detection of severe dengue.

Result: The imaging and reporting system for the detection of NS1 were successfully designed. The ladder bar format assay for the detection of severe dengue still needs further optimization.

Conclusion: The imaging system using a smartphone can help the community in dengue high-risk areas to do home self-test. Results from the testing can be converted to a report that will be useful for the patient and hospitals. While the ladder bar lateral flow test is a promising new method to detect severe dengue

Keyword : Dengue, lateral flow test, semi-quantitative, home self-test, severe dengue

Thursday 8 December 2022

S26 : Young Investigator Awards I

13.30-15.00hr

Room A

Abstract No. : ABS0001655

FEBRILE ILLNESS AMONG ADMITTED PATIENTS OF COVID- 19-ASSOCIATED RHINO-ORBITAL-CEREBRAL MUCORMYCOSIS: A PHYSICIANS' EXPERIENCE FROM A TERTIARY CARE CENTRE IN NORTHERN INDIA

Saurabh Pandey

Authors : Pandey S.[1] , Reddy D.H.[2], Priyanka R.[3], Malhotra H.S.[2], Chauhan P.[2], Agarwal V.[2]

Affillation : [1]SARITHI (Service Advocacy & Research in Infectious-Tropical disease & Health in India), Gorakhpur; [2]King Georges Medical University, Lucknow; 3- M V A state Medical College, Basti

Introduction: The epidemic of COVID 19 associated rhino-orbital-cerebral mucormycosis (CAM) involved prolonged admission and during stay they developed febrile illnesses due to variable reasons including drug fever.

Methods: All consecutive patients of CAM who developed fever were enrolled and all patients with fever persisting beyond 72 hours or showing systemic involvement were investigated for cause of fever. Patients were divided into 2 categories as localising (Lo) and non-localising (NL) cause groups.

Results: Out of 352 patients 98 (27.8%) patients experienced febrile episode. 58 (59.2%) had fever of more than 72 hours. There were 48 (85.7%) male in our study. Mean age of the patients was 50.8 years. 29.4% were localizing cause (Pneumonia, UTI, thrombophlebitis, diarrhoea, deep vein thrombosis & unkown source sepsis) whereas NL included-drug fever & long COVID syndrome. The onset of fever among drug related fever started significantly earlier than non-drug related fever (10.48 (SD= 9.82) v/s 18.93(SD=20.86); p

Conclusion: A majority of immediate fever were attributable to drug allergy & post debridement whereas majority of persistent fever were drug fever along with hospital acquired infections and thrombophlebitis. Diagnose each case clinically and prevent drug fever over-diagnosis and unnecessary withdrawal of life-saving medication like amphotericin-B.

Keyword : COVID 19 associated rhino-orbital-cerebral mucormycosis, drug fever, long COVID syndrome

Abstract No. : ABS0001764

ANTIBODY AVIDITY MATURATION FAVORS SARS-COV-2 CONVALESCENTS OVER VACCINATED INDIVIDUALS GRANTING BREADTH IN NEUTRALIZABILITY AND TOLERANCE AGAINST VARIANTS

Yu Nakagama

Authors : Yu Nakagama[1], Katherine Candray[1,2], Natsuko Kaku[1], Sachie Nakagama[1], Chihiro Watanabe[1], Yuko Nitahara[1], Evariste Tshibangu-Kabamba[1], Yasutoshi Kido[1]

Affillation : [1]Osaka Metropolitan University; [2]Centro Nacional de Investigaciones Científicas de El Salvador (CICES)

Introduction: Avidity maturation is the biological process whereby antigen-driven selection of higher affinity antibodies with better complementarity toward epitopes augment the host's protective immunity. We investigated the role of avidity maturation to determine in vitro SARS-CoV-2 neutralizability.

Methods: Convalescent individuals who had recovered from COVID-19 and recipients of the BNT162b2 vaccine were recruited. Serum samples were collected at 2- or 10-months convalescence, and 3 or 25 weeks post-vaccination. Avidity indices of serum anti-spike antibodies were measured by an ELISA platform with the addition of 5.5 M urea. The neutralizing ability of serum antibodies was assessed by surrogate virus neutralization.

Results: Compared with early-convalescent sera, the avidity index of late-convalescent sera was significantly higher ($p < 0.0001$), indicating a progressive maturation process that extends months beyond the acute phase of COVID-19. The urea-resistant, high-avidity fraction of antibodies was better predictive of in vitro neutralizability (Spearman's $r = 0.67$). Higher-avidity convalescent sera showed greater cross-neutralizability against known SARS-CoV-2 variants ($p < 0.001$ for Alpha, and $p < 0.01$ for Delta and Omicron, Mann-Whitney's). Vaccinees experienced avidity maturation following the second booster dose, though with delayed kinetics compared with convalescent individuals. The breadth of neutralizability of vaccinees' sera was limited compared with that of convalescent sera.

Conclusions: The continuous process of avidity maturation grants broader neutralizability and robust protection that is resilient against emerging SARS-CoV-2 variants. With immunopotentiation through repeat vaccinations becoming a pivotal strategy to accomplish herd immunity, it is crucial to understand the longitudinal evolution of the vaccine-induced immune response.

Keyword : SARS-CoV-2, Antibody maturation, Avidity, Neutralization breadth, Variants of concern

Abstract No. : ABS0001675

STRUCTURAL CHARACTERIZATION AND COMPARISON OF BIFUNCTIONAL HPPK-DHPS ENZYME WITH PATHOGENIC MICROBES

Rini Chaturvedi

Authors : Rini Chaturvedi[1], Jyoti Chhiber-Goel[1], Amit Sharma[1,2]

Affillation : [1]International Centre for Genetic Engineering & Biotechnology (ICGEB), New Delhi, India; [2]National Institute of Malaria Research (ICMR-NIMR), New Delhi, India

The rapid surge in reports of drug resistance in malaria threatens the gains achieved so far in its control and elimination agenda. Resistance to two validated targets of sulfadoxine(SDX) and pyrimethamine(PYR) against Pf/PvDHPS and DHFR have been emerging across the globe. The global spread of resistance and conservation of these enzymes across species is a necessity to discover potent inhibitors against these enzymes. Here, we present the global spread of resistance against Sdx-Pyr. Further, the crystal structures of the HPPK and DHPS across all pathogenic species were compared, and virtual screening of potential compounds for the HPPK active site was performed. i)The fully- and super-resistance mutants – quintuple (IRN-GE) and sextuple (IRN-GEG) are widespread in multiple African countries along with South Asian countries including India.ii)Structural analyses of DHPS protein in complexes with substrates/drugs have revealed that resistance mutations map proximal to sulfa drug binding sites. The importance of conformational changes in the protein results in similar changes in the active site of the enzyme.iii)The effective potent inhibitors against HPPK enzyme of the pathogenic species will not allow the incorporation of natural substrate in the DHPS enzyme ultimately leading to inhibition of folic acid pathway. Given the high conservation of the active site of HPPK and DHPS enzymes in organisms,the screened potent molecules against Pf/Pv HPPK enzyme might prove to be effective against all pathogens. This counteracts the rising antimalarial resistance and pave a way to a new lead of compounds that could target the validated enzymes of pathogens.

Keyword : Malaria, Plasmodium folate pathway, HPPK-DHPS, DHFR

Abstract No. : ABS0001744

DEVELOPMENT OF SELF-TEST KIT FOR DETECTION OF DENGUE FEVER

Nurfatihah Zulkifli

Authors : Nurfatihah Zulkifli[1], Naim Che-Kamarudin[1], Nurul-Atiqah Nor-Hazan[1], Nurul-Shazalina Zainudin[2], Sivalingam Rajagopal[2], Sazaly AbuBakar[1]

Affillation : [1]Tropical Infectious Diseases Research and Education Centre (TIDREC), Higher Institution Centre of Excellence (HICoE), Universiti Malaya, 50603 Kuala Lumpur, Malaysia; [2]Accobiotech Sdn Bhd, Industrial Park, 81750 Masai, Johor, Malaysia

Introduction: Dengue fever is a disease that requires early detection to help differentiate against other febrile illnesses. Currently, febrile patients suspected of having dengue are required to go to the healthcare facility to get tested for dengue. A diagnostic approach that empowers a febrile person to perform his/her own test is needed. Here, we described an approach toward democratizing diagnostics of dengue.

Methodology: A lateral flow immunochromatography test (ICT) was employed for the development of a home-based self-test dengue fever detection kit. The DENV NS1-specific monoclonal antibody (mAb) was layered on the test pad. The captured NS1 then will be visualized using a conjugate to the mAb to give the colorimetric detection on the test pad. The detection system was packaged in an easy-to-use cartridge. To enable a person to perform a self-test on his/her own, the test device, an alcohol swab, lancet, disposable dropper, assay buffer, and test manual were provided.

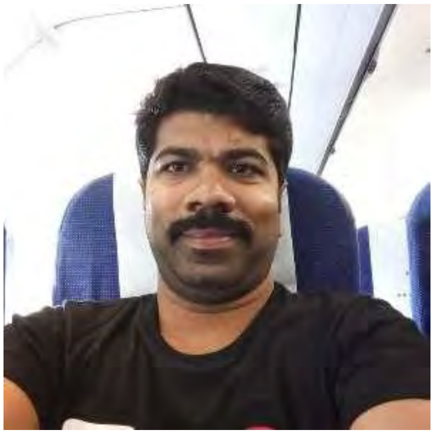
Results: A preliminary study involving three individuals was conducted. The volunteers performed the self-test and interpreted the test results according to the interpretation table. All the volunteers successfully performed the test on their own following the provided manual. All three completed the test in less than 20 minutes and accurately obtained the expected results.

Conclusion: A home-based self-test kit for the detection of dengue was established. The test was easy to perform by simply following the manual provided. This home-based self-test diagnostic could be further explored for wider application for the early detection of dengue.

Keyword : Infectious diseases, Diagnostics, Dengue, Self-test

Abstract No. : ABS0001714

IN-SILICO AND IN-VITRO APPROACH ON ANTI DENGUE ACTIVITY OF MARMELINE (AEGLE MARMELOS) AGAINST DENGUE VECTOR, AEDES AEGYPTI AND DENGUE VIRUS NS5 METHYLTRANSFERASE



Kovendan Kalimuthu

Authors : Kalimuthu Kovendan[1*], Arulsamy Jebanesan[1] and Savariar Vincent[2]
Affillation : [1]Division of Vector Biology, Department of Zoology, Annamalai University, Annamalainagar – 608 002, Tamil Nadu, India; [2]P.G. Research & Department of Advanced Zoology and Biotechnology, Loyola College, Nungambakkam, Chennai – 600 034, Tamil Nadu, India

Introduction: Insect-borne diseases continue to be a major source of sickness and death worldwide. Resistance to chemical pesticides and their risks have been regarded as a setback in mosquito vector control. Due to the presence of various phytochemical compounds in plant species, botanicals can manage and prevent vector (insect) transmitted illnesses by killing insect eggs and larvae. The objective of this study was to evaluate the mosquitocidal potential and antiviral effect of marmeline compound against Aedes aegypti and dengue viral protein NS5 methyltransferase were assessed by both in-vitro and in-silico.

Methods: Marmeline compound toxicity assays of dengue vector, Ae. aegypti larvae and adults using conventional techniques and methods (Kovendan et al., 2013). In-vitro anti-dengue activity of NS5 methyltransferase (Sujitha et al., 2015), in-silico anti-dengue activity of marmeline against NS5 methyltransferase (1L9K) (Chanprapaph et al., 2005).

Results: Larval and adult mortality was recorded after 24 h of exposure. Our findings showed that the Marmeline compound of Aegle marmelos has higher larvicidal activity (100 percent at 10 µg/mL) and adult mortality occurred 90 percent at 10 µg/mL of marmeline treatment. Marmeline have good antiviral property against Dengue virus DENV2. Moreover, we perform the Marmeline compounds were docked against the receptor protein NS5 methyltransferase, the mol dock score was-5.08 (kcal/mol).

Conclusion: Marmeline compound proved strong anti-dengue and mosquitocidal abilities that were effective against both the NS5 virus and dengue vector. Therefore, this study was found the novel drug molecules as anti-dengue compound using the structure based drug design technique.

Keyword : Aegle marmelos, Marmeline, In-vitro, In-silico, anti-dengue, Aedes aegypti

Thursday 8 December 2022

S27 : Emerging Viral Diseases

13.30-15.00hr

Room B

GLOBAL VIROME PROJECT

Dennis Carroll

Authors : Dennis Carroll

Affillation : Global Virome Project

No abstract available

Keyword : No keyword available

EMERGING VIRAL DISEASES: MILITARY CONCERNS

Stefan Fernandez

Authors : Stefan Fernandez

Affillation : AFRIMS

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001845

EYWA - EARLY WARNING SYSTEM FOR MOSQUITO BORNE DISEASES

Jonas Schmidt-Chanasit

Authors : Schmidt-Chanasit, J.[1]

Affillation : [1]Bernhard Nocht Institute for Tropical Medicine, WHO Collaborating Centre for Arbovirus and Haemorrhagic Fever Reference and Research

More than 80% of the global population lives in areas at risk of at least one major Vector-Borne Disease (VBD), with more than 700.000 deaths at a global scale. Mosquitoes are the protagonists of these vectors, carrying and transmitting various pathogens to humans. During the last decades, arthropod-borne viruses that are endemic in Europe, such as West Nile virus, have expanded their geographic range into Germany and caused an increasing number of epidemics with a total number of 4.226 WNV cases in Europe between 2008-2020 and the respective WNV cases with an upward trend imply hospitalization and relative costs as well as long term morbidity with following costs to health systems. Thus, an Early warning system for mosquito borne disease (MBD) is an urgent need in Germany. This need gave birth to the idea of EYWA, an integrated and contemporary EarlY WArning System (EWS) for MBD. The identification of MBD outbreaks in Germany is challenging and requires a high degree of awareness and laboratory capacity. In the past, translating forecast risk and observed patterns from surveillance programs into effective response plans have been hampered technically by modeling limitations and quality and rapid processing of surveillance information. EYWA was pre-operationally tested in Baden-Wuerttemberg region in Germany, forecasting Culex mosquito populations, during the mosquito season in 2020 and 2021. EYWA continues its operation in 2022, informing the local authorities and decision makers. The Report contains Culex mosquitoes abundance predictions at each trap, as produced by the MAMOTH model. In the Report you

Keyword : arbovirus, mosquito

Abstract No. : ABS0001779

TIME COURSE OF ANTIBODY RESPONSES AND NEUTRALIZATION CAPACITY IN LONGITUDINAL SERUM SAMPLES FROM PCR-CONFIRMED COVID-19 PATIENTS AND COVID-19 VACCINEES

Ronald von Possel

Authors : R. von Possel[1,2], C. Deschermeier[3], P. Emmerich[1,2]

Affillation : [1]Bernhard Nocht Institute for Tropical Medicine, Department for Virology, Hamburg, Germany; [2]Department of Tropical Medicine and Infectious Diseases, Center of Internal Medicine II, University of Rostock, Rostock, Germany; [3]Bernhard Nocht Institute for Tropical Medicine, Department for Infectious Disease Diagnostics, Hamburg, Germany

Introduction: Time-course analyses of specific antibody titers induced by natural SARS-CoV-2 infection and SARS-CoV-2 vaccination are necessary to investigate the persistence of potentially protective humoral immune responses.
Methods: Longitudinal serum samples were collected from more than 36 individuals with a PCR-confirmed SARS-CoV-2 infection as well as from individuals having received COVID-19 vaccines. Samples were analyzed using binding assays (in-house immunofluorescence testing, commercially available and in-house ELISAs, commercially available surrogate virus neutralizing ELISAs, line blotting) and in vitro virus neutralization tests.
Results: Humoral immune responses in SARS-CoV-2 infected patients with mild COVID-19 disease were monitored up to more than 500 days post infection. IgG immunofluorescence antibody titers varied widely between individual patients, peaking at approximately 1 to 2 months post infection and then subsequently waning. Nevertheless, neutralizing antibodies were still detectable in most patients at 12 - 16 months post infection. ELISA testing using both spike- and nucleocapsid protein-based tests confirmed these results, although assay sensitivity significantly influences estimated antibody persistence time frames. High anti-spike IgG antibody titers with a strong neutralizing activity were induced in convalesced COVID-19 patients already after administration of only a single dose of vaccine (BioNTech/Pfizer, Moderna, AstraZeneca).
Conclusion: Time-course analyses of specific antibody titers induced by natural SARS-CoV-2 infection revealed persistence of neutralizing humoral responses for more than 500 days post infection, but titers decline over time. Anti-spike IgG antibody titers in convalesced COVID-19 patients are strongly boosted by a spike-based mRNA and vector vaccines.

Keyword : antibody time course, neutralizing antibodies, humoral immune response

Thursday 8 December 2022

S28 : Control and Elimination of Tropical Diseases in China

13.30-15.00hr

Room C

Abstract No. : ABS0001891

SCHISTOSOMIASIS ELIMINATION IN CHINA

Xiao-Nong Zhou

Authors : Xu J, Li S-Z , **Zhou X-N**

Affillation : National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention (Chinese Center for Tropical Diseases Research), Shanghai, People's Republic of China

Introduction: Schistosomiasis, due to human infections with Schisosoma japonicum, has been prevalent in China for more than 2100 years. Schistosomiasis japonica distributed in 12 provinces in southern China. In 1950s, a total of 11.6 million human cases detected with 100 million people at risk of infection.
Methods: We reviewed the progress of the national schistosomiasis control programme, and distill the lessons learnt from the national schistosomiasis control and elimination programmes in China.
Results: Since then, the national schistosomiasis control program has been intensively implemented supported by the National Council politically and financially. With the efforts last 7 decades, the human and animal prevalence in all counties have reduced significantly. The surveillance data showed that the number of cases in 2021 was 29 041, and 99.98% (29 037/29 041) of them are advanced cases who not involving in transmission of the disease. The infection rate of schistosomiasis in bovines declined to zero in 2021. About 75.17% (339/451) counties have been validated in an elimination status, 22.17% (100/451) counties have been in a status of transmission interruption, 2.66% (12/451) counties have been in a status of transmission control.
Conclusion: Political commitment to support the program is essential by sustained recognition of the public health significance of schistosomiasis control and elimination. The control strategy has been adapted with time of the program advanced, by tailoring control interventions to the specific eco-epidemiological settings and over time as the challenge of control changes, by use of community-based multiple interventions in integrated way as well as in

Keyword : Schistosomiasis, Schisosoma japonicum; Control programme; Elimination; China

Abstract No. : ABS0001892

FROM 30 MILLION CASE TO ZERO: EXPERIENCES FROM MALARIA ELIMINATION IN CHINA

Qi Gao

Authors : Gao Qi [1], Cao Jun [1]

Affillation : Jiangsu Institute of Parasitic Diseases China

Abstract : China use to be high malaria burden country with more than 30 million cases annually in the history. China caried out national malaria elimination working plan since 2010. The last indigenous cases reported in 2016 and there were no indigenous cases since 2017. WHO certification malaria free in China in 2021. The 5 key elements of malaria elimination (Political support, financial support, multi-sector cooperation and Community participant, capacity building as well as 1-3-7 new strategy for malaria elimination) shown as China experiences for malaria elimination.

Keyword : Malaria Elimination

HOW TO CONTROL COVID-19 IN THE WORLD?

