

was administered to new TB patients, older than 15 years, who had received at least one month of TB treatment and given consent. Data was collected through informal discussions with TB coordinators and facility heads, desk top review of patient records and interviews with TB patients to assess direct costs prior to being diagnosed and direct and indirect cost of current treatment. Of the 159 patients interviewed, 64% were in the three lower socio economic quintiles with monthly income less than US\$ 42.55. Health system delay was estimated at 1.4 weeks with males taking longer to seek care than females. DOTS patients paid a mean total direct cost of US\$ 0.50 for each visit and spent of 58 minutes per DOTS visit. The mean number of days spent in the hospital was 22.7 days and direct cost of hospitalization was US\$ 48.32. Whilst 48.3% of the patients borrowed, 37.7% sold assets to cope with paying for their ill health. Reduction of monthly household and patients income due to TB was 44.5% and 82.6% respectively. Sixty-one percent of the TB patients lost their jobs, 11% got separated from their spouse/family and stopped attending public functions. Through this study, the NTP has identified constraints faced by TB patients and their families that have an effect on case finding and treatment adherence. We recommend that TB patients and their families should benefit from social protection packages that will ease the financial burden. Employers should not hesitate to take back workers who have been diagnosed and treated with TB.

## 1251

### CLINICAL OUTCOMES ASSOCIATED WITH ROUTINE USE OF INTERFERON- $\gamma$ RELEASE ASSAYS IN A CENTRAL LONDON TB SERVICE

**Dami Collier**, Andy Taylor, Steve Morris-Jones

*Hospital of Tropical Disease, London, United Kingdom*

Interferon- $\gamma$  release assay (IGRA) has been shown to have higher specificity than tuberculin skin testing (TST) for screening for latent TB and is recommended by the National Institute for Clinical Excellence (NICE). The aim of this study is to review the indications for and analyse the results of IGRA testing in our central London BCG vaccine positive population. We analysed routinely collected clinical and demographic data on patients referred for IGRA testing to a TB service at a large London teaching hospital from September 2007 to January 2012. Reasons for referral for screening included contacts of active TB, pre-mono-clonal antibody therapy, recent migrants and occupational health. Quantiferon Gold InTube was used. We used the London TB registrar to identify patients that were diagnosed with active TB either by bacteriological or clinical evidence from November 2007 to February 2012. We determined the sensitivity and specificity of IGRA for diagnosing active TB and screening for latent TB. We used univariate linear regression to assess the incremental impact of IGRA result on having a diagnosis of active TB. 961 IGRAs were performed on 917 patients. 51% were male with a median age of 30 years (IQR 19-40). There were 46 (4.8%) indeterminate, 703 (73.2%) negative and 212 (22%) positive results. Indeterminate results were more prevalent amongst immunosuppressed than immunocompetent patients 66.7% (24/36) vs. 33.3% (12/36). 46 cases of active tuberculosis were identified from the London tuberculosis register, 15 of which had a negative IGRA result. The sensitivity and specificity of IGRA for diagnosing active TB were 67% and 79% respectively. We found a direct correlation between a positive IGRA test result and active TB diagnosis ( $p < 0.00$  coefficient 1.343). The sensitivity and specificity of IGRA for latent TB screening were 55% and 89% respectively. We found an overrepresentation of indeterminate results amongst immunosuppressed patients. IGRA was used in addition or other conventional diagnostic modalities for the diagnosis of active TB, which is outside the scope of the NICE guidelines. Although the use of IGRA for this purpose is approved by the US Food and Drug Administration, caution should be exercised due to its low sensitivity for diagnosing active TB. However the usefulness of IGRA in screening for latent TB was conferred by its high specificity in our setting.

## 1252

### EVALUATION OF HOUSEHOLD LEVEL INTERVENTIONS DURING A LARGE, URBAN TYPHOID FEVER OUTBREAK - HARARE, ZIMBABWE 2011-2012

**Maho Imanishi**<sup>1</sup>, Patience Kweza<sup>2</sup>, Rachel B. Slayton<sup>1</sup>, Wellington Mushayi<sup>3</sup>, Tanaka Urayai<sup>4</sup>, Odrie Ziro<sup>5</sup>, Monica Chizororo<sup>3</sup>, Ajay Paul<sup>5</sup>, Susan M. Laver<sup>3</sup>, Clement Duri<sup>6</sup>, Stanley Mungofa<sup>6</sup>, Prosper Chonzi<sup>6</sup>, Panganai Dhliwayo<sup>7</sup>, Peter H. Kilmarx<sup>7</sup>, Portia Manangazira<sup>8</sup>, Eric D. Mintz<sup>1</sup>, Daniele S. Lantagne<sup>9</sup>

<sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States,

<sup>2</sup>National Institute of Communicable Diseases, Johannesburg, South Africa,

<sup>3</sup>United Nations Children's Fund – Collaborating Centre for Operational Research and Evaluation, Harare, Zimbabwe, <sup>4</sup>Population Services International – Zimbabwe, Harare, Zimbabwe, <sup>5</sup>German Agro Action – Zimbabwe, Harare, Zimbabwe, <sup>6</sup>Harare City Health Department, Harare, Zimbabwe, <sup>7</sup>Centers for Disease Control and Prevention - Zimbabwe, Harare, Zimbabwe, <sup>8</sup>Ministry of Health and Child Welfare, Harare, Zimbabwe, <sup>9</sup>Harvard University, Boston, MA, United States

Between October 2011 and March 2012, ~2,750 suspected cases of typhoid fever in two high-density suburbs of Harare (Dzivaresekwa and Kuwadzana) were reported to the Harare City Health Department (HCHD). To prevent outbreak spread, HCHD and non-governmental organizations conducted door-to-door health and hygiene education and distributed point-of-use water treatment (PoUWT) products beginning in October 2011. To evaluate the effectiveness of these interventions, we conducted cross-sectional household surveys in these two affected suburbs in March 2012, including free chlorine residual (FCR) testing in stored drinking water. Reported intervention coverage was high, with 351 (77%) of 458 randomly selected households having received both typhoid fever prevention information and at least one PoUWT product. Of 368 households that received at least one of the three types of chlorine tablets distributed, 326 (89%) reported ever using them, 160 (43%) reported using them daily, and 98 (27%) had stored water that was treated and had FCR  $\geq 0.2$ mg/L when tested. Only 169 (55%) of 310 household respondents who had chlorine tablets on the day of the survey knew the correct volume of water to treat with their tablets. In univariate analysis, respondents who had higher income, were older, had received PoUWT products or typhoid fever prevention information, and who reported household water treatment before the outbreak were more likely, and respondents who reported boreholes as the primary source of drinking water were less likely, to report water treatment during the outbreak or on the day of the survey, and to have treated stored water with FCR  $\geq 0.2$ mg/L ( $p < 0.05$ ). The findings highlight: 1) relatively low uptake of PoUWT after free distribution (consistent with other research); 2) the need to improve coordination of NGO response activities through consistent PoUWT product choices and communication about product use; and, 3) the need to emphasize treating drinking water from all sources daily to control and prevent typhoid fever and other waterborne disease outbreaks.

## 1253

### EFFECTS OF ENVIRONMENT ON HUMAN CYTOKINE RESPONSES: ROLE OF URBAN VERSUS RURAL RESIDENCE

**Philip J. Cooper**<sup>1</sup>, Leila D. Amorim<sup>2</sup>, Camila A. Figueiredo<sup>2</sup>, Renata Esquivel<sup>2</sup>, Fernanda Tupiza<sup>3</sup>, Silvia Erazo<sup>4</sup>, Yisela Oviedo<sup>4</sup>, Maritza Vaca<sup>4</sup>, Martha E. Chico<sup>4</sup>, Mauricio L. Barreto<sup>2</sup>

<sup>1</sup>Liverpool School of Tropical Medicine, Liverpool, United Kingdom,

<sup>2</sup>Universidade Federal da Bahia, Salvador, Brazil, <sup>3</sup>Hospital de Los Valles,

Quito, Ecuador, <sup>4</sup>Laboratorio de Investigaciones FEPI, Quinde, Ecuador

Environment may have a key role in the development of the immune system in childhood and may explain the low prevalence of allergic and autoimmune diseases in the rural tropics. To investigate the effects of urban versus rural residence on the immune response, we recruited 440 school children living in either in rural communities in the Province of Esmeraldas or in the city of Esmeraldas. We collected data on

environmental exposures by questionnaire and on intestinal parasites by examination of stool samples. Whole blood was stimulated with mitogen, parasite antigen and aeroallergens. IFN- $\gamma$ , IL-5, IL-10, IL-13, and IL-17 were measured in supernatants. Overall, urban children had mothers with greater educational levels, were more likely to have access to piped water (urban 98.7 % vs. rural 1.9%) and were more likely to use latrines or water closets for defecation (urban 94.8% vs. rural 54.7%). Rural children were more likely to be infected with geohelminths (urban 73.5% vs. rural 20.9%). The frequencies of children with ..DDDdetectable levels of cytokines were similar in urban and rural samples except for IL-10 that was significantly more frequent in the urban population when measured as spontaneous production (adjusted OR 2.56, 95% CI 1.05-6.24) and after stimulation with *Ascaris* (adj. OR 2.5, 95% CI 1.09-5.79) and house dust mite (adj. 2.24, 95% CI 1.07-4.70) antigens. Our data do not provide support for a major role for place of residence or geohelminth infections as a major determinant of the cytokine response in childhood. Surprisingly, urban residence that might be considered to be a more hygienic environment, was associated with more frequent production of the immune regulatory cytokine IL-10.

## 1254

### PROGRESS ON MDG 7.C IN THE MILLENNIUM VILLAGES AFTER THREE YEARS: IMPROVED HOUSEHOLD WATER AND SANITATION

**Elizabeth Katwan**, Lucy McClellan, Jennifer Schaefer, Uyen Huynh, Joyce Chen, Gayle Lennox

*Columbia University, New York, NY, United States*

Benefits of improving water and sanitation can influence health, educational, employment, economic and social domains. Since 1990, there have been significant global gains in access to improved water, and slower gains in sanitation. Despite commendable improvements, global progress has been uneven, with sub-Saharan Africa, and rural areas in particular, carrying a disproportionate burden of poor access. This mixed-methods implementation study assesses progress towards MDG 7.C across nine sites in rural sub-Saharan Africa in the first three years of the Millennium Villages Project (MVP), a 10-year multi-sector development project. Details of costs, variability between and within sites, challenges and lessons learned are explored in the study. Across nine MVP sites, the proportion of households not using an improved household water source reduced from 87.3% at baseline (2006/07) to 22.7% at year 3 (2009/10) (64.6% percentage-point change, 95% CI = 60.7-68.6%, p-value <0.0001). This represents a 74% reduction in the proportion of population without access to improved water, and exceeds the MDG target for water at a local level, as well as meeting the sub-Saharan African regional target of less than 25% of the population without coverage by 2015. The proportion of the population reporting not using an improved sanitation facility reduced from 98.1% at baseline to 71.4% at year 3 (26.7% percentage point change, 95% CI 24.6%-29.0%, p-value <0.0001). This represents a 27% reduction in the proportion of the population without access to improved sanitation facilities. Although not yet meeting the MDG for sanitation, if the same rate of change were to continue from today to 2015, sanitation would also be on track to meet local and regional MDG targets. These data provide promising evidence suggesting that with MDG-focused interventions, significant gains can be made in household access to improved water and sanitation facilities in a rural sub-Saharan African setting.

## 1255

### FARM WORKER HYGIENE AND HAND SANITATION IN MEXICO ASSOCIATED WITH CONTAMINATION OF FRESH PRODUCE

**Laura K. Wright**<sup>1</sup>, Elizabeth A. Adam<sup>1</sup>, Gaelle J. Gourmelon<sup>1</sup>, Faith E. Bartz<sup>1</sup>, Anna M. Fabiszewski de Aceituno<sup>1</sup>, Norma L. Heredia<sup>2</sup>, J. Santos Garcia<sup>2</sup>, Lee-Ann Jaykus<sup>3</sup>, Juan S. Leon<sup>1</sup>

<sup>1</sup>*Emory University, Atlanta, GA, United States*, <sup>2</sup>*Universidad Autonoma de Nuevo Leon, Monterrey, Mexico*, <sup>3</sup>*North Carolina State University, Raleigh, NC, United States*

Produce-related foodborne disease outbreaks lead to economic losses, illness, and death, making produce-contamination an important public health concern. In this study we investigated the pathways of produce contamination on Mexican farms, and the sanitation and hygiene practices that may contribute to contamination. We quantified the fecal contamination on produce, hands and environmental samples from 11 farms in Mexico. Produce (cantaloupe, jalapeño, tomato) rinses (161), were collected along with matched irrigation water (89), soil (55), and farm worker hand rinses (106). From these samples, fecal indicators (*E. coli*, *Enterococcus*, coliforms) and human pathogens (*Salmonella*, *E. coli* O157:H7) were enumerated. Multivariate regression modeling was used to identify associations. Data were also collected on farm sanitation and worker hygiene through surveys and interviews. Produce was frequently contaminated, 29%-100% of samples were positive for indicators, and the mean concentration of indicators ranged from 10<sup>2</sup>-10<sup>6</sup> cfu/fruit. The presence and levels of indicators on soil and water were not significantly associated with those on produce samples. Microbial indicators on hands were significantly higher (p < 0.05) than in water or soil. Presence of *E. coli* was significantly associated between hands and produce (OR 7.9, 95%CI [3.3-19.1]). The levels of *E. coli*, *Enterococcus*, and coliforms ( $\rho=0.4, 0.5, 0.6$ ) were significantly and highly correlated between hands and produce. These data show that hands are a potential source of produce contamination. Hand contamination is likely due to lack of sanitation/hygiene facilities. There were five toilets total available on all 11 farms. Only three had handwashing stations nearby. Evidence of open defecation was observed on two farms. Improved hygiene facilities and sanitation policies on farms could reduce microbial contamination of produce and improve working conditions for employees. Future study aims include the development of training modules on sanitation/hygiene behaviors tailored to farm managers and workers.

## 1256

### WASTEWATER IRRIGATED FARMS AS A COMMON DENOMINATOR FOR MALARIA AND DIARRHEAL DISEASE TRANSMISSION IN URBAN GHANA

**Razak Seidu**<sup>1</sup>, Amina Abubakari<sup>1</sup>, Robert C. Abaidoo<sup>2</sup>, Hans J. Overgaard<sup>1</sup>, Thor-Axel Stenstrom<sup>1</sup>

<sup>1</sup>*Norwegian University of Life Sciences, Ås, Norway*, <sup>2</sup>*Department of Theoretical and Applied Biology, Kumasi, Ghana*

Worldwide, wastewater use in urban agriculture is increasing at a rapid pace due to urbanization and its accompanying stress on limited freshwater resources. The economic and food security benefits associated with wastewater use in urban agriculture are enormous, but so also are the public health burden the practice exerts on the urban population. Wastewater use in urban agriculture is identified as a major risk factor for diarrhoeal disease, particularly among urban farmers and their family members and consumers of wastewater farm products. Malaria mosquito vectors also breed in wastewater farms, thus exposing nearby urban populations to increased malaria risk. In addition, agro-chemicals used in wastewater farms may contribute to development of insecticide resistance in malaria vectors, further exacerbating the malaria problem. So far, little is known of the contribution of wastewater farms to the combined risk of diarrhoea and malaria. Understanding this contribution would be important for developing integrated interventions. The main

aim of this study is to assess the contribution of urban wastewater farms as a common denominator for the transmission of malaria and diarrhoeal disease in urban Ghana. The study is being conducted in Kumasi, the second largest city in Ghana, where more than 12000 hectares of urban vegetable farms are irrigated with wastewater. The outcome of the study will lead to the development of integrated interventions for mitigating malaria and diarrhoeal disease transmission associated with wastewater irrigation.

## 1257

### ASSOCIATION BETWEEN EFFICIENTLY COLLECTED MEASURES AND OBSERVED MEASURES OF HANDWASHING BEHAVIOR IN THE IMPACT EVALUATION OF THE GLOBAL SCALING UP HANDWASHING PROJECT IN VIETNAM

Michelle W. Sahli<sup>1</sup>, Claire Chase<sup>2</sup>, Benjamin Arnold<sup>3</sup>, Bertha Briceno<sup>2</sup>, John Colford<sup>3</sup>, Paul Gertler<sup>3</sup>, Pavani K. Ram<sup>1</sup>

<sup>1</sup>State University of New York at Buffalo, Buffalo, NY, United States, <sup>2</sup>The World Bank - Water and Sanitation Program, Washington, DC, United States, <sup>3</sup>University of California, Berkeley, Berkeley, CA, United States

Handwashing reduces diarrhea incidence but is difficult to measure. Structured observation, a direct approach to measuring handwashing behavior, is costly and time-consuming. Self-report, observation of handwashing materials, and visual inspection of hand cleanliness are inexpensive and timesaving and thus efficient measures. We sought to assess whether these measures are associated with handwashing behavior measured by structured observation. With data from controls in the Impact Evaluation of the Global Scaling Up Handwashing Project in Vietnam, we used multilevel logistic regression to calculate wealth-adjusted odds ratios for associations between efficient measures of handwashing and observed handwashing behavior among caregivers, while accounting for multiple events per caregiver. We examined handwashing events overall and stratified by event type. We examined 1379 events overall; 289 fecal contact events (24% accompanied by handwashing with soap) and 569 food related events (6% accompanied by handwashing with soap). Soap and water at the handwashing places used post defecation (OR= 3.96, 95%CI: 1.61-9.53), and before food preparation (OR= 2.34, 95%CI: 1.17-4.68) as well as a rating of  $\geq 7$  on a hand cleanliness scale of 1 to 9 (OR= 3.01, 95%CI: 1.75-5.71) were significantly associated with observed handwashing with soap overall. Self-report of handwashing with soap after fecal contact (OR= 4.29, 95%CI: 1.68-11.01), observation of soap and water at the handwashing place used post defecation (OR = 8.21, 95%CI: 1.12-60.24), and hand cleanliness index  $\geq 7$  (OR = 3.48, 95%CI: 1.67 - 7.31) were all significantly associated with observed handwashing with soap after fecal contact events. Self-report of handwashing with soap before feeding a child was the only efficient measure associated with observed handwashing with soap before food related events (OR = 4.00, 95%CI: 1.14-14.02). In Vietnam, self-report of handwashing, presence of handwashing materials, and examination of hand cleanliness were associated with observed handwashing with soap overall, and handwashing after fecal contact. Where structured observation is infeasible due to cost, efficient measures of handwashing may be appropriate for measuring handwashing behavior. More importantly, promotion of handwashing with soap is required in Vietnam to improve hand hygiene at critical times relevant to pathogen transmission.

## 1258

### FAECAL CONTAMINATION OF FOOD, WATER, HANDS AND KITCHEN UTENSILS AT HOUSEHOLD LEVEL IN RURAL AREAS OF PERU

Ana I. Gil<sup>1</sup>, Claudio F. Lanata<sup>1</sup>, Stella M. Hartinger<sup>2</sup>, Daniel Mäusezahl<sup>2</sup>, Beatriz Padilla<sup>3</sup>, Theresa J. Ochoa<sup>4</sup>, Michelle Lozada<sup>1</sup>, Ines Pineda<sup>1</sup>, Hector Verastegui<sup>1</sup>

<sup>1</sup>Instituto de Investigacion Nutricional, Lima, Peru, <sup>2</sup>Swiss Tropical and Public Health Institute, Basel, Switzerland, <sup>3</sup>Wageningen University, Wageningen, The Netherlands, <sup>4</sup>Peruvian University Cayetano Heredia, Lima, Peru

The aim of this study was to evaluate sources of contamination of child's food and drinking water from rural households in the highlands of Peru. Samples from child meals, drinking water, kitchen utensils, and caregiver and child hands, were analysed for total coliforms and *Escherichia coli* counts using Petrifilm<sup>TM</sup>EC. Thermotolerant coliforms were measured in water using DelAgua<sup>®</sup> test kit. Diarrhoeagenic *E. coli* were searched by Polymerase Chain Reaction methods (PCR). Thermotolerant coliforms were found on 48% of water samples. *E. coli* was found in 23% of hands, 16% of utensils and 4% of meals. Kitchen cloths were the most frequently contaminated with total coliforms (89%) and *E. coli* (42%). Diarrhoeagenic *E. coli* was found in 33% of water, 27% of meals and 23% of kitchen utensils. There is a need to develop effective hygiene interventions focused to specific kitchen utensils and handwashing, to reduce the contamination of food, water and kitchen's environment in these rural settings.

## 1259

### WATER- AND SANITATION-RELATED RISK FACTORS FOR SOIL-TRANSMITTED HELMINTH INFECTION IN URBAN SCHOOL- AND PRESCHOOL-AGED CHILDREN IN KIBERA, NAIROBI

Caitlin M. Worrell<sup>1</sup>, Stephanie M. Davis<sup>1</sup>, Ryan E. Wiegand<sup>2</sup>, Gerard Lopez<sup>2</sup>, Leonard Cosmas<sup>3</sup>, Kennedy Odero<sup>3</sup>, Sammy M. Njenga<sup>4</sup>, Joel M. Montgomery<sup>3</sup>, LeAnne Fox<sup>1</sup>, Sharon L. Roy<sup>5</sup>

<sup>1</sup>Parasitic Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>2</sup>Division of Parasitic Diseases and Malaria, Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>3</sup>Global Disease Detection Branch, Centers for Disease Control and Prevention, Nairobi, Kenya, <sup>4</sup>Eastern and Southern Africa Centre for International Parasite Control, Kenya Medical Research Institute, Nairobi, Kenya, <sup>5</sup>Waterborne Disease Prevention Branch, Centers for Disease Control and Prevention, Atlanta, GA, United States

Individuals living in urban slums have limited access to city services, including water and sanitation (WS). Some evidence suggests that WS factors affect risk for soil-transmitted helminth (STH) infections, which disproportionately affect school-aged (SAC) and preschool-aged children (PSAC), but further characterization of WS factors and their impact in slum settings is needed to identify intervention points. Households (n=1,192) containing an index PSAC (6-59 months) or SAC (5-14 years) were randomly selected from those enrolled in CDC's International Emerging Infections Program, a population-based surveillance system in the urban slum of Kibera in Nairobi, Kenya. Data collection included a household-level questionnaire and environmental assessment for WS risk factors and index child stool specimens tested for STH ova by the Kato-Katz method. Stools of siblings living with index SACs were also tested. Household WS factors were classified by the WHO/UNICEF WS service level ladders categorizing resources in groups such as improved, unimproved, and shared, and tested for associations with STH infection. Among 130 households with sufficient data for interim analysis, household STH prevalence ( $\geq 1$  child in the household positive for any STH) was 36.2%. Of all households, 3.1% reported piped water on premises and 96.9% another improved drinking water source; 62.2% (79/127) of these sources were unofficial connections into nearby municipal pipes. Ever having

difficulty meeting household daily water needs was reported by 76.2% of households, most often due to financial barriers (69.8%). Overall, 2.3% of household sanitation facilities were improved, 87.7% shared, and 6.2% unimproved; 2.3% of households practiced open defecation. Sewage observed in the participant's yard was associated with household STH infection (Fisher's Exact Test,  $p=0.03$ ). Other associations emerging with ongoing data collection will be discussed. The Kibera population faces gaps in water availability and sanitation quality; STH control here and in similar settings requires an integrated approach.

## 1260

### A QUALITATIVE EVALUATION OF HAND DRYING PRACTICES AMONG KENYANS

**Bobbie Person**<sup>1</sup>, Katharine Schilling<sup>1</sup>, Mercy Owuor<sup>2</sup>, Lorraine Ogange<sup>2</sup>, Ibrahim Sadumah<sup>2</sup>, Alie Eleveld<sup>2</sup>, Robert Quick<sup>1</sup>

<sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States,

<sup>2</sup>Safe Water and AIDS Project, Kisumu, Kenya

Recommended disease prevention behaviors of hand washing, hygienic hand drying, and covering one's mouth and nose in a hygienic manner when coughing and sneezing appear to be simple behaviors but continue to be a challenge to promote successfully and sustain globally. We conducted a formative inquiry to better understand current hand drying behaviors associated with activities of daily living, and mouth and nose covering practices, among Kenyans. We conducted 7 focus group discussions (N=45); 30 in-depth interviews; 10 structured household observations; and 75 structured public observations in rural and urban Kenya communities. Using a grounded theory approach, we transcribed, coded, and analyzed the narrative data. Hand drying with a towel is not a common practice. Most women dry their hands on their lesa (rectangular cloth wrapped around the waist) or their clothes when cooking, eating, or cleaning a young child. When men dry their hands, they use their trousers or a handkerchief. Children rarely dry their hands but, if they do, they usually wipe them on their clothes. People drew distinctions between hand drying after sporadic sneezing and blowing their nose during a cold. Many people sneeze into their hands and wipe them on their clothes. Men and women tended to use a handkerchief when they had a cold. Drying hands on dirty clothes and lesas can compromise the benefits of handwashing. Coughing and sneezing into an open hand can help spread disease. Health education and promotion materials and messages should stress hygienic hand drying practices such as using a clean towel or cloth, or air-drying. Messages should be particularly tailored to household activities and should emphasize the potential role of dirty towels or clothes as a vector of disease. The importance of sneezing or coughing into the upper arm or a handkerchief should also be emphasized more prominently. Research into barriers to adopting these simple practices is needed.

## 1261

### POST-IMPLEMENTATION EFFECTIVENESS OF FOUR HOUSEHOLD WATER TREATMENT TECHNOLOGIES IN TYPICAL-USE CONDITIONS IN RURAL KENYA

**Onabolu Boluwaji**<sup>1</sup>, Larry Obi<sup>2</sup>, Carolyn G. Palmer<sup>1</sup>

<sup>1</sup>Rhodes University, Grahamstown, South Africa, <sup>2</sup>Walter Sisulu University, Umtata, South Africa

Household water treatment technologies are used by about 18 million of the 884 million people without adequate access to safe water. The efficacy of household water treatment technologies has been demonstrated in controlled situations such as laboratory and field trials. However some authors query the sustainability of the efficacy of HWT technologies under real-life situations after the field trials have ended. In view of the dependence of rural communities on highly polluted surface water sources; the sectoral promotion of household water treatment (HWT) systems and the lack of data on their post-intervention effectiveness, it is necessary to evaluate the effectiveness of household

water treatment technologies within a real-life context. This study was carried out one and two years after the two implementing organisations had ended their intervention. It examined the microbial efficacy of Aquatab, PUR, Waterguard and ceramic filters by carrying out three unannounced visits between March and April 2010 to each of the 37 HWT user households in five villages in the Nyanza province of Western Kenya. A total of 247 samples were collected from study households' collection and storage containers in order to determine the efficacy of the technologies on water from the 11 unimproved and improved water sources used by the study households. The findings indicate that the four HWT technologies assessed are able to improve microbial quality of the improved and unimproved water sources. However, based on the observation of inconsistent performance, none of the technologies achieved the minimum expected reduction value or can be classified as a highly protective or protective technology. It is recommended that the drinking water supply and sanitation sector should address the reasons for their reduced effectiveness in the typical-use conditions when compared to laboratory efficacy. These include incorrect usage and inappropriate selection of HWT options for water source characteristics.

## 1262

### VALIDATION OF AN INDEX OF PROXY MEASURES AND SELF-REPORTED HANDWASHING BEHAVIOR IN DHAKA, BANGLADESH

**Christina R. Crabtree-Ide**<sup>1</sup>, Kelly B. Kamm<sup>1</sup>, Michelle Sahli<sup>1</sup>, Jelena Vujcic<sup>1</sup>, Stephen P. Luby<sup>2</sup>, Pavani K. Ram<sup>1</sup>

<sup>1</sup>SUNY Buffalo, Amherst, NY, United States, <sup>2</sup>International Centre for Diarrhoeal Disease Research, Bangladesh, Centers for Disease Control and Prevention, Dhaka, Bangladesh

Handwashing with soap reduces diarrhea, a leading cause of death in young children. Structured observation permits direct measurement of handwashing, but is inefficient and costly. Measures of handwashing behavior can be efficiently collected by rapid observation and self-report, but in isolation, they are not good indicators of behavior. Using data from primary caregivers in a case-control study of pneumonia risk factors in Dhaka, Bangladesh, we sought to develop an index of efficiently collected handwashing measures, and then test the validity of the index by comparing it to handwashing behavior measured by structured observation. We used principal component analysis, a data reduction technique, to generate a handwashing behavior index score for each caregiver based on handwashing demonstration, rapid observation, and self-reported handwashing behavior. We assigned caregivers to handwashing index quintiles and used logistic regression to compare quintiles to observed handwashing with soap after fecal contact in a 5 hour structured observation, accounting for repeated events. We observed 1,958 fecal contact events, of which 773 (39%) were followed by handwashing with soap. Duration of lathering during a handwashing demonstration, use of soap during a handwashing demonstration, presence of soap at a handwashing station, and self-reported frequency of handwashing accounted for 52% of the variance in the handwashing index score. When compared to those in the lowest index quintile of handwashing scores, each quintile except the third was associated with an increased odds of observed handwashing with soap [2<sup>nd</sup> quintile OR=1.41,  $p=0.03$ , 3<sup>rd</sup> quintile OR= 0.96,  $p= 0.81$ , 4<sup>th</sup> quintile OR=1.34,  $p=0.05$ , 5<sup>th</sup> quintile OR=1.30  $p=0.08$ ]; however, there was no significant linear trend ( $p$  trend=0.11). The use of principal component analysis to develop a handwashing behavior index did not identify progressive increases in observed handwashing behavior. Alternatives for index construction, such as summing of items, factor analysis, and prediction modeling, may be considered and evaluated against structured observation and health outcomes data. The construction and validation of indices represents only one approach to addressing the pressing need for low-cost, efficient, and reliable handwashing measures for use in modestly funded studies.

## 1263

**EVALUATION OF THE MICROBIOLOGIC SAFETY OF STORED RAINWATER AS AN IMPROVED DRINKING WATER SOURCE FOR COMMUNITIES IN KHON KAEN, THAILAND**

Jacqueline S. Knee<sup>1</sup>, Christine Stauber<sup>2</sup>, Nsa Dada<sup>3</sup>, Anan Vannavong<sup>3</sup>, Hans J. Overgaard<sup>3</sup>, Thor Axel Stenstrom<sup>3</sup>, Mark D. Sobsey<sup>4</sup>

<sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States,

<sup>2</sup>Georgia State University, Atlanta, GA, United States, <sup>3</sup>Norwegian

University of Life Sciences, Ås, Norway, <sup>4</sup>University of North Carolina at Chapel Hill, Chapel Hill, NC, United States

Rainwater (RW) is considered an improved source of drinking water (DW) by the WHO and UN agencies tracking progress towards achieving the safe water access target of the Millennium Development Goals. There are, however, a paucity of data on the microbial quality of RW, making uncertain its safety as a DW source. The objective of this work was to evaluate the microbial quality of stored RW collected in a rural village in Thailand using the WHO DW quality guideline value of <1 *E. coli*/100mL as the basis for safety. In 2011, 59 households in Khon Kaen province, all of which used RW as their primary source of DW, were visited twice, once during dry season and once during rainy season. Observational data related to the physical/sanitary conditions of RW harvesting systems (RWHS) were collected during visits. Sampled containers included each household's main RW collection tank and the refillable container used to store RW for daily consumption. Samples were assayed for *E. coli* by the Colisure Quantitray 2000 method and results were scored as present if *E. coli* was ≥1/100mL. Of all samples processed (collection tank, refillable container), 39% and 82% of households had *E. coli* present in at least one container during the dry and wet seasons, respectively. *E. coli* was present in 21% and 66% of RW collection tanks during the dry and wet seasons, respectively. Initial analysis suggests that no single factor related to RWHS setup (roof, pipe, or tank material) had a statistically significant impact on the presence of *E. coli* in RW collection tanks. These results suggest that stored RW microbiologic quality may be highly seasonal, may not always meet WHO guidelines for safe DW, and that deterioration of the microbiologic quality of stored RW is likely due to a combination of collection and use practices. These results document that the UN Joint Monitoring Program's use of access to improved water supplies as an indicator of progress towards the MDG safe water target results in overestimation because improved sources, like harvested RW, may be microbiologically unsafe.

## 1264

**REDUCTIONS IN DIARRHEA AND CLINIC VISITS FOR DIARRHEA AMONG CHILDREN UNDER THE AGE OF FIVE ASSOCIATED WITH A SCHOOL-BASED WATER SUPPLY, SANITATION AND HYGIENE INTERVENTION IN WESTERN KENYA: A CLUSTER-RANDOMIZED TRIAL**

Robert Dreifelbis<sup>1</sup>, Matthew C. Freeman<sup>2</sup>, Leslie E. Greene<sup>2</sup>, Shadi Saboori<sup>2</sup>, Richard Rheingans<sup>3</sup>

<sup>1</sup>Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, United States,

<sup>2</sup>Rollins School of Public Health, Emory University, Atlanta, GA,

United States, <sup>3</sup>Center for African Studies, University of Florida, Gainesville, FL, United States

While many studies have documented reductions in diarrhea incidence in children under five associated with improvements in water, sanitation, and hygiene (WASH) in the domestic environment, the effect of institution-based interventions are not well understood. We conducted a cluster-randomized trial of school-based WASH interventions in 185 public primary schools in western Kenya. Enrolled schools with a nearby water source (<1KM) were randomized into a handwashing promotion and water treatment intervention [HP&WT], HP&WT plus an additional sanitation component [San + HP&WT], or a control group. Schools without a nearby water source were randomized to receive a water supply

intervention in addition to the San + HP&WT intervention components or to a control group. Interviews were conducted in a systematic selection of households in the catchment areas of all enrolled schools. Parent reported diarrhea episodes in the past week and clinic visits for diarrhea or vomiting in the past two weeks were recorded for all children under the age of five. Data were collected at baseline (March-April 2007) (n = 4,549) and two years after the start of the interventions (n = 4,392). There was a non-significant 33% reduction in the relative risk (RR) of diarrhea and 51% reduction in the RR of clinic visits among children under five living in the catchment areas of schools receiving water supply improvements compared to control areas (p = 0.185 and 0.075, respectively). Restricting analysis to those children under five living with at least one child attending a school enrolled in the trial increased both the magnitude and significance of this effect (RR diarrhea: 0.53, p= 0.049; RR clinic visits: 0.39, p= 0.03). The HP&WT and San + HP&WT interventions showed no effect on either outcome in both unrestricted and restricted analyses. Our findings suggest that an integrated school WASH intervention that includes the provision of improved water supply at the school can result in substantial reductions in child morbidity even among those children too young to attend school.

## 1265

**EFFICACY OF DISINFECTANTS ON VIABILITY OF FOODBORNE BACTERIA AND ON CRYPTOSPORIDIUM AND CYCLOSPORA**

Ynes R. Ortega, Venessa Chandra, Maria Torres

University of Georgia, Griffin, GA, United States

*E. coli* STEC, *Salmonella*, *Cryptosporidium*, *Cyclospora*, and microsporidia are causative agents of diarrheal illness worldwide. Most of the outbreaks associated with contaminated foods have implicated fruits and vegetables that have been consumed raw. The objective of this study was to determine the recovery efficiencies to improve the methodology detection for foodborne parasites to be used in surveillance studies, to determine efficacy of sanitizers used in the food industry on the survival of foodborne bacteria and parasites, and examine cross contamination during produce harvesting. Five *Escherichia coli* O157:H7, five *Salmonella* spp, and one isolate of each *Cyclospora cayetanensis*, *Cryptosporidium parvum*, and *Encephalitozoon intestinalis* were used for these experiments. Four different wash solutions were examined for recovery of 1000 oocysts of *Cryptosporidium* and *Cyclospora* from 25 gr basil leaves: water, 0.1M phosphate buffer, Glycine, and 3%levulinic acid/SDS. Phosphate buffer worked best. Detection of both organisms was done using nested PCR. Experimentally inoculated basil and bean sprouts were blanched (65, 88, and 100C) and determined if this process kills contaminants. The bacterial contaminants were reduced but not eliminated. The times and temperatures effective for pathogen destruction affected the fresh appearance of vegetables. Freezing did not inactivate bacterial pathogens but *Cryptosporidium* and microsporidia were very sensitive to extreme temperatures. Cross-contamination can occur when contaminated water or contaminated coring tools are used during lettuce harvesting. Reduction of contaminants in lettuce and coring tools was achieved when coring tools were rinsed with diluted chlorine (commonly used in agriculture) and more yet when rinsed with 3% LA/SDS. Sequential contamination of lettuce heads with microsporidia was also observed. Because parasites are highly resistant to chemical disinfectants, it is important to prevent crop contamination during harvesting.