Hong-Zhou Lu

Authors : Hong-Zhou Lu

Affillation : Department of Infection and Immunology, Shanghai Public Health Clinical Centre, Fudan University, Shanghai, China

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001884

TROPICAL MEDICINE DEVELOPMENT AT HAINAN MEDICAL UNIVERSITY

Guojing Yang

Authors : Guo-Jing Yang

Affillation : School of Tropical Medicine, Hainan Medical University

Hainan Medical University (HNMU) was born for the health of the Hainan people, prosperious due to the establishment of a province and a special zone in Hainan, and strengthened by the “Belt and Road” strategy and the construction of free trade ports. HMNU aims to be an international high-level medical university with distinctive tropical characteristics. The School of Tropical Medicine was officially renamed in December 2021. It integrates teaching and scientific research and is the cradle of training talents in clinical medicine (tropical disease direction), medical laboratory technology, environmental science, health inspection and quarantine. Tropical medicine discipline features tropical medicine and trains multi-level high-quality talents in junior college, undergraduate, master, doctoral, and post-doctoral students. The school actively promotes professional teaching reform, improves the teaching / research levels, and the quality of professional courses, and has achieved fruitful products. After more than 20 years of hard work, pioneering and innovating, tropical medicine disciplines at HNMU now is in a good situation with a full range of teaching, a reasonable academic echelon, and coordinated development of teaching and scientific research. HNMU will continue to strengthen the tropical medicine and serve the construction and development of Hainan Free Trade Port.

Keyword : Hainan Medical University, Tropical Medicine, Development

Thursday 8 December 2022

S29 : Epidemiological and Genetic Malaria Risk Factors

13.30-15.00hr

Room D

Abstract No. : ABS0001809

PLASMODIUM FALCIPARUM AND PLASMODIUM VIVAX RESISTANCE TO ANTI-MALARIAL DRUGS IN INDONESIA

Farindira Vesti Rahmasari

Authors : Farindira Vesti Rahmasari[1,2], Puji Budi Setia Asih[3], Farahana Kresno Dewayanti[3], Chawarat Rotejanaprasert[4], Prakaykaew Charunwatthana[5], Mallika Imwong[1], Syafruddin[3,6]

Affillation : [1]Department of Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol University, Thailand; [2]Department of Parasitology, School of Medicine, Faculty of Medicine and Health Sciences, Universitas Muhammadiyah Yogyakarta, Indonesia; [3]Eijkman Research Centre for Molecular Biology, National Research and Innovation Agency, Jakarta, Indonesia; [4]Department of Epidemiology, Mahidol-Oxford Tropical Medicine Research Unit (MORU), Mahidol University, Thailand; [5]Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol University, Thailand; [6]Department of Parasitology, Faculty of Medicine, Hasanuddin University, Makassar, Indonesia

Introduction: DHA-PPQ has been the first line anti-malarial drug that was adopted in Indonesia since 2008. The widespread reports of treatment failures indicate that the situation could change rapidly. The present study investigated the genotypic profiles of P.falciparum and P.vivax isolates following the adoption of DHA-PPQ for any uncomplicated malaria cases.

Methods: A systematic review from 1991 to the present, as well as a longitudinal research survey of 100 archived P. falciparum isolates collected through the Mass Blood Survey or TES in Sumba and Papua from 2010 to 2020. DNA sequences was analysed based on target genes such as pfK13, pfpm2, pfcrt, pfmdr1 and pfmdr2.

Results: The study revealed the absence of the SNPs associated with delayed in parasites clearance in pfK13, although several novel SNPs in pfK13 and pfcrt were detected in P. falciparum isolates during the study period. We detected a proportion of pfcrt K76T ranging from (5%-50%) to (25%–33%), revealing a significantly decreased prevalence compared to the previous study. Recently, a new background mutation pfmdr2 was found to be putatively associated with ART resistance. All the 6 recurrent P. falciparum infection isolates were observed to have no amplification in pfpm2. The I165V mutation in pvK12 and pvpm4 is not associated with ART and PPQ drug resistance based on review study.

Conclusion: DHA-PPQ continues to be effective for treatment of P. falciparum as well as of P. vivax. Consideration should therefore be devoted to identifying early dynamical changes in order to adapt chemotherapeutic treatment strategies that effectively avoid

Keyword : P.falciparum, P.vivax, Indonesia, molecular, drug resistance

Abstract No. : ABS0001805

GLUCOSE-6-PHOSEPHATE DEHYDROGENASE DEFICIENCY AND MALARIA AMONG PRIMARY SCHOOL CHILDREN IN BORDER PATROL POLICE SCHOOLS, MAE HONG SON PROVINCE

Nardlada Khantikul

Authors : Nardlada Khantikul[1], Aungkana Saejeng[1], Thunyapan Ruantip[1], Sarinee Srithep[1], Jintana Chaiwan[2], Somchat Booncamma[1], Saowanee Viboonsanti[1], Mallika Imwong[3]

Affillation : [1]The Office of Disease Prevention and Control No.1 Chiang Mai, Department of Disease Control, Ministry of Public Health, Thailand; [2]Malaria Elimination Initiative (MEI) at the University of California, San Francisco (UCSF); [3]Department of Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol University

Malaria along international border remains health crisis especially among children and young people. This was a reason to carry out phase I of a cross-sectional descriptive study to collect base-line data and to continue to conduct phase II of one-group pretest-posttest quasi-experimental design to assess causal relationship between variables before and after implementation of malaria knowledge, perception, G6PD deficiency, and preventive behaviors. The study samples were 392 students recruited from all school children grades 1-6 in eleven schools in highest endemic areas. The methods covered data collection were interviews with structure questionnaire before and after the implementation, while the screening of G6PD deficiency relied on a modified fluorescent spot test set. The data analyses had multiple approaches encompassing relationships of variables of knowing about malaria and G6PD deficiency. Assessments relied on percentages, means, S.D., χ2test, multiple logistic regression, and paired t-test. The results from phase I showed the prevalence rate of G6PD deficiency was 10.46 (41/392). It was necessitated to correct for their better awareness of G6PD deficiency, knowing malaria, perception and preventive behaviors within the rates of 95.2, 87.8, 55.6 and 80.9%, respectively. The determinants associated with the preventive behaviors were malaria risk perception, benefit of treatment, preventive methods, and daily self-care ($p<0.05$). The results from phase II revealed mean scores of knowledge, perception, G6PD deficiency, and preventive behaviors were significantly higher after implementation ($p<0.05$). Implications of the findings impressed on benefits from the implementation to pursue young school children protected themselves with correct preventive and treatment of malaria.

Keyword : Malaria Prevention, G6PD Deficiency, Communication Program

Abstract No. : ABS0001807

THE USE OF GLUCOSE -6- PHOSPHATE DEHYDROGENASE SCREENING TEST FOR MALARIA ELIMINATION IN THAILAND, 2015 – 2022

Aungkana Saejeng

Authors : Aungkana Saejeng[1], Nardlada Khantikul[1], Sarinee Srithep[1], Tanawat Kalabuch[1], Darunee Kongkarat[1], Saowanee Viboonsanti[1], Prayuth Sudatip[2], Mallika Imwong[3]

Affillation : [1]The Office of Disease Prevention and Control No.1 Chiang Mai, Department of Disease Control, Ministry of Public Health, Thailand; [2]Division of Vector Borne Disease Control, Department of Disease Control, Ministry of Public Health, Thailand; [3]Department of Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol University

Plasmodium vivax has become a predominant malaria parasite species. The great challenge for this malaria parasite species treatment is how to prevent relapse. Primaquine or tafenoquine are used for radical cure of P.vivax malaria but both cause hemolysis and severe anemia in a patient with G6PD-deficiency. G6PD testing is recommended. The aim of this study was to analyze the use of the G6PD test in Thailand from 2015 to 2022. The data was taken from malaria online data and Mae Hong Son. The result revealed that the percentage of P.vivax patients who had G6PD tested dramatically increased from 0.7% in 2015 to 11% in 2021, then decreased to 6.3% in 2022. The total number of P.vivax patients tested for G6PD were 2,189 cases with 117 (5.3%) G6PD deficiency. 50.1%, 18.0%, 17.5%, and 14.4%, of these data, were reported from Mae Hong Son, Yala, Tak, and the other of 23 provinces, respectively. The prevalence of G6PD deficiency was 2.6 % by lateral flow G6PD RDT, 3.1% by modified FST, 6.6% by methylene blue, and 7.6% by G6PD quantitative. The result suggested that methylene blue and G6PD quantitative may be better G6PD tests for the management of P.vivax malaria with higher G6PD prevalence. However, overestimating G6PD deficiency result in the underused of primaquine. Therefore, the data herein is not the endpoint for selecting the G6PD test. Although G6PD testing is improving the clinical management of P.vivax malaria, the challenge is to make it more widely available with a good quality

Keyword : Keywords: G6PD deficiency, Plasmodium vivax, G6PD testing, primaquine, tafenoquine,

Thursday 8 December 2022

S30 : Mathematical Models To Inform Health Policy Decisions In Countries In Asia

13.30-15.00hr

Room E

Abstract No. : ABS0001880

RING VACCINATION FOR A POTENTIAL YELLOW FEVER OUTBREAK IN AN ASIAN CITY

Borame L. Dickens

Authors : Lim J.T.[1], Lim N.[2], Koo J.R.[2], **Dickens B.L.[2]**

Affillation : [1]Lee Kong Chian School of Medicine, Nanyang Technological University; [2]Saw Swee Hock School of Public Health, National University of Singapore

Yellow fever is an acute viral haemorrhagic vector borne disease endemic to tropical regions of Africa and South America. Carried by the Aedes aegypti mosquito, ongoing concerns exist regarding its potential introduction into unaffected areas where this vector is established. With a suitable vector breeding environment all year round and susceptible population, Singapore requires epidemic mitigation planning to minimise spread with potential importation events. Here we discuss the simulation of yellow fever case clusters utilising an agent-based model of Singapore's population which characterises their demographics, movement behaviour and risk of vector to host transmission. We examine the spread of the epidemic outwards as individuals move from different home, work, community or school sites, and model ring vaccination strategies with vaccine coverage of 10 to 90% and 7 to 14-day delays in implementation.

Keyword : Yellow fever; outbreak control; disease transmission modelling

Abstract No. : ABS0001883

WORKING TOWARDS HEPATITIS B ELIMINATION BY 2030: MODELING APPROACH TO OPTIMISE STRATEGIES TO REDUCE MOTHER-TO-CHILD TRANSMISSION

Myka Harun Sarajan

Authors : Sarajan M.H.[1], Poovorawan K.[2], Jittamala P.[1], Wirichada Pan-ngum[1,3]

Affillation : [1]Department of Tropical Hygiene, Faculty of Tropical Medicine, Mahidol University; [2]Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol University; [3]Mathematical and Economic Modelling Group, Mahidol-Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University

Viral infections caused by Hepatitis B Virus (HBV) have been the root of significant disease burden and death globally, as chronic HBV infections can lead to cholecystitis, severe liver damage and hepatocellular carcinoma (HCC). Despite the advancement of universal immunization against HBV, public health challenges persist as chronic hepatitis B (CHB) causes a worldwide substantial disease burden associated with liver diseases. Thus, prevention of mother-to-child transmission (PMTCT) remains crucial. A transmission dynamic model, developed based on the disease progression of HBV and data found in literature, aims to examine the impact of appropriate strategies, including screening of HBV and PMTCT interventions, needed to achieve the 2030 WHO elimination goal of Hepatitis B Virus, specifically in Thailand.

Keyword : Hepatitis B virus, Hepatitis elimination goal, Mathematical modeling, Prevention of mother-to-child transmission

THE ECONOMIC IMPACT OF ROTAVIRUS VACCINATION: A COMPARATIVE MODELLING STUDY

Phetsavanh Chanthavilay

Authors : Phetsavanh Chanthavilay

Affillation : Unit for Health Evidence and Policy, Institute of Research and Education Development, UHS, Lao PDR

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001905

DATA-DRIVEN MATHEMATICAL MODEL FOR CROSS-BORDER CONTROL OF COVID-19 IN REOPENING OF THAILAND'S BORDER

Vidhyakorn Mahd-Adam

Authors : Mahd-Adam V.[1] , Thammawijaya P.[2], Rotejanaprasert C.[1], Pan-ngum W.[1,3]

Affillation : [1]Department of Tropical Hygiene, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [2]Department of Epidemiology, Ministry of Public Health, Nonthaburi, Thailand; [3]Mahidol-Oxford Tropical Medicine Research Unit (MORU), Bangkok, Thailand

From the subject review of Thailand's COVID-19 strategies against international travel and available sources of the pandemic data, we found a four-components of strategies include (1) Assessing the country's specific risk of infection from various sources of data, (2) Certification of the test of SARS-CoV-2 result and vaccine record before entry, (3) Disease screening on arrival (4) national COVID-19 quarantine strategies. Then, we proposed a data-driven mathematical model to assess the impacts of the control measures. Compartmental models are incorporated with algorithmic techniques to increase their potential in future decision-making. From the model, we quantify numbers and imported case (IC) reduction in different scenarios.

From the simulation, requiring vaccination before traveling has some impact on reducing IC. Testing at the point of departure would be the optimal testing, giving the most reduction, compared to early testing. In a combination of the control measures, quarantine was the key to reducing IC, by up to 90%. The significant reduction occurred with around 3 to 5 days of quarantine. For instance, a combination of the low-risk clusters, requiring a vaccine passport and a 3-day quarantine on arrival can reduce IC up to 80% in a 14-day quarantine.

However, in practice, the absolutes number of IC is ultimate and economic evaluation is needed to see overall impacts rather than only the IC reduction based. Collaboration among the public and private sectors is important in choosing the most optimal and efficient strategies.

Keyword : Mathematical Modelling, COVID-19, Cross-border travel, Data-driven, public health policy

Thursday 8 December 2022

S31 : Resilience Against Emerging Infectious Disease Threats

15.30-17.00hr

Room A

Abstract No. : ABS0001780

THE GLOBAL ARBOVIRUS INITIATIVE

Raman Velayudhan

Authors : Velayudhan R[1]

Affillation : [1]Veterinary Public Health, Vector Control and Environment unit (VVE), Department of Control of Neglected Tropical Diseases (UCN/NTD), World Health Organization

WHO launched a new initiative to monitor and control arthropod-borne viral diseases on March 31, 2022. The Global Arbovirus Initiative aims to “raise the global alarm on the risk epidemics of arboviruses and potential risk of outbreaks mainly affecting urban populations. The initiative provides a list of priority actions that countries and regions can implement to be prepared for the next arbovirus outbreak.

This initiative was initially discussed as a cross-cutting activity when some countries were facing severe dengue epidemics in 2019, and other Aedes-borne viruses such as chikungunya, yellow fever and Zika were well-documented. WHO secretariat prepared the draft of the initiative, and the Technical Advisory Group for Arboviruses met in December 2021 and finalized the initiative as an integrated approach that aims to collate the crucial components of the detection, prevention, and control of arboviruses.

The initiative is under the umbrella of the WHO Triple Billion Targets. It is complementary to the Eliminate Yellow Fever Epidemics strategy, Global Vector Control Response 2017-2030 and the Neglected Tropical Disease Roadmap 2021-2030. It is designed to monitor and control arboviral diseases on a global scale using six pillars. It also highlights the need for innovation in developing new diagnostics, drugs, sustainable vector control methods and vaccines.

Keyword : Arboviruses, Aedes borne diseases, Urbanization, disease burden

Abstract No. : ABS0001879

PANDASIA – A PROJECT FOR UNDERSTANDING ZOONOTIC SPILLOVER PATHWAYS FOR PANDEMIC PREVENTION AND PREPAREDNESS

Hans Overgaard

Authors : Overgaard H.J.[1,2], Treskova M.[3,4], Joacim Rocklöv[3,4]

Affillation : [1]Department of Microbiology & Tropical Medicine Research Center, Khon Kaen University; [2]Faculty of Science and Technology Norwegian University of Life Sciences; [3]Heidelberg Institute of Global Health (HIGH), Interdisciplinary Centre for Scientific Computing (IWR), Heidelberg University, Heidelberg Germany; [4]Department of Public Health and Clinical Medicine, Umeå University, Umeå, Sweden.

More than half of human emerging infectious diseases (EID) are zoonotic, caused by animal-to-human pathogen spillover. Viruses disproportionally contribute to zoonoses. Recent pandemics and outbreaks highlight the urgency of sustainable, effective, and evidence-based pandemic preparedness and prevention strategies. Improved understanding of zoonotic disease ecology, biology, reservoir-host interactions, transmission, and environmental factors can be translated into effective preventative actions and early preparedness. Research on spillover pathways at the human-animal-environment interface is crucial for creating and enhancing integrative public health measures at local and national levels. Southeast Asia presents unique settings to study spillover, as local communities are at high zoonotic risk due to high biodiversity, population movement, social practices, economic constraints, and knowledge gaps.

Methods: In the PANDASIA project we apply a One Health transdisciplinary approach for conducting systems analyses in selected study sites in spillover hotspot areas in Thailand. Data generation on human behaviors, social determinants, virus detection in wild and domestic animals, and people will provide input to analytic and predictive models informing early preparedness and design of pandemic literacy interventions to reduce viral spillover risk.

Contribution: By generating systematic scientific evidence, literacy gain and capacity building in communities, our approach will strengthen the current knowledge about spillover, contribute to know-how and enhance pandemic preparedness at local and national levels, overall contributing to global health security.

Conclusion: Zoonoses are an increasing threat to global health. Transdisciplinary research applying our approach in Southeast Asia bridges current knowledge gaps, generates action-viable evidence, and develops research know-how transferable to other settings.

Keyword : Pandemics, preparedness prevention, spillover, One Health, transdisciplinary

Abstract No. : ABS0001787

ANOPHELES STEPHENSI: CURRENT ACTIONS AND PLANS

Seth Irish

Authors : Irish S[1]

Affillation : [1]WHO GMP/Vector Control and Insecticide Resistance Unit, Geneva, Switzerland

Introduction: Anopheles stephensi was first detected on the African continent in Djibouti in 2012. It has since been found in at least four other countries (Ethiopia, Sudan, Somalia, Nigeria). Its ability to colonize urban settings is a worry for national malaria control programs. It is important to understand its distribution and plan effective interventions to prevent its spread.

Methods: The World Health Organization issued a Vector Alert (2019) to monitor the spread of An. stephensi in Africa. In addition to providing recommendations in this document, the WHO also developed a page for invasive species to share the information on the distribution of An. stephensi outside its native range. In 2022, the WHO launched an initiative against the spread of An. stephensi, and planned a regional meeting to be held in Ethiopia (November 2022).

Results: The Vector Alert and Malaria Threats Maps have proved to be valuable resources for the global community to understand the spread of An. stephensi. The launch of the initiative in 2022 focused on five key areas: 1) increasing collaboration, 2) improving information exchange, 3) strengthening surveillance, 4) developing guidance, and 5) prioritizing research.

Conclusion: The WHO aims to draw attention to the spread of An. stephensi as well as providing guidance for best practices in responding to this threat. It is up to individuals, communities, researchers, national health programs, donors, and other organizations to lead the fight against the spread of An. stephensi.

Keyword : Anopheles stephensi, invasive species, malaria, Africa

Thursday 8 December 2022

S32 : Tick-borne Pathogens Detection and Non-Pathogenic Microorganisms

15.30-17.00hr

Room B

Abstract No. : ABS0001792

HIGH-THROUGHPUT NANOTECHNOLOGIES FOR TICK-BORNE PATHOGENS DETECTION

Sara Moutailler

Authors : Moutailler S.

Affillation : ANSES, INRAE, Ecole Nationale Vétérinaire d\'Alfort, UMR BIPAR, Laboratoire de Santé Animale, Maisons-Alfort, France

Worldwide, ticks transmit more pathogens than other arthropods (around 60 bacteria, 30 parasites and 100 viruses; a third of them are responsible for zoonosis). Due to increased travel, climatic, and environmental changes, the incidence of tick-borne disease in both humans and animals is increasing throughout the world. Therefore, extended surveillance tools are desirable to better control ticks and tick-borne pathogens transmitted. To accurately screen tick-borne pathogens, new epidemiological tools were implemented in order to identify/detect 65 bacteria, 6 bacteria genus, 28 parasite species, 53 viruses and 8 tick species. Then large scale epidemiological studies were conducted through collaborative projects at the international level first in hard ticks, then in soft ticks and finally in mammals. Those advanced methodologies permitted the detection and the estimation of prevalence of expected, unexpected and rare tick-borne pathogens in different countries. Those new tools also demonstrated their ability to study tick co-infection and genetic diversity of tick-borne pathogens. Those surveillance methods represent a major improvement in epidemiological studies, able to facilitate comprehensive testing of tick-borne pathogens in ticks, mammals and humans, and which can also be customized to monitor emerging diseases.

Keyword : ticks, tick-borne pathogens, high-throughput detection, microfluidic real-time PCR

Abstract No. : ABS0001806

TOWARDS A BETTER SURVEILLANCE AND PREVENTION OF TICK-BORNE ENCEPHALITIS VIRUS ALIMENTARY INFECTIONS

Nolwenn Dheilly

Authors : Nolwenn M. Dheilly[1], Laure Matthews-Martin[2], Rayane Amaral Moraes[1], Laure Bournez[2], Marine Dumarest[1], Catherine Hennechart-Colette[3], Sandra Martin-Latil[3], Sylvie Perelle[3], Fabien Vorimore[4] , Cécile Beck[1], Gaëlle Gonzalez[1]

Affillation : [1]Anses, INRAE, Ecole Nationale Vétérinaire d'Alfort, UMR VIROLOGIE, Laboratoire de Santé Animale, Maisons-Alfort, F-94700, France;
[2]Anses, Nancy Laboratory for Rabies and Wildlife, , CS 40009, F-54220 Malzéville, France;
[3] Université Paris-Est, Anses, Laboratory for food safety, F-94700 Maisons-Alfort, France;
[4] Laboratory for Animal Health, Bacterial Zoonosis Unit, ANSES Maisons-Alfort, Paris-Est University, 94706 Paris, France

The expansion of Tick-borne encephalitis virus (TBEV) through Europe increases the risk of exposure and infection. In 2020, we witnessed the first major foodborne outbreak of TBE in France, in a department where the virus had never been detected before. We launched a One health investigation that revealed that infection was caused by the consumption of fresh cheese produced from the milk of goats that got infected through tick bites. While this mode of transmission is well documented, the actual risk that represent TBEV alimentary infections in France remains unknown. In addition, when infection occurs through the alimentary route, neurological symptoms are more frequent, and the pre-symptomatic phase is shortened.

Our objectives are therefore (i) to develop surveillance methods to better track the virus geographic circulation and transmission to dairy products during processing, and (ii) to characterize the factors that influence the clinical outcome of an alimentary infection by TBEV.

To achieve these goals we are deploying an epidemiological surveillance program in cattle and assessing the efficiency of different serological approaches, we have developed methods to detect the viral genome in dairy products and to sequence full-length genomes, and we have identified bacterial components and bacterial species isolated from fresh milk that modulate the virus infectivity. We are now investigating the damages that TBEV inflict to the gastro-intestinal tract and the role of bacteria translocation in modulating anti-viral immune responses.

This body of work opens up new prospects for the surveillance and prevention of alimentary borne TBEV infection.

Keyword : surveillance, food-borne, encephalitis, diagnostic, sequencing

Abstract No. : ABS0001794

SEVERE FEVER WITH THROMBOCYTOPENIA SYNDROME VIRUS: THE FIRST CASE REPORT IN THAILAND

Supitcha Ongkittikul

Authors : Supitcha Ongkittikul

Affillation : [1]Division of Infectious Diseases, Department of Medicine, Phyathai3 Hospital, Bangkok, Thailand; [2]Division of Neurology, Phyathai3 Hospital, Bangkok, Thailand; [3]Department of Infection Control, Phyathai3 Hospital, Bangkok, Thailand

We report a case of a 70-year-old Thai woman with severe fever and thrombocytopenia syndrome, who had lost all seven of her cats from sickness over a week. The diagnosis was established by the detection of viral RNA in serum via real-time polymerase chain reaction. Her symptoms improved after taking doxycycline orally and supportive treatment.

Keyword : severe fever with thrombocytopenia syndrome virus, Phlebovirus, encephalopathy

Abstract No. : ABS0001795

THE TICK MICROBIOME: WHY NON-PATHOGENIC MICROORGANISMS MATTER IN TICK BIOLOGY

Olivier Duron

Authors : Duron O.

Affillation : MIVEGEC Lab, French National Centre for Scientific Research

Ticks are among the most important vectors of pathogens affecting humans and animals worldwide. The list of known or potential tick-borne pathogens is constantly evolving, and includes a variety of viruses, bacteria, and protozoa. Our recent investigations in remotes ecosystems led to the description of unknown tick-borne disease agents, as in South American rainforests. However, ticks do not only carry pathogens, as a diverse group of commensal and symbiotic microorganisms are also present in ticks. Unlike pathogens, their biology and their effect on ticks remain largely unexplored, and are in fact often neglected. Nonetheless, they can confer multiple detrimental, neutral, or beneficial effects to their tick hosts, and can play various roles in fitness, nutritional adaptation, development, reproduction, defense against environmental stress, and immunity. Consequently, ticks represent a compelling yet challenging system in which to study microbiomes and microbial interactions, and to investigate the composition, functional, and ecological implications of bacterial communities. Ultimately, deciphering the relationships between tick microorganisms as well as tick symbiont interactions will garner invaluable information, which may aid in the future development of arthropod pest and vector-borne pathogen transmission control strategies.

Keyword : Ticks, Microbes, Tick-borne Diseases, Symbiosis

Thursday 8 December 2022

S33 : Improving Quantitative Decision Making for Policy in the Asia-Pacific Region

15.30-17.00hr

Room C

Abstract No. : ABS0001890

SPARK INTRODUCTION

Jodie McVernon

Authors : McVernon, J.[1]

Affillation : [1]The Peter Doherty Institute for Infection and Immunity, The University of Melbourne and Royal Melbourne Hospital, Melbourne Australia

Strengthening Preparedness in the Asia-Pacific Region through Knowledge (SPARK) is a consortium funded by the Australian Government Department of Foreign Affairs and Trade. It brings together a distributed team of Australian researchers with training partners and collaborators in Thailand (Mahidol), Vietnam (PIHCMC) and Indonesia (EOCRU). SPARK leverages additional investment from the Australian National Health and Medical Research Council through its partner Centre of Research Excellence, SPECTRUM.
Our overall approach is embedded within the structured decision-making framework, that recognises the importance of engaging with decision makers and problem owners to address challenges in their wider social, political and health systems context. While much of our work since 2020 has been focused on supporting COVID-19 response, our interests and skills span emerging infections, as well as vaccine preventable, vector borne, drug resistant and neglected tropical diseases.
SPARK and SPECTRUM support development of skills and capacity in the use of data to inform decisions about infectious diseases preparedness and response. Due to COVID-19 related disruptions, regional training activities were initially limited to online but have blossomed as borders have reopened. We are supporting post-doctoral researchers, fellows and graduate researchers, offering scholarships for training courses and workshops and developing early and mid-career researcher networks. We are focused on building in-country capability embedded in a range of disease programs to develop communities of practice across the region, with ability to pivot to future emerging infection challenges

Keyword : infectious disease modelling

Abstract No. : ABS0001893

MODELLING TO INFORM CONTROL POLICIES FOR SOIL-TRANSMITTED HELMINTH INFECTIONS

Patricia Campbell

Authors : Patricia Campbell

Affillation : Department of Infectious Diseases, Melbourne Medical School, Faculty of Medicine, Dentistry and Health Sciences

Strongyloidiasis is a parasitic disease caused by infection with the nematode Strongyloides stercoralis, a type of soil-transmitted helminth (STH). The disease spectrum ranges from asymptomatic to fatal and there is no resolution of infection without treatment. An estimated 50–100 million people are infected globally, with the prevalence of infection in tropical and subtropical settings up to 25%. Infection occurs when larvae penetrate the skin, typically entering through the feet on contact with a contaminated environmental reservoir. The life cycle of S. stercoralis is different to that of other soil-transmitted helminths, which may be important to how this pathogen spreads in a population. In addition, dogs may be infected with S. stercoralis and contribute to environmental reservoirs. We are developing mathematical models of S. stercoralis transmission that capture its unique features, such as auto-infection and the involvement of multiple hosts. Once developed, we will use these models to quantify the role of dogs in contributing to human disease and the likely impact of potential interventions, such as de-worming programs aimed at humans and/or dogs.

Keyword : modelling, helminth infections, Strongyloidiasis

Abstract No. : ABS0001900

SUPPORTING REMOTE RESEARCH WITH SPARK

Logan Wu

Authors : Wu L.[1,2,3]

Affillation : [1]Walter and Eliza Hall Institute; [2]University of Melbourne; [3]Shanghai Jiao Tong University

Research with significant overseas data collection components carry the risk of misclassification, missed opportunities for process improvement, and inaccurate inferences from data.
We discuss examples of past issues that have arisen and how we will mitigate these risks in upcoming malaria outbreak modelling work through in-country experience.
We then cover how in-country experience benefits the value chain from research aim inception to the dissemination of final outputs.
Finally, we outline the specific benefits of the SPARK consortium for graduate researchers conducting modelling studies in the Greater Mekong Subregion setting.

Keyword : spectrum, spark, Thailand, tha song yang, malaria, modelling

RESEARCH TO IMPROVE QUANTITATIVE DECISION MAKING FOR POLICY

Lauren Smith

Authors : Lauren Smith

Affillation : Walter and Eliza Hall Institute of Medical Research, Parkville Victoria, Australia

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001916

UNDERSTANDING THE IMPACT OF POPULATION IMMUNITY ON FUTURE COVID-19 WAVES: AN INDIVIDUAL-BASED MODELLING STUDY

Yasmine McDonough

Authors : TK Le[1,2], **Yasmine McDonough[3]**, Isobel Abell[1,2], Chris Baker[1,2,4], Camelia Walker[1], Alexandra Hogan[5], Michael Lydeamore[6], Eamon Conway[3], Logan Wu[3], Lauren Smith[3], Patricia Campbell[7,8,] Jodie McVernon[7,8,9], Ivo Mueller[3,10]

Affillation : [1]School of Mathematics and Statistics, The University of Melbourne, Melbourne, Victoria, Australia; [2]Melbourne Centre for Data Science, The University of Melbourne, Melbourne, Victoria, Australia; [3]Population Health & Immunity Division, Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria, Australia; [4]Centre of Excellence for Biosecurity Risk Analysis, The University of Melbourne, Melbourne, Victoria, Australia; [5]School of Population Health, University of New South Wales, Sydney, New South Wales, Australia; [6]Department of Econometrics and Business Statistics, Monash University, Melbourne, Victoria, Australia; [7]Department of Infectious Diseases, University of Melbourne, at the Peter Doherty Institute for Infection and Immunity, Victoria, Australia; [8]Melbourne School of Population and Global Health, The University of Melbourne, Victoria, Australia; [9]Victorian Infectious Disease Reference Laboratory Epidemiology Unit, The Royal Melbourne Hospital at the Peter Doherty Institute for Infection and Immunity, Melbourne, Victoria, Australia; [10]Department of Medical Biology, University of Melbourne, Melbourne, Victoria, Australia

Since its emergence in late 2019, SARS-CoV-2 (the causative agent of COVID-19) has spread worldwide, leading to a global pandemic. While much of the global community has experienced reasonably synchronous and large waves of SARS-CoV-2 infection, delayed entry of the virus into the Western Pacific Region (WPR) means that timing of epidemics has differed substantially. In many WPR countries the Omicron variant (BA1/2) was the first to establish high levels of community transmission. Subsequent importation of newer Omicron variants (e.g. BA4/5) has occurred in many countries or is anticipated. Efforts to minimise the impact of further epidemics in the WPR may include the administration of vaccines and boosters. Vaccine-acquired immunity protects against COVID-19 transmission and severe clinical outcomes. However, vaccine access and acceptance have been highly variable across populations in the WPR, and the efficacy of administered doses wanes over time. Together with variable exposure histories, the WPR exhibits a complex ‘immune landscape’, which presents challenges to understand the further spread of COVID-19. Here, we have developed a unique individual-based model that explicitly tracks individual immunity in the face of prior exposure, vaccination, and waning efficacy. Using this model, we can understand how differences in “immune landscapes” may impact the dynamics of SARS-CoV-2 variants of concern. We will discuss the application of our model using a case study of Samoa and illustrate how information gained from this model can guide decision-making.

Keyword : COVID-19, individual-based modelling, vaccination, neutralising antibodies, waning immunity, hybrid immunity, Western Pacific Region

TRAINING AND CAPACITY BUILDING WITH SPARK

Wirichada Pan-ngum

Authors : Wirichada Pan-ngum

Affillation : Faculty of Tropical Medicine, Mahidol University

No abstract available

Keyword : No keyword available

TRAINING AND CAPACITY BUILDING WITH SPARK

Zarni Lynn Kyaw

Authors : Zarni Lynn Kyaw

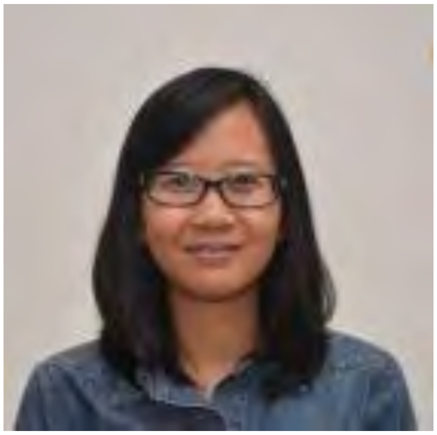
Affillation : Biomedical and Health Informatics Program (BHI), Faculty of Tropical Medicine, Mahidol University

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001917

CAPACITY BUILDING AT BIOMEDICAL AND HEALTH INFORMATICS, MAHIDOL UNIVERSITY TROUGH SPARK NETWORK



Karina Lestari

Authors : Lestari K.D.[1,2], Elyazar I.[1], Pan-ngum W.[2,3]

Affillation : [1]Oxford University Clinical Research Unit (OUCRU) Indonesia, Faculty of Medicine, Universitas Indonesia; [2]Department of Tropical Hygiene, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [3]Mahidol Oxford Tropical Medicine Research Unit (MORU), Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand.

Enrolling in Biomedical and Health Informatics at Mahidol University and joining SPARK network enables me to improve my capacity in quantitative methods and modelling. The courses are comprehensive, covering the informatics, clinical, and statistics aspects which helpful knowledge to develop methods and tools for adaptive decision-making to inform disease prevention, control, and elimination. Through SPARK network, I also experienced to learn developing simple math models in their Mathematical Modelling short course. I had the chance to meet and have discussions with people from around the world with various backgrounds which were very insightful. The experience and knowledge I gained from the courses will be used to analyse the epidemiology of malaria in Indonesia. Malaria is a vector-borne disease that continues to be a leading global health concern. The World Health Organization estimated 242 million cases of malaria in 2020. Since 2010, the number of malaria cases reported in Indonesia has decreased from approximately 500,000 to over 235,000. However, the rate of decline has been slow, impeding Indonesia\'s efforts to eradicate malaria by 2030. In Indonesia, the presence of mobile and migrant populations, such as forest workers, miners, and loggers, complicated efforts to eradicate malaria. The study will analyse the individual-based national malaria database for year 2019 to 2021, to describe the important characteristics of spatial-temporal pattern of malaria on the island of Sumatera. The finding will facilitate NMCP to develop targeted interventions.

Keyword : SPARK, capacity building, training and career development, malaria

Thursday 8 December 2022

S34 : What Makes a Good Randomized Controlled Trial

15.30-17.00hr

Room D

Abstract No. : ABS0001887

INTRODUCING THE GOOD CLINICAL TRIALS COLLABORATIVE (GCTC) GUIDANCE: FIVE PRINCIPLES OF A GOOD TRIAL TO ENHANCE TRIALS ECOSYSTEMS FOR EVERYONE

Rachel Hallett

Authors : Sir Landray M.[1,2], Medhurst, N.[2] , **Hallett R.[2]**

Affillation : [1]Nuffield Department of Population Health, Oxford University; [2]The Good Clinical Trials Collaborative

Introduction: The Covid pandemic has clearly illustrated that there is a substantial need for good Randomized Controlled Trials (RCTs) to better understand the benefits and hazards of medical interventions. The Good Clinical Trials Collaborative (GCTC), supported by Wellcome and the Bill and Melinda Gates Foundation, was set up to create new guidance to promote and enable the conduct of high-quality RCTs.
Methods: In autumn 2020, the Collaborative convened two workshops with a multi-disciplinary, multi-stakeholder group of 84 members (the Writing Group) representing a diverse, global spread to help design the guidance. Draft content was reviewed by 40 experts across 3 sessions in winter 2020, exploring scientific and ethical considerations alongside the clinical context of a RCT and quality management.
Results: Draft Guidance was launched for public consultation in summer 2021. The Guidance was finalized and published on www.goodtrials.org in May 2022. The agreed Five Principles of Good RCTs are that they:

1. are designed to produce scientifically sound answers to relevant questions.
2. respect the rights and well-being of participants.
3. are collaborative and transparent.
4. are designed to be appropriate for their context.
5. manage quality effectively and efficiently.

Conclusion: We believe The Guidance can be a foundation of common understanding that good healthcare is informed by good evidence from good trials. The Guidance can support all individuals and organizations involved at any stage of a RCT, and is applicable across all disease areas, intervention types, phases, designs and healthcare settings. The Collaborative now aims to develop a suite of educational tools that can support all stakeholders with implementing the principles of good RCTs.

Keyword : Randomized Controlled Trials, Quality, Ethical Principles

INTRODUCING THE GOOD CLINICAL TRIALS COLLABORATIVE - GCTC

Sir Martin Landray

Authors : Sir Martin Landray

Affillation : Nuffield Department of Population Health, University of Oxford

No abstract available

Keyword : No keyword available

PUTTING RESEARCH ETHICS IN CONTEXT: RETHINKING VULNERABILITY AND AGENCY WITHIN CASE STUDIES IN THAILAND, KENYA AND SOUTH AFRICA

Phaik Yeong Cheah

Authors : Phaik Yeong Cheah

Affillation : Mahidol Oxford Tropical Medicine Research Unit (MORU)

No abstract available

Keyword : No keyword available

DATA MANAGEMENT FOR CLINICAL TRIALS

Naomi Waithira

Authors : Naomi Waithira

Affillation : Mahidol Oxford Tropical Medicine Research Unit (MORU)

No abstract available

Keyword : No keyword available

LESSONS FROM THE RECOVERY TRIAL

Sir Peter Horby

Authors : Sir Peter Horby

Affillation : Nuffield Department of Medicine, University of Oxford

No abstract available

Keyword : No keyword available

Thursday 8 December 2022

S35 : Nutrition, Gut Microbiome and Immune Response

15.30-17.00hr

Room E

Abstract No. : ABS0001886

IDENTIFICATION OF PROBIOTICS WITH ANTIMICROBIAL ACTIVITY AND IMMUNE MODULATION

Narisara Chantratita

Authors : Piyaorn Chornchoem[1], Sarunporn Tandhavanant[1], Natnaree Saiprom[1], Anucha Preechanukul[1], Wasun Chantratita[2], Narisara Chantratita[1,3]

Affillation : [1]Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [2]Center for Medical Genomics, Faculty of Medicine Ramathibodi Hospital, Mahidol University, Bangkok, Thailand

Introduction: Probiotics have been formulated as dietary supplements and dairy products for treating and preventing various gastrointestinal infections, raising concerns about their biological activities. However, there was a lack of evidence of marketed probiotics used. Here, we identified and isolated probiotics from commercially dietary supplements and dairy products and assessed their antibacterial and immunomodulatory activities.
Methods: The probiotics were identified by metagenomics and isolated by culture method. The antibacterial activity against Escherichia coli and Staphylococcus aureus including antibiotic resistant strains was determined by agar overlay assay and the effect of these probiotics on cellular immune responses was evaluated in phagocytes and natural killer (NK) cell lines.
Results: Lactobacillus sp. and Bifidobacterium sp. were detected as major genera of probiotics in dietary supplements by metagenomics, whereas Streptococcus sp. was the main genus in dairy products. Only 37% of predominant microorganisms was indicated on the label of products. Seventy probiotic strains from 15 species were isolated and investigated the activities. Specific strains of Bifidobacterium longum, Lactobacillus paracasei, L. plantarum and L. rhamnosus showed high and broad antibacterial activities against the tested pathogens and also enhanced phagocytic activity of monocytic cell. In addition, L. paracasei P02.2, L. plantarum P03.1, L. plantarum P06.1 and L. rhamnosus Y01.1 activated IFN- γ production from NK cells. L. rhamnosus strains suppressed IL-6, IL-8 and TNF-α production and B. animalis activated IL-10 production in LPS-stimulated macrophages.
Conclusion: This study showed inaccurate labeling of probiotics on commercial products. Some probiotic strains can have profound antimicrobial activities while others may modulate

Keyword : probiotics, antimicrobial activity, immune modulation, dietary supplements, metagenomics

FEASIBLE BIOMARKERS FOR CORONARY HEART DISEASE RISK IN THAI HYPERLIPIDEMIA PATIENTS

Piyaorn Chornchoem

Authors : Piyaorn Chornchoem

Affillation : Faculty of Tropical Medicine, Mahidol University

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001904

GUT MICROBIOME AND CANCER IMMUNOTHERAPY RESEARCH

Supachai Topanurak

Authors : Topanurak S.[1]

Affillation : [1]Department of Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol University

Gut microbes influence host immunity by producing metabolites that promote host health. The gut microbiome has recently been intensively studied for its association with human diseases, such as infectious diseases, non-communicable diseases including cancer. The complexity of the gut microbiota has a major impact on the activation of innate and adaptive immunity at the local level in the mucosa. Cancer immunotherapy is a promising treatment for many types of cancer. Immune checkpoint inhibitors (ICIs) are antibodies that can block the deactivation of cancer cells against cytotoxic T cells, which has led to unprecedented treatment success. However, a large proportion of patients remain resistant to ICI treatment. Altering the complexity of the gut microbiome may improve outcomes. Transplantation of the fecal microbiome improved the efficacy of ICI in clinical trials. Further research is currently being updated.