1266

### CHARACTERIZATION OF THE ETIOLOGY AND EPIDEMIOLOGY OF CENTRAL NERVOUS SYSTEM INFECTIONS IN GEORGIA

Tamar Akhvediani<sup>1</sup>, Emily Rowlinson<sup>2</sup>, Margaret Farrell<sup>2</sup>, Christian Bautista<sup>3</sup>, Tinatin Kuchuloria<sup>1</sup>, Tengiz Tsertsvadze<sup>4</sup>, Roman Shakarishvili<sup>5</sup>, Nana Tatishvili<sup>6</sup>, Rusudan Chlikadze<sup>7</sup>, Matthew Hepburn<sup>8</sup>, Guillermo Pimentel<sup>2</sup>, Robert Rivard<sup>8</sup>, Brent House<sup>2</sup>

<sup>1</sup>Walter Reed Army Institute of Research/U.S. Army Medical Research Institute for Infectious Diseases Clinical Research Unit, Tbilisi, Georgia, <sup>2</sup>U.S. Naval Medical Research Unit No. 3, Cairo, Egypt, <sup>3</sup>Walter Reed Army Institute of Research, Fort Detrick, MD, United States, <sup>4</sup>Scientific Research Center of Infectious Pathology, AIDS, and Clinical Immunology, Tbilisi, Georgia, <sup>5</sup>Department of Neurology and Neurosurgery, I. Javakishvili Tbilisi State University, Tbilisi, Georgia, <sup>6</sup>Neurology Department of the Iashvili Children's Hospital, Tbilisi, Georgia, <sup>7</sup>National Center for Disease Control and Public Health, Tbilisi, Georgia, <sup>8</sup>U.S. Army Medical Research Institute of Infectious Diseases, Fort Detrick, MD, United States

Central nervous system (CNS) infections are caused by a large spectrum of viruses and bacteria, and associated with severe and disabling sequelae. Diagnosis of CNS infections and identification of the causative agents requires a complex combination of laboratory tests. In 2010, a hospital-based surveillance study was initiated in Tbilisi, Georgia to determine the incidence of infectious etiologies of acute meningitis and encephalitis, and to enhance laboratory capacity for the diagnosis of CNS infections. Cerebral spinal fluid (CSF) and acute and convalescent sera were collected for bacterial culture and real-time polymerase chain reaction (RT-PCR) testing for herpes simplex virus (HSV) types 1 and 2, mumps virus, enterovirus, varicella zoster virus (VZV), *Streptococcus pneumoniae*, *Haemophilus influenzae* type B (Hib), and *Neisseria meningitidis*. Testing for West Nile virus (WNV), tick-borne encephalitis virus, and Epstein-Barr virus (EBV) was conducted via ELISA. As of April 2012, 144 patients were enrolled. Of these, 44% were adults and 56% were children < 18 years of age. Female to male ratio was 1:1.14. The majority of the patients (75%) were from urban Tbilisi. In 89.7% of enrolled patients, the discharge diagnosis was meningitis and in 8.8% it was encephalitis. Of the meningitis cases, bacterial meningitis was the discharge diagnosis slightly more frequently than viral meningitis (52.8% and 43.4%, accordingly). *S. pneumoniae* was cultured from CSF in five patients. One of the secondary study objectives was to measure the occurrence of Hib following the initiation of a nationwide vaccination campaign that began in January 2010, shortly before the initiation of this study. None of the patients were positive for Hib. In 140 CSF samples tested by PCR, enterovirus was the most frequently detected etiology (26%). There were three cases of VZV, one case of HSV-1, and two cases of EBV. Data from this ongoing hospital surveillance study provides valuable etiologic and epidemiologic information regarding viral and bacterial acute meningitis and encephalitis in Georgia.

1267

### THIRD CASE OF FATAL YELLOW FEVER VACCINE-ASSOCIATED VISCEROTROPIC DISEASE IN A YOUNG PERUVIAN WOMAN

Gladys Turpo<sup>1</sup>, María Ticona<sup>1</sup>, Jorge Uchuya<sup>1</sup>, Alvaro Whittembury<sup>2</sup>, Stephen J. Seligman<sup>3</sup>

<sup>1</sup>Ministry of Health, Lima, Peru, <sup>2</sup>Universidad Nacional Mayor de San Marcos, Lima, Peru, <sup>3</sup>New York Medical College, Valhalla, NY, United States

Until 2001, yellow fever vaccine was considered to be the world's safest live vaccine. Since then 65 cases of Yellow Fever Vaccine-Associated Viscerotropic Disease (YEL-AVD) have been reported. YEL-AVD resembles yellow fever itself and is frequently fatal. The incidence based on a passive reporting system is 0.3 to 0.4/100,000. However, following an immunization campaign in Peru an incidence of 7.91/100,000 was observed. Known risk factors include age  $\geq$ 60 and thymectomy as

treatment for thymoma. More recently, women of childbearing age have been described as being at increased risk. Nine cases, all fatal, of YEL-AVD in young women have been reported including two from the above Peruvian campaign. Here we describe a third fatal case in a 24 year old Peruvian woman who was vaccinated in preparation for a trip to Australia. The incubation period, day of death following vaccination, and clinical course with multi-organ failure are similar to the other nine cases. RT-PCR demonstrated virus with 100% homology to vaccine virus in serum obtained on the 10th day post-vaccination. The viral load was 45 000 PFU/mL. Of interest is the evidence for concomitant leptospiral infection, lymphopenia, and family history suggesting that the death of a 2 year old male sibling was from meningo-encephalitis. The reasons for the apparent concentration of cases in young women in Peru are unclear. There was no apparent common ethnicity in the three young women. A genetic defect affecting immunity is a plausible explanation and should be investigated with additional research.

1268

### UNDERSTANDING TRICHIASIS FROM THE PERSPECTIVE OF THE PATIENT: AN ASSESSMENT OF PREVIOUSLY OPERATED AND NEVER OPERATED PATIENTS TO IMPROVE QUALITY AND EFFICIENCY OF SURGICAL SERVICES IN ETHIOPIA, NIGER AND MALI

Lisa M. Dickman<sup>1</sup>, Emily Toubali<sup>2</sup>, Stephanie L. Palmer<sup>1</sup>, Aryc W. Mosher<sup>1</sup>, Elizabeth A. Cromwell<sup>3</sup>, Paul Courtright<sup>4</sup>, Susan Lewallen<sup>4</sup>, Matthew J. Burton<sup>5</sup>, Chad MacArthur<sup>2</sup>, Mulat Zerihun<sup>6</sup>, Kadri Boubacar<sup>7</sup>, Sanoussi Bamani<sup>8</sup>, Paul M. Emerson<sup>1</sup>

<sup>1</sup>The Carter Center, Atlanta, GA, United States, <sup>2</sup>Helen Keller International, New York, NY, United States, <sup>3</sup>University of North Carolina, Chapel Hill, Chapel Hill, NC, United States, <sup>4</sup>Kilimanjaro Centre for Community Ophthalmology, Moshi, United Republic of Tanzania, <sup>5</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>6</sup>The Carter Center Ethiopia, Bahir Dar, Ethiopia, <sup>7</sup>Programme National de la Lutte Contre la Cecite, Niamey, Niger, <sup>8</sup>Programme National de la Lutte Contre la Cecite, Bamako, Mali

Ethiopia, Niger, and Mali comprise 26% of the trichiasis burden in the developing world and reported 65% of the global trichiasis surgical output in 2009. In 2011, a study was conducted in each country to understand the trichiasis experience from the patient's perspective with the aim of improving the quality and efficiency of the surgical delivery system. In each country, districts were ranked according to surgery output over the past two years and villages selected at random from the top quartile. Within selected villages all operated and un-operated patients were interviewed to a maximum of 25 and additional villages visited until 192 operated patients had been interviewed. A pre-tested standardized questionnaire asked about demographics, knowledge of trichiasis treatments, health seeking behavior, and perception of surgery; a clinical eye exam was conducted by a trichiasis surgeon. A total of 683 operated and 227 never operated cases were interviewed: Ethiopia 296 and 120; Niger 193 and 35; and Mali 194 and 72, respectively. Among those previously operated, the most common reasons for having surgery were pain, fear of vision loss, and inability to work. Post-operative trichiasis was found in 28.7% of patients in Ethiopia, 33.7% in Niger, and 26.4% in Mali; most had minor trichiasis (<5 lashes). Most patients reported satisfaction with the surgery: Ethiopia, 86%; Niger, 93%; Mali, 92%; most had recommended the surgery to others, reported improvement in vision, and no longer felt pain in the operated eye. Of those never operated, knowledge of the opportunity to receive surgery ranged from 25.0% to 73.5%; however, over 80% reported they had never presented for surgery. Major trichiasis (>5 lashes) was common: Ethiopia, 34.5%; Niger 47.1%; Mali 36.1%. The majority had lived with trichiasis for three or more years and reported pain. Study results will be used to increase community mobilization and awareness about trichiasis surgical services, boost surgical access, improve the quality of surgery, and enhance the overall efficiency of the surgical delivery system.

### PATTERN OF ACUTE POISONING AND PREDICTION OF MORTALITY: A HOSPITAL BASED SURVEY IN DHAKA, BANGLADESH

Ariful Basher<sup>1</sup>, **Robed Amin**<sup>1</sup>, Richard J. Maude<sup>2</sup>, Aniruddha Ghose<sup>3</sup>, Abdullah Abu Sayeed<sup>3</sup>, Sue Lee<sup>2</sup>, Ham Nazmul Ahasan<sup>1</sup>, M. Rajibul Alam<sup>1</sup>, M. Abul Faiz<sup>4</sup>

<sup>1</sup>Dhaka Medical College, Dhaka, Bangladesh, <sup>2</sup>Wellcome Trust Mahidol-Oxford Tropical Medicine Research Unit, Bangkok, Thailand, <sup>3</sup>Chittagong Medical College Hospital, Chittagong, Bangladesh, <sup>4</sup>Centre for Specialized Care and Research, Chittagong, Bangladesh

Poisoning is a major cause of morbidity and mortality worldwide. Different substances have variable degrees of toxicity from harmless to fatal. Treating physicians often do not know which poison has been taken. It is important to identify life threatening cases to priorities care appropriately. Few systematic investigations of poisoning have been done in the tropics. A large number of poisoning cases remains unreported due to lack of information and awareness at community level. This study collected baseline information and outcome of poisoning in Dhaka, Bangladesh. All cases of poisoning from 1/4/08-30/3/09 admitted to Dhaka Medical College Hospital (DMCH) were recruited for detailed observation. Details of clinical presentation, social background and outcome were recorded. In total, 5932 cases of poisoning in DMCH were enrolled of which 2108/5929 (35%) were female. Median age was 25 years (IQR 19-35 years). Major substances were Benzodiazepines (12%), including deliberate/"induced", organophosphates/carbamates (OPC) (12%), snake/fish/insect and medications. 36% took unknown substances. Suicidal attempt due to family disharmony was the commonest motivating cause (38%). Overall mortality was 151/5932 (2.6%) with 105/151 (70%) of deaths due to OPC (mortality 16%). Other causes of fatal poisoning included benzodiazepines, rat killer, animal/insect bites and stings, methanol, ethanol, herbal medicine and copper sulfate. Risk factors for mortality by univariate analysis were rural abode, hindu religion, illiterate, farmer, suicide attempt, accidental poisoning, GCS<9, BP<90/60mmHg, HR>100 or <60 bpm and abnormal pupils. Multivariate analysis found GCS<11 to be the best predictor of death with the addition of constricted pupils and non-muslim religion in the OPC group and systolic BP<80mmHg, economic loss/failure to pass an exam in the non-OPC group. A simple scoring system was derived using GCS and BP to predict mortality due to causes other than OPC. Poisoning is a common cause of medical admission in Bangladesh. A wide variety of substances are used. OPC poisoning is common and causes two thirds of the deaths. Those at high risk of fatal poisoning can be predicted from history and examination findings.

### 1270

### RANDOMIZED, DOUBLE-BLINDED, PHASE 2 TRIAL OF WR 279,396 (PAROMOMYCIN AND GENTAMICIN) FOR THE TREATMENT OF CUTANEOUS LEISHMANIASIS CAUSED BY LEISHMANIA PERUVIANA

**Alejandro Llanos-Cuentas**<sup>1</sup>, Ana Ramos<sup>1</sup>, Braulio Valencia<sup>1</sup>, Ana Quispe<sup>1</sup>, Mara Kreishman-Deitrick<sup>2</sup>, Karen Kopydlowski<sup>2</sup>, Diane Ullman<sup>2</sup>, William McCarthy<sup>2</sup>, Janet Ransom<sup>3</sup>, Charles Scott<sup>3</sup>, William Ravis<sup>4</sup>, Max Grogg<sup>5</sup>

<sup>1</sup>Universidad Peruana Cayetano Heredia, Lima, Peru, <sup>2</sup>U.S. Army Medical Materiel Development Activity, Fort Detrick, MD, United States, <sup>3</sup>Fast-Track Drugs and Biologics, North Potomac, MD, United States, <sup>4</sup>Auburn University, Auburn, AL, United States, <sup>5</sup>Walter Reed Army Institute of Research, Silver Spring, MD, United States

In this randomized, double-blind, parallel-group trial, 30 Peruvian patients with parasitologically confirmed cutaneous leishmaniasis (CL) lesions received either WR 279,396 (15% paromomycin + 0.5% gentamicin; n=14) or Paromomycin Alone (15% paromomycin; n=16) topical cream applied once daily for 20 days. Patients were followed

for pharmacokinetics (PK), safety, and efficacy for six months. Blood for paromomycin and gentamicin PK parameters was collected from adult subjects after the first days' and last days' drug application. The primary efficacy endpoint was cure of a parasitologically confirmed index lesion, defined as at least 50% reepithelialization of the lesion by Day 63 and 100% reepithelialization by Day 100 with no relapse. At 6 months, final clinical cure of an index lesion occurred in 9/14 (64.3%) subjects in the WR 279,306 group and 11/16 (68.8%) in the Paromomycin Alone group. In pediatric subjects, 9/10 (90%) cured with WR 279,396 and 9/11 (81.8%) with Paromomycin Alone. WR 279,396 appeared to have some benefit over Paromomycin alone as patient's lesions cured at a faster rate when treated with WR 279,396. At 6-months, efficacy of both WR 279,396 and Paromomycin Alone were comparable to historical data for first-line pentavalent antimonial treatments; WR 279,397 cured 5/5(100%) of subjects who had failed prior antimonial therapy. WR 279,396 and Paromomycin Alone creams produced only non-severe application site irritation, without systemic toxicity. PK data showed that there is limited paromomycin and gentamicin systemic absorption thus avoiding drug accumulation and toxicity. Either WR 279,396, or Paromomycin Alone may offer an advantage over first-line antimonial therapies for Peruvian CL, especially in children.

### 1271

### TRICHIASIS SURGEON PRODUCTIVITY IN ETHIOPIA, MALI AND NIGER: WHAT IS NEEDED TO REACH ELIMINATION BY 2020?

**Stephanie L. Palmer**<sup>1</sup>, Susan Lewallen<sup>2</sup>, Amir B. Kello<sup>3</sup>, Paul Courtright<sup>4</sup>, Emily Toubali<sup>5</sup>, Lisa M. Dickman<sup>1</sup>, Aryc W. Mosher<sup>1</sup>, Elizabeth A. Cromwell<sup>6</sup>, Mulat Zerihun<sup>7</sup>, Kadri Boubacar<sup>8</sup>, Sanoussi Bamani<sup>9</sup>, Paul M. Emerson<sup>1</sup>

<sup>1</sup>The Carter Center, Atlanta, GA, United States, <sup>2</sup>Kilimanjaro Centre for Community Ophthalmology, Moshi, United Republic of Tanzania, <sup>3</sup>Light for the World, Addis Ababa, Ethiopia, <sup>4</sup>Kilimanjaro Centre for Community Ophthalmology, Mosi, United Republic of Tanzania, <sup>5</sup>Helen Keller International, New York, NY, United States, <sup>6</sup>University of North Carolina, Chapel Hill, Chapel Hill, NC, United States, <sup>7</sup>The Carter Center Ethiopia, Bahir Dar, Ethiopia, <sup>8</sup>Programme National de la Lutte Contre la Cecite, Niamey, Niger, <sup>9</sup>Programme National de la Lutte Contre la Cecite, Bamako, Mali

WHO, donors and NGOs are committed to supporting National Trachoma Programs reach their elimination goals by 2020. Trachoma programs train mid-level eye care personnel and general healthcare workers to perform trichiasis surgery during routine services and outreach campaigns. Although much effort has been put into training surgeons, few studies have examined their productivity. In 2011, a standardized questionnaire was administered by phone to currently active surgeons in Ethiopia, Mali and Niger. The questionnaire asked about demographics, work facilities, supervision, training, and surgeries performed the previous year. In addition, an external ophthalmologist collected qualitative data on selection of trainees, training and supervision. A total of 445 surgeons were interviewed: 191 in Ethiopia, 60 in Mali and 194 in Niger; the majority were male (71%). Most surgeons in Ethiopia were trained <5 years ago, while in Mali and Niger, the majority were trained ≥5 years ago. While nearly 75% of Ethiopian surgeons had been retrained, 1% in Mali and 9% in Niger had been. The mean number of surgeries performed per surgeon in 2010 was: Ethiopia, 76.4; Mali, 156.4; and Niger, 55.9. Most surgery was conducted in outreach: Ethiopia, 93%, Mali, 91%; and Niger 67%. Factors significantly associated (p <0.05) with high productivity in Ethiopia included a higher proportion of time dedicated to eye care, no supervisory visit in the previous 6 months, and increasing years since training. In Mali, the only significant predictor was an increasing number of years since training, whilst in Niger predictors included percentage of time dedicated to eye care, being hospital-based, increasing years since training, and higher number of surgeries performed during training. Study results support that training dedicated eye care workers, improving the frequency and quality of supervision, providing refresher training, and

providing more outreach opportunities will support high productivity among trichiasis surgeons to enable national programs to meet their trachoma elimination targets.

## 1272

### CUTANEOUS LEISHMANIASIS AND THE EFFICACY OF AZOLES, A SYSTEMATIC REVIEW

**Wesley R. Campbell**, Joshua Hartzell, Alan Magill, Kent Dezee, Glenn Wortmann

*Walter Reed National Military Medical Center, Bethesda, MD, United States*

Cutaneous Leishmaniasis (CL) is endemic to 70 countries with 1.5 - 2 million new cases occurring annually. The majority of cases occur in the Middle East (Old World) although the disease is endemic to parts of South America (New World) as well. Travelers and military personnel are at significant risk of acquiring the disease. Its disfiguring and ulcerative lesions result in a high degree of morbidity for those infected. Despite the wide spread distribution and number of cases, debate persists with regard to the most effective treatment for CL. Antimonials have been the mainstay of therapy, but toxicity and constraints with administering the drug make it difficult to use. In recent years, evidence has been building regarding the efficacy of azole antifungals. In order to better characterize the effectiveness of azole antifungals we conducted a systematic review for azole treatment of CL. The databases used were MEDLINE, EMBASE, and Cochrane Database of Systematic Reviews. Search terms included "cutaneous leishmaniasis," "skin leishmaniasis," "therapy," "treatment," "fluconazole," "posaconazole," "ketoconazole," "itraconazole," and "voriconazole." The references from primary studies, narrative reviews and systemic reviews were reviewed to search for additional primary studies that could have been missed by the electronic search. Two investigators independently screened all citations by title and abstract and made a decision on acceptance. Disagreements were resolved by a third author. Inclusion criteria included a confirmed diagnosis of CL, monotherapy with an azole, availability of azole dosage and duration, at least 2 months of follow-up, and at least 4 patients per study. The results of the systematic review will be presented including a breakdown of effectiveness and side-effects of each azole. The aggregated data supports certain azoles as a choice for treating CL. An algorithmic approach to the treatment of CL is provided.

## 1273

### BURDEN OF SEVERE DISEASES IN THE FIRST THREE YEARS OF LIFE AMONG A BIRTH COHORT OF 1198 CHILDREN BETWEEN AGES 14 WEEKS AND THREE YEARS IN NORTHERN GHANA

**Patrick Odum Ansah**<sup>1</sup>, Nana Akosua Ansah<sup>1</sup>, Phillip K. Ayivor<sup>1</sup>, Modupe Amofa Sekyi<sup>1</sup>, Isaac Osei<sup>1</sup>, Oscar Oscar<sup>1</sup>, Timothy Awine<sup>1</sup>, Isaiah Agorinya<sup>1</sup>, Godwin Enwere<sup>2</sup>, Abraham Hodgson<sup>3</sup>, Marie-Pierre Preziosi<sup>4</sup>

<sup>1</sup>Navrongo Health Research Centre, Navrongo, Ghana, <sup>2</sup>Meningitis Vaccine Project, PATH, France, <sup>3</sup>Ghana Health Service, Accra, Ghana, <sup>4</sup>World Health Organization, Geneva, Switzerland

Reducing under-five mortality by two thirds between 1990 and 2015 according to the Millennium Development Goals is still quite elusive and efforts to control the cause of the deaths, namely, pneumonia, diarrhea, malaria and malnutrition are being revitalized. Most of these deaths occur in areas with difficulty in gathering accurate data and estimates are the only available means of assessing progress. This study assesses the incidence of serious illness episodes among children aged 14 weeks to 3 years in a cohort of 1198 children recruited into a meningitis vaccine trial in the Kassena Nankana districts in northern Ghana from November 2008 to March 2011. Surveillance teams were set up in all the communities from where children were recruited as well as the health facilities. Serious illness was assessed according to good clinical practices and according to standard clinical criteria. A substantial number had

more than one episode of illness during the period under study. Serious illness events were seasonal with over 95% due to infectious diseases. For incidence of severe illness between 14 weeks of age and 3 years, 38.3% of participants experienced at least one episode and the major causes were malaria, acute gastroenteritis and pneumonia which were 20.2%, 7.4% and 2.1% respectively. Proportion of participants who experienced at least one episode of severe illness in the first and second years of life was respectively 130(10.9%) and 175 (16.2%). In the third year of life, 103(9.7%) of participants recorded severe illness and main cause was only malaria with the others being minimal. In all 21(1.8%) of participants died over the 3 years and the main causes of death were respiratory tract infections, malaria and acute gastroenteritis. This study confirms a huge burden of preventable infectious diseases among this young age group, where more has to be done in terms of prevention. The relatively low resultant mortality presents a ray of hope that while putting in measures to prevent illnesses, affordable and effective services could be provided to control mortality in children in these age groups in areas of low illiteracy and resource constraint.

## 1274

### MULTILEVEL ANALYSIS OF TRICHIASIS AND CORNEAL OPACITY IN NIGERIA: THE ROLE OF ENVIRONMENTAL RISK FACTORS ON THE DISTRIBUTION OF DISEASE

**Jennifer L. Smith**<sup>1</sup>, Selvaraj Sivasubramaniam<sup>1</sup>, Mansur M. Rabiu<sup>2</sup>, Fatima Kyari<sup>3</sup>, Anthony Solomon<sup>1</sup>, Simon Brooker<sup>1</sup>, Clare Gilbert<sup>1</sup>

<sup>1</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>2</sup>Prevention of Blindness Union, Riyadh, Saudi Arabia, <sup>3</sup>College of Health Sciences of University of Abuja, Abuja, Nigeria

The distribution of trachoma in Nigeria is spatially heterogeneous, with the prevalence generally decreasing in a North-South gradient across the country at a larger scale and more local variation observed within these areas. Relative contributions of individual and environmental risk factors to the geographic distribution of disease remain largely unknown. The primary aim of this analysis is to assess the relationship between climatic factors and trachomatous trichiasis (TT) and/or corneal opacity (CO) due to trachoma in Nigeria, while accounting for the effects of clustering and risk factors at other levels. In addition, we explore the relative importance of clustering at different levels and the respective role of individual and environmental factors on these outcomes. Data from the 2007 National Blindness and Visual Impairment Survey were used for this analysis, which included a nationally representative sample of adults aged 40 and above. Data were available from 305 clusters selected using a multistage stratified cluster random sampling strategy. A basic eye examination was given to all participants and the presence or absence of TT and CO recorded. In addition to field-collected data on individual-level variables, remotely sensed climatic data were extracted for each cluster and used to fit Bayesian hierarchical logistic models to disease outcome. As expected, clustering was apparent at both levels in the model and there was evidence that climatic factors independently contribute to increased risk of TT/CO after accounting for available individual level risk factors. Beyond some well established individual risk factors (age, gender and occupation), there was strong evidence that environmental factors at the cluster-level (aridity, precipitation and global land cover) were also associated with the prevalence of TT/CO. This study establishes the importance of large scale geographical risk factors for later stages of trachoma, which confirms anecdotal evidence that environmental conditions are associated with increased risk of these outcomes, and highlights potential uses of risk mapping to better estimate their burden.



## DEMOGRAPHIC AND CLINICAL RISK FACTORS FOR LASSA FEVER IN SIERRA LEONE

**Donald S. Grant**<sup>1</sup>, Augustine Goba<sup>1</sup>, Jeffrey G. Shaffer<sup>2</sup>, Matthew L. Boisen<sup>2</sup>, Luis M. Branco<sup>2</sup>, Darren Ottomassathien<sup>3</sup>, Danielle Levy<sup>2</sup>, Daniel G. Bausch<sup>2</sup>, Robert F. Garry<sup>2</sup>, John S. Schieffelin<sup>2</sup>

<sup>1</sup>Kenema Government Hospital, Kenema, Sierra Leone, <sup>2</sup>Tulane University, New Orleans, LA, United States, <sup>3</sup>Corgenix, Inc, Broomfield, CO, United States

Lassa Virus (LASV) is the etiologic agent of Lassa fever (LF), an acute and frequently fatal illness endemic to West Africa. Multimammate rats (*Mastomys natalensis*) are the reservoir and are found in abundance throughout sub-Saharan Africa. LF is hyperendemic in the Eastern Province of Sierra Leone where humans are thought to acquire infection via exposure to rodent excreta. The National Lassa Fever Surveillance Program of Sierra Leone is headquartered at the Kenema Government Hospital in Kenema, Sierra Leone. All patients who present to the Lassa Fever Ward and meet criteria for suspected LF cases are evaluated using standard forms. Detailed records are kept of presenting signs and symptoms, diagnostic test results for LF, hospital course and outcome. Blood samples from all patients are tested for the presence of LASV NP antigen at the time of presentation by a recombinant-based antigen capture ELISA. Over a 25 month period (January 2010 through January 2012), 1,158 patients presenting to the Lassa Fever Ward met criteria for suspected LF. Ninety-nine (8.5%) patients tested positive for LASV antigen. Patients with an antigen positive ELISA were more likely to present with bleeding, conjunctival injection, facial or neck edema, sore throat, cough, and confusion relative to those with other diseases. In addition, patients presenting greater than 7 days after onset of illness were more likely to have LF. Outcome was known for 96 patients with LF and 230 patients with other diseases. Having LF was strongly associated with a fatal outcome (OR 4.1 CI 2.4-7.0) with a fatality rate of 64%. A fatal outcome was associated with bleeding and presenting seven or more days after disease onset.

## CLINICAL PREDICTORS OF HOSPITAL READMISSION IN UGANDAN CHILDREN WITH CEREBRAL MALARIA

**Nathan Brand**<sup>1</sup>, Robert Opoka<sup>2</sup>, Chandy C. John<sup>1</sup>

<sup>1</sup>University of Minnesota, Minneapolis, MN, United States, <sup>2</sup>Makerere University, Kampala, Uganda

Cerebral malaria (CM) affects more than 800,000 children each year in sub-Saharan Africa. Determination of clinical symptoms associated with hospital re-admission for children treated for cerebral malaria could help identify those CM children at greatest risk for severe morbidity and mortality. We conducted a study on the pathogenesis of cerebral malaria, and in this substudy, aimed to determine the clinical symptoms associated with greater risk of admission to the hospital in the first 6 months post-discharge in a cohort of Ugandan children aged 18 mo - 12 years. Clinical risk factors were assessed in 165 Ugandan children presenting to the Pediatric Acute Care Unit at Mulago Hospital in Kampala, Uganda, with cerebral malaria who completed 6 months of clinical follow-up. Twenty children (12.1%) were readmitted to the hospital for malaria during 6-month follow-up. Compared to children with CM who were not readmitted, CM children who were readmitted had a higher frequency of measured fever ( $T \geq 37.5$ , 85.0% vs. 57.9%;  $P=0.01$ ) and lactic acidosis (blood lactate  $> 5.5$  mmol/L, 60% vs. 27%,  $P=0.008$ ) on admission, and were less likely to have received antibiotics during their initial stay at the hospital (55% vs. 80%,  $P=0.02$ ). Measured fever and lactic acidosis on admission and lack of antibiotics during hospital stay predict risk of readmission in children with CM.

## HEALTH SYSTEM STRENGTHENING THROUGH COMMUNITY REFERRAL IN THE MANAGEMENT OF FEBRILE ILLNESS IN NIGERIA

Bright C. Orji<sup>1</sup>, **William R. Brieger**<sup>2</sup>, Emmanuel Otolorin<sup>1</sup>, Jones Nwadike<sup>3</sup>, Edueno V. Bassey<sup>4</sup>, Mayen Nkanga<sup>5</sup>

<sup>1</sup>Jhpiego/Nigeria, Abuja, Nigeria, <sup>2</sup>The Johns Hopkins University, Baltimore, MD, United States, <sup>3</sup>Dunamis Medical Diagnostic Services, Lagos, Nigeria, <sup>4</sup>Etebi Health Center, Etebi, Akwa Ibom State, Nigeria, <sup>5</sup>Akwa Ibom State Ministry of Health, Uyo, Nigeria

Use of Community Health Workers (CHWs) in community case management of febrile illness can improve community-clinic continuum of care, health outcomes and referral system. The main objective of this study is to ascertain the level of home visitation carried out by the CHWs, compliance rate for referrals and treatment response. The authors carried out a record review of 12 months of community registers to ascertain the level of home visitation. To determine compliance to referral, all referral slips and clients' cards at the six primary health care centers participating in the on-going Integrated Community case Management of Malaria were assessed. The CHWs made a cumulative overall home visits of 7,282 to pregnant women 4460 (61.2%) and children under-five years of age 2822 (38.8%). The median visitation for pregnant women was 406 compared to children under-five years of age 257. Overall referral was 578; pregnant women 332(57.4%) while children under-five years of age 246(42.6%). The overall median referral was 28; pregnant women (19) compared to children under-five years of age (9). Overall referral compliance rate was 79.1% (457/578) with pregnant women 73.2% (245/332) compared to children under-five years 86.2% (212/246). Median number of days for pregnant women to comply with referral was 4 compared to children under-five years of age 1.5 days. Reasons for referral for pregnant women, ANC attendance topped the list 78.4 % (192/245); malaria treatment 30.6% (75/245) and reactions to medicines Sulfadoxine-pyrimethamine 2.8% (7/245) and Artemisinin Combination Therapy 3(1.2%) while Children under-five years of age malaria treatment topped the list 60.8% (129/212); diarrhea treatment 23.6% (50/212); pneumonia treatment 14.6% (31/212) and reactions to ACT 0.94% (2/212). All cases were treated same day at the health facility. In conclusion we found relatively high compliance in community referral, and care-givers of children under-five years of age are more likely to comply with referral and very early too than pregnant women. Community health education on referral during pregnancy as a component of case management of febrile illness is recommended for program managers and implementers.

## SIGNS AND SYMPTOMS AS INDICATORS OF FEMALE GENITAL SCHISTOSOMIASIS

**Kristine Lillebø**<sup>1</sup>, Elisabeth Klepp<sup>1</sup>, Pavitra Pillay<sup>2</sup>, Sigve Holmen<sup>1</sup>, Andile Mtshali<sup>2</sup>, Myra Taylor<sup>3</sup>, Eyrun F. Kjetland<sup>1</sup>

<sup>1</sup>Oslo University Hospital, Centre for Imported and Tropical Diseases, Department of Infectious Diseases, Oslo, Norway, <sup>2</sup>University of KwaZulu-Natal, Durban, South Africa, <sup>3</sup>School of Family and Public Health Medicine, Nelson R. Mandela School of Medicine, University of KwaZulu-Natal, Durban, South Africa

Female Genital Schistosomiasis (FGS) is a neglected, poverty-related disease. Several studies also indicate higher prevalence of HIV in women with FGS. The co-existence of FGS and sexually transmitted infections (STIs) pose a diagnostic challenge for health care providers. The syndromatic management of STIs are strategies in disease prevention in developing countries. In spite of its public health implications, FGS has never been included in any of these protocols. It is therefore important to explore how self-reported symptoms, signs and behavior can be used as indicators of FGS. A school based, cluster randomized, cross-sectional study was conducted in a *Schistosoma haematobium* endemic area in rural South Africa. A total of 921 young women aged 16-22

were included. They were interviewed and asked about symptoms and behavior and gynecological examination with colposcopy was done. Samples (urine, blood and vaginal lavage) for laboratory analyses for STIs and *S. haematobium* were collected. Girls infected with schistosomiasis (cases) were compared with girls without schistosomiasis (controls). Multivariate regression was used for the statistical analyses. Female genital schistosomiasis may be a differential diagnosis to STIs in schistosomiasis endemic areas. It is of importance that health care workers consider this when adequate laboratory facilities are lacking. Symptoms could be added into an algorithm for a syndromic approach to diagnosis, the meager effect of treatment and reinfection in this age group will be discussed.

## 1279

### HIV INCIDENCE IN TEENAGE YOUNG WOMEN IN A SCHISTOSOMIASIS ENDEMIC AREA

**Elisabeth Klepp**<sup>1</sup>, Kristine Lillebø<sup>1</sup>, Sigve D. Holmen<sup>1</sup>, Myra Taylor<sup>2</sup>, Mathias Onsrud<sup>1</sup>, Svein G. Gundersen<sup>3</sup>, Eyrun F. Kjetland<sup>1</sup>  
*<sup>1</sup>Oslo University Hospital, Oslo, Norway, <sup>2</sup>University of KwaZulu-Natal, Durban, South Africa, <sup>3</sup>Sørlandet Hospital HF/University of Agder, Kristiansand, Norway*

Sub-Saharan Africa is severely affected by the HIV (Human Immunodeficiency Virus) epidemic with prevalence higher in women than in men. Young women may be especially prone to HIV infection, but there is still limited knowledge about the reasons for the high prevalence in females. Studies indicate that Female Genital Schistosomiasis (FGS) could be a risk factor. In rural KwaZulu-Natal, South Africa, an area endemic of both *Schistosoma haematobium* and HIV, school-going, sexually active young women were examined twice with an interval of approximately one year. Mean age at first visit was 18.7 years. On both visits the participants went through a detailed interview, including questions regarding water contact, age at sexual debut, alcohol consumption and number of partners. Blood and urine samples were collected, and they were offered a gynecological examination including photocolposcopy. HIV positive and seroconverting young women were compared to the HIV negative individuals. Twenty five high schools of differing schistosomiasis prevalence were included, 921 young women were investigated. Mean age at sexual debut was 16.4 years and 95% reported to have a steady partner when interviewed at first visit. Mean number of lifetime sexual partners was 2 in both groups. The overall HIV incidence was 11.7% and 25% had a genital sandy patches indicating FGS on gynecological examination. The HIV incidence in this schistosomiasis endemic area was unusually high for this age group, however one common risk factor could not be identified. Further analyses for confounders are required. These findings may have implications for the understanding of FGS' role in the different phases of the HIV epidemic.