Keyword : gut Microbiome, cancer, immunotherapy

Abstract No. : ABS0001898

FEASIBLE BIOMARKERS FOR CORONARY HEART DISEASE RISK IN THAI HYPERLIPIDEMIA PATIENTS

Yaowapa Maneerat

Authors : Yaowapa Maneerat

Affillation : Dept. of Tropical Pathology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

Introduction: Coronary heart disease (CHD) is an important complication of atherosclerosis. Biomarkers, which associate with CHD development, are potential to predict CHD risk. In this cross-sectional study, control, hyperlipidemia (H) and coronary heart disease (CHD) patients represented atherosclerosis to CHD development.

Methods: To determine whether genes showing altered expression in H and CHD patients compared with controls could be CHD risk biomarkers. Gene profiling was investigated in peripheral blood mononuclear cells using DNA microarrays. The intersected genes expressed only in H and CHD groups were selected and validated by real-time quantitative reverse transcription PCR and plasma protein determination.

Results: The findings revealed that DEFA1/DEFA3 and PPBP mRNA expression and corresponding proteins were significantly increased in H and CHD groups compared with controls.

Conclusion: PPBP and DEFA1/DEFA3 could be potential CHD biomarkers in Thai hyperlipidemia patients.

Keyword : biomarker, coronary heart disease, hyperlipidemia, DEFA1/DEFA3, PPBP

Friday 9 December 2022

S36 : Young Investigator Award II

08:30-10:00hr

Room A

Abstract No. : ABS0001746

DETECTION OF SUBCLINICAL MYCOBACTERIUM LEPRAE INFECTION THROUGH DETECTION OF ANTIBODIES (IGM) IN CHILDREN IN FAMILIES WITH A HISTORY OF LEPROSY

Khariri Khariri

Authors : Khariri[1,2*], Frans Dany[2]

Affillation : [1]Doctoral Program of Biomedical Science Faculty of Medicine Indonesia University Indonesia; [2]National Research and Innovation Agency, Indonesia

Leprosy is still a public health problem in the world, especially in developing countries. Indonesia is the third largest contributor to leprosy in the world after India and Brazil. Since 2000, Indonesia has been declared to have achieved the status of leprosy elimination with a national level of leprosy prevalence rate of 0.9 per 10,000 population. The prevalence rate of leprosy in Indonesia in 2021 was 0.45 cases per 10,000 population and the new case finding rate was 4.03 cases per 100,000 population. During the last decade, the prevalence ratio of new cases of leprosy has relatively decreased. Early detection of new cases, especially subclinical leprosy, is vital to maintain this downward trend. Serological tests can be used to detect Mycobacterium leprae infection in the body before clinical manifestations appear. This study aimed at early detection of subclinical leprosy infection in children aged 14 years who lived with family members with a history of leprosy based on the measurement of anti-PGL-1 antibody (IgM) levels. Serological examination of IgM anti-PGL-1 on 320 subjects who were in close contact with leprosy patients found that 140 subjects (46.75%) had subclinical leprosy, i.e., seropositive for leprosy-specific antibodies (titer ≥605 u/mL) without skin lesion. These results are expected to provide an illustration that even though they do not show symptoms, someone who has prolonged close contact with leprosy sufferers has the potential to be infected. The prevalence rate of subclinical leprosy in children can be used as a benchmark for the degree of leprosy endemicity

Keyword : anti-PGL-1, close contact, subclinical leprosy, children, serology

Abstract No. : ABS0001715

IMPLEMENTATION AND EFFECTIVENSS OF REACTIVE SURVEILLANE AND RESPONE STRATEGIES FOR MALARIA ELIMINATION: A SYSTEMATIC REVIEW AND META-ANALYSIS


Win Han Oo

Authors : Win Han Oo[1,2], Kaung Myat Thu[2], Nilar Aye Tun[1], Julia Cutts[1], Ei Phyu Htwe[2], Win Htike[2], May Chan Oo[2], Aung Khine Zaw[2], Paul A. Agius[1,3,4] and Freya J.I. Fowkes[1,3,4]

Affillation : [1]Disease Elimination Program, Burnet Institute, 85 Commercial Rd, Melbourne VIC 3004, Australia; [2]Health Security Program, Burnet Institute Myanmar, 226 U Wisara Road, Yangon, 11201, Myanmar; [3]Department of Epidemiology and Preventive Medicine, Monash University, Melbourne, VIC, Australia; [4]Melbourne School of Population and Global Health, The University of Melbourne, 235 Bouverie St, Carlton, Melbourne, VIC 3053, Australia

Introduction: To achieve malaria elimination, effective case-based surveillance and response system need to be developed and deployed. This study systematically reviews reactive surveillance and response strategies (RARS) for malaria, how they are implemented, and their effectiveness, in order to inform RARS guidelines.

Methods: A systematic review of published and grey literature of quantitative and qualitative studies investigating different RARS including 1-3-7 was conducted. Meta-analyses and meta-regressions were performed for each outcome overall and by geographic regions.

Results: After screening, 63 papers (n = 10 in China, n = 12 in Greater Mekong Subregion (GMS), n = 7 in other Asia-Pacific countries, n = 2 in South America and n = 32 in Africa) were included. RARS was implemented through case notification, case investigation and classification, and focus investigation and responses including reactive case detection, and there was considerable heterogeneity among the included studies (I2 > 75%). Overall, completeness and timeliness of RARS of the studies implemented in China were almost 100% and ≥80% (except one study), while the studies in GMS, South America and Africa showed ≥ 60% completeness and ≥ 50% timeliness. The secondary case yield per index case in reactive case detection was 0.02, 0.06, 0.11, 3.63 and 0.64 in China, GMS, other Asia-Pacific countries, South America and Africa respectively.

Conclusion: Implementation of diverse approaches of RARS caused high heterogenicity among the included studies. Although reactive case detection is an effective approach, completeness and timeliness of RARS may associate with malaria prevalence and overall national health system capacity.

Keyword : Reactive surveillance and response strategies, Case notification, Case investigation, Case classification, Reactive case detection, Focus investigation, Focus responses

Abstract No. : ABS0001750

TOWARDS MALARIA ELIMINATION IN MYANMAR: SCALING UP THE REACH AND UPTAKE OF PERSONAL PROTECTIVE MEASURES IN MOBILE AND MIGRANT POPULATIONS

Thae Maung Maung

Authors : Thae Maung Maung[1], Nay Yi Yi Linn[2], Kyaw Thet Aung[1], Poe Poe Aung[3],Tin Oo[1], Khin Thet Wai[1]

Affillation : [1]Department of Medical Research, Ministry of Health, Myanmar, [2]National Malaria Control Program, Department of Public Health, Ministry of Health, Myanmar, [3]Malaria Consortium,

Attempts to prevent malaria transmission among the Mobile and Migrant Populations (MMP) are still significant challenges for malaria elimination in Myanmar. This study aimed to identify the current use and preference of Personal Protective Measures (PPM) and potential solutions taking into account of scaling up the reach and uptake of PPM in MMP.

This qualitative study was conducted in four townships of four different states/regions in 2018. Data was collected from eighteen Focus group discussions with different types of MMP and twenty Key informant interviews with multi-stakeholders. Thematic analysis was applied with the aid of Atlas ti software.

The majority of MMPs knew the long-lasting insecticide nets (LLIN), but little was known about the repellent, insecticide-treated cloth (ITC) and hammock. Most participants agreed that LLIN was the most effective preventive measure that it could protect from mosquito bites. Although ITC was a preferable method for some MMPs, it was not suitable for those who were manual workers doing strenuous work with sweating and getting wet during their work. An additional concern about ITC was durability if the clothes are washed frequently. Suggestions to improve the reach of PPM, including LLIN, indicated the program should accelerate the collaboration with local authorities/ volunteers who can provide updated information about MMPs in an area where the migration pattern varies alongside seasonal or conditional situations.

Distributing different kinds of PPM according to the needs of different types and natures of MMP should be considered to improve the uptake of the PPM.

Keyword : Personal Protective Measures, Mobile and Migrant Population, Malaria

Abstract No. : ABS0001710

DESIGN AND CHARACTERIZATION OF PLASMOTAC TO INDUCE TARGET DEGRADATION IN PLASMODIUM FALCIPARUM MALARIA PARASITES

Ekkaphot Khongkla

Authors : Ekkaphot Khongkla[1], Onanong Vorasin[1], Thanawat Phumjan[1], Chariya Peeyatu[1], Chayaphat Wongsombat[1], Netnapa Charoensetakul[1], Jarunee Vanichtanankul[1], Marie Hoarau[1], Roonglawan Rattanajak[1], Thanaya Saeyang[1], Kanae Gamo[2], Yusuke Tominari[2], Yongyuth Yuthavong[1], Sumalee Kamchonwongpaisan[1], Phillip James Shaw[1] & Nitipol Srimongkolpithak[1]

Affillation : [1]National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency, Thailand Science Park, Pathumthani 12120, Thailand ; [2]FIMECS, Inc., Fujisawa, Kanagawa 251-0012, Japan

A major public health threat is the spread of Plasmodium falciparum malaria parasites that are resistant to first-line artemisinin-based combination therapies. To overcome this problem, new antimalarial drugs with new therapeutic modalities are required. Targeting protein degradation technology is an exciting new paradigm in drug discovery and development, which has not yet been exploited for tropical and neglected diseases. In this study, we describe a first-in-class “PLASMOTAC” compound that can hijack the P. falciparum ubiquitin-proteasome system (UPS) to degrade target proteins. As a proof-of-concept, we designed and synthesized a library of chimeric degrader compounds targeting P. falciparum dihydrofolate reductase-thymidylate synthase (PfDHFR-TS), a validated antimalarial target. Library compounds were synthesized by conjugating several E3 ligase-recruiting ligands with a PfDHFR-TS binding ligand (P218) as a warhead. Screening of the library by protein degradation assay revealed chimeric molecules which could reduce the PfDHFR-TS target protein in a dose-dependent manner. Moreover, degradation was rapid, with a significant reduction of PfDHFR-TS observed after 30 minutes of treatment. The requirement of both target and E3-ligase recruiting ligands in the same molecule and the role of the P. falciparum UPS in target degradation was confirmed using control compounds and chemical proteasome inhibition, respectively. Our study opens the door for the development of novel antimalarials that act by the target degradation paradigm in tropical medicine.

Keyword : PLASMOTAC, Antimalarial, P218, E3 ligase, Ubiquitin- Proteasome System

Abstract No. : ABS0001769

EXPERIENCE ON 1-3-7 SURVEILLANCE AND RESPONSE APPROACH AT THE PRIMARY HEALTH CARE SETTING IN MYANMAR

Poe Poe Aung

Authors : Poe Poe Aung[1,2,3], Zaw Win Thein[1], Zar Ni Min Hein[4], Kyaw Thet Aung[4], Nwe Oo Mon[4], Nay Yi Yi Linn[5], Aung Thi[4], Khin Thet Wai[4], Thae Maung Maung[4]

Affillation : [1]Maastricht University, Maastricht, Netherlands; [2]Duke Global Health Institute Myanmar Program, Yangon, Myanmar; [3]Malaria Consortium Asia, Bangkok, Thailand; [4]Department of Medical Research, Ministry of Health and Sports, Yangon, Myanmar; [5]National Malaria Control Program, Department of Public Health, Ministry of Health and Sports, Nay Pyi Taw, Myanmar

Background: Myanmar National Malaria Control Program (NMCP) implemented "1-3-7" surveillance and response approach to achieve the malaria elimination by 2030. This study aimed to identify the barriers to implementation in the early phase of "1-3-7" approach deployed in 2016.

Methods: A mixed-methods study was conducted in 2017-2018 with Basic Health Staff (BHS) and staff from Vector Born Disease Control Program (VBDC) in six townships targeted for sub-national elimination in Myanmar. A self-administered questionnaire was completed by 544 respondents and qualitative inquiry was conducted in four townships with 42 discussants. Bivariate analysis was performed for quantitative findings and thematic analysis was conducted for qualitative data using Atals.ti software.

Results: Less than half of respondents reported performing "1-3-7" surveillance and response activities within 3 days and 7 days (40% and 43%, respectively). Lower proportion of BHS correctly identified six categories of malaria cases (22%) and types of foci (26%). In contrast, nearly 80% of respondents correctly named the case detection methods. Major challenges included 'low community knowledge on health' (43%), 'inadequate supplies' (22%), and 'transportation difficulty' (21%). Qualitative data identified the challenges around poor knowledge of key surveillance activities, delays in reporting, differences in reporting systems and the necessity of refresher training. The dominant barrier was inability to control the influx of migrant workers into hard-to-reach areas.

Conclusions: Dispite "1-3-7" surveillance and response approach in Myanmar delivers promising results, numerous challenges are likely to slow down the progress of malaria elimination targets with the critical requirement of health system readiness.

Keyword : Malaria elimination, 1-3-7 strategy, Surveillance and response, Basic health staff, mixed methods, Myanmar

Abstract No. : ABS0001709

EVALUATION OF THE REACTIVE SURVEILLANCE AND RESPONSE STRATEGY FOR MALARIA ELIMINATION IN VIETNAM: A MIXED-METHODS STUDY

May Chan Oo

Authors : May Chan Oo[1], Win Han Oo[1,2], Nguyen Xuan Thang[3], Ngo Duc Thang[3], Ngo Thi Van Anh[4], Win Htike[1], Kaung Myat Thu[1], Julia Cutts[2], Nilar Aye Tun[1], Nguyen Vu Tuyet Mai[4], Ei Phyu Htwe[1], Aung Khine Zaw[1], Katherine O'Flaherty[2], Paul A. Agius[2,5,6], Freya J.I. Fowkes[2,5,6]

Affillation : [1] Health Security Program, Burnet Institute Myanmar, 226 U Wisara Road, Yangon, 11201, Myanmar: [2] Disease Elimination Program, Burnet Institute, 85 Commercial Rd, Melbourne VIC 3004, Australia; [3] Department of Epidemiology, National Institute of Malariology, Parasitology and Entomology, Hanoi, Vietnam; [4] Health Poverty Action, Hanoi, Vietnam; [5] Department of Epidemiology and Preventive Medicine, Monash University, Melbourne, VIC, Australia; [6] Melbourne School of Population and Global Health, The University of Melbourne, 235 Bouverie St, Carlton, Melbourne, VIC 3053, Australia

Introduction: To achieve malaria elimination in Vietnam by 2030, the National Institute of Malariology, Parasitology and Entomology, Vietnam announced a reactive surveillance and response (RASR) strategy in which malaria case notification and investigation must be completed within 2 days followed by foci investigation within 7 days. The performance of Vietnam's RASR strategy was evaluated for potential improvement.

Methods: A mixed-methods study including quantitative surveys to frontline health service providers and health stakeholders (n=74), qualitative interviews and focus group discussions with frontline providers and village malaria workers (n=98), and secondary data analysis of five-year national malaria data (2017-2021, n=12,965 records) was undertaken.

Results: Secondary data analysis of malaria data showed that the completeness and timeliness of case notifications were 100% and 65% respectively. In terms of case investigation, 79% of malaria patients were timely investigated with 97% completeness in 2021. Regarding the focus investigation and responses, reactive case detection (RACD) was a common activity with most screening done in household members of the index case (89%) and neighboring households (88%). 40% of health stakeholders reported in quantitative surveys that RACD was performed within 7 days after a positive case was recorded. In qualitative interviews, participants mentioned that there were limitations to infrastructure, budget, human resources, and poor cooperation from patients in the field implementation of RASR activities. **Conclusion:** The established guidelines and procedures of RASR strategy including case notification, case investigation, and foci investigation and responses, generally, function well in Vietnam. However, the quality of the RASR strategy could be improved by addressing limitations in its implementation.

Keyword : Reactive surveillance and response strategies, Malaria elimination, Case notification, Case investigation, Foci investigation, Reactive case detection, Vietnam

Friday 9 December 2022

S37 : Special Session: Ethics Review of Biobank and Registry Research I

08:30-10:00hr

Room B

THE US DATA PROTECTION FRAMEWORK AND RESEARCH

Holly Taylor

Authors : Holly Taylor

Affillation : Department of Bioethics, NIH Clinical Center

No abstract available

Keyword : No keyword available

EU AND GDPR RELEVANCE FOR RESEARCH

Reidar Lie

Authors : Reidar Lie

Affillation : University of Bergen

No abstract available

Keyword : No keyword available

THE NEW CHINESE DATA PROTECTION LEGISLATION AND RESEARCH

Zhai Xiaomei

Authors : Zhai Xiaomei

Affillation : Center for Bioethics, Chinese Academy of Medical Sciences

No abstract available

Keyword : No keyword available

PERSPECTIVE FROM JAPAN

Kenji Matsui

Authors : Kenji Matsui

Affillation : Division of Bioethics and Healthcare Law, National Cancer Center Japan

No abstract available

Keyword : No keyword available

PERSPECTIVE FROM SINGAPORE

Calvin Ho

Authors : Calvin Ho

Affillation : The University of Hong Kong

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001907

ETHICS REVIEW OF BIOBANK AND REGISTRY RESEARCH: PERSPECTIVE FROM THAILAND

Somruedee Chatsiricharoenkul

Authors : Chatsiricharoenkul S.

Affillation : Faculty of Medicine, Siriraj Hospital, Mahidol University

Thailand has been established biobanking system for more than 10 years but there are some questions about ethical considerations. Biobanking processes raise unanswered ethical questions about the collection, storage, and sharing of cells, tissues, biological fluid, clinical data including genetic information. As well as the attitudes and understanding of research participant are not fully understood.

The most frequently ethical aspect about biobank such as

- Informed Consent: Choosing a consent model for research involving biobanking can be challenging. Until now, there is not a best consent model that can balancing the interest of donors and research in the best possible way.
- Privacy and identifiability of the samples and data: Protection of the private information of research subjects is one of the most important ethical issues. Although biobanks have categorized levels of protection and access to data. But complete data protection cannot be guaranteed.
- Returning the results to the research subject: Each individual has “the right to know and the right not to know” the results of research. Research results that may be inaccurate or may not be relevant to subjects\' clinical symptoms may cause unnecessary concern. Biobanks should consider returning the findings of high clinical relevance to research subjects.
- Commercialization: Leveraging biobanks could lead to commercial benefits. The process to strike a balance between medical benefits and commercial benefits has not yet been clearly established.