## 1280

### COMPUTERIZED IMAGE ANALYSIS AS A TOOL FOR IDENTIFICATION OF CLINICAL MANIFESTATIONS IN FEMALE GENITAL SCHISTOSOMIASIS

**Sigve D. Holmen**<sup>1</sup>, Kristine Lillebø<sup>1</sup>, Elisabeth Klepp<sup>1</sup>, Myra Taylor<sup>2</sup>, Fritz Albrechtsen<sup>1</sup>, Eyrun F. Kjetland<sup>1</sup>  
*<sup>1</sup>University of Oslo, Norway, Oslo, Norway, <sup>2</sup>University of KwaZulu-Natal, South Africa, Oslo, Norway*

The lesions associated with Female genital schistosomiasis (FGS) consist of changes in the genital mucosa that may be described as sandy patches, characterised by their yellow colour. The gold standard for diagnosing FGS is a biopsy from cervical lesions with direct microscopic inspection for ova. However, this is an inappropriate approach in HIV endemic areas. It is therefore necessary to develop alternative methods for non-invasive, objective diagnosis of FGS that can be performed at the point of care without requiring advanced laboratory equipment or training. The image material was acquired in a study on female genital schistosomiasis in KwaZulu-Natal, South Africa. Healthy individuals were used as negative

controls. The mean colour of sandy patches was measured in a subsample of colposcopic images. The colour was represented in a range of colour spaces and compared to the values of the surrounding mucosa using the Wilcoxon signed rank test for paired samples. 7 colour channels were chosen based on the significance level in the Wilcoxon test. The mean differences were used to calculate the most appropriate threshold window in each channel. An algorithm was created in which an image is scored based on presence of pixels present in the intersection of the 7 threshold windows. The validity of the algorithm was tested by running it on a random selection of images in which 3 clinicians had agreed on the diagnosis. It was calculated that 69 pathologic images and as many controls would provide statistical significance when assuming sensitivity of 80% and specificity of 65%. This is a novel method in which computerized image analysis can be used to identify genital schistosomiasis based on the lesions' distinct colour. Further analyses should be done exploring other visual aspects of the lesions, such as morphologic features. It is also necessary to control for confounding factors such as STIs and development is required to adapt this method to socially acceptable clinical practice in a third world setting.

## 1281

### SUCCESSES AND SHORTCOMINGS OF POLIO ERADICATION: A TRANSMISSION MODELING ANALYSIS

**Bryan T. Mayer**<sup>1</sup>, Joseph N. Eisenberg<sup>1</sup>, Christopher J. Henry<sup>1</sup>, M. Gabriella M. Gomes<sup>2</sup>, Edward L. Ionides<sup>1</sup>, James S. Koopman<sup>1</sup>  
*<sup>1</sup>University of Michigan, Ann Arbor, MI, United States, <sup>2</sup>Instituto Gulbenkian de Ciencia, Oeiras, Portugal*

Polio eradication is on the cusp of success with only a few regions still maintaining transmission. Improving our understanding of why some regions have been successful and others have not will help both with global eradication of polio and with development of more effective vaccination strategies for other pathogens. To examine past eradication efforts we constructed a transmission model for wild poliovirus incorporating waning immunity, age-mediated vaccination rates, and transmission of oral polio vaccine (OPV). The model produces results consistent with the four country categories defined by the Global Polio Eradication Program: elimination with no subsequent outbreaks; elimination with subsequent transient outbreaks; elimination with detected transmission for more than 12 months; and endemic polio transmission. An analysis of waning immunity rates and OPV transmissibility suggest contrasting effects on transmission. Higher waning immunity rates make eradication harder due to increasing numbers of infectious adults. Higher OPV transmission rates make eradication easier as adults become re-immunized. Given these dynamic properties, attention should be given to intervention strategies that complement childhood vaccination. For example, improvement in sanitation can reduce the reproduction number in problematic regions, while adult vaccination can lower adult transmission.

## 1282

### SUPPORTING THE DEVELOPMENT OF RESEARCHERS IN LOW AND MIDDLE INCOME COUNTRIES IN AFRICA THROUGH PERSONAL DEVELOPMENT PLANNING AND FORMAL MENTORING

**Hazel E. McCullough**

*London School of Hygiene and Tropical Medicine, London, United Kingdom*

Building a critical mass of researchers in low and middle income countries, who are able to conduct and disseminate high quality research efficiently and effectively, and be able to use results to inform policy and practice in global health is an expectation of funders and institutions. Whilst attention is given to investing in developing the research skills of individuals through fellowship programmes, strengthening systems, infrastructure and institutions, less attention is given to the career planning and

development that is needed to help early-career researchers in these settings become sufficiently established, in order to meet this expectation. Personal Development Planning (PDP) and formal mentoring have been used to support a group of returning African researchers with their career development. The structured and supported process of PDP, assisting in empowering individuals to take ownership of their careers and develop the higher level critical thinking and reflective skills crucial to effective learning, is complemented by formal mentoring where mentors help mentees build confidence towards independence. A participatory action research approach was used to trial and explore how PDP (not used before in this context in sub-Saharan Africa) might help this group of researchers with their career development; in addition to developing an evidence-led PDP model and tools that would work for researchers in Africa. Results showed skills and knowledge gains in research methodology, techniques, communication, networking, updating clinical skills, and developing academic management skills; as well as how these gains were applied effectively in practice. With this same group of researchers, and through a self-selection process of mentees choosing their mentors, a formal mentoring programme was implemented. Whilst mentoring is a long-term process where results and benefits are not always seen immediately, initial results showed that 98% of mentees felt that their mentoring relationship was helping them to progress in their careers, and 85% of mentors were happy with their mentee's progress over the first year. Efforts to make these activities sustainable focus on working with institutions to mentor support groups in PDP and mentoring, and with the aim of embedding these strategies within institutions and programmes. This has the added value of building a network of PDP champions and mentors in Africa.

## 1283

### GETTING HEALTH CARE DELIVERY RIGHT: LEARNING FROM CASE STUDIES

Rebecca Weintraub<sup>1</sup>, Julie Talbot<sup>1</sup>, Joseph Rhatigan<sup>2</sup>

<sup>1</sup>The Global Health Delivery Project; Brigham and Women's Hospital, Division of Global Health Equity, Boston, MA, United States, <sup>2</sup>Brigham and Women's Hospital, Division of Global Health Equity, Boston, MA, United States

The future of global health lies in getting delivery right. Medical schools must prepare the next generation of leaders to confront the management challenges of disease and health programs facing an implementation bottleneck. To aid in this endeavor, we created over 25 teaching cases with accompanying teaching notes offering unique lessons and insights to the principles of global health strategy. From this new body of delivery experience, several themes have emerged: 1) context matters\_ programs must account for local factors that influence both the health of the populations and the delivery of health care in their design, implementation, and operations; 2) value\_the outcomes achieved divided by the resources invested\_is the best measure of program performance, and analysis of value using the care delivery value chain can help program managers determine how best to allocate resources and configure program activities; 3) high-value programs address the social, economic, and geographic barriers to health care delivery; they do not see their objective as "offering" services or technology but as ensuring that the population can realize the full value of the services or technology they are providing; 4) measurement should lead to meaningful learning and program improvement; 5) strategy and leadership are essential as managers face shifts in the landscape and increasing burden of disease. The global health delivery case studies are available free of charge via [www.ghdonline.org/cases](http://www.ghdonline.org/cases) and provide a tool for educators to build global health delivery competency for the next generation of leaders.

## 1284

### COMMUNITY HEALTH WORKERS FOR HOME-BASED COUNSELLING AT HOME TO IMPROVE NEONATAL SURVIVAL

Fatuma Manzi<sup>1</sup>, Donat Shamba<sup>1</sup>, Zelee Hill<sup>2</sup>, Suzanne Penfold<sup>3</sup>, Tanya Marchant<sup>3</sup>, Jennie Jaribu<sup>1</sup>, Joanna Schellenberg<sup>3</sup>

<sup>1</sup>Ifakara Health Institute, Dar es Salaam, United Republic of Tanzania, <sup>2</sup>University College London, London, United Kingdom, <sup>3</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom

Access to maternal and newborn health services in developing countries is impeded by shortages in human resources for health. We set out to study whether home-based counselling by community volunteers could change home behaviours critical to newborn survival. The objective of the study was to develop and evaluate a community intervention using village-based volunteers to improve newborn care at home. The method included a formative research involving a review of behaviours that impact on neonatal survival, a baseline survey to assess their prevalence, and qualitative work to assess barriers and facilitators of behaviour change. Key messages for home visits in pregnancy and the early newborn period were agreed with stakeholders based on the findings of the formative research, and focus on early and exclusive breastfeeding, clean delivery, and extra care for low birth-weight babies born at home. Newborn foot size was used as a proxy for birth weight to identify low birth-weight babies born at home. In 2010, over 800 volunteers were trained by district health teams, in a randomly chosen 61 of the 131 wards in the 6-district study area. Supervision was improved to involve community leader and nearby health facility staffs. In 2011, a 5,000-household survey interviewed women aged 13-49 about behaviours critical to newborn survival in control and intervention areas. The results showed that over 75% of women in intervention areas were visited by a volunteer at least once in pregnancy, and almost half received a post-natal visit at home. Key behaviours improved as a result of the intervention: tying the cord with clean thread (70% vs 39%, P=0.002), delayed bathing until 6h or more after birth (81% vs 68%, P=0.005), feeding only breast milk for the first 3 days (83% vs 71%, P=0.001), and putting nothing on the cord (87% vs 71%, P<0.001). In conclusion, home-based counselling has improved behaviours critical to newborn survival.

## 1285

### CLINICAL TRIALS OF THE MEN A CONJUGATE VACCINE CONDUCTED IN WEST AFRICA AND INDIA AMONG INFANTS, CHILDREN AND ADULTS: SHARING ETHICAL CHALLENGES AND LESSONS FOR THE FUTURE

Lionel Martellet<sup>1</sup>, Samba Sow<sup>2</sup>, Julie Chaumont<sup>1</sup>, Aldiouma Diallo<sup>3</sup>, Marie-Françoise Makadi<sup>1</sup>, Beate Kampmann<sup>4</sup>, Godwin Enwere<sup>1</sup>, Abraham Hodgson<sup>5</sup>, Siddhivinayak Hirve<sup>6</sup>, Prasad Kulkarni<sup>7</sup>, Marie-Pierre Préziosi<sup>8</sup>

<sup>1</sup>Program for Appropriate Technologies in Health, Ferney-Voltaire, France, <sup>2</sup>Centre pour le Développement des Vaccins, Bamako, Mali, <sup>3</sup>Institut pour la Recherche et le Développement, Dakar, Senegal, <sup>4</sup>Medical Research Council Laboratories, Fajara, Gambia, <sup>5</sup>Ghana Health Service, Accra, Ghana, <sup>6</sup>Shirdi Saibaba Hospital, Vadu, India, <sup>7</sup>Serum Institute of India, Pune, India, <sup>8</sup>World Health Organization, Geneva, Switzerland

Application of international ethical guidelines in order to obtain approvals when conducting vaccine trials in diverse local settings can be quite challenging. Since 2005, Meningitis Vaccine Project (a partnership between the World Health Organization and the Program for Appropriate Technologies in Health) in collaboration with the Serum Institute of India has conducted clinical trials on Men A conjugate vaccine across a diverse set of clinical trial sites located in sub-urban and rural communities in India, Mali, The Gambia, Ghana and Senegal. Our collaboration with international, national and local ethics review committees led to the accumulation of huge experiences on ethical research practices covering aspects of protocol approvals, language and communication in informed

consent, establishing processes for pregnancy testing, supporting health care, obtaining permission and providing feedback to participating communities.

## 1286

### ENHANCING ACCESS TO MEDICINES THROUGH INNOVATIONS IN WORKING CAPITAL FINANCING FOR DRUG SHOPS

Lisa Smith<sup>1</sup>, Prashant Yadav<sup>1</sup>, Sarah Alphas<sup>1</sup>, Edmund Rutta<sup>2</sup>, Keith Johnson<sup>2</sup>

<sup>1</sup>University of Michigan, Ann Arbor, MI, United States, <sup>2</sup>Management Sciences for Health, Arlington, VA, United States

Access to working capital within the different layers of the healthcare distribution network is one of the factors that limit widespread availability of key medicines and also hampers the sustainability of accredited medicine retailers in sub Saharan Africa. In OECD countries a well functioning credit provisioning system exists across the multiple entities involved in pharmaceutical distribution. Such a credit provisioning system is currently lacking in the private sector pharmaceutical distribution networks in low-income countries. The Accredited Drug Dispensing Outlets (ADDOS) in Tanzania is a very successful model for improving access to high quality medicines and similar models are now being planned in Uganda, Zambia and other countries. To ensure greater sustainability of the accredited drug shop business model and to further enhance its ability to increase access to medicines, a cross-sectional study design was employed using a comprehensive survey instrument developed for the study population of ADDO and ADS owners. The study assessed the cash-to-cash cycle, stocking practices and role of working capital credit within the accredited drug shop network. Findings revealed that accredited drug shops struggle to offer the most appropriate stock assortment at optimal levels. Analysis suggests that both drug shop owners and public health in the community would benefit from better training of shop owners on inventory and cash management and from the provision of additional working capital to the ADDO owners.

## 1287

### DENGUE RISK PERCEPTION AND BEHAVIORAL RESPONSES BY LOCAL MEMBERS IN DHAKA, BANGLADESH

Parnali Dhar Chowdhury<sup>1</sup>, C. Emdad Haque<sup>1</sup>, Robbin Lindsay<sup>2</sup>

<sup>1</sup>University of Manitoba, Winnipeg, MB, Canada, <sup>2</sup>National Microbiology Laboratory, Winnipeg, MB, Canada

Since 2000, there has been a resurgence in dengue virus in the major cities of Bangladesh. This study aimed to assess the risk perception and mitigation efforts towards dengue by analyzing entomological and socioeconomic risk factors in 12 wards within the City of Dhaka, Bangladesh. Data included in the analysis are: a) two vector surveys [i.e., pupal surveys conducted in 847 households (monsoon season 2011) and 459 households (dry season 2012)]; b) a socio-demographic survey of 300 households; c) 12 focus group discussions (FGDs) and eight key informant interviews (KIIs); and d) constructed Knowledge Models of experts and lay persons. Competent dengue vectors were detected in >40% and 12% of households during the monsoon and dry seasons respectively. The monsoon and dry seasonal pupal index were 0.40 and 0.33 respectively for the selected 12 wards. Vector indices were significantly higher for *Aedes aegypti* in this study compared to others conducted in Dhaka in the past. There are significant variations in dengue risk perception between lower (low and medium) and higher socioeconomic groups (SEG). The low and medium SEGs are concerned more about day-to-day issues than exposure to dengue whereas the higher SEG considered themselves at higher risk of dengue infection. Perceived risk from exposure to dengue virus was lower in female subjects than males. Also, experts ranked dengue risk at a much lower level than lay persons and experts emphasized the need for stronger institutional measures to control dengue outbreaks. These findings in turn signify the link between disease risk

perception and preventive responses. In consideration of significant SEG and gender variations, targeted education campaigns, vector control and community mobilization programs should be formulated to mitigate the risk of dengue in Bangladesh.

## 1288

### INCIDENCE, RISK FACTORS, AND COSTS FOR HOSPITALIZATION OF NEONATES BORN TO MOTHERS IN A MATERNAL IMMUNIZATION TRIAL IN BAMAKO, MALI

Lauren A. Orenstein<sup>1</sup>, Evan W. Orenstein<sup>1</sup>, Mahamane Djiteye<sup>2</sup>, Kounandji Diarra<sup>2</sup>, Diakaridia Sidibé<sup>2</sup>, Mahamadou Fofana<sup>2</sup>, Fadima Cheick Haidara<sup>2</sup>, Moussa Doumbia<sup>2</sup>, Fatoumata Diallo<sup>2</sup>, Flanon Coulibaly<sup>2</sup>, Ibrahima Tegueté<sup>3</sup>, Samba Sow<sup>2</sup>, Myron M. Levine<sup>4</sup>, Richard D. Rheingans<sup>5</sup>, Milagritos Tapia<sup>4</sup>

<sup>1</sup>Emory University School of Medicine, Atlanta, GA, United States, <sup>2</sup>Centre pour le Développement des Vaccins, Mali (CVD-Mali), Bamako, Mali,

<sup>3</sup>Gabriel Touré Teaching Hospital, Bamako, Mali, <sup>4</sup>University of Maryland School of Medicine, Baltimore, MD, United States, <sup>5</sup>University of Florida, Gainesville, FL, United States

Low birth weight (LBW) and prematurity are major causes of neonatal and infant morbidity and mortality worldwide, threatening the achievement of Millennium Development Goal 4. We present the incidences and hospitalization rates of LBW and prematurity among a cohort of infants born to mothers enrolled in a maternal immunization trial, as well as the first cost-analysis of hospitalizations among LBW and/or premature neonates in Bamako, Mali. Women recruited from antenatal care clinics during the 3rd trimester and enrolled after obtaining informed consent were randomly allocated to receive inactivated influenza vaccine (Vaxigrip™, Sanofi Pasteur) or quadrivalent meningococcal conjugate vaccine (Menactra™, Sanofi Pasteur), and followed thru 6 months postpartum. LBW was defined as <2.5kg measured with an infant scale prior to discharge from the maternity center. Prematurity was defined as gestational age <37 weeks by 1<sup>st</sup> trimester ultrasound if available or otherwise a Ballard exam in the first 7 days of life. All neonatal hospitalizations were identified by 24-hour surveillance. Direct and indirect costs incurred by any hospitalized neonate meeting definitions for LBW or prematurity were recorded daily. From September 2011 thru March 2012, there were 652 liveborn infants, of whom 3.4% were premature and 10.9% were LBW. The rate of hospitalization or death during the 1st month of life was 4.0% among all infants, compared to 17.7% for newborns <2.5kg (RR: 8.2, 95% CI: 3.9-16.8) and 36.4% for newborns <37 weeks (RR: 13.4, 95% CI: 6.3-26.2). Complete cost data were available for 22 hospitalized infants, of whom 14 were LBW and premature, 7 were LBW only, and 1 was premature only. The median duration of hospitalization was 7 days (IQR: 5-11), with a median cost of 94.44 USD (IQR 56.43-157.25). Direct expenditures accounted for 79% of all costs, with medication purchases responsible for the majority. In addition to mortality, prematurity and LBW cause substantial morbidity and economic hardship for families in Mali. Interventions that can reduce the risk for prematurity or LBW are urgently needed.

**CAN COMMUNITY HEALTH WORKERS PROVIDE QUALITY INTEGRATED COMMUNITY MANAGEMENT OF FEBRILE ILLNESSES: A CASE STUDY OF COMMUNITY HEALTH WORKERS IN TWO SELECTED LOCAL GOVERNMENT AREAS OF AKWA IBOM STATE, NIGERIA**

Bright C. Orji<sup>1</sup>, William R. Brieger<sup>2</sup>, Emmanuel Otolorin<sup>1</sup>, Jones Nwadike<sup>3</sup>, Edueno V. Bassey<sup>4</sup>, Mayen Nkanga<sup>5</sup>

<sup>1</sup>Jhpiego/Nigeria, Abuja, Nigeria, <sup>2</sup>The Johns Hopkins University, Baltimore, MD, United States, <sup>3</sup>Dunamis Medical Diagnostic Services, Lagos, Nigeria, <sup>4</sup>Etebi Health Center, Esit Eket, Akwa Ibom State, Nigeria, <sup>5</sup>Akwa Ibom State Ministry of Health, Uyo, Nigeria

The World Health Organization has recommended improved quality of care as key elements in strengthening health systems in poor resource countries. Engagement of Community Health Workers (CHWs) can reduce challenges such as weak public sector, human resource constraints, and variable quality of the private sector. Efforts to improve access to quality case management of febrile illness in Nigeria included the engagement of Community Health Workers (CHWs) to use Rapid Diagnostic tests as a component of home management of malaria, dispense ACTs and manage pneumonia and diarrhea. This current effort monitored and measured the performance of CHWs in providing quality management of febrile illnesses in two selected LGAs. The authors trained one hundred and fifty-two CHWs and developed simple quality performance standards (one-page tool) for CHWs providing community services in Akwa Ibom State, Nigeria. All 152 trained CHWs providing malaria, pneumonia and diarrhea case management were monitored and assessed using the standards. The tool has 37 performance criteria (PC) to measure CHW knowledge, skills and competence in 3 sections: History taking and Examination; Conducting RDTs for Malaria; and Illness Management. Trained assessors observed CHWs providing services. Each correctly performed criterion was scored 1 point. Four rounds of assessments were conducted at an interval of two months from June 2011 - March, 2012. During Round 1 CHWs achieved an average of 19 (52.2%) PC. This rose to 25 (67.5%) PC at Round 2; 28 (75.6%) at Round 3 and 30 (81.1%) and ( $p = 0.00$ ). PC that needed most improvement included reinforcement on checking RDT expiry date, entering results on records, and safe disposing of sharps. CHWs can provide quality case management of febrile illness in the current efforts to reduce annual deaths of people at risk while contributing to the achievement of targets numbers 4, 5 and 6 of the Millennium Development Goals (MDGs). In conclusion CHW supervisors can use this tool to enhance the quality of services provided by the CHWs and improve CHW training.

**REGULATION OF VACCINES TO PROTECT AGAINST GLOBAL INFECTIOUS DISEASES: A ROADMAP TO WORKING WITH THE UNITED STATES FOOD AND DRUG ADMINISTRATION**

**Roshan Ramanathan**

*Food and Drug Administration, Rockville, MD, United States*

Global infectious diseases (GID) such as tuberculosis, malaria, dengue and hookworm affect more than one billion people worldwide. The development of safe and effective vaccines for the prevention of these diseases is of critical importance not only for global humanitarian reasons but also for United States (U.S.) public health. The submission of an investigational new drug application (IND) for a vaccine or biologic to the US FDA can provide sponsors with important scientific and regulatory advice on products that are critical to the advancement of world health. If pursued, U.S. licensure signifies to the global medical and regulatory community that the FDA has made the determination that the vaccine is safe and effective. This finding by the FDA may assist other National Regulatory Authorities in their evaluation of the vaccine. The US FDA recently updated the Guidelines for the Development of Vaccines to Protect Against Global Infectious Diseases. This presentation aims to

introduce vaccine developers to these recently updated recommendations and to the regulatory review process at the Division of Vaccines and Related Products Applications (DVRPA) in the Office of Vaccine Research and Review at the Center for Biologics Evaluation and Research (CBER), U.S. FDA. The following issues will be discussed: acceptability and utility of non U.S. studies to support product licensure; the use of clinical bridging studies and how these data may be used to determine interregional acceptance of foreign data; safety monitoring during international vaccine clinical trials. Regulatory issues in the manufacture and pre-clinical testing of new vaccines for global health will be presented. Finally, general principles pertaining to evaluation of vaccine safety and effectiveness, and common concerns related to vaccine manufacturing submissions will be reviewed.

**THE WORLD INTELLECTUAL PROPERTY ORGANIZATION (WIPO RE:SEARCH) PARTNERSHIP HUB: GENERATING NEW COLLABORATION OPPORTUNITIES TO ACCELERATE NEGLECTED TROPICAL DISEASE R&D**

Jennifer Dent<sup>1</sup>, Thomas Bombelles<sup>2</sup>, Konji Sebati<sup>2</sup>, Anatole Krattiger<sup>2</sup>, Rianna Stefanakis<sup>1</sup>, Roopa Ramamoorthi<sup>1</sup>, Don Joseph<sup>1</sup>

<sup>1</sup>BIO Ventures for Global Health, San Francisco, CA, United States, <sup>2</sup>World Intellectual Property Organization, Geneva, Switzerland

Collaborations are a key mechanism to more effectively and efficiently discover and develop new drugs, vaccines, and diagnostics to help the more than 1 billion people suffering from neglected tropical diseases (NTDs), malaria, and tuberculosis. Recognizing the need for more progress in neglected disease research, the WIPO Re:Search Consortium was formed in October 2011. The World Intellectual Property Organization (WIPO) in partnership with BIO Ventures for Global Health and several of the world's leading pharmaceutical companies, renowned academic and other neglected disease research organizations provide access to intellectual property for pharmaceutical compounds, compound libraries, technologies, and importantly expertise and knowledge to support research and development for NTDs, malaria and tuberculosis. WIPO Re:Search aims to expand the number of drug, vaccine, and diagnostic technology candidates for NTDs by sharing these valuable resources and knowledge to accelerate product development. The WIPO Re:Search Partnership Hub facilitates research collaborations among WIPO Re:Search members by fielding requests for specific targets or compounds of interest, identifying collaboration opportunities among key biopharmaceutical and neglected disease research institutions, and providing scientific expertise to proactively match contributions in WIPO Re:Search with members' research program needs. The Partnership Hub establishes mutual interest in exploring a collaboration opportunity and then connects members so that scientists can discuss their research and collaborate. This presentation will focus on the WIPO Re:Search Partnership Hub as an innovative model in global health. We will explain how the Hub has facilitated successful collaborations, and will highlight the impact that the Partnership Hub model has had in accelerating product development for NTDs, malaria, and tuberculosis.

**THE DRUG DRUG INHIBITION POTENTIAL OF ANTI-MALARIAL AGENTS**

**Mark B. Baker**

*Medicines for Malaria Venture, Geneva, Switzerland*

Therapeutic regimes for malaria involve the co-administration of two or more compounds. The patient can also have additional therapy of which HIV therapy is an example. These combinations have the potential to cause drug-drug interactions (DDIs) leading to drug exposures that vary from that intended. This can be critical when determining combination partners and if the drugs in question have narrow therapeutic indices. A weakness of published  $IC_{50}$ s is that they are dependent on experimental

conditions which are often not comparable or able to be transformed into  $K_i$  values. The inhibition of the following CYP450 isoforms - 1A, 2B6, 2C8, 2C9, 2C19, 2D6, and 3A4 - were investigated using the metabolism of their specific substrates. Mefloquine, piperazine, pyronaridine, OZ439, naphthoquine, dihydroartemisinin, primaquine, amodiaquine, chloroquine and lumefantrine were the marketed or MMV proprietary drugs investigated. They were investigated in concentration response experiments where the test compound (0.1  $\mu\text{M}$  - 25  $\mu\text{M}$ ) was incubated with human liver microsomes and NADPH in the presence of a cytochrome P450 isoform-specific probe substrate. Potent inhibition was considered as  $IC_{50} < 1 \mu\text{M}$ , moderate inhibition was considered as  $IC_{50}$  between 1 and 10  $\mu\text{M}$ , and no or weak inhibition was considered as  $IC_{50} > 10 \mu\text{M}$ . All of the isoforms tested were inhibited by at least one of the test compounds except for 2C9 which was not inhibited. The majority of the inhibition observed was determined to be moderate except for 1A where primaquine caused potent inhibition. The most affected isoform was 2D6 (4/10 compounds inhibited). Piperazine, OZ439 and lumefantrine did not cause any inhibition of the isoforms tested. This data can be used as a first guide in forming antimalarial combinations and when combining several therapeutic approaches. Further work will be done to augment these results. This will include widening the set of compounds tested, determining the metabolic pathways of the pathways tested and determining  $K_i$  values for inhibition where the  $IC_{50}$  values warrant it.

## 1293

### MATHEMATICAL MODELING OF THE EFFECTS OF DRUGS ON MALARIA TRANSMISSION IN LOW TRANSMISSION AREAS

Geoffrey L. Chi-Johnston

*Columbia University, New York, NY, United States*

Malaria eradication is now the ultimate objective of many organizations, including the Roll Back Malaria Partnership, the Bill and Melinda Gates Foundation, and the Global Fund. Achieving this objective will require utilizing the three pillars of malaria control: insecticide-treated bed nets, spraying, and antimalarial drugs. However, the impacts of drugs on malaria transmission are not yet fully understood. We describe the development and application of a new mathematical modeling framework to simulate the effects of drug treatment on transmission in low transmission settings. We find that the addition of gametocytocidal drugs to standard treatment regimens may play an important role in reducing transmission. However, we find that the reductions are not large when only symptomatic individuals are treated. Further, the reductions in transmission from the addition of gametocytocidal drugs can be achieved by other means, such as increasing the fraction of individuals treated and reducing the time to treat. These three methods of reducing transmission can be combined, depending on context of malaria transmission in an area. We also present preliminary results using our modeling framework to predict the effects of artemisinin resistance on treatment outcomes with a variety of artemisinin-based therapies.

## 1294

### HEMATOLOGIC COMPLICATIONS AFTER INTRAVENOUS ARTESUNATE IN PATIENTS WITH SEVERE MALARIA

Jakob P. Cramer

*Bernhard-Nocht-Institute for Tropical Medicine, Hamburg, Germany*

Fast acting anti-malarials are essential to treat severe malaria. Existing evidence shows that intravenous artesunate is significantly more effective in parasite clearance but also with respect to survival compared to quinine. Clinical benefits of artesunate appear to be most prominent in patients with high parasitemia. However, previously unknown complications like delayed hemolysis has been described in an increasing number of patients with imported severe malaria. There appears to be an association of post-treatment hemolysis with high parasite levels. We have seen similar hematologic complications after treating three patients with imported severe malaria during a prospective follow-up in our center in Hamburg,

Germany. Post-treatment hemolysis occurred in all patients and reached its peak around 14 days after initiating intravenous artesunate. In addition to signs of hemolysis like a second rise in LDH levels, there was a low reticulocyte production index in all patients indicating prolonged impairment of erythropoiesis. We are currently investigating this relevant complication in children with severe malaria in Africa. In addition, pathophysiologic analyses including murine models are underway. Evidence of post-treatment hemolysis, potential pathogenesis and clinical relevance both for imported as well as endemic severe malaria are discussed.

## 1295

### TRENDS IN U.S. MILITARY HEALTH SYSTEM (MHS) MALARIA CHEMOPROPHYLAXIS PRESCRIBING PATTERNS FROM 2007-2011

Colleen M. Kersgard, Patrick W. Hickey

*Uniformed Services University of the Health Sciences, Bethesda, MD, United States*

No systematic reviews describing malaria chemoprophylaxis prescription trends within U.S. primary care settings have been conducted. The MHS, with its 9.7 million beneficiaries, represents an enormous pool of potential travelers to be considered for malaria prevention measures. Military force health protection policies target active duty forces but may affect all beneficiaries if providers implement policy guidance comprehensively. In 2009, the Department of Defense released malaria prophylaxis policy guidance limiting the use of mefloquine in deployed personnel. A systematic search of the MHS electronic medical record was performed for all prescriptions of atovaquone-proguanil (AP), chloroquine (CQ), doxycycline (DC), and mefloquine (MQ) to adult patients from 2007-2011. For CQ and DC, search parameters were filtered to target malaria chemoprophylaxis. Absolute and proportional prescribing rates for the total, active duty (AD) and dependent/retiree (DR) populations were assessed for changes over time. Trends for prescriptions originating from primary care (PC) clinics versus specialty travel (ST) clinics were also compared. A total of 624,416 prescriptions (AP 7%, CQ 3%, DC 76%, MQ 14%) were identified during the study period, including 156,150 DR patients (25%). Prescription volume rose from 64K (AP 11%, CQ 8%, DC 45%, MQ 36%) in 2007 to 180K (AP 6%, CQ 1%, DC 89%, MQ 4%) in 2011, with DC representing the majority of the increase ( $p < 0.001$ ). MQ use diminished in all clinics over time. Whereas ST clinics predominantly and increasingly prescribed AP (58% in 2007 and 71% in 2011), PC clinics predominantly and increasingly prescribed DC (54% in 2007 and 96% in 2011). Trends were similar for AD and DR populations, suggesting that health policies influence prescription practices in both groups. This study is the first longitudinal systematic review of malaria chemoprophylaxis patterns in the U.S. adult population. Health policies and provider specialty influence malaria chemoprophylaxis choices.

## 1296

### MALARIA KNOWLEDGE AND USE OF MALARIA PREVENTION IN THE UNITED KINGDOM POPULATION AND BY UNITED KINGDOM TRAVELERS TO MALARIA ENDEMIC COUNTRIES

Ron Behrens, Neal Alexander

*London School of Hygiene and Tropical Medicine, London, United Kingdom*

Few data exist on travellers' knowledge and practices regarding malaria and its prevention, or the numbers of travellers receiving advice or taking chemoprophylaxis when visiting malaria-endemic areas. This study was undertaken to evaluate British adults' knowledge of malaria, and utilisation of anti-malarials through a face to face questionnaire. Two groups were surveyed; a sample of Great Britain's adult population through an IPSOS MORI's Capibus survey of 1,991 adults aged  $\geq 15$  years old, of whom 548 had previously visited a malaria-endemic country. The 2nd group were 500 passengers in departure areas of Heathrow

Airport departing to a malaria endemic areas, by the airport authority (CAA). All were questioned about their malaria knowledge and used of prophylaxis and other measures. 40% were travelling to W Africa and 38% East and Central Africa. Knowledge and advice scores based on respondents' knowledge of symptoms, seriousness, curability of malaria were calculated. The IPSOS cohort's mean knowledge score was 3.21, versus 2.98 in non-travelled (n=548 & 1443),  $p < 0.001$  with a similar score in the CAA travellers of 3.23. The source of advice obtained was categorized scored as a) professional and b) non-professional or no advice. Most had had obtained professional advice - 55% of IPSOS and 61% of CAA travellers - while most travellers not using prophylaxis had not. Prophylaxis use was reported by 77% of Kenyan, 81% of Ghanaian and 49% Nigerian departing passengers. In the CAA travellers, mean knowledge score was similar in those who used prophylaxis or not (3.3 and 3.2 respectively) and the same was true in the IPSOS travellers (mean 3.2 whether used prophylaxis or not). Statistical analysis will be presented of chemoprophylaxis and other factors which may be associated with knowledge of malaria.

## 1297

### DISCOVERY OF A NOVEL TARGET FOR ANTIMALARIAL THERAPY: CYTOPLASMIC PROLYL TRNA SYNTHETASE IS THE TARGET OF HALOFUGINONE IN *PLASMODIUM FALCIPARUM*

Jonathan D. Herman<sup>1</sup>, Lauren Pepper<sup>2</sup>, Joseph F. Cortese<sup>1</sup>, Kevin Gallinsky<sup>3</sup>, Tracey L. Keller<sup>4</sup>, Malcom Whitman<sup>4</sup>, William Sullivan<sup>5</sup>, Susan Lindquist<sup>2</sup>, Ralph Mazitschek<sup>6</sup>, Dyann Wirth<sup>1</sup>

<sup>1</sup>Harvard School of Public Health, Boston, MA, United States, <sup>2</sup>Whitehead Institute for Biomedical Research, Cambridge, MA, United States, <sup>3</sup>Broad Institute, Cambridge, MA, United States, <sup>4</sup>Harvard School of Dental Medicine, Boston, MA, United States, <sup>5</sup>Indiana University School of Medicine, Indianapolis, IN, United States, <sup>6</sup>Massachusetts General Hospital, Boston, MA, United States

Many current anti-malarial drugs work within the same biological pathways leading to shared resistance mechanism. We have taken the methodology of chemogenomics to identify potential antimalarials that target novel pathways. Understanding the anti-plasmodial mechanism of halofuginone (HFG), a febrifuginone analogue, informs our understanding of parasite biology and directs the future creation of novel therapies. To interrogate mechanism, we selected parasites that are resistant to halofuginone and then used whole genome sequencing to identify the causative mutation (SNPs) and developed high resolution melting (HRM) genotyping assays to follow up those most promising. We found two nonsynonymous mutations in the active site of the cytoplasmic prolyl-tRNA synthetase (*PfcPRS*) in independent selections. Using a heterologous *S. cerevisiae* model, we have confirmed the sufficiency of *PfcPRS* to confer sensitivity to halofuginone. In addition, the two nonsynonymous SNPs abrogate sensitivity to halofuginone. Amino acid deprivation of *Plasmodium falciparum* activates the amino acid starvation response (AASR) – a highly conserved stress pathway that inhibits cell-wide translation. To determine the involvement of AASR, we then performed western blot analysis of the phosphorylation of eukaryotic initiation factor 2  $\alpha$  (eIF2 $\alpha$ ) in the presence or absence of excess proline. We have found that halofuginone and febrifugine block *P. falciparum* proline metabolism. Treatment of parasites with halofuginone and febrifugine also results in increased phosphorylation of a *P. falciparum* eIF2 $\alpha$  analogue. Furthermore, proline supplementation in the media decreases sensitivity to halofuginone in a dose-dependent fashion. In a similar dose dependent manner, the phosphorylation of eIF2 $\alpha$  is dependent on the level of exogenous proline in the presence of halofuginone. Overall, these results demonstrate halofuginone-induced proline starvation via an interaction with *PfcPRS* leads to translational inhibition. Thus we posit that the potential of amino acid supply and aminoacyl tRNA synthetases as a new promising and potential target for chemotherapeutic intervention.

## 1298

### QUANTIFYING THE ANTIMALARIAL MARKET IN AFFORDABLE MEDICINES FACILITY (AMFM) PILOT COUNTRIES THROUGH ANALYSIS OF IMPORT, EXPORT AND LOCAL MANUFACTURING RECORDS

Caitlin F. Dolkart, Aaron M. Woolsey, Justin M. Cohen

Clinton Health Access Initiative, Boston, MA, United States

The Affordable Medicines Facility for malaria (AMFm), an innovative financing mechanism which aims to increase access to artemisinin-based combination therapies (ACTs) on a multi-national scale through an ex-factory subsidy, launched in July 2010. Since the first private sector order was placed in July 2010, over 158 million ACTs have been ordered by private sector buyers across all active AMFm countries. While these figures likely represent a significant increase in ACT volumes procured in the private sector from pre-AMFm years, understanding the market share and implications for national and global drug forecasts requires better understanding of the total antimalarial market size in these countries. In this investigation, a quantification of the antimalarial markets in 7 of the 9 AMFm pilot countries was performed through a top of the supply chain analysis. For each country, antimalarial import, export, and local manufacturing data were gathered and analyzed. The number of treatment doses procured and manufactured over a three year period was combined and exports deducted to estimate the net market size. The results of this analysis describe the antimalarial market, including ACT market share, before and during initial implementation of the AMFm. For example, an initial analysis of imports, exports and local manufacturing records showed that the total market size in Kenya for 2008 was 43.8M: 25.4M in the private sector and 18.4M in the public sector, representing a significant increase from previous antimalarial demand estimates. This analysis provides context for better understanding the impact of the AMFm and offers a baseline for future analysis of antimalarial demand.

## 1299

### TRACKING MALARIA CASE MANAGEMENT COVERAGE IN THE ERA OF ACT AND RDT SCALE-UP: POSSIBILITIES AND LIMITATIONS WITH USING HOUSEHOLD SURVEYS

Megan Littrell, Stephen Poyer, Hellen Gatakaa, Kathryn O'Connell

Population Services International, Nairobi, Kenya

Global malaria control targets focus on coverage of appropriate case management of suspected malaria among children under five. The key indicator for measuring progress towards targets in endemic countries has been presumptive treatment of all fevers among children under five measured using population-based surveys. Access to diagnostic testing and policy change focused on diagnosis before treatment diminish the relevance of the presumptive treatment indicator. This presentation focuses on the value of population-based surveys in the context of scaling up access to treatment and diagnosis. Nationally-representative household surveys focused on treatment-seeking behavior for suspected malaria were conducted in 2012 in Uganda, Madagascar and Nigeria as part of the ACTwatch research program. The timing of these surveys falls at the end of the Affordable Medicines Facility malaria (AMFm) pilot which aimed to increase access to artemisinin-based combination therapy (ACT) in the public and private sectors. Detailed information on treatment-seeking behavior was collected, including where treatment was sought, services and medicines received, and perceived quality of care received at each source. Perceptions regarding dimensions of quality of care were also assessed across local options for fever treatment. Results from questions on type and result of blood testing, and treatment based on test results will be discussed - including issues with respondent recall and respondent awareness of diagnostic test results and treatments received in the context of patient-provider interactions that characterize these settings. While household surveys can provide information on where treatment is sought

and to some extent why, complementary data are necessary to improve case management of suspected malaria and to track progress towards global targets. Methods and measures will be discussed.

### 1300

#### REACH OF THE GREEN LEAF: EXPOSURE, AWARENESS, AND REPORTED USE OF AFFORDABLE MEDICINES FACILITY (AMFM)-BRANDED MEDICINES IN THREE COUNTRIES

Stephen Poyer<sup>1</sup>, Megan Littrell<sup>1</sup>, Hellen Gatakaa<sup>1</sup>, Peter Buyungo<sup>2</sup>, Ekundayo Arogundade<sup>3</sup>, Jacky Raharinjatovo<sup>4</sup>, Julius Ngigi<sup>1</sup>, Illah Evance<sup>1</sup>, Emily Carter<sup>1</sup>, Kathryn O'Connell<sup>1</sup>

<sup>1</sup>Population Services International, Nairobi, Kenya, <sup>2</sup>Population Services International, Kampala, Uganda, <sup>3</sup>Population Services International, Abuja, Nigeria, <sup>4</sup>Population Services International, Antananarivo, Madagascar

The Affordable Medicines Facility - malaria (AMFm) is a global initiative aiming to expand access to affordable artemisinin combination therapy (ACT). The AMFm seeks to reduce consumer prices through price negotiations and a buyer co-payment for which both public and private first-line buyers at the country level are eligible. Reduced prices are expected to extend down the antimalarial supply chain so that effective medicines are available and affordable for consumers. Changes in household treatment-seeking behavior and improved household fever management are expected as access to effective antimalarials increases. Subsidized quality-assured treatments are marked with a green leaf logo to facilitate product promotion and consumer recognition. The first phase of the AMFm began in 7 sub-Saharan African countries in 2010/11. The ACTwatch research program conducted nationally representative household surveys in 2012 in 3 AMFm countries: Uganda, Nigeria, and Madagascar. The studies investigated treatment-seeking behavior for recent fever in children under five. Questions to assess awareness of the AMFm program and the green leaf logo were administered to caregivers in all households with children under five. In households where children had fever in the past 2 weeks, questions on use of antimalarial medicines included recall of the green leaf logo on drug packaging. Information on type, timing, and source of antimalarial treatments obtained was also collected. Results on the reach AMFm communications and the green leaf logo, and implications for treatment-seeking behavior and treatment outcomes will be discussed.

### 1301

#### PRIVATE SECTOR DEMAND AND AVAILABILITY OF ARTEMISININ-BASED COMBINATION THERAPIES UNDER THE AFFORDABLE MEDICINES FACILITY FOR MALARIA

Aaron M. Woolsey, Caitlin F. Dolkart, Justin M. Cohen  
Clinton Health Access Initiative, Boston, MA, United States

Phase 1 of the Affordable Medicines Facility for malaria (AMFm), a buyer-subsidy program that aims to increase consumer access to artemisinin-based combination therapies (ACTs), launched across nine countries in 2010 and 2011. This program is likely to have a significant impact on the ability of consumers to purchase previously unaffordable ACTs in the private sector, where many seek treatment for malaria-like illness. As of early April 2012, private sector buyers had procured 158M ACTs through the AMFm mechanism. Despite these substantial ACT volumes, it's unclear how well private sector procurement has met consumer demand. Using a dynamic sub-national market forecasting model based on data collected during routine household surveys along with assumptions drawn from the published literature and ongoing operational research, we forecasted private sector consumer demand for antimalarial medicines, including ACTs, following the launch of AMFm. We validated our model using a 2012 analysis of antimalarial import, export, and local manufacturing records in 7 of the 9 AMFm countries. Finally, we estimated the portion of private sector treatments that are likely used to treat true malaria infections and the average cost per treated malaria episode. Results demonstrate that across AMFm countries in 2012, private sector consumer

demand for ACTs is significantly greater (165M) than the projected private sector procurement volumes (83M) through AMFm. The mean cost per ACT-treated malaria episode varied widely across the eight AMFm countries, with highest per-infection ACT costs in regions with low malaria prevalence (\$6.37 in Kenya) and the lowest in areas with high prevalence (\$2.27 in Nigeria). The substantial demand for ACTs in the private sector in AMFm countries suggests that the ACT subsidy's goal of crowding out inferior antimalarial medicines will be difficult to achieve with current procurement rates. In addition, this study provides an indication of the potential cost savings that could result from implementation of improved diagnostic methods in the private sector.

### 1302

#### EFFICACY AND TOLERABILITY OF DIHYDRO-ARTEMISININE-PIPERAQUINE (DUOCOTEXCIN\*) VERSUS ARTEMETHER-LUMEFANTRINE (COARTEM\*) FOR THE TREATMENT OF UNCOMPLICATED PLASMODIUM FALCIPARUM MALARIA IN SENEGAL: OPEN RANDOMIZED TRIAL

Khadime Sylla

Dakar University Cheikh Anta Diop, Dakar, Senegal

Malaria remains a major public health problem in Sub-Saharan Africa. Prompt an effective treatment is essential for malaria control. Malaria treatment requires the use of Artemisinin Combination Therapies (ACT). In Senegal, ACT are widely in health care units. In the context of the scaling up of antimalarial treatment, there is a need to monitor ACT efficacy. The study was carried out from November 2011 to January 2012 in Deggo health center within the district health of Pikine (located at 20 from Dakar the capital city). Study end points included (i) PCR corrected adequate clinical and parasitological response (ACPR) at day 28, (ii) ACPR at days 35 and 42, (iii) parasites and fever clearance time, (iv) incidence of adverse events and patients biological profile at day 7. The WHO 2003 protocol for antimalarial drug efficacy evaluation was used to assess each outcome. Overall, 240 patients were randomized to receive either Dihydro-Artemisinin-Piperazine (Duocotexcin\*) (n=120) or Artemether-lumefantrine (Coartem\*) (n=120). PCR corrected ACPR at day 28 was at 93.3% in the Dihydro-Artemisinin-Piperazine group while that was at 97.5% in the Artemether-Lumefantrine group (p=0.21). Therapeutic efficacy was at 100% in Dihydro-Artemisinin-Piperazine group versus 99% in Artemether-lumefantrine group at day 35 (p=0.44). At day 42 ACPR at 100% was obtained in the two treatments group. The two treatments were well tolerated with similar clinical and biological profile. Abdominal pain, vomit and dizziness were the most frequent adverse event in two treatment group. No serious adverse event was noted in the two study groups. In conclusion, Dihydro-Artemisinin-Piperazine (Duocotexcin\*) and Artemether-lumefantrine (Coartem\*) are still efficacious and well tolerated and are suitable for the treatment of uncomplicated *P. falciparum* malaria in Senegal.



## 1303

### EFFECTS OF PLASMA PIPERAQUINE LEVEL ON THE ELECTROCARDIOGRAM IN PATIENTS WITH UNCOMPLICATED MALARIA RECEIVING A TWO- VERSUS THREE-DAY COURSE OF DIHYDROARTEMISININ-PIPERAQUINE IN NORTHERN CAMBODIA

Pattaraporn Vanachayangkul<sup>1</sup>, Chanthap Lon<sup>2</sup>, Soklyda Chann<sup>2</sup>, Sabaithip Sriwichai<sup>1</sup>, Youy Se<sup>2</sup>, Darapiseth Sea<sup>3</sup>, Mashamon Mitprasat<sup>1</sup>, Raveewan Siripokasupkul<sup>1</sup>, Paktiya Teja-isavadharm<sup>1</sup>, Duong Socheat<sup>4</sup>, Satharath Prom<sup>5</sup>, Louis Cantilena<sup>6</sup>, David Saunders<sup>1</sup>

<sup>1</sup>Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand, <sup>2</sup>Armed Forces Research Institute of Medical Sciences, Phnom Penh, Cambodia, <sup>3</sup>National Center for Entomology, Parasitology and Malaria Control, Phnom Penh, Cambodia, <sup>4</sup>Ministry of Health, Phnom Penh, Cambodia, <sup>5</sup>Ministry of National Defense, Phnom Penh, Cambodia, <sup>6</sup>F. Edward Hebert School of Medicine, Bethesda, MD, United States

DHA-piperaquine is currently recommended as a first line treatment for uncomplicated *Plasmodium falciparum* and *P. vivax* in Cambodia, and worldwide (WHO 2010). A post-treatment prophylactic effect of DHA-PIP up to 63 days has been reported, making it potentially valuable in malaria eradication efforts. However, cardiotoxicity is an important potential concern with PIP due to QTc interval prolongation. While a 3-day course is widely recommended, the Cambodian military currently employs a 2-day regimen in order to improve compliance. As part of a clinical trial comparing therapeutic efficacy of 2 versus 3 day dosing regimens of DHA-PIP, cardiac safety was evaluated by comparing plasma PIP levels to EKG results. In an open-label clinical trial, 80 patients developing uncomplicated malaria infections of any species were randomized 1:1 to receive a directly observed cumulative dose of 320mg DHA/2880mg PIP divided into either a 2 or 3 day course as inpatients. Plasma piperaquine levels from all volunteers receiving DHA-PIP were collected at pre-dose, 4, 24, 48, 72 hr, 7, 14, 21, 28, 35 and 42 days after the first dose, and on the day of recurrence. Patients had 12 lead EKGs at screening, pre-dose, daily for 3 days and then weekly for 4 weeks if prolongation was more than 10 ms during dosing. Pharmacokinetic analysis is currently in process. Of 35 out of 80 completed subjects with levels measured by high performance liquid chromatography-mass spectrometry to date, there were 8/23 (34.8%) from the 2-day and 2/12 (16.7%) from the 3-day regimen with a positive correlation between the change in QTcB from baseline and the log of the piperaquine concentration. Final results will be presented to determine if either regimen posed a greater risk for QTc prolongation.

## 1304

### STABILIZING SUPPLY AND AVOIDING NATIONAL LEVEL STOCK OUTS OF ACTS IN AN ERA OF WIDE ACT SCALE-UP

Rima Shretta<sup>1</sup>, Prashant Yadav<sup>2</sup>

<sup>1</sup>Management Sciences for Health, Arlington, VA, United States, <sup>2</sup>William Davidson Institute, University of Michigan, Ann Arbor, MI, United States

The global market for ACTs has been fraught with volatile demand due to poor planning and supply chain management, uncertainties in funding, and uncertainties in supply due to the long lead times involved in production and the vagaries of an agricultural starting material. Unless appropriately managed these uncertainties have the potential to disrupt global supply of ACTs and hamper the the scale-up efforts achieved in the last few years. Better matching of demand and supply and building resilience in the ACT supply chain may require new approaches. Policy makers have begun to discuss buffer stocks, volume guarantees and other mechanisms to ensure an uninterrupted supply of ACTs to meet the fluctuating demand. However, to date no detailed and rigorous analysis of these mechanisms has been performed to understand their suitability, benefit and cost effectiveness for the ACT supply chain. This paper attempts to address this issue. Models such as a regional ACT

buffer stocks, a buffer capital fund, and minimum volume guarantees to ACT manufacturers are discussed for their effectiveness, efficiency and feasibility for this context.

## 1305

### AN EVALUATION OF TREATMENT RESPONSE TO ARTESUNATE-MEFLOQUINE FIXED-DOSE COMBINATION IN CHILDREN DURING A DEPLOYMENT STUDY IN AMAZON BASIN COMMUNITIES OF BRAZIL

André Daher<sup>1</sup>, Ana Carolina Santelli<sup>2</sup>, Mariana S. Xavier<sup>3</sup>, Simone D. da Silva<sup>4</sup>, Izabela Magalhães<sup>5</sup>, Isabela Ribeiro<sup>6</sup>

<sup>1</sup>Drugs for Neglected Diseases Initiative, Rio de Janeiro, Brazil, <sup>2</sup>Secretaria de Vigilância em Saúde, Ministério da Saúde, Brasília, Brazil, <sup>3</sup>Instituto de Tecnologia em Fármacos - Farmanguinhos, Fundação Oswaldo Cruz, Rio de Janeiro, Brazil, <sup>4</sup>Centro de Endemias, Secretaria Municipal de Saúde, Cruzeiro do Sul, Brazil, <sup>5</sup>Secretaria Estadual de Saúde do Acre, Rio Branco, Brazil, <sup>6</sup>Drugs for Neglected Diseases Initiative, Rio de Janeiro, Brazil

The World Health Organization currently recommends the use of five Artemisinin Combination Therapies (ACTs) for the treatment of uncomplicated malaria. The Drugs for Neglected Disease initiative (DNDi), together with the Special Program for Research and Training in Tropical Diseases (TDR) and the Drugs Technology Institute of the Oswaldo Cruz Foundation (Farmanguinhos/Fiocruz) developed an artesunate-mefloquine fixed-dose combination (ASMQ FDC). The public health impact of ASMQ FDC was evaluated between 2006-2008 in a total of 23,845 patients in the Amazon basin of Brazil, in collaboration with the Brazilian Ministry of Health and RAVREDA-AMI/PAHO. As a large number of these patients (8880/37,2%) were patients under the age of 14, we decided to conduct a post-hoc assessment of treatment outcomes in this specific patient population in the municipality of Cruzeiro do Sul, in order to gather data on the use of ASMQ FDC in children. Cruzeiro do Sul was selected because it is an urban area in which patient follow-up smears are more readily accessible. A total of 584 patients under the age of 14 presented for a follow-up slide until day 40 - the time defined as the interval for recrudescence by the study protocol. Less than 2% of the originally tested patients (8/584; 1.4%) had positive thick smears for the malaria parasite, equally distributed among different age categories. Asexual forms of the parasite were detected in a total of 4 cases (0.68%); among which a case with both asexual and sexual forms. These positive malaria smears could represent either re-infections or recrudescence of the initial infection. Our data represent important additional information on the effectiveness of ASMQ FDC in children, and support its use in this specific population. They are consistent with results of other clinical studies, performed in different epidemiological settings and populations.

## 1306

### CLEARANCE OF PLASMODIUM FALCIPARUM AS ASSESSED BY RAPID DIAGNOSTIC TESTS, MICROSCOPY AND PCR FOLLOWING ANTI-MALARIAL TREATMENT IN TANZANIAN CHILDREN

Berit Aydin-Schmidt<sup>1</sup>, Marycellina Mubi<sup>2</sup>, Zul Premji<sup>2</sup>, Billy E. Ngasala<sup>2</sup>, Ulrika Morris<sup>1</sup>, Andreas Mårtensson<sup>1</sup>, Anders Björkman<sup>1</sup>

<sup>1</sup>Karolinska Institutet, Stockholm, Sweden, <sup>2</sup>Muhimbili University of Health and Allied Science, Dar es Salaam, United Republic of Tanzania

Rapid Diagnostic Test (RDT) has become an important tool for confirmatory malaria diagnosis. Until recently most tests have been based on detection of Histidine Rich Protein 2 (HRP2), a sensitive and stable marker for *Plasmodium falciparum* (Pf) malaria. However, the usefulness of HRP2 based RDT detection of Pf is hampered by persistent antigenemia causing false positivity even after successful treatment. Conversely, Pf-specific Lactate Dehydrogenase (LDH) based RDT has been proposed to detect only live parasites. Our aim was to study Pf clearance as assessed by these two antigens (HRP2 and LDH) in comparison with microscopy and PCR after artemisinin-based combination therapy in Tanzanian children.

Some 50 children <5 years with uncomplicated *Pf* malaria were enrolled. The children were examined on nine occasions during a 42-day follow-up period. At each visit blood was collected for the two RDTs (ParaHit® and CareStart®), Giemsa and Acridine Orange staining of blood slides for microscopy and filter papers for real time-PCR based detection of parasite DNA. A majority of children cleared their parasitemia  $\leq 3$  days as assessed by microscopy and PCR. Median HRP2 and LDH positivity time after treatment initiation was 21 (range 3-42) and 3 (range 1-7) days, respectively. Due to the remaining HRP2 positivity, this RDT was unable to identify recurrent malaria infections that occurred during follow-up in 10/50 (20%) of the children, whereas the LDH based RDT identified eight of these recurrent infections. The results suggest LDH based RDTs to be more suitable for *Pf* detection in high endemic areas.

### 1307

#### HRP2 AND PLDH RDTs COMPARED WITH MICROSCOPY, PCR AND HISTOLOGY FOR DETECTION OF PLACENTAL MALARIA DURING PREGNANCY AND AT DELIVERY IN AREAS OF VARIED TRANSMISSION

Heidi Hopkins<sup>1</sup>, Jane Cunningham<sup>2</sup>, Issaka Zongo<sup>3</sup>, Patrick Angutoko<sup>1</sup>, John Ategeka<sup>1</sup>, Yves-Daniel Compaoré<sup>3</sup>, Michal Fried<sup>4</sup>, Michelle Gatton<sup>5</sup>, Sandra Incardona<sup>6</sup>, Daniel Kyabayinze<sup>1</sup>, Atis Muehlenbachs<sup>7</sup>, Jerry Mulondo<sup>1</sup>, Miriam Nakalembe<sup>8</sup>, Aminata Ouattara<sup>3</sup>, Wellington Oyibo<sup>9</sup>, Noel Rouamba<sup>3</sup>, Fabrice Some<sup>3</sup>, Silvère Zaongo<sup>3</sup>, Jean-Bosco Ouedraogo<sup>3</sup>, David Bell<sup>6</sup>

<sup>1</sup>Foundation for Innovative New Diagnostics, Kampala, Uganda, <sup>2</sup>UNICEF/UNDP/World Bank/WHO Special Programme for Research and Training in Tropical Diseases (TDR), Geneva, Switzerland, <sup>3</sup>Institut de Recherche en Sciences de la Santé (IRSS), Bobo-Dioulasso, Burkina Faso, <sup>4</sup>National Institute of Allergy and Infectious Diseases, National Institutes of Health, Rockville, MD, United States, <sup>5</sup>Queensland Institute for Medical Research, Brisbane, Australia, <sup>6</sup>Foundation for Innovative New Diagnostics, Geneva, Switzerland, <sup>7</sup>Department of Pathology, University of Washington, Seattle, WA, United States, <sup>8</sup>Department of Obstetrics and Gynaecology, School of Medicine, Makerere University, Kampala, Uganda, <sup>9</sup>Department of Medical Microbiology and Parasitology, University of Lagos, Lagos, Nigeria

Malaria prevention measures for pregnant women are critical and available, but the effectiveness of intermittent preventive treatment in pregnancy (IPTp) with sulfadoxine-pyrimethamine (SP) is declining with increasing parasite resistance. Diagnostic testing may allow better targeting of efficacious antimalarial treatment to asymptomatic women with demonstrated malaria infection. Light microscopy of peripheral maternal blood misses a large proportion of cases, and PCR is unavailable in routine care. Early data show that detection of parasite antigen in maternal blood may indicate clinically significant infection and predict pregnancy outcomes. Therefore, screening with RDTs may offer a practical way to identify pregnant women who will benefit from targeted therapy for placental malaria infection. We assessed the detection of asymptomatic malaria infection in pregnancy by highly-characterized RDTs in two African clinical settings (Uganda, hyperendemic, and Burkina Faso, seasonal transmission). We enrolled 995 (345 Uganda, 650 Burkina Faso) HIV-negative women in the second or third trimester of pregnancy and followed them to delivery. On the standard IPTp schedule and at delivery, participants' blood was collected for RDTs detecting histidine-rich protein 2 (HRP2) and plasmodium lactate dehydrogenase (pLDH), malaria microscopy and PCR; placental tissue for histology was obtained at delivery. Participants with negative RDT results received SP; those with a positive RDT received artemether-lumefantrine or quinine, and SP. Preliminary data show that 130 (38%) and 112 (32%) participants were positive by HRP2 and pLDH, respectively, at enrollment in Uganda; 134 (21%) were positive by either RDT at enrollment in Burkina Faso. Quality controlled interpretation of peripheral and placental blood microscopy, PCR and histology samples is on-going. Data will be presented on the accuracy of these diagnostic testing methods for detection of asymptomatic malaria during pregnancy and on the potential utility of RDT screening for management of such infections.

### 1308

#### ABSOLUTE QUANTIFICATION AND DETECTION OF PLASMODIUM PARASITE BY qPCR

Edwin Kamau, Saba Alemayehu, Karla C. Feghali, Christian F. Ockenhouse

Walter Reed Army Institute of Research, Silver Spring, MD, United States

Determining precise parasite quantification in real time PCR has been a challenging aspect in malaria diagnostics. In general, quantification of *Plasmodium* by qPCR is done by serially diluting a standard of a known parasite density where the source can be from a cultured parasites or clinical samples. The parasites density is determined by microscopy and described in parasite/ $\mu$ l which is known as a relative standard. A relative standard can lead to incorrect quantification because it may have difference on the source, parasite culture or clinical samples. It relies on microscopy being performed accurately and consistently. Absolute quantification is based on known concentration of DNA standard molecules such as plasmid DNA. We have developed an absolute quantitative multiplex qPCR for detection of *Plasmodium* spp., *P. falciparum* and *P. vivax* described in parasite/ $\mu$ l. Plasmid DNAs are constructed for qPCR assays by amplifying PCR fragments from genomic DNA from either clinical samples or cultures and cloned into TOPO TA vectors. The concentration of each plasmid DNA was determined in genomic equivalence (GE) and was used for subsequent experiments. All of the absolute qPCR assays performed with efficiency of more than 94%,  $R^2$  values greater than 0.99 and the STDEV of each replicate was <0.167. Correlation of genomic equivalence to parasite/ $\mu$ l was established using standard clinical samples and or cultures. One copy of plasmid DNA was established to be equivalent to 0.12 parasite/ $\mu$ l for *Plasmodium* spp. assay, 0.54 parasites for *P. falciparum* assay and 0.16 parasite/ $\mu$ l for *P. vivax* assay. From this data, absolute qPCR can be expressed in parasite/ $\mu$ l. An absolute quantitative qPCR assay is better than a relative qPCR because it is more accurate and consistent. Plasmid DNAs are stable, can be easily produced in large quantities and stored for a long period of time. In addition, plasmid DNA production and quantification can be highly standardized ensuring more uniform quantification. Accurate quantification of parasites can have great impact on malaria diagnosis in clinical trials as confirmatory method to microscopy.

### 1309

#### DEVELOPMENT OF LOCAL EXPERTISE FOR PLACENTAL MALARIA HISTOPATHOLOGY IN TORORO, UGANDA: FROM COLLECTION TO INTERPRETATION

Atis Muehlenbachs<sup>1</sup>, Patrick Angutoko<sup>2</sup>, John Ategeka<sup>2</sup>, Michal Fried<sup>3</sup>, Heidi Hopkins<sup>2</sup>, Daniel Kyabayinze<sup>2</sup>, Miriam Nakalembe<sup>4</sup>, Lynnette Tumwine<sup>5</sup>, David Bell<sup>6</sup>, Jane Cunningham<sup>7</sup>

<sup>1</sup>Department of Pathology, University of Washington, Seattle, WA, United States, <sup>2</sup>Foundation for Innovative New Diagnostics, Kampala, Uganda, <sup>3</sup>National Institute of Allergy and Infectious Diseases, National Institutes of Health, Rockville, MD, United States, <sup>4</sup>Department of Obstetrics and Gynaecology, School of Medicine, Makerere University, Kampala, Uganda, <sup>5</sup>Department of Pathology, School of Biomedical Sciences, Makerere University, Kampala, Uganda, <sup>6</sup>Foundation for Innovative New Diagnostics, Geneva, Switzerland, <sup>7</sup>UNICEF/UNDP/World Bank/World Health Organization Special Programme for Research and Training in Tropical Diseases (TDR), Geneva, Switzerland

Placental histology is a valuable technique to evaluate malaria epidemiology and control during pregnancy. Histology laboratories and expertise are usually confined to urban tertiary care hospitals and facilities are rare in Africa. The process of preparation requires specialized skills and training. As part of a study of malaria rapid diagnostic tests (RDTs) in pregnancy, placental specimens were collected in rural eastern Uganda (n=267) and southwestern Burkina Faso (n=548), areas of high and seasonal transmission, respectively. Specimens were fixed in 10% neutral buffered formalin and after 24 hours transferred to 70% ethanol for shipping and storage (4-8°C). On site in Uganda, paraffin blocks were

manually generated, and sections were Giemsa stained. Concurrently 30 biopsies per site, 30 paraffin blocks and stained slides were shipped to Seattle, USA, for external quality control (QC). Tissue was well preserved with no formalin pigment artifact. Blocks and stained slides were well prepared with minimal artifact. Processing and staining problems detected early were rapidly addressed. After one-on-one training on reference slides, study samples were interpreted by two trained technologists, with cross-checking against placental blood smears. A subset of all positive cases and 10% of negative cases were reviewed at University of Washington. The majority of supplies were locally available, however a microtome was imported by another research group at the same site, and microtome knives, charged slides and paraffin wax were imported. Challenges included exposure to alcohol, xylene, and formalin, and the physical distance to the nearest experienced histopathologist. The exercise demonstrated development of placental malaria histopathology expertise with robust QC in an inexpensive laboratory in a rural district hospital, showing successful implementation of capacity-building for a highly skill-dependent activity critical to study success, and providing potential for long-term reference-level histology for pregnancy studies in Africa.

### 1310

#### POINTING OUT MALARIA INFECTIONS WITH LASER POINTERS

**Brian T. Grimberg**, Robert J. Deissler, Jason Jones, Richard F. Bihary, D'Arbra R. Blankenship, William C. Condit, Robert W. Brown

*Case Western Reserve University, Cleveland, OH, United States*

Detecting the presence of malaria parasites primarily relies upon; the highly accurate but time consuming method of PCR, the use of expensive and subjective RDT card tests, or the inexpensive but slow (up to 1 hr) microscopy-based methods which can yield false positives for 36% of samples and false negatives as high as 18% of the time. Inter-operator error in creation, staining, and visual analysis of the slides may contribute to this high error rate. Therefore, there is a need for novel malaria diagnostic techniques to identify which samples are potentially infected and help confirm negative diagnoses. Through a multidisciplinary effort we have designed an inexpensive, rapid malaria detection device (3 minutes) that detects the presence of hemozoin, a parasite byproduct of hemoglobin digestion. We place blood samples into the path of a polarized light beam in the presence and absence of a magnetic field. When the partially magnetic malaria hemozoin is present, it aligns with the magnetic field and acts as a reflector thus decreasing the amount of light reaching a light level detector on the far side of the sample. This decrease in light is directly proportional to parasitemia ( $R^2=0.996$ ) which can be detected at parasitemias as low as 0.00033% (17 parasites per microliter) which exceeds detection levels for microscopy without the need for staining or trained microscopists. Our long term goal is to translate this technology into a field ready, low-cost device, which can be used in malaria-endemic regions to enable rapid malaria diagnosis at the point-of-care.

### 1311

#### TRENDS IN PRESCRIBER ADHERENCE TO MALARIA TESTS IN HEALTH FACILITIES RECEIVING JOINT CLINICAL AND LABORATORY SUPERVISION VISITS

**Nicole E. Whitehurst**, Isaac Bediako, Timothy Nzangwa, Petros Chirambo, Ramani Saliou, Christopher Petrucci, Sean Fennell, Luis Benavente

*Medical Care Development International, Silver Spring, MD, United States*

During 2008-2012, the President's Malaria Initiative made considerable investments towards improving malaria diagnostics to promote the rational use of anti-malaria drugs in health facilities in sub-Saharan Africa. Through the Improving Malaria Diagnostics (IMaD) project, Ministries of Health in Benin, Ghana, Malawi, and Zambia, implemented

quality assurance programs based on Outreach Training and Support Supervision (OTSS). In Ghana, laboratory supervisors implemented routine supervision and observed laboratory specific topics such as malaria microscopy (MM) and RDT performance. The same laboratory supervisors addressed prescriber compliance during their visit. In Benin, Malawi, and Zambia, supervision was implemented together by a laboratory and clinical supervisor. Laboratory supervisors focused on MM and RDT performance while clinical supervisors addressed fever diagnosis and prescriber adherence. Standardized checklists were used during each visit and improvements were tracked using a Microsoft Access database. In countries implementing joint supervision, general positive trends in prescriber adherence to microscopy and RDT results were observed: Benin 38% (MM) and 39% (RDT) percentage point improvement between visits 1-7, Malawi 17% (MM) between visits 1-3, and Zambia 23% (MM) and 21% (RDT) improvement between visits 1-4; In Ghana, where supervisory visits were implemented by laboratory supervisors only, no discernible trend was observed in prescriber adherence to negative tests: changes of 3% (MM) and -7% (RDT) were observed. Trends in prescriber adherence from OTSS data show that a joint approach to supervision had a greater impact on prescriber adherence to negative blood slide and RDT results than supervision conducted by laboratory supervisors alone, provider confidence improves when laboratory results are quality assured, and communication between the two cadres is strengthened. It should be noted that not all facilities have received a full cycle of visits due to the staggered nature of the roll-out of the OTSS program.

### 1312

#### CLINICAL SIGNS AND SYMPTOMS OF *PLASMODIUM FALCIPARUM* MALARIA INFECTION (PATENT AND SUB-PATENT) IN PREGNANT WOMEN LIVING IN AN AREA OF HIGH SEASONAL TRANSMISSION

**Marc Christian Tahita**

*Clinical Research Unit of Nanoro, IRSS, Burkina Faso*

Malaria in pregnancy is a major public health concern in endemic countries. There a paucity of data on the association between peripheral parasitaemia and the presence of signs and symptoms of malaria during pregnancy. The objective of this study is to document the frequency of the attendance of pregnant women at health facilities with clinical complaints suggestive of malaria and to assess their parasitological status. To attend this objective, a hospital-based descriptive study at the maternity clinic was conducted in the rural district of Nanoro in Burkina Faso. A total of 600 pregnant women attending the antenatal care (ANC) were recruited, 200 pregnant women with signs and symptoms suggestive of malaria and 400 others without signs and symptoms were control group. The women were matched by gestational age and parity. For each woman, a capillary blood sample was taken for rapid diagnostic test, microscopy and hemoglobin test. A multivariate model was used to access each predictor of malaria. The overall prevalence of malaria was 42.6% (256/600) using the microscopy while anemia was found in 60.8% (365/600). Nearly a half (49.5%) of the women who displayed symptoms was parasitaemic and 39.5% of the asymptomatic women were parasitaemic. The most frequently encountered signs and symptoms were fever 36% (72/200), history of fever 29% (58/200) and headache 52% (104/200). The predictive positive values for fever were 53% (95%CI 41-64), history of fever 58% (95%CI 37-63) and headache 51% (95%CI 41-61). Signs and symptoms suggestive of malaria are quite frequent in pregnant women in intense transmission area. A large number of asymptomatic but parasitaemic women were found. For a better management of malaria in pregnancy, active case detection of all pregnant women attending the ANC should be performed to detect and treat earlier malaria infection.