Keyword : Biobank, Ethic, Inform consent, privacy, commercialization

Friday 9 December 2022

S38 : Free Paper IV: Tropical Diseases: Surveillance and Treatment

08:30-10:00hr

Room C

Abstract No. : ABS0001836

CROSS TRANSMISSION OF TRICHURIS TRICHIURA AND TRICHURIS VULPIS BETWEEN HUMANS AND ANIMALS IN CARAGA REGION, PHILIPPINES

Angelou Marie Aquino

Authors : Angelou Marie O. Aquino[1], Erika Joy U. Ancayan[1], and Vachel Gay V. Paller[1]

Affillation : [1]Animal Biology Division, Institute of Biological Sciences, University of the Philippines Los Banos

Parasitic infections caused by intestinal helminths are one of the public health concerns affecting developing countries where adequate water and proper sanitation are lacking. Among these parasites of public health challenge, is the whipworm or Trichuris spp. which is the etiological agent for trichuriasis in humans. Trichuris displays a wide range of hosts and are diverse in terms of species with reported cases of zoonotic transmission. Thus, it is important to understand the dynamics of its transmission by identifying factors which may be associated with infection and proper identification of this parasite. This study aims to molecularly characterize infections by using stool samples to investigate prevalence of both whipworms in humans and dogs in selected rural communities in Caraga Region, Philippines. Initial detection was conducted through quantitative polymerase chain reaction by amplification of ITS1 gene regions. This was followed by semi-nested PCR of small subunit ribosomal RNA sequences of both species for species-specific diagnosis. The PCR-based diagnosis revealed that 23 human samples were infected with T. trichiura, three infected with T. vulpis and three showed co-infections. Meanwhile, six dog samples were infected with T. trichiura, two samples with T. vulpis with no co-infections. Findings in the study highlights the cross transmission of whipworms among dogs and humans. Thus, control measures must be taken to control zoonotic transmission from companion animals.

Keyword : Trichuris, zoonosis, whipworm, STH

Abstract No. : ABS0001824

PREVALENCE OF HEAD LICE WITH RESISTANCE GENE AND RISK FACTORS OF HEAD LICE INFESTATION IN THAI RURAL AREA

Natthamongkol Sanganate

Authors : Sanganate N[1], Sata N[1,] Srithanundorn K[1], Tirapornchai J[1], Chearsakul C[1], Suparatchatpan N[1], Wonggungwan T[1], Saipia P[1], Na Lampang P[1], Tangtaveerat P[1], Jongkongkiat W[1], Kittiwijit W[1], Sealow W[1], Suwannahitatorn P[2], Ruangareerate T[2], Thitthiwong P[3]

Affillation : [1]Phramongkutklao College of Medicine; [2]Department of Parasitology, Phramongkutklao College of Medicine; [3]Department of Pediatrics Phramongkutklao Hospital

Head lice infestation problems are increasing worldwide. Significant problems are re-infestation and treatment failure associated with inadequate or misused pediculicides. The extensive use of Permethrin as a first-line treatment for Pediculosis capitis in Thailand has caused many failure-to-treat cases and has established evidence of resistance. The knockdown resistance (kdr) mutation at the voltage-sensitive sodium channel (VSSC) gene is a molecular biomarker for Permethrin resistance. This study aims to determine how often head lice are found and what factors are associated with infestation and kdr mutation.

This study was a cross-sectional study. In March 2022, head lice were collected from 104 elementary school kids in Sra Kaew, Thailand. Questionnaires analyzed demographics and risk. The head lice samples were collected before and after treatment with 1% Permethrin. After DNA extraction and PCR of the VSSC gene with kdr-F and kdr-R primers, the sample was tested for the kdr gene by restriction fragment length polymorphism (RLFP) with SsPI restriction enzyme.

Head lice infection was 46.15 % (n = 48) among 104 participants, with a strong correlation with females (AORs 51.67, 95%CI 6.62-403.20) and ages 10-12 (AORs 4.136, 95%CI 1.01.-16.95). The genotypic forms of the kdr gene mutation are RR, RS, and SS, with the first two being drug-resistant. 51 of 69 infected samples were positive for the VSSC gene (73.91%), while 35 were mutant (68.62%).

The kdr mutation was detected in head lice in rural Thailand, raising awareness of the fail-to-treat condition. Long-term, effective management requires identifying resistance mechanisms.

Keyword : Permethrin Resistance, Head Lice, kdr gene mutation, VSSC gene

Abstract No. : ABS0001829

PHARMACOKINETIC-PHARMACODYNAMIC ANALYSIS OF BENZNIDAZOLE IN A PRE-CLINICAL ANIMAL MODEL OF CHAGAS DISEASE

Frauke Assmus

Authors : Frauke Assmus[1,2], Ayorinde Adehin[1,2], Richard M. Hoglund[1,2], Amanda Fortes Francisco[3], Michael D. Lewis[3], John Kelly[3], Susan Charman[4], Karen L. White[4], David M. Shackleford[4], Fanny Escudié[5], Eric Chatelain[5], Ivan Scandale[5], Joel Tarning[1,2]

Affillation : [1]Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [2]Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, United Kingdom; [3]Department of Pathogen Molecular Biology, London School of Hygiene and Tropical Medicine, London, United Kingdom; [4]Centre for Drug Candidate Optimisation, Monash University, Parkville, Australia; [5]Drugs for Neglected Disease initiative, Geneva, Switzerland

The pharmacokinetic/pharmacodynamic (PK/PD) relationship for benznidazole, the first line treatment for Chagas disease, is poorly understood. The aims of this study were i) to characterise the population pharmacokinetic properties of benznidazole in mice and ii) to investigate the relationship between plasma exposure and antitrypanosomal activity in T. cruzi infected mice. A population pharmacokinetic model for benznidazole was developed in NONMEM (v 7.4), based on plasma concentration-time data in uninfected Balb/c mice (n=52), receiving a single dose of 10, 30 or 100 mg/kg benznidazole as oral gavage. Highly sensitive in vivo bioluminescence imaging was used to monitor antitrypanosomal activity against chronic stage T. cruzi infections in Balb/c mice, following 5 to 20 days of treatment with 10 to 100 mg/kg benznidazole. Sterile parasitological cure (absence of bioluminescence in vivo and ex vivo after immunosuppression) was used as a PD endpoint. The relationship between simulated drug exposure and parasitological cure was evaluated by binomial regression analysis in R (version 4.0). Benznidazole pharmacokinetics in mice were well described by a one-compartment disposition model with first-order absorption. Higher dose was associated with slower absorption. Total plasma exposure of benznidazole, when given for more than 5 days, was identified as a better predictor of antiparasitic activity compared to peak plasma drug concentration, daily dose or dose per dosing occasion. In summary, the exposure-response relationship for benznidazole in T. cruzi-infected mice was successfully quantified. Our results provide a valuable tool to aid the dosing selection and design of prospective pre-clinical and clinical trials for Chagas.

Keyword : Benznidazole, Chagas, bioluminescence imaging, PK/PD modelling, mice

Abstract No. : ABS0001653

BIOLOGICAL EVALUATIONS OF EXTRACT AND FRACTIONS OF COMBRETUM DOLICHOPETALUM LEAF FOR THE MANAGEMENT OF SOME TROPICAL DISEASES (TDS)

Thaddeus H. Gugu

Authors : Gugu T.H.[1],*, Berebon P.D.[1], Onyi P.N.[1] and Attama A.A.[2]

Affillation : [1]Department of Pharmaceutical and Microbiology, University of Nigeria, Nsukka. Enugu State, Nigeria.
[2]Department of Pharmaceutics, University of Nigeria, Nsukka. Enugu State, Nigeria.

Introduction: The emergency of drug resistance against some tropical diseases among rural dwellers has necessitated the use of some herbal product from medicinal plant origin in management and treatment of these menace.
Methods: The active principle of the plant was extracted upon pulverization and fractioned using cold maceration and colume chromatography. The phytochemistry, acute toxicity, antibacterial, antifungi, antidiarrheal, in vitro- in vivo anti-trypanosomiasis, iv vitro anti-trypanosomiasis, anti-leishmaniasis, anti-plasmodiasis and cytotoxicity studies were carried out on both crude and fractions following standard methods.
Results: The LD50 >5000 mg/kg, the extracts had significant activity against bacteria and fung. The anti-diarrhea had a significant water absorption on animal feaces within 4 hours with maximum percentage inhibition of 88.3% of the crude at 200 mg/kg and up to 100% for some fractions while the in vitro and in vivo anti-trypanosoma, anti-plasmodia and anti-leishmania study revealed that, there was significant reduction of parasite ($P>0.05$) within 8 days of post infection treatment with both crude and fractions. The cytotoxicity studies showed that both crude extract and some fractions are safe.
Conclusion: The study showed effective activity of Combretum dolichopotelum against tested organisms which are responsible for most of tropical diseases as an alternative in the management of such ailments.

Keyword : Combretum dolichopotelum, phytochemistry, bio-evaluations and cytotoxicity

Abstract No. : ABS0001651

SURFACE-MODIFIED LIPID NANOPARTICLES FORMULATED WITH BIOCOMPATIBLE EXCIPIENTS ENHANCED THE PHARMACODYNAMICS OF ARTEMETHER IN MICE EXPERIMENTALLY INFECTED WITH PLASMODIUM BERGHEI MALARIA

Franklin Chimaobi Kenechukwu

Authors : Kenechukwu F.C.[1],*, Momoh M.A.[1], Agbo C.P.[1], Ugwuoke W.I.[2], Nwagwu S.C.[1], Echezona A.C.[1], Uzondu S.E.[1], Attama A.A.[1]

Affillation : [1]Drug Delivery and Nanomedicines Research Group, Department of Pharmaceutics, Faculty of Pharmaceutical Sciences, University of Nigeria, Nsukka 410001, Enugu State, Nigeria; [2]Department of Veterinary Anatomy, Faculty of Veterinary Medicine, University of Nigeria, Nsukka 410001, Enugu State, Nigeria

Introduction: Malaria is a global health problem which affects most developing nations, especially sub-Saharan Africa, Asia and Southern America. Given the problems associated with the use of first-line drugs (artemisinin derivatives) in malaria treatment, researchers are seeking new ways to enhance malaria treatment. Surface-modification is a promising technique for improving the biopharmaceutical properties of active pharmaceutical ingredients. Thus, the aim of this study was to develop and evaluate artemether-loaded surface-modified nanoparticles as an improved oral malaria therapy.

Methods: The artemether-loaded surface-modified lipid nanoparticles were prepared from tailor-made lipid matrices, using high shear hot-homogenization, and thereafter evaluated in-vitro for physicochemical performance. In-vivo antimalarial activity was done using a standard protocol in Wistar mice infected with Plasmodium berghei, while hematological and histological studies were performed on major organs implicated in malaria vis-a-vis commercial sample of artemether.

Results: Results revealed enhanced loading of artemether in the formulations, as well as compatibility of the drug and excipients employed in the preparation of the formulations. The optimized formulation was stable and nanomeric, had higher clearance of parasitemia and more sustained antimalarial activity than market formulation (reference/control) with minimal effect on the hematological parameters tested, and also ameliorated the liver and kidney complications of the malariogenic mice.

Conclusions: Surface-modified lipid-based nanotool designed with biocompatible excipients improved the pharmacodynamics of artemether in murine model of Plasmodium berghei malaria. This novel nano-platform can be pursued as a new sustained-release nanomedicine for improved oral malaria treatment.

Keyword : Surface-modified lipid nanoparticles, pharmacodynamics, oral malaria therapy, artemether, Plasmodium berghei.

Friday 9 December 2022

S39 : Recent Advance in Leptospirosis

08:30-10:00hr

Room D

Abstract No. : ABS0001909

MULTIPLEX qPCR FOR SCREENING LEPTOSPIROSIS AND OTHER TROPICAL INFECTIOUS DISEASES

Janjira Thaipadungpanit

Authors : Wongrattanapipat S.[1], Huangsuranun W.[1,2], Perrone C.[1,2]; Robinson M.T.[2,3], Suputtamongkol Y.[4], Batty E.M.[1,2], Day NPJ1,2, Lubell Y1,2, **Thaipadungpanit J**

Affillation : [1]Mahidol-Oxford Tropical Medicine Research Unit (MORU); [5]Department of Clinical Tropical Medicine, Faculty of Tropical Medicine; [4]Faculty of Medicine, Siriraj Hospital, Mahidol University, Bangkok, Thailand; [2]Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, UK; [3]Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit (LOMWRU);

Introduction: Leptospirosis and rickettsiosis (LR) are endemic in South and Southeast Asia (SEA). Pathogenic Leptospira causes human leptospirosis. R. typhi of typhus group rickettsiae causes murine typhus. Orientia tsutsugamushi causes human scrub typhus. R. conorii, R. felis, R. honei, and R. rickettsii of the spotted fever group were also commonly found in SEA. These diseases show a wide range of symptoms from flu-like to severe diseases. Serology assays are used for disease confirmation using paired sera. Even the window of positivity is in days 1-5 post-onset acute infection; nucleic acid amplification tests (NAAT) are developed for early diagnosis and treatment. Sometimes there was no agreement between serology and NAAT results. It might be the diversity of bacterial serotypes or target sequences. In this study, we aim to develop multiplex real-time PCR detecting these bacterial infections to investigate the fever aetiology in SEA populations in rural areas.

Methods: Three modified primer and probe sets (used previously to screen leptospirosis, scrub typhus, and eubacteria infections) were combined with newly designed primers targeting Rickettsia spp. commonly identified in SEA. The multiplex PCR was optimised to archive the amplification efficiency and analytic sensitivity comparable to the simplex PCR assays. The assay accuracy was validated using clinical specimens confirmed LRD by serology tests or NAAT.

Results and Conclusion: The diagnostic accuracy of multiplex PCR to screen leptospirosis and scrub typhus was comparable to the corresponding simplex PCR. Further optimisation and an increase in the accuracy of rickettsial diseases and other bacteria infections are needed.

Keyword : multiplex real-time PCR, leptospira, scrub typhus, murine typhus, spotted fever, rickettsial diseases

Abstract No. : ABS0001832

PATHOPHYSIOLOGY OF LEPTOSPIROSIS ASSOCIATED AKI

Chih-Wei Yang

Authors : Chih-Wei Yang

Affillation : Chang Gung Kidney Research Center, Chang Gung Memorial Hospital, Chang Gung University
Taoyuan, Taiwan

Acute Kidney Injury (AKI) is one of the severe manifestations of leptospirosis. Kidney involvement can range from abnormal urine sediment to severe AKI necessitating hemodialysis. Leptospirosis-related AKI is frequently asymptomatic and hypokalemia is present in 45 percent of cases and has been linked to a variety of potential processes. Sodium and potassium losses in the urine can be explained by decreased sodium-hydrogen exchanger isoform 3 (NHE3) in the proximal tubule and decreased sodium-potassium-2-chloride cotransporter (NKCC2) in the medullary thick ascending loop. The polyuria could be a result of the decreased aquaporin 2 expression and the resulting urine concentrating deficiency. Numerous more proximal tubular dysfunctions have been described, including bicarbonaturia, glucosuria, reduced proximal sodium reabsorption, and excessive excretion of phosphate and uric acid. In addition, hypotension and hypovolemia are significant causes of AKI and are present in the vast majority of patients. Sonography indicates enlarged kidneys with relatively normal parenchymal echogenicity, consistent with interstitial edema and nephritis. Early diagnosis and antibiotic therapy may save individuals with leptospirosis-induced multiple organ failure. Traditional treatment for severe leptospirosis is intravenous penicillin, but oral antibiotics such as doxycycline can be used for mild cases. Cephalosporins of the third generation, such as ceftriaxone, appear to be effective as well. After a successful treatment, Jarisch-Herxheimer responses may develop. This reaction is characterized by an immediate inflammatory response to spirochete removal from circulation. These situations need to be immediately reversed. Leptospirosis AKI should be treated as early as possible where clinical alertness is always eminently encouraged.

Keyword : Leptospirosis; AKI

ZERO DEATH IN LEPTOSPIROSIS

Nattachai Srisawat

Authors : Nattachai Srisawat

Affillation : Tropical Medicine Cluster, Chulalongkorn University

No abstract available

Keyword : No keyword available

Friday 9 December 2022

S40 : Free Paper V: Bacterial Diseases

08:30-10:00hr

Room E

Abstract No. : ABS0001711

GENOTYPIC VIRULENCE PROFILES AND ASSOCIATIONS IN SALMONELLA ISOLATED FROM MEAT SAMPLES IN WET MARKETS AND ABATTOIRS OF METRO MANILA, PHILIPPINES

Rance Derrick Pavon

Authors : Pavon R.D.[1]

Affillation : [1]Pathogen-Host-Environment Interactions Research Laboratory, Institute of Biology, College of Science, University of the Philippines Diliman

Salmonella are pathogenic foodborne bacteria with complex pathogenicity from numerous virulence genes housed in Salmonella pathogenicity islands (SPIs), plasmids, and other gene cassettes. However, Salmonella virulence gene distributions and mechanisms remain unestablished. Philippine studies mainly report Salmonella incidences and antimicrobial resistance, but none on virulence profiles and associations including Salmonella serogroups, animal source and collection sites. Hence, this study screened Salmonella virulence genes by multiplex polymerase chain reaction and determined significant associations through statistical analyses. The use of animal sources and location types in addition to serogroups to predict virulence genes prevalence were also determined. High frequencies (64 to 98%) of SPI virulence genes were detected among 799 Salmonella isolates namely mgtC, pipB, avrA, hilA, spi4R and sseC, from most to least. Meanwhile, only one isolate was positive for plasmid-borne spvC and spvR. The highest virulence gene pattern involving SPIs 1-5 suggests the wide distribution and high pathogenic potential of Salmonella. Statistical analyses showed five virulence gene pair associations. Animal source predicted presence of virulence genes sseC and pipB, whereas location type for hilA and spi4R, suggesting that these factors contribute to the type and pathogenicity of Salmonella present. Diversity in virulence genes across Salmonella serogroups was also demonstrated, particularly for avrA, hilA, sseC, and mgtC. The high prevalence of virulence genes among Salmonella in the study suggest the high pathogenic potential of Salmonella from abattoirs and wet markets of Metro Manila, Philippines which poses food safety and public health concerns and threatens the Philippine food animal industry.

Keyword : Association, Pathogenicity islands, Prevalence, Salmonella, Virulence genes

Abstract No. : ABS0001735

FECAL CONTAMINATION AND ANTIMICROBIAL RESISTANCE IN URBAN GARDENS IN METRO MANILA, PHILIPPINES

Pierangeli Vital

Authors : Vital P. and Lopez M.

Affillation : Natural Sciences Research Institute, University of the Philippines Diliman, Quezon City, 1101, Philippines

Antibiotics have been used in different fields, most commonly in agriculture. They are used on plants and animals, aiding in combating diseases. Because antibiotics are not completely absorbed, they settle in excrement and are used as fertilizer in the soil. However, long-term use promotes antimicrobial resistance (AMR) of bacteria in the environment. Urban gardening also promotes this type of environment, defined as growing and harvesting produce in an urban setting, making them hotspots for antimicrobial resistant bacteria (ARB) due to the use and misuse of antibiotics. Thus, this study aims to determine AMR in Escherichia coli collected from urban gardens. Antibiotic susceptibility testing on 6 antibiotics is performed on 32 samples previously collected in Metro Manila. The data showed that E. coli samples showed high resistance to tetracycline, low resistance to nalidixic acid and ciprofloxacin. For ciprofloxacin, 11 isolates showed intermediate results, suggesting a higher dosage is needed to prevent the growth of bacteria. In conclusion, urbanization leads to excess use and excretion of antibiotics used by humans and their products and may promote more ARB in their community.