## 1313

### BLOOD SMEAR TEST FOR MALARIA CONFIRMATION AT THE COMMUNITY LEVEL: FEASIBILITY AND LESSONS LEARNED FROM SARAYA HEALTH DISTRICT, SENEGAL

Jean louis Ndiaye<sup>1</sup>, Youssoupha Ndiaye<sup>2</sup>, Mamadou S. Ba<sup>1</sup>, Akhenaton Manga<sup>2</sup>, Maguette Ndiaye<sup>1</sup>, Pape Moussa Thior<sup>2</sup>, Badara Cisse<sup>1</sup>, Omar Gaye<sup>1</sup>, Paul Milligan<sup>3</sup>

<sup>1</sup>University Cheikh Anta Diop, Laboratory of Medical Parasitology, Dakar, Senegal, <sup>2</sup>Ministry of Health and Prevention, Dakar, Senegal, <sup>3</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom

Following Rapid Diagnostic Test (RDT) and ACT introduction in 2009, health units were asked to confirm all malaria cases; this has been partially scaled up to the community level where Community Health Workers (CHWs) were trained to use RDT. Smear blood tests were realized only in the laboratories with laboratory technicians. In Saraya district thick and thin blood smears were introduced to confirm all malaria cases in 24 villages involved in a Seasonal Malaria Chemoprevention research project. The objective of the study was to assess the feasibility of smear blood tests at the community level. Saraya district is located in South East Senegal, bordering Mali and Guinea Republic. Health staff was very limited, and with a strong network of community health workers and malaria village volunteers called DSDOM. Twenty four CHWs and malaria volunteers were trained by staff from the medical school, parasitology laboratory for 3 days to perform Blood smears with practical sessions. They were asked to complete RDT, thick and thin blood smears for all patients under 10 with fever. Blood smear tests were kept in a box and collected by supervisors. Close follow up were made by supervisors, mainly in the first month for continued training and improvements. Slides were read at the Medical school, parasitology laboratory. CHW performed 1635 blood smear tests between July and November 2011; 68.47% were positive, 31.47% negative, 0.06% not readable. Parasite density mean was 22.8 [13, 521] and nearly all malaria cases were due to *Plasmodium falciparum* (98%) with only 2% of malaria due to *P. malariae* and *P. ovale*. Blood smears can be performed at the community level by lower educated personnel with formal training and close follow up; this would be helpful to be more accurate on malaria diagnosis and non malaria febrile illnesses as well in remotest under served areas.

## 1314

### A REVIEW OF MALARIA RAPID DIAGNOSTIC TESTS (RDT) GUIDELINE IMPLEMENTATION IN A DISTRICT HOSPITAL IN GHANA: HAS RAPID TESTING BEEN PRIORITIZED?

Nana Yaa A. Boadu<sup>1</sup>, Daniel Ansong<sup>2</sup>, John H. Amuasi<sup>3</sup>, Samuel B. Nguah<sup>4</sup>, Bernard Arhin<sup>2</sup>, Stephen Somuah<sup>5</sup>, Stephanie K. Yanow<sup>6</sup>

<sup>1</sup>University of Alberta, Edmonton, AB, Canada, <sup>2</sup>Research and Development Unit, Komfo Anokye Teaching Hospital; Kwame Nkrumah University of Science and Technology, Kumasi, Ghana, <sup>3</sup>University of Minnesota School of Public Health, Minneapolis, MN, United States, <sup>4</sup>Komfo Anokye Teaching Hospital, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana, <sup>5</sup>Atwima Nwabiagya District Directorate of Health Services, Kumasi, Ghana, <sup>6</sup>University of Alberta School of Public Health, Edmonton, AB, Canada

Rapid diagnostic tests (RDTs) can improve timeliness and accuracy of malaria diagnosis. This can help to slow down the development of antimalarial drug resistance by promoting appropriate treatment. Since 2009, revised malaria management policies in Ghana promote testing by microscopy or RDTs, before treating all suspected malaria cases aged five years and above. In this study we reviewed the use of RDTs in a district hospital over a two-year period following the implementation of 'test-before-treat' policies for malaria in Ghana. A random sample of 500 malaria cases recorded at the Nkawie-Toase District Hospital from January 2010 to December 2011 were identified and reviewed. For reference visits where the clinician made a differential diagnosis of malaria, only 3.6%

(95%CI: 2.2-5.7) of reviewed cases were tested with RDTs compared to 13% (95%CI:10.2-16.3) by microscopy. For cases with repeat visits within 6 months of the reference attendance, percentage RDT-use decreased to 0.6% (95%CI: 0.01 - 3.5), while testing by microscopy increased to 26.1% (95%CI:19.3-33.8). RDT use ranged from 1.6% to about 4% (p=0.09), from low to high malaria incidence months. Testing with microscopy appeared strongly associated with seasonality of malaria, almost doubling from 10% in non-peak, to 19.3% (p=0.005) in peak malaria incidence months. Testing by microscopy was more frequent than RDT use during the period under review. These findings suggest that rapid malaria testing was poorly implemented in this district hospital over the study period, despite existing policy revisions in Ghana. Investigating RDT utilization in similar referral level facilities is essential to understand and to improve the implementation of current malaria testing guidelines in Ghana. This information will be useful to advise investments in rapid diagnostics for malaria, and to improve their application in limited resource settings.

## 1315

### RAPID DIAGNOSTIC TEST (RDT) PERFORMANCE OF THE MALARIA GOLD MINING PROGRAM IN SURINAME: A COMPARISON BETWEEN RDT AND BLOOD SMEAR RESULTS

Deborah Stijnberg<sup>1</sup>, Hedley Cairo<sup>2</sup>

<sup>1</sup>Ministry of Health, Paramaribo, Suriname, <sup>2</sup>Ministry of Health Malaria Program; "Looking for gold, finding malaria", Paramaribo, Suriname

Currently malaria infections occur mainly among persons (ca. 15,000) engaged in small-scale gold mining and related activities. The mining areas are remote from the existing healthcare services. To address this problem, a system of quick diagnosis and treatment was established by training lay persons (e.g. shopkeepers) in gold mining areas to perform malaria diagnosis and to treat uncomplicated malaria. They are called Malaria Service Deliverers (MSD). Also in the city, in the gold miners' neighborhood, the Tourtonne laboratory was established to provide similar services. For each RDT performed a blood smear is taken and examined by Tourtonne Laboratory (TL) for quality control of the RDT. Good RDT performance is the cornerstone of the MSD system. The RDT results from 2007 through the first quarter of 2012 were compared with the Blood Smear results. 4489 slides received from the MSD were readable for comparison. The overall sensitivity was 83.3% (81.2 - 85.2%), and the overall specificity 91.8% (90.8 - 92.7%); a PPV of 80.8% was calculated. For the TL 6761 RDT results were available for comparison. The sensitivity was 81.3% (79.7 - 82.8%), the specificity was 96.2% (95.6 - 96.7%) and the PPV was 92.7%. Looking specifically at the performance of RDT related to *Plasmodium falciparum*, the sensitivity, specificity and PPV were respectively 83.1%, 94.2% and 62.6% for MSD versus 84.8%, 95.6% and 82.7% for Tourtonne laboratory. The sensitivity of both the MSD system and TL were lower than the expected sensitivity (95.3%) calculated by the manufacturer. The specificity of both on the other hand was according to expectations. As the accurate diagnosis and treatment for especially *falciparum* malaria is of paramount importance, false negative tests should be avoided. Further research e.g. parasitaemia level, storing conditions, reader variability is needed to explain the difference found between the expected and found sensitivity.

### INVESTIGATING THE OPTIMAL SAMPLING SCHEME FOR MEASURING PARASITE CLEARANCE WITH THE PARASITE CLEARANCE ESTIMATOR

Jennifer A. Flegg<sup>1</sup>, Philippe J. Guerin<sup>1</sup>, Francois Nosten<sup>2</sup>, Arjen M. Dondorp<sup>3</sup>, Rick M. Fairhurst<sup>4</sup>, Duong Socheat<sup>5</sup>, Steffen Borrmann<sup>6</sup>, Anders Björkman<sup>7</sup>, Andreas Mårtensson<sup>7</sup>, Mayfong Mayxay<sup>8</sup>, Paul N. Newton<sup>9</sup>, Delia Bethel<sup>9</sup>, Youry Se<sup>9</sup>, Harald Noedl<sup>10</sup>, Abdoulaye A. Djimde<sup>11</sup>, Nicholas J. White<sup>3</sup>, Kasia Stepniewska<sup>1</sup>

<sup>1</sup>WWARN, Oxford, United Kingdom, <sup>2</sup>Shoklo Malaria Research Unit, Mae Sot, Thailand, <sup>3</sup>Mahidol-Oxford Tropical Medicine Research Unit, Bangkok, Thailand, <sup>4</sup>National Institute of Allergy and Infectious Diseases, Bethesda, MD, United States, <sup>5</sup>Center for Parasitology, Entomology and Malaria Control, Phnom Penh, Cambodia, <sup>6</sup>Kenya Medical Research Institute/ Wellcome Trust Research Programme, Kilifi, Kenya, <sup>7</sup>Karolinska Institutet, Stockholm, Sweden, <sup>8</sup>WellcomeTrust-Mahosot Hospital-Oxford Tropical Research Collaboration, Vientiane, Lao People's Democratic Republic, <sup>9</sup>Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand, <sup>10</sup>Medical University of Vienna, Vienna, Austria, <sup>11</sup>University of Bamako, Bamako, Mali

The emergence of artemisinin resistance in South East Asia threatens the efficacy of artemisinin derivatives (AD). Since the pharmacodynamic hallmark of AD is rapid parasite clearance, the clinical phenotype of slow clearance characterises resistance. Frequent parasite counts are needed to define clearance rate but it is uncertain what sampling frequency is required to ensure reliable estimates. We selected 2841 parasitaemia-time profiles from clinical studies in which 6-hourly parasite counts were available in the first 48 hours (h). Patients were treated with an artesunate alone or in combination with a partner drug. WWARN's Parasite Clearance Estimator estimated the median (range) parasite half-life (HL) as 3.2 (0.7 - 17.5) h. Four measurement schedules (at 0,6,12,24 or 0,6,18,24 or 0,12,18,24 or 0,12,24 h and then every 12h) were investigated. The median (range) for the difference between the original HL estimate and that from the 4 schemes were -0.02 (-3.4 to 3.8), -0.06 (-3.3 to 3.5), -0.09 (-3.6 to 3.4), -0.15 (-5.0 to 3.6) h, respectively. The overestimation of the HL by the restricted schemes was greater for profiles with short reference HL. Bootstrapping was then used to estimate the sampling distribution of HLs for two subsets of the population with: (A) fast clearance (20% of reference HL>3h) and (B) slow clearance (50% of reference HL>3h). In both subsets, the median HL was overestimated by the 4 schemes (A:91 -100%, B: 79-97% of bootstrap samples), but by ≤0.5h for nearly all samples. The schemes overestimated the proportion (%) of profiles with HL >3h, on average by 39, 44, 54, 72% (A) and 6, 7, 9, 12% (B), relative to the scheme with 6 hourly measurements, respectively. The proportion of profiles with HL longer than 6h in bootstrap samples was very similar for all restricted schemes. Our data indicate that HL can be best estimated by including samples at 6 and 12h while every 12h counting is satisfactory in patients with slow clearance.

### WORLDWIDE ANTIMALARIAL RESISTANCE NETWORK (WWARN) TOOLKIT: PROMOTING HARMONIZATION OF ANTIMALARIAL RESISTANCE EPIDEMIOLOGICAL OUTPUTS

Emmanuelle Denis, on behalf of the WWARN Toolkit Development Team

*WorldWide Antimalarial Resistance Network, Oxford, United Kingdom*  
To meet the known threat of parasite resistance to artemisinin-based therapies, the WHO's Global Plan for Artemisinin Resistance Containment stresses the need for more quality-assured antimalarial efficacy data. The WorldWide Antimalarial Resistance Network (WWARN) response is an online Toolkit that guides research scientists to collect the reliable, comprehensive evidence needed by the public health community to identify and contain antimalarial drug resistance. The Toolkit contains a growing portfolio of essential tools and services to promote high-quality

antimalarial efficacy and laboratory testing. These include guidance on study protocol design, tools for data collection and analysis and technical procedures, supported by proficiency testing and reference material programmes, training workshops and online courses. The Toolkit will assist researchers - particularly those working in resource-limited environments - in the design, conduct and interpretation of their studies, thereby facilitating high-quality prospective data collection, and reducing data heterogeneity. The standardised Toolkit data outputs from *in vivo* studies and laboratory tests can be pooled - across studies, time, and place - uncovering subtle trends or sub-population effects with higher statistical certainty. Increasing the ease and potential for data mining in turn allows complex issues, like antimalarial resistance, to be understood more quickly and cost-effectively and with less duplication of effort. We will describe the components of the Toolkit and present the 'roadmap' that guides scientists progressively through the steps to plan and run antimalarial resistance research projects and how to use the various tools and services.

### LONGITUDINAL STUDY OF SULFADOXINE-PYRIMETHAMINE (SP) RESISTANCE IN TURBO, COLOMBIA

Stella Chenet<sup>1</sup>, Silvia Blair<sup>2</sup>, Lina M. Zuluaga Idárraga<sup>2</sup>, Ananias A. Escalante<sup>1</sup>

<sup>1</sup>Center for Evolutionary Medicine and Informatics, Arizona State University, Tempe, AZ, United States, <sup>2</sup>Malaria Group, Universidad de Antioquia, Medellín, Colombia

Pyrimethamine was introduced in the 1950s in South America as a mass treatment in Venezuela. By 1968, pyrimethamine-resistant parasites were found in Colombia and resistance rapidly disseminated in the Amazon and Orinoco basins. However, SP resistance in Colombia is unevenly distributed, showing high resistance in the Amazon basin to moderate levels in the Caribbean, the Cauca Valley and northwestern regions. In this study we characterized a total of 145 *Plasmodium falciparum* samples from Turbo, a port town in Antioquia Department, collected during years 2002 to 2009 and characterized point mutations in two genes that have been implicated in resistance to SP, dihydrofolate reductase (*dhfr*) and dihydropteroate synthase (*dhps*). The treatment given to the patients in this area during 2002 until 2006 was a combination therapy of amodiaquine and SP, which was changed to artesunate and mefloquine in 2007 and then to Coartem in 2008. We found that pyrimethamine-resistant double mutants (50C/51I/59C/108N/164I) are nearly fixed in the population, while both sensitive and resistant sulfadoxine genotypes (436S/437G/540K/581A/613A) were present in the population. We also assayed neutral microsatellite markers around the *dhfr* (chromosome 4) and *dhps* (chromosome 8) loci to get an idea of the strength of selection. According to the microsatellite haplotypes for the *dhfr* and *dhps* SP-resistant alleles, the *dhfr* double and *dhps* single mutants seem to have a single origin. Further studies are required to determine the increased in frequency of SP sensitive parasites, as well as to characterize the gene flow between the southwestern populations, where SP is still efficacious, and the northwestern populations of Colombia where moderate resistance has been documented.

### WORLDWIDE ANTIMALARIAL RESISTANCE NETWORK (WWARN) IN VITRO PROFICIENCY PILOT PROJECT: DETERMINATION OF THE INTERLABORATORY VARIABILITY OF IC<sub>50</sub> ESTIMATES IN PLASMODIUM FALCIPARUM REFERENCE CLONES

Sabina Dahlström, on behalf of WWARN In Vitro Proficiency Pilot Project Group

*WorldWide Antimalarial Resistance Network, Paris, France*

*In vitro* testing is a key component of resistance surveillance as drug susceptibility can be tested without the influence of human confounders, such as immunity and pharmacokinetic parameters. Furthermore the

effect of single compounds in a combination therapy can be evaluated. Currently a wide range of methodologies and conditions are being used to perform drug susceptibility testing in the global community of *in vitro* laboratories. Although there is no gold standard *in vitro* protocol that is suitable for all drugs in all different settings, several aspects of *in vitro* methodology can be standardised to reduce variability. In this study we assessed whether the inter-laboratory variability of drug susceptibility testing could be minimized by introducing simple standardisation measures. Fifteen participating laboratories used their established methodology to test the drug susceptibility of *Plasmodium falciparum* reference clones 3D7 and W2 on several occasions. WWARN provided the following measures to improve standardisation: 1) genetic validation of reference clones by microsatellites and *pfmdr1* gene copy number at the start and close of the pilot project; 2) validated test drugs – chloroquine, mefloquine, desethylamodiaquine and dihydroartemisinin – supplied from the WWARN Reference Material Programme; 3) standardised data analysis using the WWARN *In Vitro* Analysis and Reporting Tool (IVART). Comparing data from different laboratories improves understanding of the range of variability encountered with different *in vitro* readout methods when other parameters have been standardized. These results will be presented and used to design a Proficiency Testing programme to improve standardisation of *in vitro* assessment across the malaria community.

### 1320

#### GENOMIC APPROACH FOR TARGET IDENTIFICATION OF ANTIMALARIAL CYCLOPROPYL CARBOXAMIDES

Cristina de Cózar, Maria G. Gomez-Lorenzo, Laura M. Sanz, Jose L. Llergo, Ane Rodríguez, **Francisco-Javier Gamo**  
GlaxoSmithKline, Tres Cantos (Madrid), Spain

One of the current antimalarial drug discovery approaches is focused on whole cell screening. One of the greatest challenges working with compounds identified in phenotypic screenings is the complete lack of knowledge of the molecular target responsible for antimalarial activity. Cyclopropyl carboxamides (CCAX), a chemical class not described previously as antimalarial drugs, have been identified recently from a whole-cell screening as potent inhibitors of *Plasmodium falciparum* drug-sensitive and resistant strains, as reported previously. Moreover, this series shows a promising *in vivo* oral efficacy in *P. falciparum* mouse models. This might indicate an antimalarial mode of action different from already known resistant mechanisms, although only the identification of the target responsible for the antimalarial activity could confirm it. Despite a potent *in vitro* activity, further characterization of the molecules has revealed an unusual propensity to develop resistance. The frequency of spontaneous resistance is one order of magnitude higher than in the case of atovaquone when using W2 strain. To investigate the resistance mechanisms of this series and to achieve the identification of the cyclopropyl carboxamide antimalarial target we have selected seven independent pure clones that have been extensively characterized. Despite of the high level of resistance (two orders of magnitude) none of them shows sensitive differences in terms of growth rate compared with the parental strain. We have purified genomic DNA of the different clones and started a full genome sequencing approach in order to identify the determinants responsible of CCAX resistance. The identification of this target would help to the progression of this chemical series and to a better understanding of antimalarial resistance.

### 1321

#### PHARMACODYNAMICS OF ARTEMISININ-BASED COMBINATION THERAPIES (ACTS) IN A RODENT MODEL OF ARTEMISININ-RESISTANT MALARIA

**Philipp P. Henrich**<sup>1</sup>, Connor O'Brien<sup>1</sup>, Kyle Dennis<sup>2</sup>, David A. Fidock<sup>1</sup>

<sup>1</sup>Columbia University, New York, NY, United States, <sup>2</sup>University of South Florida, Department of Global Health, Tampa, FL, United States

The emergence of the delayed parasite clearance phenotype in *Plasmodium falciparum* parasites present in the Greater Mekong subregion, as reported previously, highlights the urgent need to identify antimalarial therapies and regimens that can adequately treat these infections. In this study, we have employed an animal model to monitor the course of rodent malaria infection after treatment with Artemisinin-based Combination Therapies (ACTs). In addition to providing insight into the pharmacodynamic properties of existing ACTs when used against artemisinin-resistant strains, our work shows that the artemisinin-resistant *Plasmodium berghei* SANA strain can be treated successfully with an artesunate-pyronaridine combination therapy at similar drug concentrations that are curative for infections with the parental drug-sensitive N strain. The 30-day outcomes indicate that SANA resistance to artemisinin can be overcome with the combination of pyronaridine-artesunate. Piperaquine, which is currently used in combination with dihydroartemisinin in Southeast Asia, also proved to be effective in clearing parasite infections after three doses in the animal model. Of the five partner drugs tested, pyronaridine was the most effective at suppressing the recrudescence of SANA parasites.

### 1322

#### EFFICACY AND EFFECTIVENESS OF ARTEMETHER-LUMEFANTRINE AFTER FIVE YEARS OF WIDE SCALE USE IN TANZANIA

**Billy E. Ngasala**<sup>1</sup>, Andreas Martensson<sup>2</sup>

<sup>1</sup>MUHAS, Dar es Salaam, United Republic of Tanzania, <sup>2</sup>Karolinska Institutet, Stockholm, Sweden

Artemether-lumefantrine (AL) is the most widely adopted ACT in sub-Saharan Africa. The recent emergency of artemisinin resistance in *Plasmodium falciparum* malaria in South East Asia, characterized phenotypically by slow parasite clearance following ACT treatment, highlights the need for both detailed follow up monitoring of efficacy/effectiveness of AL, including detailed assessment of parasite clearance time, and surveillance . identification of molecular markers of resistance to AL as an early warning system. This study is conducted in two rural sites in Bagamoyo and Kibaha Districts, We are conducting a randomised clinical trial to assess the efficacy and effectiveness of AL in children with uncomplicated malaria, including parasite clearance time, selection of molecular markers of resistance, identify factors associated with poor adherence after five years of wide scale use in Tanzania. We are enrolling patients 6 months-10 years with confirmed malaria by finding parasites in blood samples. Patients are randomly allocated to either supervised (admitted to the health facility for 3 days) or unsupervised (at home) artemether-lumefantrine (Coartem®) treatment, and then they are reviewed every week for 42 days, to monitor treatment outcomes. Study nurses make home visits to assess treatment adherence through parent/caretaker interview and blister pack pill count. Standardized procedures recommended by WHO are used to accurately detect and document drug resistant malaria and lumefantrine drug levels on day 7. Data collecting will be completed August 2012.

### PLASMODIUM FALCIPARUM IN VIVO EARLY RESPONSE TO ARTEMETHER-LUMEFANTRINE THERAPY IS ASSOCIATED WITH ABC TRANSPORTER TRANSCRIPTS

**Maria Isabel Veiga**

Columbia University College of Physicians and Surgeons, New York, NY, United States

Increased expression of ABC transporters has been associated with decreased clinical drug response in several different pathologies. *Plasmodium falciparum* malaria is no exception and increased copy number of the parasite P-glycoprotein homologue has been associated with resistance against several antimalarials, including lumefantrine and artemisinins. The aim of this work was to investigate the expression of *P. falciparum* ABC transporters in a clinical setting, upon treatment with artemether-lumefantrine (AL), the most used treatment against *P. falciparum* malaria. The clinical trial was conducted at Fukayosi Primary Health Care Centre, Bagamoyo District, Tanzania in 2006. A total of 50 patients: age 1-10 years were included, hospitalized and treated with standard 6 doses of AL. Venous blood samples were taken at 0,2,4,8,16,24,36,48,60,72 hour and preserved for nucleic acid extraction. RNA was extracted and quality controlled at Karolinska Institutet. For the time points up to 24h cDNA was synthesised and analysed by Real-time PCR for relative quantification of pfmdr1, pfcr, pfmrp1, pfmrp2 using the endogenous control seryl-tRNA synthetase (PF07\_0073). Gene expression relative to the control was calculated using the  $\Delta\Delta C_t$  method. After initiation of AL treatment the expression of pfmrp1 increased significantly whereas the expression of pfmdr1, pfcr and pfmrp2 significantly decreased. Our results emphasises the likely importance of pfmrp1 in artemisinin combination therapy drug resistance.

### EVALUATING THE ROBUSTNESS OF PARASITE CLEARANCE RATE MEASURES USING HERITABILITY

**Standwell Nkhoma**<sup>1</sup>, Shalini Nair<sup>1</sup>, Kasia Stepniewska<sup>2</sup>, Elizabeth Ashley<sup>3</sup>, Rose McGready<sup>4</sup>, Aung Pyae Phyo<sup>4</sup>, François Nosten<sup>4</sup>, Tim Anderson<sup>1</sup>

<sup>1</sup>Texas Biomedical Research Institute, San Antonio, TX, United States, <sup>2</sup>WWARN, Oxford, United Kingdom, <sup>3</sup>Mahidol University, Bangkok, Thailand, <sup>4</sup>Shoklo Malaria Research Unit, Mae Sot, Thailand

Measurement of malaria parasite clearance rates following artemisinin treatment requires sequential parasite counts taken at intervals following treatment. Frequent sampling is ideal, but extremely labor intensive, and the optimal strategy for obtaining robust clearance rate estimates while minimizing sampling effort is poorly understood. We evaluate a variety of metrics (24 and 48hr parasite reduction ratios, time to parasite clearance, clearance half-lives ( $t_{1/2}$ ) measured using 6-24 hourly sampling until clearance or for the first 48 hrs only). We also evaluate the effect of different slope fitting procedures (ignoring or incorporating time lags) on the robustness of clearance estimates. We perform these analyses using parasite clearance data collected from 1731 hyperparasitemic patients from a region of emerging resistance on the Thai-Burma border. All parasites were genotyped using 96 single nucleotide polymorphisms, and we used heritability (the proportion of variation attributable to parasite genetics) to evaluate the robustness of each measure. Our assumption is that the most robust measure will show the highest heritability, while less useful measures will show lower heritability due to measurement error. The results of these analyses will be presented.

### SUPPRESSING ANTIMALARIAL DRUG RESISTANCE WITH COMPLEMENTARY INHIBITORS: CATCHING *PLASMODIUM FALCIPARUM* BETWEEN A ROCK AND A HARD PLACE

**Leila S. Ross**<sup>1</sup>, Amanda Lukens<sup>2</sup>, Francisco Javier Gamo Benito<sup>3</sup>, Maria Jose Lafuente-Monasterio<sup>3</sup>, Piotrek Sliz<sup>4</sup>, Michael Booker<sup>5</sup>, Dyann F. Wirth<sup>1</sup>, Roger C. Wiegand<sup>2</sup>

<sup>1</sup>Harvard School of Public Health, Boston, MA, United States, <sup>2</sup>Infectious Disease Initiative, Broad Institute, Cambridge, MA, United States, <sup>3</sup>GlaxoSmithKline, Tres Cantos, Spain, <sup>4</sup>Harvard University, Boston, MA, United States, <sup>5</sup>Genzyme Corporation, Waltham, MA, United States

Managing drug resistance is a core problem in anti-malarial drug therapy. Resistance has arisen to all drugs in clinical use. Combination therapy is a key tool for delaying the development and spread of resistant parasites. Most combinations use two drugs with different mechanisms of action. We explore here the possibility of using two agents acting on the same target - one drug that selectively inhibits the wild-type target, and a complementary partner drug that selectively inhibits the most likely drug-resistant mutations. Selection of malaria parasites resistant *in vitro* to either alkylthiophene- or triazolopyrimidine-based Dihydroorotate Dehydrogenase (DHODH) inhibitors resulted in mutations in the drug-binding pocket of DHODH, which had been previously determined through crystallography and biochemical characterization of purified protein. Using those mutants resistant to both the alkylthiophene and triazolopyrimidine inhibitors we re-screened a library of DHODH inhibitors. This screen yielded several compounds 10-100-fold more potent against the mutants than the wild-type parasites. Subsequent selection of resistance to these selectively potent compounds in the alkylthiophene-resistant strains resulted in reversion of the DHODH gene back to wild-type, confirming the key role of the mutation. Modeling and molecular dynamics simulations are being used to probe the mechanisms of heightened sensitivity to different compounds. Combination therapy that exploits target reciprocity traps malaria: escape from the primary drug results in increased sensitivity to the secondary drug. Selective pressure on the partner compound is predicted to be reduced; it acts only against the small population of parasites that become resistant to the primary compound. In targets that tolerate few mutations, the fitness costs of becoming resistant to both complementary inhibitors may provide a path for suppressing drug resistance.

### EMERGING COARTEM RESISTANCE ASSESSED BY DAY THREE PARASITEMIA IN SURINAME

**Jeetendra K. Jitan**<sup>1</sup>, Stephen G. Vredon<sup>2</sup>, Malti R. Adhin<sup>3</sup>

<sup>1</sup>Ministry of Health Suriname, Paramaribo, Suriname, <sup>2</sup>Foundation for Scientific Research Suriname (SWOS), Paramaribo, Suriname, <sup>3</sup>ADEK Universiteit van Suriname, Paramaribo, Suriname

In 2004 Suriname changed its first line treatment for *Plasmodium falciparum* malaria to an artemisinin based combination therapy (ACT), introducing Coartem. This and other measures resulted in a more than 90 percent decrease of malaria. Currently malaria cases are mainly seen in gold miners in the interior. In this population adherence to treatment is poor and also the use of counterfeit medication is widespread. Following WHO recommendations, the efficacy of the treatment was evaluated in 2006 and found to be adequate. A study was undertaken to assess Coartem efficacy in patients with *P. falciparum* malaria. Consenting patients with *P. falciparum* malaria mono-infection were enrolled and followed to assess the course of clinical symptoms and parasitemia. Because of the current low number of cases available for a 28 days follow up, in this assessment we also included day 3 parasitaemia, as a clinical endpoint. The treatment was directly observed; patients were followed until parasite clearance plus one day and then on day 7, 14, 21 and 28. 67 Patients were enrolled, of whom 9 were withdrawn because of protocol violations. There were no reports of serious side effects. From the

remaining 58 patients, 5 were lost to follow up before parasite clearance. Only 11 patients were followed for the full 28 days period, none of whom had recurrent parasitaemia. From the 53 patients that were followed at least until parasite clearance, 15 (28.3%) had still parasites on day 3. From 11 patients that were followed until day 28 only 1 had a positive slide on day 3, which became negative on day 4. Comparing these results to those of 2006 we found that at that time the incidence of day 3 parasitaemia was 1.6 percent, with 95% of cases with a negative slide on day 28. We conclude that the rate of day 3 parasitaemia has significantly increased in 2011 ( $p < 0.001$ ). This may be an indication for emerging resistance to Coartem. It is suspected that this may be due to the (improper) use of counterfeit ACT.

### 1327

#### MALARIA AS A CAUSE OF ACUTE FEBRILE ILLNESS IN AN URBAN PEDIATRIC POPULATION IN GHANA

**Keziah L. Malm<sup>1</sup>**, Constance Bart-Plange<sup>2</sup>, George Armah<sup>3</sup>, John Gyapong<sup>4</sup>, Seth Owusu Adjei<sup>5</sup>, Kojo Koram<sup>6</sup>, Fred N. Binka<sup>6</sup>

<sup>1</sup>University of Ghana, Accra, Ghana, <sup>2</sup>National Malaria Control Programme/Ghana Health Service, Accra, Ghana, <sup>3</sup>Noguchi Memorial Institute for Medical Research, Accra, Ghana, <sup>4</sup>University of Ghana, Research and Development Department, Accra, Ghana, <sup>5</sup>Kintampo Health Research/Ghana Health Service, Kintampo, Ghana, <sup>6</sup>University Ghana, School of Public Health, Accra, Ghana

Annually about 500 million people become severely ill with malaria. Over 90% of cases and deaths occur in Sub-Saharan Africa with children under five years and pregnant women being affected mostly. In Ghana, about 3.7 million cases of malaria were reported in 2010 out of which only 26% were confirmed by laboratory testing. Most febrile cases are treated as malaria sometimes with fatal consequences though they may not be malaria. This could explain the high proportion of funds that the Ghana Health Insurance Authority spends on the treatment of malaria. This study sought to determine the proportion of acute febrile illness in children under five years due to malaria. A hospital based surveillance system recruited children less than five years who reported at the out-patient department of an urban hospital with fever  $\geq 37.5^{\circ}\text{C}$  at the time of visit from February 2009 to February 2010. Parents/guardians who consented were interviewed using a structured questionnaire and the child examined by a clinician. Capillary blood through a finger prick was used for a thick blood film using Giemsa and viewed under the microscope for malaria parasites. Out of the 605 children with fever whose blood samples were taken for microscopy, only 68 were positive for malaria, giving an overall positivity rate of 11.2%. Malaria was equally distributed among males and females, the proportion malaria cases increased as age increased. Of the 492 children whose reports were available, 80% of the children were diagnosed by clinicians as having malaria either alone or in combination with other diseases and were treated with anti-malarials. The treatment of febrile cases based solely on clinical symptoms has been shown to be less cost effective than confirming the diagnosis with a laboratory test and also promotes the occurrence of drug resistance. Clinicians should look out for other causes of fever rather than treating almost all febrile cases as malaria. The National Malaria Control Programme has intensified efforts to increase laboratory testing before treatment.

### 1328

#### A COMPREHENSIVE RISK MAP FOR MALARIA IN KINSHASA, DEMOCRATIC REPUBLIC OF CONGO

**Giovanfrancesco Ferrari<sup>1</sup>**, Henry Maggy Ntuku<sup>2</sup>, Sandro Schmidlin<sup>1</sup>, Christian Lengeler<sup>1</sup>, Antoinette K. Tshetu<sup>2</sup>

<sup>1</sup>Swiss Tropical and Public Health Institute, Basel, Switzerland, <sup>2</sup>School of Public Health, Kinshasa, Democratic Republic of the Congo

The Democratic Republic of Congo (DRC) is the second most malarious country in the world. However, there is a paucity of epidemiological data on the risk pattern of malaria. In 2009 (dry season) and 2011 (end

of the rainy season) two two-stage cluster sampling malaria surveys were conducted in the capital city Kinshasa with the twofold aim of (1) assessing malaria parasite prevalence, anemia and associated malaria risk factors, and (2) producing a malaria risk map using a geographic information system (GIS). A total of 6410 children aged 6-59 months (3058 in 2009 and 3352 in 2011) were tested for both malaria (using rapid diagnostic tests) and anemia (by HemocueTM). Nine health zones (HZ) were sampled in 2009 with an average prevalence for malaria and anemia of 6.6% (95% CI 5.8-7.5) and 66.0% (64.5-67.4) respectively, while in the 25 HZs in 2011 the prevalence was 17.0% (15.7-18.3) and 64.2% (62.6-65.9). Overall, the prevalence rate for both surveys was 11.9% (11.2-12.8) for malaria and 65.1% (63.9-66.7) for anemia. To ensure comparability of the results between surveys, two HZs from 2009 were resampled in 2011. Prevalence for malaria in 2009 and 2011 was: Ngiri Ngiri 1.0% versus 0.8% and Selembao: 14.1% versus 26.8%. Prevalence for anemia was: Ngiri Ngiri 62.5% versus 55.4% and Selembao: 67.1% versus 61.4%. In a multivariate analysis of the 2011 data significant protective factors for malaria risk were: educational level of the respondent (OR = 0.12, 95% CI: 0.03 - 0.56) and sleeping under an ITN (OR = 0.52, 95% CI: 0.43 - 0.63). All key parameters were mapped to the level of the HZs (n=35). Malaria parasitemia, anemia and fever prevalence were found to be much lower in the city center than in the peri-urban suburbs, where transmission rates remain high. ITN usage showed the opposite pattern. These maps provide for the first time a comprehensive picture of the epidemiology of malaria in Kinshasa and provide solid baseline information for planning future malaria control interventions.