Keyword : Antibiotics, Antimicrobial Resistance, Escherichia coli, Urban Gardens

Abstract No. : ABS0001697

MULTI-DRUG RESISTANT BACTERIAL CONTAMINATION ALTERING HEALTHY FRUITS AND VEGETABLES INTO DANGEROUS SOURCE OF INFECTION

Suraj Khatri

Authors : Suraj Khatri[1,2], Deepika Shrestha[1,2], Prasamsha Thapa[1,2], Prativa Bhatta[1,2], Hemanta Kumari Chaudhary[1], Jenny Shah[1], Mitesh Shrestha[1], Ashish Bhusal[1*]

Affillation : [1]Research Institute for Bioscience and Biotechnology (RIBB); [2]Kantipur Valley College

Introduction: Raw fruits and vegetables are the preferable sources of high nutrition. However, when consumed raw, they could also be a source of foodborne illnesses which could be further aggravated through the presence of multi-drug resistant bacteria. It is estimated that annually 1.27 million deaths occur due to antibiotic resistance which would extend to 10 million by 2050.

Methods: Samples of fresh fruits and vegetables were collected from major markets (n=7) and vendors around the hospital (n=10) in Kathmandu. The samples were rinsed in MRD (Maximum Recovery Diluent) solution before being plated on VRBG (Violet Red Bile Glucose) and MacConkey agar. Once pure colonies were isolated, antibiotic susceptibility testing was done using 20 different antibiotic discs. PCR was done for various extended spectrum beta-lactamases (ESBLs) and carbapenem resistance causing genes.

Results: A total of 166-gram negative bacteria were isolated. Out of which, 28 (16.1%) bacteria were carbapenem-resistant, 55 (31.6%) bacteria were found to be ESBL producers and 68 (39.1%) bacteria were multi-drug resistant. PCR detected blaKPC (n=10), blaNDM (n=8), bla CTX (n=4), blaOXA (n=3), blaSHV (n=3), blaIMP(n=1), and blaTEM (1) genes.

Conclusion: We report the presence of carbapenem-resistant & extended-spectrum beta-lactamases (ESBLs) producing bacteria in fruits and vegetables. Several factors including but not limited to poor sanitation of places or people and antibiotic abuse in the clinical as well as agricultural settings could be contributing to this contamination. Hence, effective control measures and policies should be adopted for enhancing food safety.

Keyword : KEYWORDS: Antibiotic resistance, Carbapenem resistance, Extended spectrum beta-lactamases (ESBLs),Multi-Drug resistance, Markets, and Hospital vendors.

Abstract No. : ABS0001771

RESISTANCE MECHANISMS AMONG THE NON-CARBAPENEMASE-PRODUCING CARBAPENEM-RESISTANT KLEBSIELLA PNEUMONIAE

Yee Qing Lee

Authors :
Yee Qing Lee[1], Sasheela Sri La Sri Ponnampalavanar[2], Chun Wie Chong[3], Rina Karunakaran[1], Cindy Shuan Ju Teh[1,*]

Affillation : [1]Department of Medical Microbiology, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, Malaysia.; [2]Department of Medicine, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, Malaysia.; [3] School of Pharmacy, Monash University Malaysia, Jalan Lagoon Selatan, 47500 Bandar Sunway, Selangor, Malaysia.; [*]Correspondence: cindysjteh@um.edu.my; Tel.: +6012-515 1989

Introduction: An increase of non-carbapenemase-producing carbapenem-resistant Klebsiella pneumoniae (NC-CRKP) has been reported in a tertiary teaching hospital in Malaysia. NC-CRKP confers carbapenem resistance through a combination of chromosomal mutations and acquired non-carbapenemase resistance mechanisms. In this study, we determined the resistance mechanisms among the NC-CRKP.

Methods: A retrospective study of NC-CRKP was conducted from January 2013 to October 2019. The minimum inhibitory concentration (MIC) testing was performed for ciprofloxacin, imipenem, meropenem, ertapenem, and colistin using broth microdilution method, while the sensitivity toward seven other selected antimicrobials was identified using the Vitek®2 system. The presence of resistance genes and the loss of porin-associated genes were determined using polymerase chain reaction (PCR), while the efflux pump contribution was determined by the MIC reduction assay, with and without phenylalanine-arginine β-naphthylamide (PaβN).

Results: All strains were resistant to amoxicillin/clavulanate, ampicillin, cefuroxime, ertapenem, and ciprofloxacin. 61.1% and 33.3% of the strains were susceptible to imipenem and meropenem respectively. Two colistin-resistant strains were identified. Resistance genes detected were bla_{TEM}, bla_{SHV}, $bla_{CTX\text{-}M}$, bla_{OXA}, and bla_{DHA}. Porin loss was detected in 46.3% of the strains. No active efflux contribution to carbapenem resistance was observed.

Conclusions: Since all the strains isolated had at least one ESBL-associated gene and no active efflux contribution of PAβN-inhibited efflux pumps to carbapenem resistance was detected, other potential chromosomal mutations could contribute to the carbapenem resistance. As only 46.3% of strains had porin loss, further investigation of the expression and alteration of outer membrane porin or penicillin-binding protein is pivotal to reveal more information about the mechanisms of carbapenem resistance.

Keyword : Efflux pump inhibitor (EPI), non-carbapenemase-producing carbapenem-resistant Klebsiella pneumoniae, PAβN, porin loss

Abstract No. : ABS0001835

MOLECULAR DIAGNOSIS OF BACTERIAL INFECTION IN NEGATIVE BLOOD CULTURE FLUID

Yasithirra Devi Kirishnan

Authors : Yasithirra Devi Kirishnan[1], Mohammad Ridhuan Mohd Ali[2], Nur Ayuni Kadir[1], Zahrul Laili Abd Hadi[3], Padmaloseni @ Nur Humairah Thangarajah[4], Julina Abd Aziz[5], Murnihayati Hassan[2].

Affillation : [1]Faculty of Health Science, University Sultan Zainal Abidin, Gong Badak Campus, 21300 Kuala Nerus, Terengganu, Malaysia; [2]Bacteriology Unit, Infectious Disease Research Centre, Institute of Medical Research (IMR), 40170 Setia Alam, Malaysia; [3]Department of Pathology, Hospital Raja Permaisuri Bainun, 30450 Ipoh, Perak Malaysia; [4]Department of Pathology, Hospital Melaka, Jalan Mufti Haji Khalil, 75400 Melaka, Malaysia; [5]Department of Pathology, Hospital Taiping, Jalan Taming Sari, 34000 Taiping, Perak, Malaysia.

Introduction: Bacterial infection is a leading cause of morbidity and mortality globally. Currently, blood cultures are the main diagnostic technique for identifying the aetiologic agents of bacteremia. However, in many instances, blood cultures are negative in patients despite distinctive clinical symptoms of infections. This study investigates the potential of PCR to detect bacterial DNA from negative blood cultures.

Methods: Retrospectively, blood culture fluid with negative growth were collected. Total DNA was extracted using PrimeWay Genomic DNA Extraction Kit with a prior neutralization method using guanidine hydrochloride and benzoyl alcohol. The extracted DNA was subjected to broad-range 16s rRNA conventional PCR. Amplicons were sequenced and analyzed using the BLAST program to determine the bacterial species.

Results: Of the 80 samples, 12 (15%) were positive for bacterial DNA. Two samples were positive for Staphylococcus aureus and two more for Staphylococcus capitis. Enterobacter mori was identified in two samples. The remaining samples were positive for Prescottela equi, Escherichia coli, Enterobacter sp., Bacillus sp., and Burkholderia pseudomallei.

Conclusions : The broad – range 16s rRNA PCR is potentially useful for the pathogens from negative blood culture fluids. The resulting information, however, need to be correlated clinically and validated on larger sample size.

Keyword : Keywords : Infection; bacteraemia; blood culture; PCR, pan-16s rRNA

Abstract No. : ABS0001772

SURVIVAL OF HYPERMUCOVISCOUS CARBAPENEM RESISTANT K. PNEUMONIAE IN A SERUM KILLING ASSAY

Zhi Xian Kong

Authors : Zhi Xian Kong[1], Sasheela Ponnampalavanar[2], Rina Karunakaran[1], Kartini Abdul Jabar[1], Chun Wie Chong[3], Cindy Shuan Ju Teh[1]

Affillation : [1]Department of Medical Microbiology, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, Malaysia; [2]Department of Medicine, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, Malaysia; [3]School of Pharmacy, Monash University Malaysia, Jalan Lagoon Selatan, Bandar Sunway 47500, Selangor, Malaysia;
*Corresponding author: Associate Professor Dr. Cindy Teh Shuan Ju, Department of Medical Microbiology, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, Malaysia, +603-79676660, cindysjteh@um.edu.my

Introduction: The emergence of hypervirulent variants among K. pneumoniae has been a great concern as these strains are more frequently associated with serious infection in healthy host with metastatic spread. Previously, we have isolated a hypermucoviscous carbapenem-resistant K. pneumoniae (CRKp) from a male patient. This strain harboured ybtS, entB, kfu and mrkD gene and was resistant to serum killing. In this study, we further analysed the response of this hypermucoviscous CRKp that contributed to serum killing.
Methods: An aliquote of the hypermucoviscous CRKp at 1.5 hours of serum killing assay was subjected to RNA extraction. The extracted RNA was sent for commercial sequencing service. The regulation of genes that responsible for serum killing was identified.
Results: When exposed to serum, 709 genes were up-regulated while 815 genes were down-regulated. Genes in the iron uptake systems, such as ybt, ent and kfu were significantly up-regulated. In addition, the strain also tended to increase the pathogenicity activity by upregulating genes such as Shikimate dehydrogenase, biotin synthesis, invasion-like, glutaredoxin-like protein and tonB protein encoding genes.
Conclusion: The significant up-regulation of iron-acquisition genes in the hypermucoviscous CRKp during serum killing activity indicated the importance of multiple iron-acquisition systems (tonB-dependent and independent) and their roles in preventing killing by human serum.

Keyword : Hypermucoviscous, carbapenem resistant K. pneumoniae, serum killing, RNA sequencing

Friday 9 December 2022

S41 : Vertical Transmission in the Tropics

10.30-12.00hr

Room A

Abstract No. : ABS0001919

VERTICAL TRANSMISSION IN THE TROPIC

Thanyawee Puthanakit

Authors : Thanyawee Puthanakit

Affillation : Division of Infectious Diseases, Department of Pediatrics, Faculty of Medicine, and Center of Excellence for Pediatric Infectious Diseases and Vaccines, Chulalongkorn University, Bangkok, Thailand

Vertical transmission is defined as infection that transmits from mother to infant, of which can occur in utero, during peripartum or breast feeding. Most transmission occurs during the peripartum when the baby is in direct contact with mother's blood and secretion. There are several pathogens with vertical transmission such as blood born virus (HIV, Hepatitis B, Hepatitis C), SCROTCH (syphilis, CMV, Rubella, Toxoplasmosis, Cytomegalovirus, Herpes simplex), and mosquito-borne virus in tropical countries (dengue virus, chikungunya, zika virus). The global health policy is aimed for triple elimination of vertical transmission of HIV, hepatitis C and syphilis. Elimination criteria for HIV include vertical transmission rate < 2% in non-breastfeeding population or < 5% in breastfeeding population. HIV vertical transmission can achieve zero transmission if mother receives antiretroviral treatment and had undetectable plasma HIV RNA prior to conception. Elimination goal for hepatitis B is prevalence of children under 5 years of age, had < 0.1% prevalence of chronic hepatitis B infection. Many countries implemented birth dose of hepatitis B vaccine promptly within 24 hours post-delivery and complete 3-dose vaccine course in first 6 months of life. In high-risk of HBV transmission, pregnant women had high plasma hepatitis B DNA (or HBeAg positive as a surrogate), WHO recently commends to give tenofovir as antiviral agent during third trimester. The Syphilis elimination goal is lower than 50 per 100,000 live births. During the session, we will discuss clinical management, programmatic implementation, public health policy to prevent and manage the important vertical transmission.

Keyword : vertical transmission, mother to infant

Abstract No. : ABS0001827

CONGENITAL SYPHILIS: IS IT POSSIBLE TO ELIMINATE?

Suvaporn Anugulruengkitt

Authors : Suvaporn Anugulruengkitt

Affillation : Division of Infectious Diseases, Department of Pediatrics, Faculty of Medicine, and Center of Excellence for Pediatric Infectious Diseases and Vaccines, Chulalongkorn University, Bangkok, Thailand

Syphilis in pregnancies and transmission to infants remains as one of the significant health concerns worldwide. The recent global estimation of congenital syphilis cases was 473 per 100,000 live births. World Health Organization sets a goal of elimination of mother-to-child transmission of syphilis at a target of Gaps to elimination of congenital syphilis are late access to antenatal care, late timing of infection and/or diagnosis of syphilis during pregnancy. Strengthening diagnosis and treatment cascade of syphilis during antenatal care should be improved to achieve congenital syphilis elimination goal. There are multiple interventions on a basis of WHO four pillars for elimination of congenital syphilis. First, increasing access to early antenatal care and improving quality of maternal health services such as same day result of syphilis testing. Second, syphilis testing should be conducted in all pregnant women with at least two times during antenatal care, at the first and early third trimester, and at delivery. Third, case management programs corresponded with elimination of mother-to-child transmission of HIV and hepatitis B, as triple elimination, should be implemented.

Keyword : congenital syphilis; elimination; mother-to-child transmission; prevention; syphilis

ELIMINATION OF VERTICAL TRANSMISSION OF HEPATITIS B

Suchada Jiamsiri

Authors : Suchada Jiamsiri

Affillation : Department of Disease Control, Ministry of public health, Thailand

No abstract available

Keyword : No keyword available

Friday 9 December 2022

S42 : Special Session: Ethics Review of Biobank and Registry Research II

10.30-12.00hr

Room B

THE US DATA PROTECTION FRAMEWORK AND RESEARCH

Holly Taylor

Authors : Holly Taylor

Affillation : Department of Bioethics, NIH Clinical Center

No abstract available

Keyword : No keyword available

EU AND GDPR RELEVANCE FOR RESEARCH

Reidar Lie

Authors : Reidar Lie

Affillation : University of Bergen

No abstract available

Keyword : No keyword available

THE NEW CHINESE DATA PROTECTION LEGISLATION AND RESEARCH

Zhai Xiaomei

Authors : Zhai Xiaomei

Affillation : Center for Bioethics, Chinese Academy of Medical Sciences

No abstract available

Keyword : No keyword available

PERSPECTIVE FROM JAPAN

Kenji Matsui

Authors : Kenji Matsui

Affillation : Division of Bioethics and Healthcare Law, National Cancer Center Japan

No abstract available

Keyword : No keyword available

PERSPECTIVE FROM SINGAPORE

Calvin Ho

Authors : Calvin Ho

Affillation : The University of Hong Kong

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001907

ETHICS REVIEW OF BIOBANK AND REGISTRY RESEARCH: PERSPECTIVE FROM THAILAND

Somruedee Chatsiricharoenkul

Authors : Chatsiricharoenkul S.

Affillation : Faculty of Medicine, Siriraj Hospital, Mahidol University

Thailand has been established biobanking system for more than 10 years but there are some questions about ethical considerations. Biobanking processes raise unanswered ethical questions about the collection, storage, and sharing of cells, tissues, biological fluid, clinical data including genetic information. As well as the attitudes and understanding of research participant are not fully understood.

The most frequently ethical aspect about biobank such as

- Informed Consent: Choosing a consent model for research involving biobanking can be challenging. Until now, there is not a best consent model that can balancing the interest of donors and research in the best possible way.
- Privacy and identifiability of the samples and data: Protection of the private information of research subjects is one of the most important ethical issues. Although biobanks have categorized levels of protection and access to data. But complete data protection cannot be guaranteed.
- Returning the results to the research subject: Each individual has “the right to know and the right not to know” the results of research. Research results that may be inaccurate or may not be relevant to subjects\' clinical symptoms may cause unnecessary concern. Biobanks should consider returning the findings of high clinical relevance to research subjects.
- Commercialization: Leveraging biobanks could lead to commercial benefits. The process to strike a balance between medical benefits and commercial benefits has not yet been clearly established.

Keyword : Biobank, Ethic, Inform consent, privacy, commercialization

Friday 9 December 2022

S43 : Plasmodium knowlesi: Situation and Challenges (Thai language) [MOPH]

10.30-12.00hr

Room C

MALARIA ELIMINATION AND CHALLENGES (THAI SESSION)

Apinya Niramitsantipong

Authors : Apinya Niramitsantipong

Affillation : Bureau of Vector Borne Disease, Department of Disease Control, Ministry of Public Health

No abstract available

Keyword : No keyword available

MALARIA ELIMINATION AND CHALLENGES (THAI SESSION)

Pathomporn Prikchoo

Authors : Pathomporn Prikchoo

Affillation : Office of Diseases and Prevention Control Region 12 Songkhla

No abstract available

Keyword : No keyword available

MALARIA ELIMINATION AND CHALLENGES (THAI SESSION)

Suravadee Kitchakarn

Authors : Suravadee Kitchakarn

Affillation : Bureau of Vector Borne Disease, Department of Disease Control, Ministry of Public Health

No abstract available

Keyword : No keyword available

Friday 9 December 2022

S44 : Free Paper VI: Vector Borne Diseases

10.30-12.00hr

Room D

Abstract No. : ABS0001798

THE PARASITE GENETIC AND HOST IMMUNOLOGICAL DETERMINANTS OF IMMUNE ESCAPE IN PLASMODIUM FALCIPARUM MALARIA

Myo Naung

Authors : Myo T. Naung[1,2,7], Somya Mehra[3,10], Swapnil Tichkule[1,2], Andrew J. Guy[4], Ramin Mazhari[1], Eamon Conway[1], Zahra Razook[9], Somesh Mehra[9], Paolo Bareng[9,10], Matthew Adam[8], Brendan Ansell[1,2], Wilson Wong[1,2], Eizo Takashima[5], Takafumi Tsuboi[5], Rory Bowden[7], Shannon Takala Harrison[8], Ivo Mueller[1,2,6], and Alyssa E. Barry[1,2,9,10]

Affillation : [1]Population Health and Immunity Division, Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria, Australia; [2]Department of Medical Biology, University of Melbourne, Parkville, Victoria, Australia; [3]School of Mathematics and Statistics, The University of Melbourne, Melbourne, Australia; [4]School of Science, RMIT University, Melbourne, Victoria, Australia; [5]Division of Malaria Research, Proteo-Science Center, Ehime University, Japan; [6]Department of Parasites and Insect Vectors, Pasteur Institute, Paris, France; [7]Advanced Genomics Facility, Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria, Australia; [8]Center for Vaccine Development and Global Health, University of Maryland School of Medicine, Baltimore, Maryland, United States of America;
[9]School of Medicine, Deakin University, Geelong, Victoria, Australia; [10]Disease Elimination and Maternal and Child Health, Burnet Institute, Melbourne, Victoria, Australia

Human malaria remains a major global public health problem with an estimated 241 million clinical cases and 627,000 deaths in 2020, expected to increase in future years. Highly effective vaccines are urgently needed to progress the control and elimination of the disease. There are dozens of candidates in development, however only one vaccine (RTS, S) targeting Plasmodium falciparum, has reached Phase-4 implementation trials with less than 50% efficacy. The limited efficacy of malaria vaccines to date has been in part attributed to the extreme diversity of parasite antigens being developed as ‘subunit' vaccines, with only one or two randomly selected allelic variants as the basis for inducing immune responses. Antigen diversity has evolved to evade host immune responses - a process known as an immune escape. Pinpointing specific antigen polymorphisms that drive immune escape would help to prioritise antigens and alleles for inclusion in vaccine formulations. We focused on two cohorts of children from malaria endemic regions of Papua New Guinea conducted during moderate and high transmission periods. We analysed samples from 758 children, conducting multiplexed serological assays to measure IgG responses against 27 antigens, and targeted amplicon sequencing of 38 parasite antigen genes in sequentially collected samples from each child to measure the rate of allelic turnover for each antigen. The analysis identified critical immune escape genes and their specific polymorphisms that contribute to immune escape. This research provides a vital framework for the prioritization of vaccine candidate antigens and a platform to identify immune escape polymorphisms.