### 1329

#### LINKING THE INCIDENCE AND AGE PATTERNS OF CLINICAL MALARIA TO PARASITE PREVALENCE USING A MATHEMATICAL MODEL

**Jamie T. Griffin**, Neil M. Ferguson, Azra C. Ghani  
*Imperial College, London, United Kingdom*

Estimating the changing burden of malaria disease remains difficult due to limitations in health reporting systems in those countries with the largest burden of disease. Methods extrapolating from parasite prevalence data are therefore often employed. We present an approach to estimating disease incidence from prevalence data accounting for the changing age distribution of cases that occurs as transmission declines. We use a transmission model to capture the shifting age-pattern of disease at different transmission intensities through dynamically modelling the acquisition and loss of immunity. The model is fitted to age-stratified data on the incidence of uncomplicated malaria due to *Plasmodium falciparum* from 24 sites in 9 sub-Saharan African countries. We used Bayesian methods, and accounted for variation in treatment rates and reporting methods (active versus passive case detection). We estimate that passive case detection picks up 32% (95% credible interval: 18-56%) as many cases as daily active detection, and weekly detection 77% as many (95% CrI: 63-88%). However, there was wide variation in incidence between studies that cannot be explained by differences in case-finding or case definitions such as parasitaemia thresholds, and so substantial uncertainty remains in the incidence at any given transmission intensity. We estimate that at a parasite prevalence in 2 to 10 year-olds of 60%, 50% of cases occur in under-fives and 10% in over 15s; at a prevalence of 20%, 21% are in under-fives and 38% are in over 15s; and at a prevalence of 5%, 11% are in under-fives and 59% in over 15s. As our transmission model includes the principal control measures, these results will allow us to predict the impact of interventions on the incidence of clinical malaria.



### RATIONALE AND DESIGN OF CCM IN SARAYA DISTRICT: RESULTS AND IMPLICATIONS FOR POLICY IN RURAL SENEGAL

**Youssoupha Ndiaye**<sup>1</sup>, Jean Louis Ndiaye<sup>2</sup>, Jonas Bassene<sup>1</sup>, Mansour Ndiath<sup>2</sup>, Akhenaton Manga<sup>1</sup>, Paul Milligan<sup>3</sup>, Demetri Blanas<sup>4</sup>, Sylvain Faye<sup>5</sup>, Mouhamed Ndiaye<sup>2</sup>, David Schellenberg<sup>3</sup>, Badara Cisse<sup>2</sup>, Omar Gaye<sup>2</sup>

<sup>1</sup>Ministry of Health and Prevention, Dakar, Senegal, <sup>2</sup>University Cheikh Anta Diop, Laboratory of Medical Parasitology, Dakar, Senegal, <sup>3</sup>London School of Hygiene & Tropical Medicine, London, United Kingdom, <sup>4</sup>Mount Sinai College of Medicine, New York, NY, United States, <sup>5</sup>University Cheikh A. Diop, Department of Sociology, Dakar, Senegal

Following the Abuja conference, malaria control strategies improved malaria patterns in Senegal with 3% of prevalence in outpatients in 2009. Figures hid disparities between Northern regions where morbidity was low and the southeast with high malaria incidence. Furthermore the data came only from health units only. To fill the gap in most under served areas, Community Case Management (CCM) was scaled up in rural Senegal with Community Health workers (CHW) and village volunteers called DSDOM. The objective of the study was to evaluate CCM at larger scale and identify policy implications for malaria. The project was held in Saraya district located in south east Senegal. It covers 6837 km<sup>2</sup> for 102 villages with an estimated 40000 population; 70% lived at more than 15 km of the nearest health unit. CCM was done in 47 villages with CHW or village volunteers, trained in malaria diagnosis and treatment. A Community Households cluster survey with Knowledge, Attitude, Practices (KAP) and Treatment seeking behavior were completed, quality of data assessed and traditional healers involved from June 2010 to December 2011. 683 heads of household were interviewed. Mosquito as the malaria vector was recognized by 81% of household heads, 93% cited mosquito nets as protective, RDT was well known (71%) and ACT as well (62%); 33% of respondents knew of potential adverse events, and use of LLINs the night before the survey was reported by 80% of respondents. In 73% of households 1 member was ill during the last 15 days, 91% had fever, and first visits were done by CHWs (34%), nurses (17%), DSDOM (15%) and traditional healers (7%); 44% of patients completed consultations within 24 hours. ACT was administered to 55% of patients. Few patients (N=52) sought second treatment mainly from CHW (36%) and traditional healers (18%). 15.491 visits were documented. 80% were reported by CHWs, about 50% were children under 10 years; 11.479 RDT were completed and 74% were positive; referrals (2005) were made and 6 deaths recorded. 36 traditional healers were visited by 67 patients. They referred 65 patients, 63% were RDT positive. The study revealed the central place of CHWs and the need to re-evaluate policy in under served areas, especially CHW status, the training curriculum and discussions on incentives to sustain filling the gap.

### 1331

### IMPACT OF PLASMODIUM FALCIPARUM INFECTION ON HEMATOLOGICAL PARAMETERS IN CHILDREN WITH ABNORMAL HEMOGLOBIN LIVING IN A MALARIA ENDEMIC AREA OF BURKINA FASO

**Edith C. Bougouma**<sup>1</sup>, Adama Gansane<sup>1</sup>, Alfred Tiono<sup>1</sup>, Noelle B. Henry<sup>1</sup>, Alphonse Ouedraogo<sup>1</sup>, Amidou Diarra<sup>1</sup>, Issiaka Soulama<sup>1</sup>, Souleymane Sanon<sup>1</sup>, AndreLin Ouedraogo<sup>1</sup>, Jean B. Yaro<sup>1</sup>, Esperance Ouedraogo<sup>1</sup>, Amadou T. Konate<sup>1</sup>, Megan Sansa<sup>2</sup>, Tina J. Dube<sup>2</sup>, Issa Nebie<sup>1</sup>, Sodiomon B. Sirima<sup>1</sup>

<sup>1</sup>Centre National de Recherche et de Formation sur le Paludisme, Ouagadougou, Burkina Faso, <sup>2</sup>EMMES Corporation, Rockville, MD, United States

Malaria is the most common cause of childhood morbidity in Africa, having varied haematological consequences. The high prevalence of HaemoglobinS/C is associated with the protection against malaria during

childhood. Much less is known about the effect of HbS and HbC on malaria infection and haematological parameters. Susceptibility of the human host to malaria infection and haematological parameters has been reported to be influenced by some genetic factors as abnormal haemoglobin. The aim of this study was to evaluate haematological parameters in children less than fifteen years of age with abnormal haemoglobin genotypes and malaria infection. The study was conducted in 2008 in rural villages. It consisted of a combination of 2 cross-sectional surveys during the low and high malaria transmission. During each survey, each child was clinically examined, and thick and thin blood films were prepared for malaria diagnosis. The full blood count was performed with a haematology analyzer and an additional blood specimen was taken to determine the haemoglobin genotypes by PCR. In total, 406 children were recruited, 176 and 230 during the high and low seasons, respectively. Prevalence of Hb genotypes during the high and low season was: normal haemoglobin AA (76.7 and 65.7%) and abnormal haemoglobin (22.2 and 25.3%). There was no difference between the two groups in terms of leucocyte count and haemoglobin level if the subject was infected or not. However, during the low season, abnormal haemoglobin children without parasitemia tended to have higher lymphocyte counts ( $p=0.02$ ), monocyte counts ( $p=0.02$ ), red blood cell counts ( $p=0.03$ ) and neutrophil counts ( $p=0.01$ ), as compared to normal haemoglobin group. The platelet counts differed between the two groups for healthy children during the high season ( $p=0.002$ ). The comparison of haematology parameters within haemoglobin type showed that basophil, lymphocyte and monocyte counts were significantly lower during high season. Basophil, eosinophil, red blood cells, haematocrit, haemoglobin and monocyte counts in the malaria-infected normal haemoglobin group were significantly lower. In conclusion, these findings suggest that malaria parasites may affect the haematopoiesis of children living in malaria endemic area. Genetic factors, such as abnormal haemoglobin genotype, also influenced haematological parameters if subjects were not infected.

### 1332

### ANTHROPOMETRIC GROWTH TRENDS DETERMINED BY WHO (2006) AND CDC (2000) GROWTH CRITERIA FOR CLINICALLY WELL INFANTS ENROLLED INTO A TRIAL OF SINGLE DOSE FANSIDAR FOR PRESUMPTIVE TREATMENT OF MALARIA IN RURAL NORTHEASTERN GHANA

**David J. Fryauff**<sup>1</sup>, Abraham R. Oduro<sup>2</sup>, Francis Anto<sup>3</sup>, Frank Atuguba<sup>2</sup>, Joseph Flanagan<sup>4</sup>, Abraham Hodgson<sup>5</sup>, Francis Nkrumah<sup>6</sup>, Kwadwo A. Koram<sup>6</sup>

<sup>1</sup>Naval Medical Research Center, Silver Spring, MD, United States, <sup>2</sup>Navrongo Health Research Centre, Navrongo, Ghana, <sup>3</sup>University of Ghana, Accra, Ghana, <sup>4</sup>Naval Medical Research Unit No. 3, Cairo, Egypt, <sup>5</sup>Ghana Health Service, Accra, Ghana, <sup>6</sup>Noguchi Memorial Institute of Medical Research, Accra, Ghana

Current benefits of Fansidar-based intermittent preventive treatment for malaria during pregnancy (IPTp), and infancy (IPTi), prompted us to look retrospectively for evidence of a positive Fansidar effect on growth in clinically well young children that were randomized into a placebo-controlled, single-dose Fansidar trial at the peak of malaria season in rural Ghana. Growth charts from CDC (2000) and the newer WHO (2006) growth standards were used to determine within- and between-group differences at treatment baseline (Aug. 2001) and follow-up endpoint (Jan. 2002) among girls ( $n = 261$ ) and boys ( $n = 237$ ) enrolled in that four month trial. Weight-for-Age Z (WAZ) and Weight-for-Height Z (WHZ) scores derived from CDC growth charts were significantly lower (worse) than those derived from the WHO growth standards, while Height-for-Age (HAZ) Z scores were significantly higher by the CDC scale. Consequently, frequencies of underweight and wasting based on the CDC growth curve were greatly inflated over those derived from WHO standards and estimates of stunting were much lower by the CDC scale. Surprisingly, baseline and endpoint comparisons between sexes for mean WAZ, WHZ, and HAZ scores by both CDC and WHO growth criteria revealed better, more normative growth for girls-significantly improved over boys for all

three indices according to WHO criteria whereas by CDC criteria only HAZ was significantly improved. Endpoint comparison based on the newer WHO growth standards found no change in either sex for WAZ and % underweight, but WHZ and % wasting were improved significantly in boys. In boys and girls HAZ and % stunting worsened significantly; a result reflected by the two growth scales but which disappeared when sexes were combined. Analyses that combined sexes found no significant differences in growth indices that were associated with Fansidar or bednet effect, but comparison with a non-enrolled age-, sex-, and location-matched control revealed highly improved growth indices, by both CDC and WHO standards, for the cohort that had been subjects during this brief study.

### 1333

#### COMMUNITY HEALTH WORKERS AS AN EFFECTIVE CHANNEL FOR DELIVERY OF CHILD HEALTH INTERVENTIONS: EXPANDING THE KNOWLEDGE BASE

Lucy Paintain<sup>1</sup>, Barbara Willey<sup>1</sup>, Alyssa Sharkey<sup>2</sup>, Julia Kim<sup>2</sup>, Valentina Buj<sup>2</sup>, Jayne Webster<sup>1</sup>, David Schellenberg<sup>1</sup>, Ngashi Ngongo<sup>2</sup>

<sup>1</sup>London School of Hygiene & Tropical Medicine, London, United Kingdom, <sup>2</sup>UNICEF, New York, NY, United States

A systematic literature review was conducted to assess the published and unpublished evidence on the effectiveness of strategies to improve community case management (CCM) of malaria. Specific objectives were to investigate interventions to (i) increase the coverage and quality of services provided by community health workers (CHWs) responsible for malaria case management; (ii) strengthen referrals from community to facility-based providers; (iii) increase the capacity of health systems (HS) to support CCM; and (iv) integrate malaria diagnosis and case management with other health services at the community level. Thirty-six studies were included in the review, the majority (32) reporting reasonably standard indicators of CHW performance. Findings show that CHWs are able to provide good quality of care, including performing simple procedures such as rapid diagnostic tests. Appropriate training and regular supportive supervision are important facilitating factors. However, crucial to the sustainable success of CHW programmes is the strengthening of HS capacity to support commodity supply, supervision, and appropriate treatment of referred cases. The little evidence available on referral systems from the community to health facility level suggests that this is a priority area that needs attention. There are few published studies on integrated CCM, although this is now the direction that policy and programmes are moving. Adding additional tasks does not reduce the quality of malaria CCM, provided sufficient training, supervision and support is maintained. However, with the exception of pneumonia treatment, reporting on the quality of delivery of additional interventions is limited. Amongst included studies, 11 reported on referral, 11 on HS capacity and 9 on iCCM; however not all data was quantitative and indicator definitions varied, making direct comparisons challenging. There is a need to encourage implementers to evaluate programmes robustly using standardised indicators and share their findings with other programmes to enable broader lesson learning.

### 1334

#### RISK FACTORS ASSOCIATED WITH MULTIPLE MALARIA INFECTIONS IN BANGLADESH

Ubydul Haque, Gregory E. Glass, Hans J. Overgaard  
Department of Molecular Microbiology and Immunology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, United States

Malaria is endemic in Bangladesh. In 2011, there were 51,773 episodes and 36 deaths attributed to malaria with most cases occurring in the Chittagong Hill Tracts (CHT), Bangladesh. This study identifies environmental and socioeconomic malaria risk factors and determines the spatial distribution of malaria in an endemic area in CHT. Longitudinal

data on malaria incidence were collected from 1634 households in 54 villages (total population 7922) from January 2009 to December 2010. Hydrological, topographic, climatic and socioeconomic risk factors were used as potential predictors for malaria infection. Spatial malaria patterns were observed. Relative risk ratios were calculated to identify possible reasons for zero, one and >1 malaria infections in the study population. There were 509 malaria cases (6.4%) during the study period. These were distributed heterogeneously between villages. Children were most vulnerable to malaria infection. About 21.8% of homesteads accounted for all the malaria cases in the study area. The multivariate analysis with socioeconomic risk factors showed that bed net ratio (number of nets per person per household), ethnicity, house wall construction material, and household density had significant relationships with malaria incidence. Among the topographic and hydrological risk factors, households within two kilometers of a 4<sup>th</sup> order streams were at highest risk of malaria infection. In multinomial analysis belonging to the Bengali ethnic group, house walls made of mud and high household density were associated with a high risk for multiple malaria infections. High bed net ratio, belonging to the Tripura ethnic group, household heads having a non-specific ('other') occupation were associated with a low risk for multiple malaria infections. No clear relationship was observed between climatic and topographic parameters and malaria. Prioritizing the risk zones and identified risk factors will assist in cost effective targeting of malaria interventions and may contribute to a further reduction in malaria burden in the region.

### 1335

#### HEMOGLOBIN C TRAIT PROVIDES PROTECTION FROM CLINICAL FALCIPARUM MALARIA COMPARABLE TO THAT PROVIDED BY HEMOGLOBIN S TRAIT IN MALIAN CHILDREN

Mark Travassos<sup>1</sup>, Drissa Coulibaly<sup>2</sup>, Matthew B. Laurens<sup>1</sup>, Ahmadou Dembélé<sup>2</sup>, Youssouf Tolo<sup>2</sup>, Abdoulaye K. Koné<sup>2</sup>, Karim Traoré<sup>2</sup>, Amadou Niangaly<sup>2</sup>, Aldiouma Guindo<sup>2</sup>, Andrea A. Berry<sup>1</sup>, Shannon Takala Harrison<sup>1</sup>, Bourema Kouriba<sup>2</sup>, Kirsten E. Lyke<sup>1</sup>, Dapa A. Diallo<sup>2</sup>, Ogobara K. Doumbo<sup>2</sup>, Christopher V. Plowe<sup>1</sup>, Mahamadou A. Thera<sup>2</sup>

<sup>1</sup>Howard Hughes Medical Institute/Center for Vaccine Development, University of Maryland School of Medicine, Baltimore, MD, United States, <sup>2</sup>Malaria Research and Training Center, University Science, Techniques and Technology, Bamako, Mali

Hemoglobin (Hb) C trait, like Hb S trait, appears to protect against severe malaria in children. Recent work examining whether Hb C trait also protects against uncomplicated malaria has produced conflicting results. We hypothesized that children with Hb C trait would have a longer time to the first clinical malaria episode than children with Hb AA in a cohort study of malaria incidence in Bandiagara, Mali. Three hundred children aged one to six years were enrolled in a longitudinal follow-up study of malaria incidence that included scheduled monthly blood smears and unscheduled follow-up for sick visits. Hb electrophoresis was measured at baseline. Excluding those participants with mutations for glucose-6-phosphate dehydrogenase deficiency, 216 children had Hb AA, 35 children had Hb AC, nine children had Hb AS, three children had Hb SC, and two children had Hb CC. Children with Hb AC had a longer time to first clinical malaria episode than children with Hb AA (P=0.002; 309 mean malaria-free days versus 227 days). Children with Hb AS also had a longer time to first clinical malaria episode than children with Hb AA (P=0.03; 334 mean malaria-free days versus 227 days). Children with Hb AC had fewer episodes of clinical malaria in a single season than did children with Hb AA (0.2 episodes versus 0.7 episodes, P=0.002). However, children with Hb AC or AS experienced the same number of anemia episodes (Hb<8.4 g/dL) as children with Hb AA. Children with Hb AS experienced more asymptomatic malaria episodes (1.44 episodes versus 0.57 episodes, P=0.009) and a lower cumulative parasitemia than children with Hb AC (P=0.02). Thus, while both Hb C and S traits exerted a protective effect

against clinical malaria episodes, they appeared to do so by distinct mechanisms that differentially affected a subject's response to infecting malaria parasites.

## 1336

### HIGH BURDEN OF MALARIA IN UGANDAN ADULTS AND INCREASED RISK OF SEVERE MALARIA AND DEATH IN ADULT MEN AS COMPARED TO WOMEN

Anne E. Frosch<sup>1</sup>, Paul Bangirana<sup>2</sup>, James Keck<sup>3</sup>, Francis Tintani<sup>4</sup>, Robert O. Opoka<sup>5</sup>, Tracy L. Bergemann<sup>4</sup>, Chandy C. John<sup>6</sup>

<sup>1</sup>University of Minnesota, Minneapolis, MN, United States, <sup>2</sup>Makerere University College of Health Sciences, Kampala, Uganda, <sup>3</sup>Partners in Health, Boston, MA, United States, <sup>4</sup>School of Public Health, University of Minnesota, Minneapolis, MN, United States, <sup>5</sup>Department of Paediatrics and Child Health, Mulago Hospital/Makerere University Medical School, Kampala, Uganda, <sup>6</sup>Center for Global Pediatrics, University of Minnesota, Minneapolis, MN, United States

Malaria prevention has targeted young children and pregnant women because of the disproportionate burden of disease in these populations. Few studies have assessed the frequency and severity of malaria in adult males. To examine the relative impact of gender and age on malaria outcomes, we conducted a chart review of all individuals admitted with a primary diagnosis of malaria to three Ugandan public hospitals between January 2000 and June 2005. The hospitals included Kabale Hospital (hypoendemic malaria transmission), Mulago Hospital (mesoendemic), and Soroti Hospital (holoendemic). 45,176 charts were reviewed. Adult males  $\geq 14$  years accounted for 17.2% (Kabale), 8.1% (Mulago) and 8.6% (Soroti) of all malaria admissions, but 35.3% (Kabale), 14.5% (Mulago) and 16.5% (Soroti) of all deaths in persons admitted with malaria. Among persons  $< 14$  years, there was no difference in the risk of severe malaria or death in males as compared to females in any hospital. In contrast, among persons  $\geq 14$  years of age, males had a significantly higher risk of severe malaria and death than females at two of the three hospitals (risk expressed as odds ratio, 95% confidence interval): Mulago (severe malaria, 1.31, 1.11-1.55,  $P=0.001$ ; death, 1.54, 1.25-1.90,  $P<0.0001$ ) and Soroti (severe malaria, 1.56, 1.34-1.82,  $P<0.0001$ ; death 2.15, 1.72-2.68,  $P<0.0001$ ). Among persons admitted to Mulago Hospital with a primary diagnosis of pneumonia, risk of death was also higher in males than females in persons  $\geq 14$  years (1.50, 1.23-1.83,  $P<0.0001$ ) but lower in males than females for persons  $< 14$  years (0.86, 0.76-0.98,  $P=0.02$ ). Among persons  $\geq 14$  years of age hospitalized for malaria in Uganda, males have a significantly greater risk of severe disease and death. Given that adult males are largely neglected in malaria control and prevention efforts, further study is needed to understand the reason for this observation.

## 1337

### GAMETOCYTE DYNAMICS IN AN AREA WITH SEASONAL MALARIA TRANSMISSION

Bronner P. Goncalves<sup>1</sup>, Mahamadoun Hamady Assadou<sup>2</sup>, Ruth Ellis<sup>3</sup>, Agnes Guindo<sup>2</sup>, Charles Luswata<sup>3</sup>, Nafomon Sogoba<sup>2</sup>, Mamady Kone<sup>2</sup>, Diakit  Moussa Lamine<sup>2</sup>, Michael Fay<sup>4</sup>, D. Rebecca Prevots<sup>5</sup>, Ogobara Doumbo<sup>2</sup>, Yimin Wu<sup>3</sup>, Issaka Sagara<sup>2</sup>, Patrick E. Duffy<sup>3</sup>

<sup>1</sup>Laboratory of Malaria Immunology and Vaccinology/Laboratory of Clinical Infectious Diseases - Epidemiology Unit, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Rockville, MD, United States, <sup>2</sup>Malaria Research and Training Center, University of Bamako, Bamako, Mali, <sup>3</sup>Laboratory of Malaria Immunology and Vaccinology, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Rockville, MD, United States, <sup>4</sup>Biostatistics Research Branch, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Rockville, MD, United States, <sup>5</sup>Laboratory of Clinical Infectious Diseases - Epidemiology Unit, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD, United States

Renewed interest in malaria elimination has underscored the need for understanding malaria transmission. Gametocytes, the sexual stage of malaria parasites, are responsible for disseminating malaria infection. To better comprehend the epidemiology of gametocytes, including transmission reservoir and "hotspot", in an area with seasonal malaria transmission, we recruited 250 individuals, from ages of 3 months to 50 years, in Bancoumana, Mali. During one year, study subjects were surveyed for parasite carriage every 4 weeks. Children aged 5-15 years had gametocytes more frequently (8%) during their monthly visits compared with individuals in younger or older age groups (2.5-4%). This might be a consequence of a higher proportion of visits with infection in this age group (24% in 5-15 age group compared 7-13% in other age groups) as opposed to a higher probability of having gametocytes when infected. At the beginning of transmission season (July and August), individuals between 5 and 20 years of age were more likely to carry gametocytes than other individuals. However, at the peak of transmission (September through November), individuals from different age groups also presented gametocytes during scheduled visits. There was a strong correlation between proportions of visits with infection in a compound and proportions of visits with gametocytes in the same compound ( $P<0.01$ ). There was evidence for familial aggregation of gametocyte positivity during follow-up (odds ratio 4 [95% CI 1.04 - 15.3]) but we could not rule out that this might be solely due to infection aggregation. Three compounds that represented 12.4% of the study population had 35.5% of all visits with gametocytes, mostly because of chronic infections in asymptomatic young children. Taken together, the data suggests that children aged between 5 to 15 years carry gametocytes more frequently; whether this is related to longer average duration of infection or to higher incidence of infection in this age group still requires further investigation. Similarly, the identification of factors present in compounds where most gametocyte positivity clusters would guide studies to understand malaria transmission dynamics and possibly the design of clinical trials to test transmission-blocking interventions.

## 1338

**PLASMODIUM FALCIPARUM MALARIA HAS INCREASED IN BISSAU IN RECENT YEARS, MAINLY AMONG OLDER CHILDREN**

Johan Ursing<sup>1</sup>, Lars Rombo<sup>2</sup>, Amabelia Rodrigues<sup>3</sup>, Poul-Erik Kofod<sup>4</sup>

<sup>1</sup>Karolinska Institutet, Stockholm, Sweden, <sup>2</sup>Centre for Clinical Research, Sörmland County Council, Eskilstuna, Sweden, <sup>3</sup>Bandim Health Project, Bissau, Guinea-Bissau, <sup>4</sup>University of Southern Denmark, Kolding, Denmark

*Plasmodium falciparum* malaria was holo-endemic in Guinea-Bissau during the early 1990's. We have undertaken back to back clinical trials at the Bandim Health Centre in Bissau since 1994. The health centre serves the population living within the Bandim Demographic Surveillance Site and has been well staffed throughout the study period. The annual number of children aged <15 years, seeking medical attention with at least 20 *P. falciparum* per 200 leukocytes from 1994 to 2011 (except 2009) were as follows: 116, 214, 211, 172, 125, 377, 266, 301, 256, 343, 180, 172, 109, 40, 141, (no data 2009), 316 and 362. Data are lacking Jan-May 1994 (prior to study start), July, August and Nov 1998 (due to civil war), October 2006 (in-between studies) and the whole of 2009 (laboratory staff were not available). The median age of children the same years were: 48, 58, 47, 46, 43, 58, 61, 65, 57, 68, 60, 64, 61, 59, 79, (no data), 107 and 115 months. There was a significant increase of age between 1994 and 2007 as well as between 2007 and 2011 (non parametric test for trend  $p < 0.0001$  for both). The number of children aged 5-15 years with malaria were 188/377 (50%) in 1999, 20/40 (50%) in 2003 and 307/362 (85%) in 2011. The annual total rainfall varied with peaks of 1980 mm and 1839 mm in 2003 and 2010, respectively and a trough of 1085 mm in 2007. The overall decrease of malaria after the war in 1999 until 2007 (377 to 40 cases) is in line with findings in neighbouring The Gambia. The decrease was not due to artemether-lumefantrine, as the drug did not replace efficacious high dose chloroquine until 2008. Contrary to the situation in The Gambia, the number of children with malaria has increased ~9 fold since 2007 (40 to 362 cases). The increase consisted of a doubling (20 to 40) of cases amongst children under 5 years of age and a 15 fold (20 to 307) increase in children aged 5-15 years.

## 1339

**MALARIA IN PREGNANCY IN SOUTHERN PROVINCE, ZAMBIA**

Kojo Yeboah-Antwi<sup>1</sup>, Katherine Semrau<sup>1</sup>, Julie Herlihy<sup>1</sup>, Arthur Mazimba<sup>1</sup>, Caroline Grogan<sup>1</sup>, Manka Nkimberg<sup>2</sup>, Lauren Owens<sup>1</sup>, Davidson H. Hamer<sup>3</sup>

<sup>1</sup>Center for Global Health and Development, Boston University, Boston, MA, United States, <sup>2</sup>Department of International Health, Boston University School of Public Health, Boston, MA, United States, <sup>3</sup>Zambia Centre for Applied Health Research and Development (ZCAHRD), Lusaka, Zambia

Malaria in pregnancy (MIP) in areas of stable malaria transmission is responsible for maternal anemia and adverse pregnancy outcomes such as low birth weight and preterm birth. In recent years, Zambia has received substantial funding for malaria and has scaled up activities to control MIP. This study assessed institutional capacity to prevent MIP and the utilization of MIP services in Southern Province of Zambia. We conducted comprehensive health center (HC) surveys in Southern Province, Zambia. Pregnant women recruited at the same HCs during routine antenatal care to participate in a neonatal study (ZamCAT) were interviewed at the time of recruitment and 4 days post-delivery about their use of MIP services. Of the 90 primary HCs surveyed, only 25.6% had a functional microscope, 16.7% had supplies to prepare blood smear and 94.4% had rapid diagnostic tests (RDTs). In terms of antimalarials, 96.6% had oral quinine, 96.6% had artemether-lumefantrine and 87.8% had sulfadoxine-pyrimethamine (SP) for intermittent preventive treatment (IPTp) in stock on the day of the survey. Among 9,816 women interviewed, 55.3% reported sleeping under an insecticide-treated net

(ITN) on the night before recruitment and 62.7% reported sleeping under ITN with the baby the night before the post-delivery interview. The average number of antenatal visits made by the women was 3.3; however only 52% received the Zambia Ministry of Health -recommended 3 doses of SP during pregnancy. Women who attended facilities that had SP available were 1.2 times more likely to have completed 3 doses of SP during pregnancy compared to women who attended facilities without stock (95% CI: 1.03, 1.40). Despite appropriate stocking of SP and an adequate number of antenatal visits by pregnant women, many women did not receive the recommended number of doses of IPTp, a situation of missed opportunities. An evaluation of factors responsible for the missed opportunities is needed to improve IPTp coverage.

## 1340

**USING HEALTH MANAGEMENT INFORMATION SYSTEM DATA ON PARASITOLOGICALLY-CONFIRMED MALARIA CASES TO EVALUATE THE EFFECT OF VECTOR CONTROL COVERAGE**

Adam Bennett<sup>1</sup>, John Miller<sup>2</sup>, Mercy Mwanza Ingwe<sup>3</sup>, Hawela B. Moonga<sup>3</sup>, Busiku Hamainza<sup>3</sup>, Mulakwa Kamuliwo<sup>3</sup>, Joshua Yukich<sup>1</sup>, Thomas A. Smith<sup>4</sup>, Richard W. Steketee<sup>5</sup>, Thomas P. Eisele<sup>1</sup>

<sup>1</sup>Tulane University School of Public Health, New Orleans, LA, United States, <sup>2</sup>PATH-MACEPA, Lusaka, Zambia, <sup>3</sup>National Malaria Control Centre, Lusaka, Zambia, <sup>4</sup>Swiss Tropical and Public Health Institute, Basel, Switzerland, <sup>5</sup>PATH-MACEPA, Seattle, WA, United States

Routine health management information system (HMIS) data are an under-utilized source for evaluating the effect of malaria control program intensity on the malaria morbidity burden. Since 2009, facilities in Zambia have reported both clinical and parasitologically confirmed (by RDT or microscopy) malaria through the HMIS on a monthly basis. We sought to evaluate the association between vector control coverage and monthly confirmed malaria cases at the district level in Zambia for the period 2009-2011. We first used Bayesian geo-statistical models to create smoothed estimates of insecticide-treated net (ITN) ownership from MIS data and to estimate differences in fever treatment-seeking behavior by district from 2009-2011. We incorporated programmatic data on the distribution of ITNs and indoor residual spraying (IRS) to improve district-level coverage estimates. We included mean monthly rainfall and temperature from remote sensing data to control for climate variability, and additionally controlled for differences in reporting and testing by district and month. We then modeled the association between confirmed cases and vector control coverage with conditional autoregressive models in a Bayesian framework to account for spatial and temporal correlation. After adjusting for reporting, total malaria outpatient cases increased from 3.3 million in 2009 to 4.3 million in 2010, and decreased to 3.8 million in 2011. Confirmed cases represented 29% of total cases in 2009, the first year parasitological confirmations were recorded in the HMIS, 30% in 2010, and 48% in 2011. After controlling for reporting, testing, climate, and district level factors influencing treatment seeking, we estimate that an increase in district level ITN coverage of 1 ITN per household is associated on average with a 19% reduction in population-standardized confirmed case incidence. We did not find an association with IRS. HMIS data, if improved through comprehensive parasitologically confirmed-case reporting, can become an important data source for evaluating associations between malaria program scale-up and spatial and temporal trends in disease burden.

## 1341

**CLINICAL AND LABORATORY FEATURES OF SEVERE MALARIA IN PERU**

**Dalila Y. Martínez**, Fiorella Llanos, Frine Samalvides, Alejandro Llanos-Cuentas

*Universidad Peruana Cayetano Heredia, Lima, Peru*

Malaria is a vector-borne disease considered as one of the main public health concerns by the World Health Organization (WHO). It causes close to 1 million deaths annually. For this reason, WHO established criteria to define severe malaria (SM), in order to reduce the morbidity and mortality. These criteria were based on features of severe malaria cases due to *Plasmodium falciparum*, however reports of SM due to *P. vivax* have been rising during the last years. *Vivax* and *falciparum* malaria are endemic in Latin America, but the features and prognosis of SM caused by them are poorly characterized. We describe the epidemiological, clinical and laboratory features of patients with SM, in a national reference center of an endemic area of malaria in Peru. Case reports. Patients admitted at Hospital Nacional Cayetano Heredia (HNCH), from 2005 to 2011, with diagnosis of SM according to the 2000 WHO guidelines. The inclusion criteria was to have a full medical record. We identified 40 cases of SM, from which 34 full medical records were available. The mean age for these patients was 39 years (range from 14-64 years) and the male/female ratio was 2.8. Most of the cases came from the Amazon region (47.1%), and few imported cases from Africa (14.7%). *P. vivax* was the most common agent identified in 70.6% of our patients, followed by *P. falciparum* (17.6%) and mixed infection (11.8%). Among the criteria of severity showed by this group of patients, 54.2% (13/34) presented with jaundice and hyperbilirubinemia, followed by 47.1% (16/34) with severe thrombocytopenia, 32.4% (11/34) with hyperpyrexia and 14.7% (5/34) with shock. Only one patient, with renal failure, respiratory insufficiency and multifactorial refractory shock, died of SM caused by *P. falciparum*. No fatal case of *P. vivax* was reported. *P. vivax* is a frequent cause of severe malaria in countries of the Latin America region such as Peru, even if it is not the most common agent reported in the worldwide. The most common complications were liver injury, severe thrombocytopenia, hyperpyrexia and shock.

## 1342

**COSTING A LARGE-SCALE IMPLEMENTATION OF SEASONAL MALARIA CHEMOPREVENTION IN CHILDREN DELIVERED THROUGH COMMUNITY HEALTH WORKERS IN SENEGAL**

**Mouhamed Ndiaye**<sup>1</sup>, Catherine Pitt<sup>2</sup>, Lesong Conteh<sup>3</sup>, El Hadj Ba<sup>4</sup>, Ousmane Sy<sup>1</sup>, Papa Ibrahima Camara<sup>5</sup>, Cheikh Sokhna<sup>4</sup>, Jean Louis Ndiaye<sup>1</sup>, Jules-Francois Gomis<sup>4</sup>, Badara Cisse<sup>1</sup>, Oumar Gaye<sup>1</sup>, Paul Milligan<sup>2</sup>

<sup>1</sup>Faculty of Medicine UCAD, Dakar, Senegal, <sup>2</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>3</sup>Imperial College London, London, United Kingdom, <sup>4</sup>Institute of Research for Development, Dakar, Senegal, <sup>5</sup>Ministry of Health, Dakar, Senegal

Seasonal Malaria Chemoprevention in children (SMC) is a new strategy for malaria control in areas where transmission is strongly seasonal. In Senegal, a pilot implementation of SMC was conducted by four district health teams from 2008 to 2010 in order to evaluate the feasibility of delivering SMC, its safety and effectiveness, when administered on a large scale using community health workers (CHWs). In 2010, SMC was delivered by 46 health-posts to a rural population of 175,000 children under 10 years of age in 1097 villages, and costing data were collected from each health facility in order to estimate the financial and economic costs of delivery. Delivery was coordinated by the head nurse in each health-post who assigned CHWs to a circuit of villages to visit over a 5-day period in September, October and November, to deliver SMC house to house to all children 3-120 months of age. Tools were developed to collect data on costs and resource use at four levels: the project, the district, the health post, and the CHW. Data was collected from both

“top-down”, and “bottom-up” (using facility-based costs and extensive interviews on resource use). Data were collected from all 46 health-posts after each round of administration. The study takes a provider perspective with a focus on costs of SMC at the district level. Each health-post employed from 4-68 CHWs and delivery each month took from 2-5 days. High coverage was achieved with about 90% of eligible children treated each month. When the financial cost of delivery was estimated, it cost \$233,714 to administer SMC to a population of 175,000 children under 10 years of age at a cost of \$0.50 per course. The main cost driver was the incentives paid to CHWs (44%). High coverage of SMC can be achieved at moderate cost. As SMC is now a recommendation from the World Health Organization and each year CHWs may visit households a number of times for distribution of Vitamin A, bednets, mass vaccination and other programs, this will be an opportunity for economies of scope by combining SMC with delivery of other interventions.

## 1343

**OPERATIONAL METHODS TO OBTAIN GEOLOCATION INFORMATION TO TRACK COMMON DISEASES FOR PATIENTS PRESENTING AT HEALTH FACILITIES IN AREAS WHERE ADDRESSES ARE NOT AVAILABLE: A CROSS-SECTIONAL SURVEY IN FIVE HEALTH FACILITIES IN THE WESTERN KENYAN HIGHLANDS**

**Gillian H. Stresman**<sup>1</sup>, Teun Bousema<sup>2</sup>, Jennifer Stevenson<sup>1</sup>, Chrispin Owaga<sup>3</sup>, Elizabeth Marube<sup>3</sup>, Wycliffe Odongo<sup>3</sup>, Wendy P. O'Meara<sup>4</sup>, Chrispin Drakeley<sup>1</sup>, Jonathan Cox<sup>1</sup>

<sup>1</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>2</sup>Radboud University Nijmegen, Nijmegen, The Netherlands, <sup>3</sup>Center for Global Health Research, Kenya Medical Research Institute/Centers for Disease Control and Prevention, Kisumu, Kenya, <sup>4</sup>Duke Global Health Institute, Duke University, Durham, NC, United States

The spatial distribution of cases is an important component of understanding the epidemiology of diseases, including malaria, and is valuable in planning and evaluating disease control. Spatial surveillance of cases facilitates targeted control, monitoring for potential epidemics, and evaluation of spatially heterogeneous transmission levels. In countries where no organized network or geocoded database exists, locating where patients come from can be problematic. Obtaining individual coordinates for a health facility attendee is operationally unattractive and less labour intensive methods should be developed that can accurately locate individuals. Such a system would facilitate research and enable disease control interventions to be targeted. To do this, we explored operational approaches to geolocate health facility attendees and determined their relative accuracy. We conducted a cross-sectional survey for malaria in 5 health facilities in the Western Kenyan highlands in October 2011. Of the 1659 people sampled, approximately 30% were followed-up to their compound with coordinates recorded. Information on various geolocation strategies was collected: 1) nearest landmarks to the compound as indicated by the patient, 2) patients identifying the names of heads of compound and 3) of nearest neighbours as well as 4) asking patients to indicate their area of residence on a poster sized satellite image. The effectiveness of the methods was assessed using ArcGIS to create zones around the landmarks where people are more likely to come. A database from previous studies in the area was used as a baseline and the proportion of participants followed-up during the health facility survey that were correctly located was calculated. Preliminary results indicate that of the names of the head of compound and nearest neighbors that were matched, 60% of patients were geolocated to within less than 500 meters of their compound. The results on the optimum approach, or combination of approaches to achieve the most accurate method to the finest possible resolution as assessed by spatial area and population density will be discussed.

## 1344

**CHANGING OF MALARIA PREVALENCE AND AGE OF INFECTED CHILDREN IN DIFFERENT AREAS OF GABON FROM 2005 TO 2011**

**Denise Patricia Mawili Mboumba**, Marielle K. Bouyou Akotet, Eric Kendjo, Joseph Nzamba, Matthieu Medang Owono, Mrcru Team, Maryvonne Kombila

*Department of Parasitology, Faculty of Medicine, Libreville, Gabon*

In Libreville, the capital city of Gabon, a reduction of malaria prevalence and a trend towards a higher risk of *Plasmodium falciparum* infection in children aged more than five years have been reported after new malaria control strategies implementation. With the support of Global Fund allocations, Malaria national control program organized the deployment of bednets and Artemisinin based combination therapeutic within the country from 2005. The aim of the study was to estimate the disease burden among children and to characterise malaria transmission intensities based on *PfPR*<sub>2-10</sub> in various areas of Gabon. Prospective cross sectional surveys were conducted at the Malaria Clinical Research Unit in Libreville and in four public health facilities at Melen, Port\_Gentil, Oyem and Owendo. Febrile pediatric patients, aged less than 11 years old were screened for malaria using microscopic examination. A total of 14293 febrile children were enrolled; 78.5% were less than five years. Between 2005 and 2008, there was a significant drop of malaria prevalence from 35.1% to 16.8%; followed by a raise reaching 26.6% in 2011. Before 2011, *PfPR*<sub>2-10</sub> was low in urban areas: 20% at Libreville in 2005 and 2008 and under 5% in 2005 at Port-Gentil. In the rural and semi urban areas of Oyem and Melen, it was above 40.0%. The mean age of infected patients, increased from 37.0 to 48.0 months between 2005 and 2008. From 2008, children above 5 years old were the most infected in all sites. The risk of being infected in this group was 3.21 fold to 5.05 fold higher in urban areas. These data confirm a shift in the age of infected patients towards older children and a large heterogeneity of malaria epidemiology suggesting the need to maintain malaria control strategies in Gabon; and to redefine their implementation throughout the country.

## 1345

**THE IMPACT OF ACADEMIC DETAILING ON PRESCRIBING AND ACCESSIBILITY OF ACTS IN THE PRIVATE SECTOR IN MADAGASCAR**

**Abigail Ward**, Pierre-Loup Lesage, Alexandra Morris, Felix Lam, Justin Cohen

*Clinton Health Access Initiative, Boston, MA, United States*

Madagascar is participating in the first phase of the Affordable Medicines Facility for malaria, a multi-national subsidy for artemisinin-based combination therapies (ACTs). It is unclear, however, whether subsidized drugs will reach rural areas of the country without additional intervention. We piloted a supporting intervention to encourage prescribing, stocking and purchasing of subsidized ACTs in rural areas of Madagascar by employing "academic detailers" to share scientifically accurate knowledge about ACT effectiveness with doctors and shopkeepers. Baseline cross-sectional surveys on factors related to prescription practices and antimalarial stocking were conducted in five regions of Madagascar in July 2011, covering 160 medical providers and 234 outlets. Additionally, exit interviews were conducted with antimalarial drug shoppers at 128 outlets to identify drug choice. Doctors and outlets in intervention regions were visited by academic detailers with educational ACT materials from October 2011 to March 2012. At baseline, 80.9% of urban outlets were stocked with subsidized ACTs compared to 50.3% of rural outlets. About 80% of providers reported ever prescribing ACTs. Of 279 customers interviewed at outlets that stocked subsidized ACTs, only 27% purchased them. Logistic regression models suggested purchase decisions were predicted by ACT awareness, urban versus rural location, and whether or not the outlet was visited by a representative for subsidized ACTs in the six months

prior to the interview. These results suggest the potential for a low-cost intervention involving academic detailers to improve the proportion of treatment-seekers who receive effective antimalarial drugs.

## 1346

**MALARIA AND ANEMIA PREVALENCE AND INSECTICIDAL NET OWNERSHIP AND USE IN PLATEAU AND ABIA STATES, NIGERIA (2010): RESULTS FROM REPRESENTATIVE HOUSEHOLD SURVEYS**

**Amy E. Patterson**<sup>1</sup>, Patricia M. Graves<sup>2</sup>, Adamu Sallau<sup>3</sup>, Emmanuel Emukah<sup>4</sup>, Emmanuel Miri<sup>3</sup>, Abel Eigege<sup>3</sup>, Jeremiah Ngondi<sup>5</sup>, Gregory Noland<sup>1</sup>, Iheanyichi Okorofor<sup>6</sup>, Mary Umar<sup>7</sup>, Olusola Oresanya<sup>8</sup>, Masayo Ozaki<sup>9</sup>, Elizabeth Cromwell<sup>10</sup>, Frank O. Richards<sup>1</sup>

<sup>1</sup>The Carter Center, Atlanta, GA, United States, <sup>2</sup>James Cook University, Cairns, Australia, <sup>3</sup>The Carter Center, Jos, Nigeria, <sup>4</sup>The Carter Center, Owerri, Nigeria, <sup>5</sup>University of Cambridge, Cambridge, United Kingdom, <sup>6</sup>Abia State Ministry of Health, Umuahia, Nigeria, <sup>7</sup>Plateau State Ministry of Health, Jos, Nigeria, <sup>8</sup>Federal Ministry of Health, Abuja, Nigeria, <sup>9</sup>University of Alabama, Birmingham, AL, United States, <sup>10</sup>University of North Carolina, Chapel Hill, NC, United States

There have been few recent surveys of malaria prevalence and net coverage in Nigeria. In September 2010, The Carter Center worked with the ministries of health of Abia (Southeast Nigeria) and Plateau (North Central Nigeria) states to conduct a modified Malaria Indicator Survey prior to mass LLIN distribution. In 58 systematically selected clusters (census enumeration areas or segments thereof) of 25 households per state, the average household size was 4.4 persons in Abia (1305 households, 5754 persons) and 6.2 in Plateau (1337 households, 8312 persons). All children <10 years of age were tested for malaria and anemia, and persons of all ages in every third household were tested for malaria. The percentage of households owning  $\geq 1$  net was much lower in Abia (10.2%) than Plateau (34.8%). The majority of nets were LLIN: 68% (N=123) in Abia and 89.6% (N=489) in Plateau. The percentage of persons using nets the previous night were: Abia: 3.4% of all ages, 6.0% of children under 5 years and 3.6% of pregnant women; Plateau: 14.7% of all ages, 19.1% of children under 5 years, and 21.0% of pregnant women. Crude malaria prevalence by RDT was 36.2% in Abia (95% CI 30.5-41.8, N=2619) and 40.5% in Plateau (95% CI 33.7-47.7, N=4242). Age specific prevalence peaked in the 5-9 year age group at 47.5% in Abia and 58.9% in Plateau, with second highest prevalence among 10-14 year-olds (Abia 43.0%, Plateau 50.1%). The percentage of children <10 with moderate to severe anemia (hemoglobin < 8 g/dl) was higher in Abia (13.2%, 95% CI 10.3-16.8%, N=1556) than Plateau (5.1%, 95% CI 3.9-6.5%, N=2835). The results reveal high malaria prevalence in these states, and low baseline net ownership. Additional work is needed to explain the fact that anemia prevalence is higher in Abia, though malaria prevalence is comparable to Plateau. A possible contributing factor could be differences in treatment coverage for neglected tropical diseases. Nigeria's universal coverage distribution policy and on going national LLIN distribution campaigns should increase access to LLIN among children 5-14 years of age, but other determinants of use in this age group remain poorly understood.

## 1347

**LOOKING FOR GOLD, FINDING MALARIA: 2011 MALARIA SURVEILLANCE IN GOLD MINERS' COMMUNITIES IN SURINAME**

**Hedley Cairo**<sup>1</sup>, Deborah Stijnberg<sup>2</sup>

<sup>1</sup>Ministry of Health Malaria Program; "Looking for gold, finding malaria", Paramaribo, Suriname, <sup>2</sup>Ministry of Health, Paramaribo, Suriname

Despite the marked reduction of malaria incidence in Suriname, malaria continues to affect the migrants' population (n= 15,000) involved in gold mining. Miners have been trained in the use of RDTs and treatment of

uncomplicated malaria to provide services in their communities. Blood films are prepared for the quality control of all RDTs performed. They report to the Tourtonne laboratory (TL). The TL in the epicenter of the Brazilian gold miners' community in the city is the other component of malaria surveillance in gold miners' communities. The TL staff executes Active Case Detection Campaigns on a regular basis in gold mining areas. The surveillance data serves as the basis of this paper. In 2011, 646 cases were recorded, representing a decrease of 54% ( $p < 0.0002$ ) from the 1403 recorded in 2010. *Plasmodium falciparum*, *P. vivax* and *P. malariae* were identified in 42.7%, 49.8% and 2.5% of cases respectively. 5.0% had a mixed infection. 484 (75%) cases were imported; the 162 autochthonous cases signify a reduction of 66.3% compared to the 480 reported in 2010. Of the autochthonous cases, 83 (51.2%) were acquired in the Lawa region, 48 (29.7%) around the Lake, Tapanahoni had the lowest number of cases 1 (0.6%). The 162 cases were dispersed over 44 locations. Only 3 (6.8%) locations, all on the Lawa River had more than 10 cases; 47.7% of the locations had only 1 malaria case in 2011. The mean prevalence measured during ACDs was 1.9% (0% - 6.0%). The SPR was 15.1%, ABER 19.9% and API 10.8 per 1000. 97.4% of the infections occurred in Brazilians. 22 cases were reported in pregnant women of which 6 were *P. vivax* relapse. One possible explanation for the tremendous reduction in malaria cases from 2010 to 2011 could be the fact that LLINs have been distributed in 2010 among the populations at risk in the gold mining areas. We have to find innovative ways including cross-border cooperation to deal with the high incidence of imported cases in Suriname.

### 1348

#### THE ESSENCE OF ACCURATE SURVEILLANCE IN A LOW INCIDENCE ERA: REASSESSING AUTOCHTHONOUS CASES THROUGH MALARIA CASE INVESTIGATION IN SURINAME

Hedley Cairo<sup>1</sup>, Deborah Stijnberg<sup>2</sup>

<sup>1</sup>Ministry of Health Malaria Program; "Looking for gold, finding malaria", Paramaribo, Suriname, <sup>2</sup>Ministry of Health, Paramaribo, Suriname

The persistent low prevalence measured at any time during 2010 and the low incidence through 2010 of autochthonous cases recorded by the malaria notification points in mining areas brought the authors to the hypothesis that malaria transmission in Suriname is lower than is being captured by the regular surveillance system at the Tourtonne laboratory (TL) in the city. The Malaria Case Investigation form (CI) used by the Bureau of Public Health extended with questions relevant to gold miners was introduced at the TL in February 2011. The CI form captures amongst others, a detailed travel history. The travel history, malaria endemicity and the incubation period for the different species were taken into account to classify the cases either as imported or autochthonous. To test the hypothesis the classification by CI was compared to the classification by general surveillance. 415 malaria cases were diagnosed at TL from February through December 2011. According to the regular surveillance 94 cases were classified as autochthonous. 376 forms were completed, representing 47.2% of all cases ( $n=797$ ) diagnosed in Suriname. 53 ( $n=376$ ) cases were classified as autochthonous based on the CI forms. The proportion of autochthonous cases 14.1% based on the CI form was lower ( $p < 0.003$ ) than the proportion (22.7%) calculated from the general surveillance data. Several possible explanations might account for this difference, including the fact that *Plasmodium vivax* with the ability to relapse if not treated radically, is the predominant infection in Suriname. Self-medication could suppress clinical symptoms and favors the relapse of *P. vivax* and recrudescence of *P. falciparum*. If the patient acquiring an infection abroad stays long enough in Suriname and develops symptoms, the infection might erroneously be recorded as an autochthonous case. Since information on the possible location of transmission is identically captured by all the malaria surveillance systems in Suriname, the authors assume that the over estimation of autochthonous cases is country wide.

### 1349

#### MALARIA CASE INVESTIGATION AT THE TOURTONNE LABORATORY

Hedley Cairo<sup>1</sup>, Deborah Stijnberg<sup>2</sup>

<sup>1</sup>Ministry of Health Malaria Program; "Looking for gold, finding malaria", Paramaribo, Suriname, <sup>2</sup>Ministry of Health, Paramaribo, Suriname

Malaria incidence in Suriname has decreased tremendously in the past decade. In order to get a better understanding of the malaria epidemiology and the habits of the persons at risk the need for detailed information on every case becomes more pressing. The Malaria Case Investigation form (CI) used by the Bureau of Public Health extended with questions relevant to gold miners was introduced at the Tourtonne Laboratory in February 2011. The CI form captures amongst others, detailed information on the travel history, symptoms and medical history. Also basic knowledge on malaria prevention is evaluated and the health seeking behavior is assessed. 415 malaria cases were diagnosed at TL from February through December 2011. 376 (90.6%) forms were completed, representing 47.2% of all cases diagnosed in Suriname. Vendors (35%) and gold miners (21.4%) were the groups most affected; CSW 3% were the group least affected. The mean interval between onset of symptoms (Sx) and testing was 5.9 days. The mean interval between onset of Sx and treatment was 6 days. 54.8% ( $n=312$ ) of the patients used self-treatment. 34.1% ( $n=314$ ) did not know that malaria is transmitted by a mosquito. 49.4% did not know how to protect oneself against malaria. 13.3% ( $n=369$ ) used a bed net. Conveying the importance of adhering to appropriate preventive measures for malaria and seeking early detection and effective treatment is a prerequisite to sustain the reduction of malaria. The use of ACT for self-treatment is a concern since it contributes to the emergence and spread of resistance.

### 1350

#### MALARIA IN PREGNANCY IN RWANDA AS THE COUNTRY TARGETS PRE-ELIMINATION

Corine Karema<sup>1</sup>, William R. Brieger<sup>2</sup>, Aline Uwimana<sup>1</sup>, Beata Mukarugwiro<sup>3</sup>, Irene Umulisa<sup>1</sup>

<sup>1</sup>Malaria and Other Parasitic Diseases Program, Rwanda Ministry of Health, Kigali, Rwanda, <sup>2</sup>The Johns Hopkins University, Baltimore, MD, United States, <sup>3</sup>Jhpiego/Maternal and Child Health Integrated Project, Kigali, Rwanda

Rwanda has made strides toward lowering malaria transmission with universal coverage of long-lasting insecticide treated nets and easy access to artemisinin based combination treatment. National prevalence is estimated at 1.4% among children 6-59 months and 0.7% among women aged 15-49 years according to the 2010 DHS. Slide positivity rates from the national health management information system continue to drop and yet malaria persists. Pregnant women thus remain vulnerable even as prevalence drops. While Rwanda no longer practices IPTp it is concerned it is interested in offering the best malaria protection to pregnant women. In order to plan appropriately, there is need for a malaria in pregnancy prevalence study. Pregnant women were studied at first antenatal care registration visit in low, moderate and relatively higher transmission areas using rapid diagnostic test and microscopy. Ethical clearance was provided by the ethical review board within the Ministry of Health. ANC staff were trained to obtain data during normal client visits. Among nearly 4000 women studied, prevalence with RDT was 2.4% ranging from 6.6% in the higher border districts in the east to 0% in the areas designated as low transmission based on the HMIS. For microscopy the overall prevalence was 1.6% and also varied from 4.5% to 0.1%. RDT positivity showed reducing trend with increasing parity and with LLIN use the night before the interview. Results show need to continue to protect pregnant women and their unborn children in Rwanda through increased use of LLINs and identification and tracking women of low parity.

## 1351

### PLASMODIUM FALCIPARUM PARASITE CLEARANCE IN PATIENTS TREATED WITH ARTESUNATE-AMODIAQUINE VS. COMPARATOR GROUPS, SUB-SAHARAN AFRICA

Julien Zwang<sup>1</sup>, Grant Dorsey<sup>2</sup>, Abdoulaye Djimdé<sup>3</sup>, Corine Karema<sup>4</sup>, Andreas Mårtensson<sup>5</sup>, Jean-Louis Ndiaye<sup>6</sup>, Jean-Paul Guthmann<sup>7</sup>, Sodiomon Sirima<sup>8</sup>, Philippe Brasseur<sup>9</sup>, **Piero L. Olliaro**<sup>10</sup>

<sup>1</sup>Drugs for Neglected Diseases Initiative, Geneva, Switzerland, <sup>2</sup>Department of Medicine, University of California, San Francisco, CA, United States, <sup>3</sup>Malaria Research and Training Center, Department of Epidemiology of Parasitic Diseases, Faculty of Medicine and Pharmacy, University of Science, Techniques and Technology of Bamako, Bamako, Mali, <sup>4</sup>Malaria and Other Parasitic Diseases Division-RBC, Ministry of Health, Kigali, Rwanda, <sup>5</sup>Infectious Diseases Unit, Department of Medicine, Karolinska University Hospital, Karolinska Institutet, Karolinska, Sweden, <sup>6</sup>Department of Parasitology, Faculty of Medicine, Cheikh Anta Diop University, Dakar, Senegal, <sup>7</sup>Epicentre, Paris, France, <sup>8</sup>Centre National de Recherche et de Formation sur le Paludisme, Ministère de la Santé, Ouagadougou, Burkina Faso, <sup>9</sup>Institut de Recherche pour le Développement (IRD), Dakar, Senegal, <sup>10</sup>World Health Organization, Geneva, Switzerland

Monitoring response to artemisinin combination therapy (ACT) worldwide is particularly important now that artemisinin resistance is reported in Southeast Asia. Delayed parasite clearance is considered the best practical surrogate for artemisinin resistance. Artesunate-amodiaquine (ASAQ) is the second most widely used ACT. We analysed 11,570 patients (81% children under 5 years of age) from 41 sites from 20 countries sub-Saharan. The median parasite clearance on ASAQ by site varied from one to two days; a third of the patients cleared their parasitaemia on Day 1; the decrease in mean log parasitaemia between Day 0 and Day 1 was -58% (range: -44% to -83%); between Day 0 and Day 2 it was -96% (-77% to -100%). Using multivariate logistic regression with random effects and controlling for treatment, the risk for a delayed parasite clearance (still parasitaemic on Day 2) was higher in children under five (AOR 1.34, 95%CI 1.10-1.63,  $p=0.004$ ) as well as in patients with higher parasitaemia at enrolment (AOR 2.56, 95%CI 2.26-2.90,  $p=0.001$ ). No difference was detected between ASAQ and other ACT (artemether-lumefantrine, dihydroartemisin-piperazine, AS+SP), but non-ACT (AQ, AQ+SP, chloroquine+SP) carried a higher risk of delayed parasite clearance ( $p<0.005$  for all comparisons vs. ASAQ). The analysis provides a platform for future comparisons of antimalarial performance across sub-Saharan Africa.

## 1352

### THE DEMOGRAPHICS OF WITHIN-COUNTRY POPULATION MOVEMENT NETWORKS IN EAST AFRICA: IMPLICATIONS ON MALARIA TRANSMISSION AND CONTROL

Deepa K. Pindolia<sup>1</sup>, Andres J. Garcia<sup>1</sup>, Roshni R. Vaghjiani<sup>2</sup>, Andrew J. Tatem<sup>1</sup>

<sup>1</sup>University of Florida, Gainesville, FL, United States, <sup>2</sup>University of Southampton, Southampton, United Kingdom

Human population movement plays an important role in the transmission and importation of malaria. Movement between areas of differing transmission may risk importation of infection from high to low transmission zones. Different demographic and socioeconomic groups are likely to have different movement patterns and infection rates and therefore different risks of importing infections upon travel. It is therefore relevant to quantify and compare movement patterns between varying transmission areas, for different sub-populations. At a national level, household surveys and population census data provide records for individual-level migration. Together with malaria endemicity maps, population distribution maps, mathematical models and network analysis tools, Kenyan, Ugandan and Tanzanian migration data was analysed to construct within country population movement networks, useful for

malaria importation assessment. The models were further stratified for different demographic and socioeconomic groups to identify and compare movement patterns relevant for malaria importation. Network characteristics, such as cumulative degree distributions and network diameter, were calculated to quantify and compare network structure. Movement networks were different between countries and between demographic and socioeconomic groups. Some demographic groups however, were had similar network characteristics. For example, children under 10 years and adults between 15-24 years had overlapping cumulative degree distributions, illustrating that children were likely to move with their parents. After including malaria in the movement analysis, certain population groups were more likely to contribute to imported infections in certain geographical locations. Census and survey data include migration and demographic data useful for nationwide population movement assessments. Together with national malaria maps and quantitative techniques, malaria importation estimates provide a unique evidence base to inform control policy.

## 1353

### COMMUNITY ACCEPTANCE OF LARVICIDING FOR MALARIA CONTROL IN RURAL TANZANIA

Leonard Mboera<sup>1</sup>, Randall Kramer<sup>2</sup>, Elizabeth Shayo<sup>1</sup>, Keshini Senkoro<sup>1</sup>, Adriane Lesser<sup>2</sup>, Stella Kilima<sup>1</sup>, MarieLynn Miranda<sup>3</sup>

<sup>1</sup>National Institute for Medical Research, Dar es Salaam, United Republic of Tanzania, <sup>2</sup>Duke University, Durham, NC, United States, <sup>3</sup>University of Michigan, Ann Arbor, MI, United States

Larval source management, including the application of larvicides, is a lesser-used intervention for malaria control yet holds promise as a safe, effective, and environmentally sustainable component of a successful integrated vector management strategy. Recent research has supported the feasibility and effectiveness of larviciding in the urban setting of Dar es Salaam, but its application in rural areas remains understudied. One key element of determining feasibility of larviciding in a rural setting is community acceptance of the method. Community acceptance of larviciding in rural east-central Tanzania was assessed through a range of methods in April-May 2011, including surveys of 962 randomly-selected households from 24 villages, 12 focus group discussions, and in-depth interviews with local leaders and community health workers in each village. The household survey found that the majority of household heads surveyed (82.3%) were not familiar with larviciding as a way to control mosquito larvae in water bodies. Most households (93.8%) indicated that they would grant permission for larvicide to be applied in water bodies where mosquitoes breed near their homes based on a brief standardized description of the process. There was a high level of trust in the safety (74.6%) and efficacy of larviciding, both to control mosquitoes around the home (92.6%) and to reduce the risk of malaria infection (92.9%). Survey questions following up on these attitudes using a Likert scale allow for a more nuanced interpretation of villagers' perceptions. Also, in structured key informant interviews, respondents indicated that community members would be receptive to larviciding in the area, but that community sensitization efforts should be a key component of such an intervention. Household surveys indicated a willingness among community members to make a nominal household contribution (1800 TZS on average, or \$1.20 USD) every 3 months. Overall the results of the assessments indicate a receptive environment for future efforts directed at larviciding for malaria control in a rural setting in Tanzania.



## 1354

### EFFECTIVE PARTNERSHIP DURING HOUSEHOLD CAMPAIGN WITH HANG UP OF INSECTICIDE TREATED NETS MAKE NETS AVAILABLE TO PEOPLE IN GHANA

**Keziah L. Malm**<sup>1</sup>, Kwame Gakpey<sup>2</sup>, Ivy Forson<sup>2</sup>, Aba Baffoe-Wilmot<sup>2</sup>, Constance Bart-Plange<sup>2</sup>

<sup>1</sup>University of Ghana, Accra, Ghana, <sup>2</sup>National Malaria Control Program/Ghana Health Service, Accra, Ghana

Malaria continues to be the cause of significant morbidity and mortality in the country. In 2011, there were Cases and attributed to malaria in Ghana. Insecticide treated nets (ITNS) have been shown avert about 50% of malaria cases. In order to increase ownership and use of ITNs, a household door-to-door campaign to distribute ITNS and hang them in households was instituted. A partnership made up the government, multilateral, bilateral, non-governmental agencies, private sector, political heads, chiefs and elders and the community was formed to ensure the implementation of this campaign. To paper is to describe the partnership at play during the hang up campaign. Partnership started right from the planning stage through the implementation to the post implementation evaluation stages. Looking at the financial and technical capabilities of partners, roles were agreed on and assigned to ensure a coordinated activity. Some partners procured specific quantities of ITNS to cover particular sections the country; others provided funds for procuring other logistics, whilst others provided technical support for quantification, registration, supervision and evaluation. The Chiefs and political leaders contributed through advocacy, conflict resolution and transporting the logistics to the needed sites for distribution. The household campaign, which involved community sensitization, training, registration of households, actual hanging, supervision and monitoring has been undertaken in nine out of ten regions in the country. By end of April 2011, 9,683,160 ITNs had been handed in the homes of 19,366,320 in the country. Through the effective partnership at play, Ghana is likely to achieve universal coverage of ITNS by July 2012. Resources can be mobilized with the appropriate partnership to achieve health targets and objectives.

## 1355

### INVESTIGATING MALARIA VECTOR-PARASITE GENOTYPE-GENOTYPE INTERACTIONS AND HOW THEY MIGHT INFLUENCE THE USE OF GENETICALLY-MODIFIED MOSQUITOES IN MALARIA CONTROL

**Hannah C. Slater**, Thomas S. Churcher, Jacob C. Koella, María-Gloria Basáñez

Imperial College, London, United Kingdom

Typically, malaria transmission models do not consider genotypic structure in the mosquito or the *Plasmodium* population. However, there is evidence that the interaction between malaria parasites and their *Anopheles* vectors is dependent on the specific genotype-genotype (g2g) combination. Here, we initially develop a simple 2 vector - 2 parasite malaria model to explore the impact of g2g interactions on transmission dynamics. This model is then extended to include a greater number of vector and parasite types. In particular, we assume that transmission (from human to vectors) and vector mortality rates are specific for each vector-parasite g2g combination. Motivated by results from experimental infections, we consider whether there is an evolutionary trade-off between transmission and virulence (to the vector) for each vector-parasite combination, and the conditions under which both parasite and vector types can co-exist. The more complex model is used to investigate how introducing a genetically-modified (GM) *Anopheles* population into the system affects the abundance of the other mosquitoes and parasites. Specifically, we consider the case where the GM mosquito is refractory to most, but not all, of the parasite strains. We investigate under which conditions it would be possible for the GM mosquito to replace all other *Anopheles* of the same species, or the conditions under which all malaria parasites could be

eliminated. Applications of this work will be helpful to assess the feasibility of using GM mosquitoes to reduce or eliminate malaria in the presence of genotype interactions.

## 1356

### HOW MANY BEDNETS PER HOUSEHOLD NEED TO BE DISTRIBUTED? EVALUATION OF A UNIVERSAL COVERAGE BED NET DISTRIBUTION CAMPAIGN IN FOUR DISTRICTS IN SOFALA PROVINCE, MOZAMBIQUE

**Silvia Chicuecue**<sup>1</sup>, Juliette Morgan<sup>2</sup>, Abdul Mussa<sup>3</sup>, Samuel Mabunda<sup>3</sup>, Patrick Kachur<sup>4</sup>, Eusébio Macete<sup>1</sup>, Caterina Guinovart<sup>5</sup>

<sup>1</sup>Manhiça Health Research Centre, Manhiça, Mozambique, <sup>2</sup>Centers for Disease Control and Prevention, Maputo, Mozambique, <sup>3</sup>National Malaria Control Program, Ministry of Health, Maputo, Mozambique, <sup>4</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>5</sup>Barcelona Center for International Health Research (CRESIB), Hospital Clinic/IDIBAPS, Barcelona, Spain

Malaria remains a priority public health problem in Mozambique. The National Malaria Control Program (NMCP) is conducting universal coverage (UC) distribution campaigns for long lasting insecticide-treated nets (LLINs), among other control measures. However, given the lack of a standard UC distribution model, countries embarking on UC distribute different number of LLINs per household. Setting a fixed number of LLINs per household (HH) is a common strategy, with the risk of these being insufficient or excessive to cover all family members or sleeping spaces. The NMCP piloted a new UC distribution model in 4 districts in Sofala Province (Central Mozambique), using information gathered from the community on the HHs composition (sex, age and relation among each HH member) to determine the number of LLINs to be allocated to each HH based on assumed sleeping patterns. The objective of this model was to maximize the efficiency of the LLIN campaign and cover all sleeping spaces. We conducted an evaluation of these sleeping patterns assumptions, the coverage of sleeping spaces with LLINs (ownership coverage) and the individual use of LLINs by household members (usage coverage). A community-based two-stage cluster random cross sectional survey, including 35 clusters and 32 households per cluster, was performed in May 2010, shortly after the LLIN distribution, and one year later, in June 2011, in the area where the UC campaign had been conducted. Informed consent was obtained from the head of each selected HH and a standardized questionnaire was filled out with information on the LLIN ownership and frequency of use as well as the number of HH members and their sleeping patterns. Analysis of data is ongoing and results will be available in October. This information will be used to validate the assumptions of the distribution model (assumed sleeping patterns within a HH) and to evaluate the effectiveness of the model in covering all sleeping spaces with an LLIN right after the distribution campaign and one year later, as well as to assess other uses of the nets.

## 1357

### INCREASING ACCESS TO MALARIA PREVENTION IN SOUTH SUDAN BY INTEGRATING NET DISTRIBUTION AND INTERMITTENT PREVENTIVE TREATMENT WITH ANTENATAL CARE AND IMMUNIZATIONS

**Fredrick Hartman**<sup>1</sup>, John Rumunu<sup>2</sup>, Victor Guma<sup>2</sup>, Erin Polich<sup>2</sup>, Angela Lee<sup>1</sup>

<sup>1</sup>Management Sciences for Health, Cambridge, MA, United States, <sup>2</sup>Management Sciences for Health, Juba, South Sudan

Increasing access to malaria prevention by integrating malaria control and prevention services with existing services like antenatal care and routine childhood immunizations is feasible in a post-conflict country like South Sudan where malaria is the leading cause of morbidity and mortality. Pregnant women and children under five are especially at risk. Sleeping under a long-lasting insecticide-treated net (LLIN) may reduce child mortality by as much as 20%. Intermittent preventive treatment

(IPT) reduces the risk of malaria during pregnancy, which may cause complications such as anemia or illness for the mother, and low birth weight or spontaneous abortion for the fetus. In 2010, a household survey reported only 51.6% of pregnant women received one dose of IPT, and only 22.7% received the two doses (IPT2) recommended by the World Health Organization. The second phase of the USAID-funded Sudan Health Transformation Project (SHTP II) targets children and pregnant women by distributing LLINs during antenatal care (ANC) visits as well as during routine immunization for children under five. Between April 2010 to December 2011, SHTP II-supported facilities distributed 79,885 LLINs during routine immunization and ANC visits. There were corresponding increases in ANC1, DPT3 (immunization indicator), and LLIN distribution, culminating in a 97% increase in net distribution. Although an influx of refugees during the 2011 referendum resulted in intermittent stock outs of LLINs, numbers of ANC and DPT3 immunizations continued to rise, demonstrating a consistent increase in access to services and awareness. To prevent malaria during pregnancy, IPT2 services were integrated into ANC visits. IPT2 services increased by 38%, from 4,815 to 6,636 after the first two years of the project. A corresponding increase during this time period was noted in both ANC1 and ANC4 visits (7,638 to 10,301, a 35% increase, and 3,284 to 5,743, a 75% increase, respectively), showing a greater access to primary care as well as an increase in the perceived importance of ANC as well as malaria prevention. The conclusion is that it is possible to make significant progress on malaria prevention in a challenging post-conflict, fragile state like South Sudan, by focusing on key interventions that can be integrated with existing services like antenatal care and immunization programming.