Keyword : Plasmodium falciparum, vaccines, immune escape, diversity, malaria

Abstract No. : ABS0001756

ACCEPTABILITY AND FEASIBILITY OF COMMUNITY-DELIVERED INTEGRATED MALARIA ELIMINATION MODEL FROM PERSPECTIVES OF VOLUNTEERS AND COMMUNITY LEADERS IN YANGON REGION, MYANMAR

Ei Phyu Htwe

Authors : Ei Phyu Htwe[1], Win Han Oo[1,2], Win Htike1, May Chan Oo[1], Kaung Myat Thu[1], Khaing Wai Wai Phyo[1], Aung Khine Zaw[1], Galau Naw Hkawng[1], Pwint Phyu Phyu[3], Julia Cutts[2], Freya J.I. Fowkes[2,4,5]

Affillation : [1]Health Security Program, Burnet Institute Myanmar, Yangon, Myanmar; [2]Disease Elimination Program, Burnet Institute, VIC, Australia; [3]Myanmar National Malaria Control Program; [4]Department of Epidemiology and Preventive Medicine, Monash University, VIC, Australia; [5]Melbourne School of Population and Global Health, University of Melbourne, VIC, Australia

Introduction: As the malaria burden declines, the motivation of malaria volunteers also declines. Therefore, the Community-delivered Integrated Malaria Elimination (CIME) Model that provides services for malaria elimination, and prevention and referral of dengue, tuberculosis, childhood diarrohea, and febrile illness was developed and evaluated in three townships in Yangon Region, Myanmar. In this study, from the perspectives of CIME volunteers and community leaders, the acceptability and feasibility of the model in the community were explored qualitatively.
Methods: Six focus group discussions (FGD) with six CIME volunteers per FGD and six semi-structured interviews with community leaders were conducted at the end of the CIME model implementation in March/2022 and June/2022. Deductive followed by inductive thematic analysis was employed.
Results: The CIME volunteers accepted the CIME model because it provided integrated health services that fulfilled the community's needs and helped the volunteers earn more community acceptance. The community leaders also claimed that the community members were satisfied with the service quality and the integrated health services provided by CIME volunteers. Additionally, community demand for volunteer services and volunteer motivations, due to integrated health services together with its relevant supports, made the model more feasible to implement. However, it had some challenges due to the COVID-19 pandemic, politics, the community context, and health system factors in implementation.
Conclusion: Overall, CIME volunteers and community leaders accepted the CIME model, and it was feasible to implement at the community level. Nevertheless, it still needs to be addressed its challenges, and scientifically and programmatically evaluated to document its effectiveness at the national level.

Keyword : Acceptability, Community-delivered Integrated Malaria Elimination Model, Malaria elimination, Community-based Health Worker, Feasibility, Volunteer

Abstract No. : ABS0001684

THE INAPPROPRIATE ANTIMICROBIAL AGENT PRESCRIPTIONS AMONG CONFIRMED DENGUE CASES IN HOSPITAL FOR TROPICAL DISEASES: A RETROSPECTIVE COHORT STUDY

Ashley Siribhadra

Authors : Siribhadra A.[1], Ngamprasertchai T.[1], Rattanaumpawan P.[2], Lawpoolsri S.[3], Luvira V.[1], Pitisuttithum P.[1]

Affillation : [1]Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand; [2]Department of Medicine, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok 10700, Thailand; [3]Department of Tropical Hygiene, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand

Introduction: Dengue is common viral infection predominantly in Asia which required supportive treatment without antimicrobial agent prescriptions. The overuse of antimicrobial agents leads to antimicrobial resistant threats. This study aimed to determine the appropriate use of antimicrobial agents and clinical characteristics of bacterial co-infections among dengue confirmed cases.

Methods: This retrospective cohort study included dengue confirmed cases by serological or molecular tests from Hospital for Tropical Diseases during 2016-2021. Systematic random sampling was conducted to select the numbers of participants that was proportionate to annual case prevalence before dengue severity stratifications. Clinical characteristics were retrieved from hospital database and evaluated by two independent reviewers including infectious disease physician. Disagreement will be resolved by third reviewer. The appropriateness was defined as antimicrobial agents properly prescribed in all following aspects, indications, choice, duration, dosage, and route of antimicrobial agents.

Results: A total of 249 subjects were included in study and analyses. Overall rate of inappropriate antimicrobial agent prescriptions was 57%. The main reason for inappropriateness was indication. The rate of definite bacterial co-infections among confirmed dengue cases was 32.1%. Urinary tract infections followed by primary bacteremia, then skin and skin structure infections were the common source of infections, respectively. Cephalosporin groups were the most empirical antimicrobial agent prescriptions (66.7%), followed by carbapenems (10.0%), and fluoroquinolones (6.4%).

Conclusions: The inappropriateness of antimicrobial agents in dengue patients was high. Antimicrobial stewardship should be endorsed in all dengue cases. Promptly antibiotics cessation should be performed in cases without evidence of bacterial infections.

Keyword : dengue, antimicrobial stewardship, antibiotics, antimicrobial agents, appropriateness, and inappropriateness

Abstract No. : ABS0001823

A PUTATIVE NEW SPECIES OF RICKETTSIA SP. HL-1 IN HAEMAPHYSALIS HYSTRICIS FROM DOMESTIC ANIMALS IN HUALIEN, EASTERN TAIWAN

Jing-Syuan Huang

Authors : Jing-Syuan Huang[1], Tzu-Ling Lin[1], Hsi-Chieh Wang[1], and Kun-Hsien Tsai[1,2]

Affillation : [1] Institute of Environmental and Occupational Health Sciences, College of Public Health, National Taiwan University, Taipei 100025, Taiwan ; [2]Department of Public Health, College of Public Health, National Taiwan University, Taipei 100025, Taiwan

Introduction: Ticks and cat fleas are the primary ectoparasites of companion animals and serve as vectors for Rickettsia spp. Rickettsioses caused by companion animals were neglected in Taiwan. Rickettsiae have been studied in metropolitan cities in northern, central and southern Taiwan but not in eastern Taiwan. The study reported both the identification of ticks and cat fleas, to determine the prevalence and species of Rickettsia spp. collected from Hualien city, east Taiwan.

Methods: Ticks and fleas were identified by morphological and molecular methods. Gene primers of ITS2, 16S and COI genes were applied for species identification. For rickettsia detection, genes of gltA, OmpA, OmpB and sca4 were amplified to perform the gene diversity and prevalence rate of Rickettsia spp.

Results: The specimens were collected from 10 veterinary hospitals in Hualien city including 2 tick species (Rhipicephalus sanguineus and Haemaphysalis hystricis) and 1 cat fleas species (Ctenocephalides felis) were collected. The prevalence rate of Rickettsia spp. in ticks and fleas was 2.7% (1/36) and 3.7% (14/377). This study identified one novel Rickettsia spp. HL-1 in H. hystricis based on the genes of gltA, OmpA, OmpB and sca4 which showed 99%, 95%, 94% and 97% gene sequence similarity to Rickettsia sp. (KM386690.1), Rickettsia slovaca (JX683121.1), Candidatus Rickettsia tasmanensis (GQ223393.1).

Conclusion: This study indicated a putative new Rickettsia species in H. hystricis based on molecular analysis, whether it can infect the humans or not are unknown. There should be continuous monitoring to ensure the health and safety of both humans and animals in east Taiwan.

Keyword : Rickettsia, Tick, Flea, East Taiwan

Abstract No. : ABS0001778

DYNAMICS OF WNV INFECTION IN CULEX MOSQUITOES

Sylvie Lecollinet

Authors : Naomie Pature[1], Lise Fiacre[1;2], Catherine Hermant[4], Olivier Gros[5], Emmanuel Albina[3], Gaelle Gonzalez[2], Nonito Pages[1], **Sylvie Lecollinet[1]**

Affillation : [1]CIRAD, UMR ASTRE, F-97170 Petit Bourg, Guadeloupe, France; [2]UMR 1161 Virology, ANSES, INRAE, ENVA, ANSES Animal Health Laboratory, EURL for Equine Diseases, 94704 Maisons-Alfort, France

Introduction: West Nile virus (WNV) is a mosquito-borne flavivirus and a reemerging zoonotic pathogen, reported in Americas, Europe, Africa, Australia, South-East Asia and the Middle East. WNV is maintained in an enzootic cycle between ornithophilic Culex mosquitoes and wild birds, while infections in mammals, in particular in humans and equids, result from spill-overs from bridge mosquitoes. While vector competence in North-American mosquito populations and anatomical barriers regulating virus dissemination and transmission are well-documented, molecular mechanisms modulating WNV infection in mosquitoes are not well characterized.

Method: In order to monitor the dynamic of WNV infection in Culex mosquitoes, both spatially and temporally, WNVs integrating fluorochrome-encoding gene in the viral genome were engineered through reverse genetic tools and confocal microscopy images were acquired after chemical transparization of mosquito cuticles.

Results: WNV encoding either eGFP or mCherry fluorochrome were generated by the ISA method. Replication kinetics in Vero cells evaluated at early and late timepoints (3 and 26 hours post-infection) were identical for the genetically modified viruses and the parental strain. Moreover, eGFP and mCherry fluorescence was recovered from Vero cells infected with eGFP and mCherry recombinant viruses respectively.

Discussion: Thanks to reverse genetics tools, WNV integrating fluorochrome-encoding gene in the viral genome were rapidly generated and characterized in in vitro models. They will be used to infect laboratory-adapted Slab strain as well as natural Culex populations from Guadeloupe to study WNV tropism and infection dynamics in these species.

Keyword : Culex mosquitoes, fluorescent protein, tropism

Abstract No. : ABS0001727

GENETIC DETERMINANTS OF THE VIRULENCE OF MEDITERRANEAN WNV ISOLATES

Lise FIACRE

Authors : Lise Fiacre[1;2], Steeve Lowenski[1], Céline Bahuon[1], Maelle Bayet[2], Maha Dridi[4], Emmanuel Albina[2;3], Nonito Pages[2], Benedicte Lambrecht[4], Nathalie Pardigon[5], Gaelle Gonzalez[1], Sylvie Lecollinet[2]

Affillation : [1]UMR 1161 Virology, ANSES, INRAE, ENVA, ANSES Animal Health Laboratory, EURL for Equine Diseases, 94704 Maisons-Alfort, France; [2]CIRAD, UMR ASTRE, 97170 Petit Bourg, Guadeloupe, France; [3]ASTRE, University Montpellier, CIRAD, INRAE, F-34398 Montpellier, France; [4]Operational Direction of Viral Diseases, CODA-CERVA-Veterinary and Agrochemical Research Centre, 99 Groeselenberg, 1180, Brussels, Belgium; [5]Unité de Recherche et d\'Expertise Environnement et Risques Infectieux, Institut Pasteur, Paris, France.

Introduction: West Nile virus (WNV) is a mosquito-borne flavivirus maintained in enzootic transmission cycles between Culex mosquitoes and wild avifauna and largely spread in tropical regions. Horse vaccines exist but no human vaccines have been developed. With the objectives to develop WNV human vaccine, molecular determinants of virulence are investigated especially through reverse genetic approaches. We used classical bacterial plasmid-based approach and ISA, an innovative bacteria-free method developed in 2014, to produce WNV chimeras between two Mediterranean WNV strains with varying virulence for birds, to identify genetic determinants of WNV virulence.
Methods: Eight chimeric constructs between two different Mediterranean WNV strains (WNV Israel 1998 - GenBank: AF481864.1 and WNV Italy 2008 - GenBank: FJ483549.1) were produced. Replication kinetics were characterized in vitro on mammalian (Vero) and mosquito (C6/36) cells, and virus multiplication and virulence were assessed in vivo for two chimeras and the parental strains in Balb/cByJ mice and SPF chicks.
Results : Exchange of genetic regions between WNV Israel 1998 and Italy 2008 in the produced chimeras was confirmed by Next generation Sequencing (SISPA method, IonTorrent). Viral replication proved to differ in Vero cells for chimeric constructs modified in NS3 -NS4A/NS4B or NS1, suggesting that these non-structural proteins can be responsible for the differential virulence observed between the two parental strains. In vivo analyzes suggested a major role of NS5 protein and 3’UTR in neurovirulence in chicks and a role of NS4A/NS4B/5’NS5 in the virulence in mice.
Discussion : Additional analyses in in vivo models (mice, mosquitoes) will allow to better understand the role of WNV proteins.

Keyword : West Nile, molecular determinants, virulence, reverse genetics

Friday 9 December 2022

S45 : Free Paper VII: Diseases Surveillance Tools

10.30-12.00hr

Room E

Abstract No. : ABS0001767

A NEW SEROLOGIC APPROACH FOR ESTIMATING THE POPULATION-LEVEL INCIDENCE OF SCRUB TYPHUS

Kristen Aiemjoy

Authors : Aiemjoy K.[1], Kutawal N.[2], Vaidya K.[1], Shrestha S.[2], Teunis P.[3], Varghese G.[4], Trowbridge P.[5], Paris D.[6], Blacksell S.[7], Bogoch I.[8], Maude R.[7], Tamrakar D.[2], Andrews J.[7]

Affillation : [1]University of California Davis School of Medicine; [2]Dhulikhel Hospital, Kathmandu University Hospital; [3]Rollins School of Public Health, Emory University; [4]Christian Medical College Vellore; [5]Tufts University; [6]Swiss Tropical Institute; [7]Mahidol Oxford Tropical Medicine Unit, Oxford University; [8] University of Toronto

Introduction: Scrub typhus is an acute febrile illness caused by Rickettsiaceae Orientia tsutsugamushi. Characterizing the population-level burden of scrub typhus has been challenging due to the lack of accessible and accurate diagnostics. We describe a new approach using information about antibody dynamics after infection to generate population-level scrub typhus seroincidence estimates.

Methods: We use data from two clinical studies of scrub typhus patients enrolled in Chiang Rai, Thailand, and Vellore, India, and representative population data from two representative serosurveys in the Kathmandu Valley, Nepal, and Vellore, India. The samples were tested for IgM and/or IgG responses to Orientia tsutsugamushi-derived recombinant 56-kDa antigen using commercial ELISA kits. We used Bayesian hierarchical models to fit two-phase models to the antibody responses from scrub typhus cases and used the joint distributions of the peak antibody titers and decay rate to estimate population-level incidence rates in the cross-sectional serosurveys. We compared this new method to a traditional cut-off-based approach for estimating seroincidence.

Results: Among 18 to 29-year-olds, the seroincidence of scrub typhus was 886 (95% CI 432-1817) per 100,000 person-years in India and 945 (95% CI: 616-1449) in Nepal. Seroincidence rose with age, reaching a rate of 3231 (95% CI: 2630-3969) among 50 to 89-year-olds in Vellore, India. The seroincidence rates estimated using a cutoff were half the rates we estimated using antibody dynamics.

Conclusion: The approach described here can be used to rapidly characterize scrub typhus burden and generate scrub typhus seroincidence estimates that are comparable across populations, regions, and time.

Keyword : Orientia tsutsugamushi, Scrub Typhus, Antibody kinetics, Seroepidemiology, incidence

Abstract No. : ABS0001782

NS1-BASED FcγR IgG COMPETITION ELISAs ALLOW DIFFERENTIATION OF FLAVIVIRUS-INDUCED HUMORAL IMMUNE RESPONSES

Christina Deschermeier

Authors : Christina Deschermeier[1], Christa Ehmen, Rutineia Ferraz-Jansen, Ronald von Possel, Neele Pekarek, Ana Bispo de Filippis, Patricia Brasil, Aline Silva Santos, Marcelle Aline Santos, Patricia Carvalho de Sequeira, Jörg Blessmann, Latdamone Keoviengkhone, Vatsana Sopraseuth, Simone Kann, Leonardo J Maya Amaya, Gadith E Rivera Salcedo and Petra Emmerich

Affillation : [1]Bernhard Nocht Institute for Tropical Medicine

Background: Serosurveillance of flavivirus infections in countries where several human-pathogenic flaviviruses are co-circulating is hampered by strong antigenic cross-reactivity, compromising the reliability of serological assay results.
Methods: Based on a patented platform technology employing a recombinant human Fcγ receptor as capture molecule, enzyme-linked immunosorbent assays (ELISAs) for the detection of IgG antibodies elicited by contact with Dengue virus (DENV), Zika virus (ZIKV), and Yellow Fever virus (YFV) were developed. As antigens, horseradish peroxidase - labeled recombinant flavivirus NS1 proteins were used. Cross-reactivity of antibodies induced by other flaviviruses was eliminated by a competitor approach using unlabeled flavivirus NS1 proteins. Assays were comprehensively validated using serum panels from flavivirus endemic areas in Asia (Lao PDR) and South America (Colombia, Brazil) as well as longitudinal samples from European travelers having contracted Dengue or Zika fever abroad.
Results: The DENV, ZIKV, and YFV IgG FcγR ELISAs reliably detected antibodies elicited by the respective flavivirus infections. Strong cross-reactivity with the labeled NS1 antigens was observed for a fraction of sera originating from flavivirus-endemic areas. The addition of competitor molecules allowed the efficient suppression of these false-positive signals and thus significantly improved assay specificity.
Conclusions: Due to their high specificity, the developed DENV, ZIKV, and YFV IgG FcγR ELISAs allow the performance of conclusive seroprevalence studies in countries with several co-circulating human-pathogenic flaviviruses.

Keyword : flavivirus, DENV, ZIKV, YFV IgG FcRγ ELISAs

Abstract No. : ABS0001753

SCHISTOSOMA JAPONICUM (KATSURADA, 1904) DETECTION IN HUMANS AND ANIMALS IN SELECTED ENDEMIC AREAS IN CARAGA REGION, MINDANAO, PHILIPPINES USING MICROSCOPY, QPCR, AND MITOCHONDRIAL NAD1 GENE ANALYSIS

Vachel Gay Paller

Authors : Vachel Gay V. Paller[1], Jasmin Ayyah T. Samudio[1], Ericka Anacayan[1], Allen Jethro Alonte[1], Kim Louisse A. Patagnan[1], Vicente Y. Belizario, Jr.[2], Billy DIvina[3], Joaquin Prada[4], Martha Betson[4]

Affillation : [1]Animal Biology Division, Institute of Biological Sciences, College of Arts and Sciences, University of the Philippines Los Baños; [2]Department of Veterinary Paraclinical Sciences, University of the Philippines Los Baños, Laguna, the Philippines; [3]Department of Parasitology, College of Public Health, University of the Philippines Manila, Manila, the Philippines; [4]School of Veterinary Medicine, University of Surrey

The underestimation of the zoonotic contribution of mammalian reservoirs promotes the persistence of Schistosoma japonicum, the causative agent of schistosomiasis (SCH), in endemic areas. The infection status of S. japonicum in 606 humans and 302 animals from eight endemic sites in Agusan del Sur and Surigao del Norte was determined using real-time PCR (qPCR), with comparative findings by stool-based microscopic examinations using Kato-Katz (KK) technique for humans and flotation and sedimentation techniques for animals. The genetic relationships of S. japonicum within and among different host species and endemic sites based on the mitochondrial (mt) nad1 gene were also examined. A higher prevalence of S. japonicum infection was obtained for both humans and animals using qPCR compared to microscopic techniques. The overall prevalence of human SCH determined by qPCR was 69.8% and 10.1% using KK. While the overall prevalence of S. japonicum infection using qPCR in dogs, cats, pigs, and water buffaloes was 88.4% (vs. 1.8% in microscopy), 65.2% (vs. 4.4% in microscopy), 69.8% (vs. 4.7% in microscopy), and 65.8% (vs. 0% in microscopy), respectively. The analysis of partial mt nad1 gene suggested that dogs are a major reservoir and possibly the main contributor to SCH transmission to humans in Caraga Region. These findings highlight that the animals contribute to the transmission and persistence of S. japonicum and that microscopy-based diagnostic techniques underestimate the disease burden in the region. Therefore, a multi-sectoral approach, using molecular detection methods for active disease surveillance in humans and animals, and targeted treatment of infected animals

Keyword : Schistosomiasis, Schistosoma japonicum, zoonosis, transmission, qPCR, mitochondrial nad1 gene, Caraga Region, Philippines

Abstract No. : ABS0001694

DEVELOPMENT OF AN APTAMER-BASED SANDWICH ASSAY FOR THE DETECTION OF LEPTOSPIROSIS

Marjo Mendoza

Authors : Mendoza M.V.[1], Almazar C.A.[1], Montala Y.B.[1], Rivera W.L.[1]

Affillation : [1]Pathogen-Host-Environment Interactions Research Laboratory, Institute of Biology, College of Science, University of the Philippines Diliman, Quezon City, Philippines

Increasing global incidence of leptospirosis were noted recently as numerous outbreaks occurred particularly in endemic countries where relative risks were associated with habitat and extreme weather conditions. Although the disease is considered a major public health concern, diagnosis remains a challenge, thus, the development of a reliable and fast diagnostic tool is imperative. In this study, aptamers, which are synthetically produced single-stranded nucleotides with high specificity and affinity to a wide array of molecules, were used as an alternative to antibodies for the detection of Leptospira antigen. A sandwich enzyme-linked aptamer assay (ELAA) was developed to test the sensitivity and specificity of cell SELEX-derived aptamers and to identify the best aptamer pair for diagnostics application. Direct ELAA was performed to test the binding affinity of four aptamers against a commercially available vaccine. Optimization of sandwich ELAA conditions was done followed by aptamer pair assessment. From the 16 aptamer combinations, five candidate aptamer pairs (AP1/AP1, AP5/AP1, AP5/AP5, AP5/AP10, AP10/AP5) were further evaluated to test their sensitivity and specificity. Screening revealed AP1 and AP5 aptamer combinations have the highest affinity to Leptospira antigen as supported by molecular modelling. The dual aptamer sandwich assay detected 1.9 x 108 cells/mL. Cross-reactivity with other known bloodborne pathogens, specifically E. coli and Klebsiella pneumoniae, was relatively high but low compared to the Leptospira antigen. Although additional optimization is required to improve the aptamer pairs diagnostic performance, the prototype successfully detected Leptospira. Further evaluation is recommended to determine its applicability in clinical diagnostics settings.

Keyword : Leptospirosis, aptamers, enzyme-linked aptamer assay, diagnostics

Abstract No. : ABS0001817

A VGG16 CONVOLUTIONAL NEURAL NETWORK MODEL-BASED WEB APPLICATION TO INTERPRET THE IGM LATERAL FLOW DIAGNOSTIC TEST OF ACUTE LEPTOSPIROSIS DIAGNOSIS

Santi Maneewatchararangsri

Authors : Worarat Krathu[1], Charnyote Pluempitiwiriyawej[2], Thanapon Noraset[2], Kulachart Jangpatarapongsa[3], Charin Thawornkuno[4], Panyawat Boontanom[5], **Santi Maneewatchararangsri[4]**

Affillation : [1]School of Information Technology, King Mongkut's University of Technology Thonburi, Bangkok, 10140, Thailand; [2]Faculty of Information and Communication Technology, Mahidol University Salaya campus, 73710 Nakhon Pathom, Thailand; [3]Center for Research and Innovation, Faculty of Medical Technology, Mahidol University Salaya Campus, 73710 Nakhon Pathom; [4]Department of Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol University, Bangkok, 10400, Thailand; [5]Division of Education Technology and arts, Faculty of Tropical Medicine, Mahidol University, Bangkok, 10400, Thailand.

Background: Leptospirosis continues to be a global public health burden, afflicting a million cases annually. Accurate lateral flow rapid diagnostic test (RDT) results are required for effective treatment and the prevention of disease complications that can lead to death. Usually, faintly visible test lines among early leptospirosis patients and residents in the endemic area are difficult to interpret by human reading. In this invention, a convolutional neural network (CNN) model-based web application was deployed to interpret the accurate RDT image results and overcome the limitations of visual interpretation.

Methods and Results: Among trained CNN models, VGG16 trained with the original image dataset presented high prediction sensitivity of 98.38% (n = 3,456) and specificity of 96.28% (n = 2,070), 99.44% (n = 1,988), and 99.99% (n = 3,000) among different validation datasets. A VGG16 model web application was deployed through the URL: https://lepto.cscms.me/. The web application performance increased diagnostic interpretation accuracy to 98.38% sensitivity and 96.28% specificity with clinical evaluation compared with optical reading. The platform enables registered users to perform tests, record subject/patient, sample, and test information upload RDT test image photographs, and collect user/subject/sample/RDT test information and results. A downloaded file of the prediction result can be sent to the user by e-mail.

Conclusion: A VGG16 model-based web application provides accurate test results for IgM antibody RDT kits, i.e., Lep-M PLUS, for leptospirosis diagnosis in the first week of fever. It allows healthcare professionals to perform accurate diagnoses by themselves in laboratories, bedside, and other settings, i.e., fieldwork.

Keyword : Leptospirosis diagnosis, Rapid diagnostic test, Artificial intelligence, VGG16 convolutional neural network model, Web application

Friday 9 December 2022

S46 : Small Molecules Drug Discovery for Tropical Diseases

13:00-14:30hr

Room A

Abstract No. : ABS0001788

OPPORTUNITIES AND CHALLENGES OF NEXT-GENERATION ANTIFOLATES AGAINST PROTOZOAL INFECTIONS – TARGET-BASED DESIGN TO OVERCOME ANTIFOLATE RESISTANCE

Jarunee Vanichtanankul

Authors : Vanichtanankul J., Taweechai S., Saeyang T., Jantra T., Pengon J., Talawanich Y., Kongkasuriyachai D., Kamchonwongpaisan S., and Yuthavong Y.

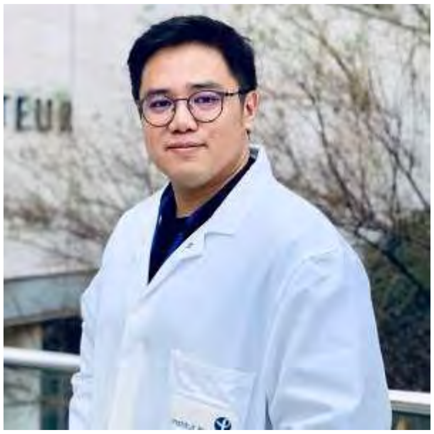
Affillation : National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), 113 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khlong Luang, Pathum Thani 12120, Thailand

Current chemotherapies for the treatment of protozoan parasitic diseases, such as malaria, African sleeping sickness, and toxoplasmosis, are based on drugs discovered several decades ago. For example, pyrimethamine (Pyr), an antifolate drug developed in 1953, is still used in combination with sulfa drugs to treat toxoplasmosis and malaria. However, the efficacy of this drug is compromised by parasite resistance. Pyr targets dihydrofolate reductase (DHFR), an essential enzyme in the folate pathway. Competitive inhibitors of DHFR can be rationally designed to be effective against Pyr-resistant variants using structural data, as demonstrated by the development of compound P218. Clinical Phase I trial demonstrated that P218 is safe with chemopreventive activities against Pyr-resistant Plasmodium falciparum (Pf) malaria. Although the DHFR function is conserved, parasite species vary in their susceptibility to Pyr, which can be attributed to DHFR structural differences. Pyr is markedly less effective against Trypanosoma brucei (Tb) and Toxoplasma gondii (Tg) than Pf and P. vivax. We obtained Tb and Tg DHFR X-ray structures to understand the basis of Pyr resistance in these species. Wild-type Tb- and Tg-DHFR shared structural similarities with Pyr-resistant PfDHFR mutants, suggesting that antifolates developed against Pyr-resistant PfDHFR mutants could be potent inhibitors of both TbDHFR and TgDHFR. Indeed, a series of antifolates rationally designed for Pyr-resistant PfDHFR showed strong inhibit against TbDHFR and TgDHFR with a mode of enzyme-ligand binding similar to that of PfDHFR. Our study opens the door for the development of novel, effective, and safe antifolate drugs against Tb and Tg.

Keyword : Antifolate drug, Antifolate resistance, Dihydrofolate reductase, Drug development, Parasitic diseases

Abstract No. : ABS0001815

TARGETING 'UNDRUGGABLE TARGET' – HIJACKING PLASMODIUM PROTEIN DEGRADATION SYSTEM



Nitipol Srimongkolpithak

Authors : Srimongkolpithak N., Khongkla E., Vorasin O., Peeyatu C., Phumchan T., Vanichtanankul J., Charoensetakul N., Saeyang T., Rattanajak R., Taweechai S., Kamchonwongpaisan S., Shaw P., and Yuthavong Y.

Affillation : National Center for Genetic Engineering and Biotechnology (BIOTEC)

The efficacy of artemisinin combination therapy for treating malaria is compromised by parasite resistance to artemisinin and partner drugs. More effective drugs and combinations are thus needed. Heme-activated artemisinin promiscuously alkylates many parasite proteins and irreversibly damages them by forming covalent adducts, following degradation through the ubiquitin-proteasome system (UPS). Although the artemisinin mode of action is rapid and powerful, the selectivity is lacking. Plasmodium thymidylate synthase, linking with dihydrofolate reductase as a bifunctional enzyme called PfDHFR-TS, could be an undruggable target due to the high similarity to a human one. We hypothesize that chimeric compounds with two pharmacophores, one UPS-degradation inducer and another DHFR binder can lead to the degradation of PfDHFR-TS.

A series of chimeric compounds were designed and synthesized. The first prototype compound, bearing artemisinin and folate recruiter, showed desired binding affinity and killing activities (Ki = 0.60±0.02 nM and IC50 = IC50 = 3.5±0.2 nM). The inhibition of PfDHFR activity of the first prototype is potentiated by heme in a time-dependent manner suggestive of irreversible inactivation. However, the degradation in parasites could not be observed from western blot analysis due to the inferior selectivity in the cellular environment. Therefore, we recently developed novel chimeric compounds based on proteolysis targeting chimeric technology in Plasmodium spp., called PlasmoTAC. The new chimeric compounds work by direct hijacking E3 ligase in UPS in order to degrade PfDHFR-TS. The second prototype revealed promising data by inducible degradation. Therefore, our new technology could be applied to other undruggable targets as well.

Keyword : Plasmodium, Protein Degradation, PlasmoTAC, Drug Discovery

ESTABLISHING MODELS FOR ASSESSING PROPHYLAXIS AND TRANSMISSION-BLOCKING ACTIVITIES TO SUPPORT MALARIA ELIMINATION POLICIES

Natapong Jupatanakul

Authors : Natapong Jupatanakul

Affillation : National Center for Genetic Engineering and Biotechnology (BIOTEC)

No abstract available

Keyword : No keyword available

Abstract No. : ABS0001696

PRIORITIZING PLASMODIUM FALCIPARUM ESSENTIAL GENES FOR ANTIMALARIAL DEVELOPMENT BY ANALYSIS OF CONDITIONAL LOSS-OF-FUNCTION MUTANTS

Philip Shaw

Authors : Shaw P.J.[1], Prommana P.[1], Pengon J.[1], Wongsombat C.[1], Laohasinnarong S.[1], Suwanakitti N.[1], Kamchonwongpaisan S.[1]

Affillation : [1]National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency

The spread of Plasmodium falciparum malaria parasites resistant to antimalarial drugs, including artemisinin-based combination therapies presents a public health threat. Hence, new antimalarials, particularly those with novel mechanisms of action are urgently needed. To achieve this goal, drug discovery efforts should be focused on novel and vulnerable targets for which even partial loss of function is lethal.

In this study, we modified 13 P. falciparum genes annotated as essential by genome editing to insert the glmS ribozyme regulatory element. Conditional loss-of-function mutants were generated by treating transgenic parasites with the ribozyme inducer glucosamine (GlcN), and loss of gene function was assessed by RNA-seq and immunoblot experiments. We tested whether the loss of target gene function affected parasite proliferation by a GlcN dose-response assay. The GlcN sensitivities of transgenic parasites were compared with a control P. falciparum 3D7 parasite.

Mutants of the DHFR-TS, DHFS-FPGS, MDR1, MUS81, and cPheRS genes were significantly more sensitive to GlcN than the control, suggesting that the loss of function of these genes causes an acute proliferation defect. In contrast, the GlcN sensitivities of the mutants of other genes were not significantly different from the control.

From these data, we suggest that loss of function for some essential genes is less deleterious in the short term than for others. These data can be used to prioritize the most vulnerable gene targets in medicinal chemistry programs to develop potent and rapidly acting antimalarials.

Keyword : Plasmodium falciparum, malaria, glmS ribozyme, target vulnerability, drug

Friday 9 December 2022

S47 : Introduction to Scholarly Publishing for Researchers: What are editors, reviewers and publishers looking for?

13:00-14:30hr

Room B

Abstract No. : ABS0001914

INTRODUCTION TO SCHOLARLY PUBLISHING FOR RESEARCHERS: WHAT ARE EDITORS, REVIEWERS AND PUBLISHERS LOOKING FOR?

Dale Seaton

Authors : Dale Seaton[1]

Affillation : [1]Elsevier Publishing, New York, USA

In this talk I will go through the best practices for writing scientific articles, the peer review process, and handling a rejection. I will explore key points that journal Editors and Reviewers look for in submitted manuscripts. I will also review Ethics in Publishing, including plagiarism and sceintific misconduct.

Keyword : Scientific Writing; Peer Review: ECR: Plagiarism

INTRODUCTION TO SCHOLARLY PUBLISHING FOR RESEARCHERS: WHAT ARE EDITORS, REVIEWERS AND PUBLISHERS LOOKING FOR?

Bilge San

Authors : Bilge San

Affillation : Elsevier Life Sciences Publishing

No abstract available

Keyword : No keyword available

Friday 9 December 2022

S48 : Climate Change and Vector Borne Disease [MOPH]

13:00-14:30hr

Room C

S48 : Climate Change and Vector Borne Disease [MOPH]

Invited speakers :

1. Surapong Sarapa
Division of Research and Development for Meteorological Information

2. Piti Mongkalangoon
Bureau of Vector Borne Diseases, Department of Disease Control, Ministry of Public Health

No abstract available

Keyword : No keyword available

Friday 9 December 2022

S49 : EDCs (Endocrine Disrupting Chemicals) and Health: A Challenge for Our Society

13:00-14:30hr

Room D

Abstract No. : ABS0001863

EDCs AND HEALTH: A CHALLENGE FOR OUR SOCIETY

Vichit Supornsilchai

Authors : Vichit Supornsilchai

Affillation : Division of Endocrinology, Department of Pediatrics, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand

The data about EDCs exposure in Thai children are scanty. Our group reported BPA detection in children of 75.3% during 2013-2014. The study in 2020-2021, Bisphenol metabolites; BPA, BPF and BPS, were detected 78.4, 88.5 and 89.9%, respectively, in Thai children. We also reported some phthalate metabolites detection; monomethyl phthalate (MMP) and monobutyl phthalate (MBP) as 28.5 and 88.6%, respectively. The association between EDCs (BPA and Phthalates) and common Pediatric endocrine problems for example, obesity, body compositions, precocious puberty and type1 Diabetes mellitus (T1DM), have been conducted by our group. BPA exposure appears to be related to an earlier age at onset of puberty especially in obese girls. Precocious puberty girls had an association with increased monoethyl phthalarte (MEP) concentration. Higher urinary BPA level is one of the possible risk factors for T1DM. Higher urinary phthalates concentration were significantly associated with elevated total fat mass and were not mediated through the degree of obesity defined by BMI. Thailand has some regulations for BPA use especially in newborns and infants, however, we do not have any regulation for phthalate use. Our group have been trying to do research about common EDCs exposure particularly in children and aim to collect the evidence and ask for a proper regulation for EDCs in Thailand. The association studies with common pediatric endocrine disorders have been done, however, more study must be further analyzed in in vitro model systems (in cell biology, in vitro settings) or animal studies.

Keyword : Endocrine-disrupting chemicals (EDCs)

Abstract No. : ABS0001693

THYROID DISRUPTING CHEMICALS AND ENVIRONMENTAL HEALTH IMPLICATIONS IN HUMAN POPULATION

Kyungho Choi

Authors : Choi K.

Affillation : Graduate School of Public Health, Seoul National University

Increasing prevalence of thyroid related diseases are worldwide phenomenon. Depending on the stages of life, thyroid disruption may lead to different types of health outcomes as well. Evidence linking chemicals that are encountered in general population and thyroid endocrine disruption is accumulating. These chemicals include not only consumer chemicals like phthalates and phenolic compounds, but also persistent and naturally occurring chemicals such as halogenated organics and inorganic metals. We have conducted several human observation studies and identified chemicals with significant associations with thyroid outcomes in general human populations. We have also noticed that many of thyroid disrupting chemicals could influence other target organs and were associated with different health outcomes such as kidney function, neurobehavior, and lipid metabolism, in humans. Using zebrafish (Dania rerio) and different cells, we have identified potential mechanisms underlying such observations made in human populations. In addition, many thyroid disrupting chemicals also show toxicological potentials that are related to kidney function and neurobehavior, while direct links between thyroid disruption and other toxicological pathways are not well-characterized. Significant health and societal burden of thyroid related diseases emphasize that the efforts to identify and manage thyroid disrupting chemicals should be given a priority. Exposure assessments are an essential approach to identify major sources of exposure and to design appropriate mitigation measures for these chemicals of growing public health importance.

Keyword : Thyroid, Chemical, Exposure, Human, Observation, Experiment

Abstract No. : ABS0001814

THE HOKKAIDO STUDY ON ENVIRONMENT AND CHILDREN’S HEALTH: OVERVIEW AND CHILDREN’S CHEMICAL EXPOSURE LEVELS

Atsuko Ikeda

Authors : Atsuko Ikeda-Araki[1,2,3], Yu Ait Bamai[2,4], Rahel Mesfin Ketema[1,2,3], Chihiro Miyashita[2,3], Reiko Kishi[2,3]

Affillation : [1]Faculty of Health Sciences, Hokkaido University; [2]Center for Environmental and Health Sciences; [3]WHO Collaborating Centre for Environmental Health and Prevention of Chemical Hazards; [4]Toxicological Centre, University of Antwerp

The Hokkaido Study on Environment and Children’s Health is an ongoing study consisting of two birth cohorts of different sizes, the Sapporo cohort and the Hokkaido cohort, which were established in 2001. This presentation provides an ongoing progress, summarize recent results of children’s chemical exposure, and future directions. Prenatal environmental exposure to chemicals such as polychlorinated biphenyls and dioxins, organochlorine pesticides, per- and polyfluorinated compounds, and phthalates has been measured. Information on physical growth, neurodevelopment, allergy and infections, and onset of puberty has been collected to analyze health outcomes. In this webinar, results of children’s chemical exposure are focused. When participating children of the Hokkaido cohort reached 7 years old, morning void urine samples were collected to investigate the current internal exposure levels of shorter half-life compounds or their metabolites: phthalates, phosphate flame retardants and plasticizers (PFRs), bisphenols, and nonylphenol (NP). The prevalence of asthma and allergies were also examined by ISAAC questionnaire. When comparing the levels of these chemicals in the urine collected from 2012 to 2017, increasing secular trend of PFRs and BPS was found, while decreasing trend in BPA and NP. The levels of phthalates did not show any secular trends during the study periods suggesting stable exposures. Finally, single metabolite as well as mixture of phthalates were positively associated with increased risk of wheeze and eczema of 7 years old children. For further examination and follow-up, we are now conducting face-to face health check-up with blood and urine sample collections at one’s adolescence.The Hokkaido Study on Environment

Keyword : birth cohort, children, asthma and allergies, endocrine disrupting chemicals, exposure

Friday 9 December 2022

K2 : Closing Ceremony and Keynote Address

14:30-15:30hr

Room A

Abstract No. : ABS0001899

NUCLEOSIDE-MODIFIED mRNA THERAPEUTICS

Drew Weissman

Authors : Drew Weissman

Affillation : Director of Vaccine Research, Infections Diseases Division, Perelman School of Medicine, University of Pennsylvania

No abstract available

Keyword : no keywords available