### 1358

#### BIOINFORMATICS SYSTEMS FOR UNDERSTANDING MALARIA TRANSMISSION AND CONTROL

**Samson S. Kiware**<sup>1</sup>, Alpha Malishee<sup>1</sup>, George Corliss<sup>2</sup>, Tanya Russell<sup>3</sup>

<sup>1</sup>Ifakara Health Institute, Dar es salaam, United Republic of Tanzania, <sup>2</sup>Marquette University, Milwaukee, WI, United States, <sup>3</sup>James Cook University, Maroochydore, Australia

Innovative control strategies that target the entire mosquito life cycle may be required to achieve malaria elimination. Researchers need to analyze huge quantities of ecological data collected from multiple experiments to understand malaria transmission for the development of control strategies. The data preparation process for analysis is very time consuming. We present a bioinformatics system for understanding malaria transmission and control that integrates mosquito densities, infectious status, phenotypic observations, and sample archiving with capabilities to securely store and share data. A relational database schema is designed based on commonly used procedures by mosquito entomologists, which are experiment design followed by sample sorting, observation, constitution, and archiving. Our system handles the data preparation process by providing users with the ability (1) To upload raw data using standardized customizable templates, (2) To download cleaned data for analysis, (3) To generate summarized scientific reports, and (4) To archive and share data locally and globally. Our secure bioinformatics system reduces data preparation time, thus increasing research output. The system provides researchers with field and lab mosquito data rich in information such as densities, species type, and infectious status to address different scientific questions. Researchers upload data using customizable templates that handle data collected using different portable or paper based field collection forms but adhering to standardized terminologies. Users can download cleaned data linking a sample from the field, to the lab, and to a storage location with a data dictionary for analysis. Also, researchers are able to share data and/or to generate quick summaries such as mean catches per mosquito species per infectious status. The system is securely accessible online, but users may opt to run the system locally for data uploading, cleaning, and linking. Our relational schema is extensible to store and link other data such as environmental data and easily can be linked to other databases e.g., demographic

surveillance systems (DSS). An extensible bioinformatics system for understanding malaria transmission and control is developed to increase research output. Our system allows users to store field- and lab-based mosquito data, download them for analysis, and share them, with an ability to generate quick reports.

### 1359

#### EVIDENCE-BASED BEHAVIOR CHANGE COMMUNICATIONS (BCC) ENHANCE LONG-LASTING INSECTICIDAL NET (LLIN) UPTAKE AND UTILIZATION IN SOUTHEAST NIGERIA

**Amy E. Patterson**<sup>1</sup>, Adamu Sallau<sup>2</sup>, Emmanuel Emukah<sup>3</sup>, Omeni Nkwocha<sup>4</sup>, Lawrence Nwankwo<sup>5</sup>, Gift Opara<sup>4</sup>, Adaku Echebima<sup>4</sup>, Rita Otozi<sup>3</sup>, Mgbodochi Onyia<sup>4</sup>, Masayo Ozaki<sup>6</sup>, Paul M. Emerson<sup>1</sup>, Patricia M. Graves<sup>7</sup>, Frank O. Richards<sup>1</sup>

<sup>1</sup>The Carter Center, Atlanta, GA, United States, <sup>2</sup>The Carter Center, Jos, Nigeria, <sup>3</sup>The Carter Center, Owerri, Nigeria, <sup>4</sup>Imo State Ministry of Health, Owerri, Nigeria, <sup>5</sup>Ebonyi State Ministry of Health, Abakaliki, Nigeria, <sup>6</sup>University of Alabama, Birmingham, AL, United States, <sup>7</sup>James Cook University, Cairns, Australia

Long-lasting insecticidal net (LLIN) ownership is often the strongest determinant of net use, but having a net does not guarantee use. Net distribution should be accompanied by evidence-based interventions to address other key determinants. To inform the development of BCC strategies, we asked about social and behavioral determinants of net use during a 2010 survey of 1290 adults in 1192 households located within randomly selected clusters in Imo and Ebonyi States (Southeast Nigeria). Knowledge that mosquitoes transmit malaria was widespread (83%), but 66% reported that malaria was only a risk during the rainy season, and 65% that malaria is caused by eating certain foods. Though 72% reported that LLINs protect against mosquito bites, only 15% mentioned malaria prevention as a benefit. When asked about disadvantages of LLINs, 42% said there are none, but 15% said they were hot and 5% that they cause allergies. More people agreed with the statement that LLINs are safe to sleep under (90%), than that it is safe to hang them where you store food (54%). Only 2.4% knew that LLINs do not need re-treatment. Nets have some negative connotations: 39% agreed that they are "old fashioned;" 33% that they are for poor farmers; and 27% that they are a Western plot to reduce African populations. Low literacy (46%), limited comprehension of languages used for malaria communications, and widespread distrust of many sources of information suggested that home visits by trusted community members would be the most appropriate channel for BCC. The data informed the development of a community-based net monitoring and BCC intervention piloted in six sentinel villages in Ebonyi State in 2011 to improve LLIN ownership, use and care. We stressed the safety and effectiveness of LLINs for both malaria and lymphatic filariasis prevention, and taught skills to make it easier to hang nets at the appropriate height, over any sleeping space. Messages were tailored to fit household behaviors and barriers to use. After six months, 100% of households owned  $\geq 1$  net (N=1240); 95% of nets were hanging and 94% had been used the previous night (N=2982). 97% of people reported net use (N=5912). All were statistically significant improvements from baseline. Household net data collected by community volunteers provided motivation and direction for an LLIN "mop-up" campaign. This strategy can be modified for implementation by community directed distributors of treatments for neglected tropical diseases.

## 1360

**THE AFFORDABLE MEDICINES FACILITY-MALARIA (AMFM): ARE REMOTE AREAS BENEFITING FROM THE INTERVENTION?**

**Yazoume Ye**<sup>1</sup>, Fred Arnold<sup>1</sup>, Abdisalan Noor<sup>2</sup>, Ruilen Ren<sup>1</sup>, Catherine Kyobutungi<sup>3</sup>, Blessing Mberu<sup>3</sup>, Marilyn Wamukoya<sup>3</sup>, Frederick Wekesah<sup>3</sup>, Yohannes Kinfu<sup>3</sup>, John Amuasi<sup>4</sup>, Samuel Blay<sup>4</sup>, Hellen Gatakaa<sup>5</sup>, Mitsuru Toda<sup>5</sup>, Illah Evance<sup>5</sup>, Julius Njogu<sup>5</sup>, Kate O'Connell<sup>5</sup>, Tanya Shewchuk<sup>5</sup>, Sarah Tougher<sup>6</sup>, Andrea Mann<sup>6</sup>, Barbara Willey<sup>6</sup>, Catherine Goodman<sup>6</sup>, Kara Hanson<sup>6</sup>

<sup>1</sup>ICF International, Calverton, MD, United States, <sup>2</sup>KEMRI/Wellcome Trust, Nairobi, Kenya, <sup>3</sup>APHRC, Nairobi, Kenya, <sup>4</sup>Komfo Anokye Teaching Hospital, Kumasi, Ghana, <sup>5</sup>The ACTwatch project (Population Service International), Nairobi, Kenya, <sup>6</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom

In most cases, remote areas are less likely to be covered by health interventions despite often exhibiting the worst health indicators. One aim of the Affordable Medicines Facility - malaria (AMFm) is to ensure that people in remote areas have access to effective and affordable malaria treatment by making subsidized quality - assured artemisinin-based combination therapies (ACTs) available in these areas. AMFm, hosted by the Global Fund to Fight AIDS, Tuberculosis and Malaria, is a financing mechanism which subsidizes quality-assured ACTs for distribution to the public and private sectors, complemented by supporting interventions to promote rational drug use. AMFm has been in operation since mid-2010 in eight national-scale operational pilots in Ghana, Kenya, Madagascar, Niger, Nigeria, Tanzania mainland, Uganda and Zanzibar. By March 2012, over 220 million co-paid ACT treatment doses had been ordered. The Independent Evaluation of AMFm Phase 1 was commissioned by the Global Fund to assess the impact of AMFm on availability, price, market share and use of quality-assured ACTs in all the operational pilots. The assessment is based on a pre- and post-test design with detailed documentation of the implementation process and context, treating each pilot independently. In each pilot, a nationally representative survey of outlets stocking antimalarial medicines was conducted at the baseline (2009/10) and the endline (2011). At the endline, an additional sample of outlets was selected in remote areas in Kenya and Ghana, where availability, price and market share of quality-assured ACTs were measured. Areas were classified by remoteness based on an index computed from estimated travel times to three levels of service centers. The composite index was computed from the sum of the standardized travel times which was used to generate remoteness quintiles with areas in 4<sup>th</sup> and 5<sup>th</sup> quintiles considered remote. The number of outlets screened in non-remote and remote areas, respectively, was 501 and 194 in Ghana and 9,980 and 2,353 in Kenya. We compare remote and non-remote areas in each country with respect to availability, price and market share of quality-assured ACTs. The significance of the differences is assessed using Chi-squared tests for proportions and Wilcoxon rank tests for price indicators, expressed as medians.

## 1361

**INSULIN SIGNALING IN THE MOSQUITO: UNDERSTANDING AKT PHYSIOLOGY IN THE FAT BODY REGULATION AT THE MOLECULAR LEVEL**

**Lewis Hun**

*University of Arizona, Tucson, AZ, United States*

Lifespan is a key factor in determining the transmission efficiency of mosquito borne diseases. Finding a novel mechanism affecting mosquito lifespan could be a valuable tool to control mosquito-borne disease transmission. In mosquitoes, the insulin/insulin growth factor 1 signaling (IIS) cascade regulates lifespan, reproduction, and innate immunity. To better understand the impact of IIS in mosquitoes we induced IIS in the fat body of transgenic *Anopheles stephensi* mosquitoes. To accomplish this we used the vitellogenin promoter to express a myristoylated form of An. stephensi Akt (AsteAkt), a key component of the IIS cascade. Myr-AsteAkt

transcript and protein expression occurred as expected with expression only in the fat body, following a bloodmeal. We characterized how changes to IIS specifically in the fat body effects egg production during multiple reproductive cycles and the impact is has on mosquito lifespan. Although myr-AsteAkt expression had little effect on total egg production, lifespan was significantly extended in the transgenic mosquitoes, an effect that was opposite of the anticipated result. Ongoing work on this transgenic mosquito may yield unique insights into how IIS regulates lifespan in mosquitoes and other eukaryotes.

## 1362

**CHARACTERIZATION OF CARBONIC ANHYDRASES AND ION REGULATORY PROTEINS IN Aedes Aegypti FEMALE MOSQUITOES PRE- AND POST-BLOOD MEAL**

**Daniel P. Dixon**<sup>1</sup>, Leslie VanEkeris<sup>2</sup>, Paul Linsler<sup>2</sup>

<sup>1</sup>University of Florida, Department of Microbiology and Cell Science, Gainesville, FL, United States, <sup>2</sup>The Whitney Laboratory for Marine Biosciences, Saint Augustine, FL, United States

Mosquitoes represent a major threat to human health due to their capacity to spread diseases, such as malaria and dengue, to both humans and livestock. Blood feeding plays an important role in reproduction and pathogen transmission. Blood meals represent a significant challenge to digestive and ion regulatory processing mechanisms due to the protein, ion, water, and carbon dioxide-rich nature of the blood. This nutrient rich meal needs to be processed during and shortly after a blood meal to facilitate post-blood-meal flight and prevent toxic levels of sodium and CO<sub>2</sub> from remaining in the mosquito. This research determines the respective roles ion transport proteins and carbonic anhydrases play in ion transport and pH maintenance post-blood meal, specifically in the female midgut and hindgut tissues. The ion transporters analyzed include sodium proton antiporters, sodium dependent anion exchangers, and chloride-bicarbonate exchangers. The carbonic anhydrases analyzed fall into the alpha carbonic anhydrase family, with two genes at the focus of our studies. Immunohistochemical analyses reveal that CA9 is localized to the anterior and posterior midgut of the adult, while CA10 is localized to the nervous system and the hearing organ, the Johnston's organ. Immunocytochemical analyses also indicate that the sodium proton antiporter, NHA1, is localized to the apical membranes of the ileum and the stellate cells of the malpighian tubules. We hypothesize that if a female mosquito is fed blood, the expression of ion transport proteins and carbonic anhydrases in the gut will modulate in such a way as to maintain the alkaline pH within the posterior midgut and rapidly transport sodium out of the gut lumen and into the hemolymph. Also, we hypothesize that if ion regulatory or carbonic anhydrase gene expression is perturbed via reverse genetics, the gut and ion regulatory systems will not be able to properly digest the blood meal and regulate ion secretion, thus reducing reproductive capacity and fitness.

## 1363

**CLIP-SERINE PROTEINASE CLIPB8 SUPPLEMENTS A SRPN2/CLIPB9 REGULATORY UNIT THAT CONTROLS MELANIZATION IN AFRICAN MALARIA MOSQUITO, ANOPHELES GAMBIAE**

**Xin Zhang**, Chunju An, Kara J. Jones, Kristin Michel

*Kansas State University, Manhattan, KS, United States*

Melanization immune response encapsulates and kills invading pathogens in insects and other arthropods. Melanization is regulated by the activation of prophenoloxidase (PPO), which is controlled by a proteinase cascade and its serpin inhibitors. To date, the molecular composition of this system is partially understood especially in mosquitoes. Recently, a regulatory unit of melanization in *Anopheles gambiae* was documented comprising an inhibitory serpin-clip-serine proteinase pair: serpin2-CLIPB9. Partial reversion of SRPN2 phenotypes in melanotic tumor formation and adult survival by SRPN2/CLIPB9 double knockdown suggests other target proteinases of SRPN2 in regulating melanization. Here we report that

CLIPB8 is identified as a target proteinase of SRPN2 and supplements SRPN2/CLIPB9 regulatory unit in controlling melanization in *An. gambiae*. Heterologously expressed SRPN2 forms a complex with activated recombinant proCLIPB8 and directly inhibits CLIPB8 activity *in vitro*. Similar as CLIPB9, double knockdown SRPN2 and CLIPB8 also partially reversed the pleiotrophic phenotype induced by SRPN2 silencing both in adult survival and melanotic tumor formation. Differently, CLIPB8 does not cleave and does not activate PPO *in vitro* as CLIPB9 did either by using purified *M. sexta* PPO or *M. sexta* plasma. Biochemical analysis showed that CLIPB8 and CLIPB9 can not activate each other *in vitro*. In addition, reverse genetic analysis by triple knockdown of SRPN2, CLIPB8, and CLIPB9 did not show accumulative effect in reverting the pleiotrophic phenotype by SRPN2 silencing. These results suggest CLIPB8 is on the further upstream of CLIPB9 in activation of melanization.

## 1364

### A MULTIPLEX REAL-TIME PCR ASSAY FOR DETECTION AND QUANTIFICATION OF *PLASMODIUM* SPP INFECTION IN MALARIA VECTORS

Maurice Marcel Sandeu<sup>1</sup>, Azizath Moussiliou<sup>2</sup>, Nicolas Moiroux<sup>3</sup>, Achille Massougbodji<sup>4</sup>, Vincent Corbel<sup>1</sup>, Nicaise Tuikue Ndam<sup>2</sup>

<sup>1</sup>Research Institute for Development: UMR 224, Cotonou, Benin,

<sup>2</sup>Research Institute for Development: UMR 216, Cotonou, Benin,

<sup>3</sup>Research Institute for Development: UMR 224, Montpellier, France,

<sup>4</sup>Centre d'Etudes et de Recherche sur le Paludisme Associé à la Grossesse et à l'Enfant (CERPAGE), Faculté des Sciences de la Santé (FSS), Cotonou, Benin

The enzyme linked immunosorbent assay specific for circumsporozoite protein (CSP-ELISA) is the gold standard method for the detection of malaria parasites in the vector despite several limitations. Here, we developed a new multiplex PCR-based method to detect and quantify the mixed infection rates of *Plasmodium* species in the African malaria vectors to better estimate the level of parasite infection in field populations and to ensure more accurate evaluation of the level of transmission following the implementation of vector control interventions. TaqMan duplex real-time PCR was first evaluated using different ranges of plasmids. The efficiency of real-time PCR was compared with the CSP ELISA using field caught *Anopheles gambiae* and *An. funestus* mosquitoes collected from two localities in southern Benin. Finally, quantification of DNA of *Plasmodium* spp was performed and normalized using a housekeeping gene RS7. A total of 200 mosquito samples (100 *An.gambiae* and 100 *An.funestus*) were used to develop and validate the RT-PCR method. The validation of these oligonucleotides this technique on the mosquito homogenates showed that RT-qPCR was more sensitive than the ELISA-CSP for the detection of *P. falciparum* (RT-PCR RT-PCR= 97% and CSP (RT-PCR RT-PCR= 97% and CSP-Elisa=87%). These results indicated high specificity of the multiplex real-time PCR to detect the other *Plasmodium* species (notably *P. malariae* and *P. ovale*) in anophelinae mosquitoes. The relative quantification shows that the amount of DNA varies between 3 and 90 copy number/ng per samples. The average number of copies / ng in *An. gambiae* is (28.35767) and (7.16700) in *An. funestus* (p-value = 0.1045). This study describes a new method for the detection and quantification of the four *Plasmodium* species in the African malaria vectors. This will ensure a better diagnostic of malaria parasite's infection in field populations and allow for new basic research on the fitness cost associated with malaria infection during the life of the mosquito.

## 1365

### PARAQUAT FEEDING FOR STUDY OF MOSQUITO DEFENSE CAPACITY AGAINST OXIDATIVE STRESS

Jinjin Jiang, Celeste Alvarez, Phanidhar Kukutla, Wanqin Yu, Jiannong Xu

New Mexico State University, Las Cruces, NM, United States

Anautogenous female mosquitoes take blood meals for egg production. Digestion of hemoglobins is accompanied with heme associated oxidative stress, which is potentially detrimental to lipids, proteins and DNA. As an adaptation, mosquitoes have evolved certain antioxidant mechanisms to cope with this oxidative stress. However, little is known about the extent of defense capacity that mosquitoes have. Paraquat is an herbicide known to causes extensive damage to the mitochondria through the production of free radicals and oxidative stress. In this study we used Paraquat feeding to add extra oxidative stress to the mosquitoes, and examine the antioxidant capacity in the gut ecosystem. Mosquitoes were fed on sugar diet with different concentration of Paraquat (2mM, 10mM and 20mM) after emergence. Paraquat causes mosquito death in a dose dependent manner. Interestingly, blood feeding increased the mortality of mosquitoes that had been fed on 2 mM Paraquat, suggesting that the bloodmeal increased the stress to a level that exceeds the defense capacity of mosquitoes. The expression patterns of mosquito and bacterial catalase and SOD, and bacterial AhpC, Paraquat inducible protein A and B genes were assayed by qPCR. These mosquito and microbial anti-oxidant genes responded to the stress in various settings, such as blood-fed, Paraquat-fed and Paraquat-plus blood-fed mosquitoes. The data suggest that gut redox homeostasis is managed collaboratively by both mosquito and its microbial community.

## 1366

### TRANSCRIPTIONAL MEDIATORS KTO AND SKD ARE INVOLVED IN THE REGULATION OF THE IMD PATHWAY ANTI-*PLASMODIUM* DEFENSES IN *ANOPHELES GAMBIAE*

Yang Chen, Yuemei Dong, Simone Sandiford, George Dimopoulos

W. Harry Feinstone Department of Molecular Microbiology and Immunology, Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD, United States

Malaria is responsible for the deaths of over one million people annually. *Anopheles* mosquitoes are the main vectors for the malarial parasites. We have shown that the IMD pathway is the most important arm used by the mosquitoes to resist infection with the human malaria parasite *Plasmodium falciparum*. In this study, we showed that the transcriptional mediators Kto and Skd are involved in the regulation of the IMD pathway. Transcriptional mediators serve as transcriptional co-activators, which are a group of evolutionally conserved proteins that can form complexes to bridge regulatory regions to the RNA polymerase II initiation complex in eukaryotic cells. Studies with *Drosophila*, zebrafish and *Caenorhabditis elegans* have shown that Kto and Skd are required for several specific developmental processes. Here we show that knocking down Kto and Skd in the *Anopheles gambiae* cell line down-regulate the expression level of Cec1 which is controlled by the IMD pathway. However, Kto and Skd are not transcriptional co-activators of Rel2 and are not involved in the transcription of the main IMD pathway components. Silencing the two genes *in vivo* would lead to increased susceptibility of mosquitoes to bacterial and *P. falciparum* infection, but not to infection with *P. berghei*. Together the results suggest that Kto and Skd are involved in the regulation of the IMD pathway, which is crucial for the mosquito's defense against *P. falciparum*.

### FRAGMENTATION MECHANISMS OF ARGININE ISOBUTYL ESTER APPLIED TO ARGININE QUANTIFICATION IN EXCRETA FROM INDIVIDUAL *Aedes aegypti* FEMALES

David R. Bush, Vicki H. Wysocki, **Patricia Y. Scaraffia**

*The University of Arizona, Tucson, AZ, United States*

Our laboratory is interested in uncovering the metabolic regulation of arginolysis and uricolysis in mosquitoes. For this purpose, it is necessary to have a rapid and efficient method to monitor arginine (Arg) levels in excreta from individual *A. aegypti* females. Thus, the fragmentation patterns of the isobutyl esters of Arg and  $^{15}\text{N}_2$ -Arg (labeled at the guanidino group) were studied by electrospray ionization-tandem mass spectrometry, and fragmentation pathways not described before were characterized. In addition, Arg,  $^{18}\text{O}_2$ -Arg,  $^{15}\text{N}_2$ -Arg and  $^{15}\text{N}_2$ - $^{18}\text{O}_2$ -Arg were analyzed to elucidate some of the minor fragments in greater detail. Mosquito excreta from individual females were collected before and at different times after feeding a blood meal, mixed with  $^{15}\text{N}_2$ -Arg, an internal standard, and derivatized as isobutyl esters. Based on the fragmentation mechanism of Arg standards studied by MS<sup>2</sup> and MS<sup>3</sup>, Arg levels in the mosquito excreta were analyzed by multiple-reaction monitoring (MRM) in a triple-quadrupole mass spectrometer. Arg excretion was quantified at 1, 6, 12, 18, 24, 36, 48, 72, 96 and 120 h before and after feeding female mosquitoes with a bovine blood meal. As expected, Arg is not present in the sugar-fed female excreta and only a very small amount is observed in blood-fed female excreta at the beginning of the time course. At 12 h, the Arg concentration is approximately 20 nmol/female mosquito. This value increases significantly during the time course, reaching the highest levels between 36 and 48 h (about 60 nmol/female) and remains constant through the end of the time course (120 h after a blood meal). These data correlate well with the periods of intense blood meal digestion and maximal excretion of nitrogen compounds in the blood-fed females. The quantification of Arg by mass spectrometry provides a rapid, sensitive and accurate method to investigate the metabolic regulation of nitrogen wastes in individual *A. aegypti* females.

### MOLECULAR AND FUNCTIONAL CHARACTERIZATION OF INWARD-RECTIFYING POTASSIUM (KIR) CHANNELS IN THE 'KIDNEYS' OF MOSQUITOES: TOWARDS THE DEVELOPMENT OF NEW INSECTICIDES

**Matthew F. Rouhier**<sup>1</sup>, Jerod S. Denton<sup>2</sup>, Klaus W. Beyenbach<sup>3</sup>, Peter M. Piermarini<sup>1</sup>

<sup>1</sup>*Department of Entomology, The Ohio State University, Wooster, OH, United States*, <sup>2</sup>*Department of Pharmacology, Vanderbilt University Medical Center, Nashville, TN, United States*, <sup>3</sup>*Department of Biomedical Sciences, Cornell University, Ithaca, NY, United States*

The evolution of insecticide resistance in mosquitoes has led to an urgent need to develop new chemical control agents with novel mechanisms of action. In the present study, we evaluate the inward-rectifying potassium (Kir) channels of mosquitoes (*Aedes aegypti*) as potential insecticidal targets by characterizing their molecular and functional expression. We focus our study on the Kir channels expressed in the Malpighian tubules, because this renal epithelium is a key component of the mosquito excretory system and has not been exploited as a physiological target for controlling mosquitoes. We show that (1) Malpighian tubules express a combination of at least 3 different Kir channel genes that is distinct among mosquito tissues, (2) at least two of the Kir channels encode barium-sensitive potassium channels when expressed in *Xenopus* oocytes, and (3) injecting a small-molecule antagonist of Kir channels into mosquitoes elicits desirable sub-lethal effects that are consistent with perturbed Malpighian tubule function.

### THE ROLE OF APOPTOSIS IN DENGUE-2 INFECTION OF THE MOSQUITO VECTOR *Aedes aegypti*

**Matthew W. Eng**, David W. Severson

*University of Notre Dame, Notre Dame, IN, United States*

*Aedes aegypti* is the primary vector for dengue virus (DENV). An understanding of host-pathogen interaction is important in understanding what factors contribute to vector competence. Our previous global transcriptional analysis has suggested the induction of apoptotic proteins in the involvement of resistance and susceptibility to DENV infection. However the mechanism through which this happens is largely unknown. Here we analyze the possibility that programmed cell death is actively involved in the defense of *A. aegypti* host cells to DENV infection. The effector caspase, *CASP2L2*, has been previously shown to be part of the core apoptotic pathway involved in the response to drug and UV-induced DNA damage in *A. aegypti*. Here we use siRNA interference to show that *CASP2L2* is also involved in apoptotic signaling for DENV-2, and that silencing of this gene affects virus titer at early and late points of infection. Silencing of *CASP2L2* also affected dissemination and transmission of the virus. In addition, we investigate the possibility that by delaying programmed cell death in susceptible individuals, DENV-2 can manipulate this process for its benefit.

### P38 MAPK SIGNALING IN *ANOPHELES STEPHENSII*: A MECHANISM FOR TOLERANCE OR RESISTANCE DURING PARASITE INFECTION?

**Bo Wang**, Shirley Luckhart

*University of California, Davis, Davis, CA, United States*

Among the mitogen-activated protein kinases, p38 MAPK-dependent signaling is critical to the regulation of the balance between resistance and tolerance to infection. However, little is known about the functional biology of p38 MAPK signaling in vector mosquitoes. Our data demonstrated that inhibition of *Anopheles stephensi* p38 MAPK signaling can reduce malaria parasite development, including oocyst burden in the midgut as well as infection prevalence. Further, p38 MAPK signaling regulates a wide variety of known mosquito anti-parasite effector genes in patterns that suggest a balance between tolerance and resistance. This work indicates that the essential roles of p38 MAPK signaling identified in mammals are conserved in mosquitoes. More importantly, however, our data provide new insights into regulatory mechanisms that can be manipulated to control suites of anti-parasite genes as the basis for a novel strategy for the development of transgenic, parasite-resistant mosquitoes.

### CHARACTERIZATION OF A G PROTEIN COUPLED RECEPTOR (GPCR) THAT BINDS TO THE ANTI-*PLASMODIUM* IMMUNE FACTOR FBN9

**Simone L. Sandiford**<sup>1</sup>, Jinfei Ni<sup>2</sup>, Andrew Pike<sup>1</sup>, Craig Montell<sup>2</sup>, George Dimopoulos<sup>1</sup>

<sup>1</sup>*Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, United States*, <sup>2</sup>*Johns Hopkins School of Medicine, Baltimore, MD, United States*

In *Anopheles gambiae* mosquitoes, the fibrinogen related protein family (FREP, also known as FBN) is the largest group of pattern recognition receptors. We have previously reported that one of its members FBN9, interacts directly with various species of bacteria and also exhibits anti-*Plasmodium* activity. To further understand the role of FBN9 in the mosquito's innate immune system, a yeast two hybrid screen was performed to identify novel binding partners. In addition to a number of other interacting proteins, we have discovered a G protein coupled receptor (GPCR) that binds to FBN9. Interestingly, this GPCR has been

identified as a rhodopsin receptor (GPROP10) and has no previously described immune related function. Rnai studies show that GPROP10 may also participate in controlling *Plasmodium* development in the mosquito midgut. Here we describe the characterization of GPROP10 and its potential function in the innate immune system of *An. gambiae* mosquito's defense against pathogens.

### 1372

#### TRANSCRIPTOMIC COMPARISON OF LABORATORY AND GEOGRAPHICALLY DISTINCT FIELD-DERIVED *Aedes aegypti* POPULATIONS TO IDENTIFY GENES THAT REGULATE VECTOR COMPETENCE FOR DENGUE VIRUS2

Seokyoung Kang<sup>1</sup>, Shuzhen Sim<sup>1</sup>, Natapong Jupatanakul<sup>1</sup>, Jose L. Ramirez<sup>1</sup>, Claudia Romero-Vivas<sup>2</sup>, Hamish Mohammed<sup>3</sup>, George Dimopoulos<sup>1</sup>

<sup>1</sup>Johns Hopkins University, Baltimore, MD, United States, <sup>2</sup>Fundacion Universidad del Norte, Barranquilla, Colombia, <sup>3</sup>University of Trinidad and Tobago, Arima, Trinidad and Tobago

Dengue virus (DENV) is the most important mosquito-borne virus affecting humans today, and is vectored primarily by the mosquito *Aedes aegypti*. Since no vaccine against DENV is currently available, there is interest in transmission control strategies that target the mosquito vector. Most studies of mosquito immune responses have been performed with the laboratory strains of *Ae. aegypti*, which have been maintained under insectary conditions for decades. As compared to natural mosquito populations, laboratory mosquito strains are exposed to lower doses and a much narrower range of microbes; this together with the genetic bottleneck of a small initial parental population size often results in a loss of genetic variability. Although most field studies have focused on genetic polymorphisms, natural and laboratory mosquito populations are also likely to differ in their transcriptomic responses to pathogen infection, either in terms of the magnitude of gene regulation or in the subsets of regulated genes. We established field colonies of *Ae. aegypti* from geographically-distinct dengue-endemic regions, spanning South America, the Caribbean, and Southeast Asia, and evaluated their and vector competences for DENV2. This analysis identified both refractory and susceptible strains to DENV2 infection. A genome-wide gene expression microarray was then performed to compare the transcriptomes of field-derived strains to our laboratory Rockefeller strain. Several candidate genes were identified that may regulate vector competence in field-derived strains; we are currently functionally testing the role of these genes through RNAi-mediated gene knockdowns. This study will not only provide valuable information about immune gene regulation and usage in natural mosquito populations, but will also allow us to identify novel pathogen recognition receptors and effector genes that control DENV in field mosquitoes.

### 1373

#### HIGH PREVALENCE OF HTLV-1 AND HTLV-2 INFECTIONS IN PERUVIAN AMAZONIAN COMMUNITIES

Nicanor Mori<sup>1</sup>, Silvia M. Montano<sup>1</sup>, Magaly M. Blas<sup>2</sup>, Isaac E. Alva<sup>2</sup>, Jorge O. Alarcon<sup>3</sup>, Drake H. Tilley<sup>1</sup>, Joseph R. Zunt<sup>4</sup>

<sup>1</sup>U.S. Naval Medical Research Unit No. 6, Lima, Peru, <sup>2</sup>Epidemiology, HIV and STD Unit, School of Public Health, Universidad Peruana Cayetano Heredia, Lima, Peru, <sup>3</sup>Instituto de Medicina Tropical "Daniel A. Carrion", Universidad Nacional Mayor de San Marcos, Lima, Peru, <sup>4</sup>Departments of Neurology, Global Health, Medicine (Infectious Diseases) and Epidemiology, University of Washington, Harborview Medical Center, Seattle, WA, United States

HTLV-1 and HTLV-2 infections are distributed worldwide and endemic to regions of Japan, sub-Saharan Africa, the Americas, Melanesia, and the Middle East. Peru has reported HTLV-1 and HTLV-2 infections in indigenous Amazonian populations and among African-Peruvian and mestizo populations. To assess the prevalence, risk factors and neurological

manifestations associated with HTLV-1 and -2 infections, we conducted a cross-sectional study of 878 adult participants, ages 15-64 years, from 14 indigenous communities near Pucallpa. 94 (10.7%) participants were infected with HTLV: 56 (59.6%) had HTLV-1, 35 (37.2%) HTLV-2, and 3 (3.2%) were infected with both HTLV-1 and HTLV-2. Seven patients had indeterminate test results and were excluded from further analysis. The median age for all participants was 34 (SD  $\pm$  13.8) years. HTLV positive participants were older than HTLV negative participants (mean 43.1 vs. 32.9 years ( $p < 0.0001$ )). HTLV-1 and -2 infections increased with age ( $p < 0.0001$ ) but decreased for participants aged 50 years or older. Factors significantly associated with HTLV infection included age  $\geq$  38 years ( $p < 0.0001$ , OR: 3.07), female gender ( $p = 0.008$ , OR: 1.82), illiteracy ( $p = 0.002$ , OR: 2.85), education of 7 years or less ( $p < 0.0001$ , OR 2.22), having had a relative with gait difficulties affecting both legs ( $p = 0.036$ , OR 2.4), prior episode of chronic scabies (significant only for males;  $p = 0.046$ , OR: 2.1), and being pregnant more than four times ( $p = 0.027$ , OR 1.88). Surprisingly, no participant had clinical evidence of HTLV-associated myelopathy/tropical spastic paraparesis (HAM/TSP). To our knowledge, this is one of the highest reported prevalences of HTLV infection among native Amazonian ethnic groups. Although not measured in this study, the high prevalence of helminthic coinfection reported among Amazonian inhabitants may potentially attenuate immune responses and thus impede the development of HAM/TSP.

### 1374

#### AUSTRALIAN ARBOVIRUSES AND A NOVEL RHABDOVIRUS IN ANOPHELINE MOSQUITOES IDENTIFIED USING METAGENOMICS

Lark L. Coffey<sup>1</sup>, Belinda Herring<sup>2</sup>, Richard Russell<sup>3</sup>, Stephen Doggett<sup>4</sup>, John Haniotis<sup>4</sup>, Eric L. Delwart<sup>1</sup>

<sup>1</sup>University of California San Francisco, San Francisco, CA, United States, <sup>2</sup>Griffith University, Gold Coast Campus, Queensland, Australia, <sup>3</sup>Sydney Medical School, University of Sydney and Centre for Infectious Diseases and Microbiology, Westmead Hospital, New South Wales, Australia, <sup>4</sup>Centre for Infectious Diseases and Microbiology, Westmead Hospital, New South Wales, Australia

Identifying viruses as etiologies of human and animal disease is an important initial step in preventing and treating illness. The success of many previous virus identification strategies has been impeded by the requirement for prior knowledge of the viral genome, which dictates the testing assay. Deep sequencing, by contrast, is a cutting-edge metagenomics technique that detects and characterizes known and unknown viruses in a specimen nonspecifically and with high sensitivity, without prior knowledge of the viral genome. We used deep sequencing to identify virus genomes in pools of mosquitoes from New South Wales, Australia, that were antigenically negative for known Australian flaviviruses and alphaviruses. Full genome characterization and phylogenetic analyses revealed sequences of several viruses in a least one pool each: 1) strains of Liao Ning virus (LNV, *Reovirus*, *Seadornavirus*), heretofore only detected in Indonesia and China where it is the etiological agent of encephalitis in humans, 2) strains of Stretch Lagoon virus (SLOV, *Reovirus*, *Orbivirus*) a mosquito-borne virus that infects livestock and has previously been isolated only in Northern Australia and once in Sydney, and 3) a novel rhabdovirus in *Anopheles annulipes* that diverges by  $\approx 40\%$  at the amino acid level compared to other members of the *Vesiculovirus* genus and probably represents a new species. To our knowledge, this is the first report of LNV outside China, and we extend the distribution of SLOV to central New South Wales. This study highlights the power of metagenomics for identifying novel RNA viruses in field-collected mosquitoes. The new rhabdovirus may eventually be linked to human or veterinary disease, and follow-up epidemiological arbovirus studies will address this possibility.

### LASSA FEVER OUTBREAK INVOLVING HEALTHCARE WORKERS IN TARABA STATE, NIGERIA: MARCH 2012

**Kabiru I. Getso**<sup>1</sup>, Muhammad S. Balogun<sup>1</sup>, Saheed S. Gidado<sup>2</sup>, John Oladejo<sup>2</sup>, Abdussalam Nasidi<sup>3</sup>, Patrick M. Nguku<sup>1</sup>, Henry Akpan<sup>2</sup>, Simeon Ajisegiri<sup>2</sup>

<sup>1</sup>Nigeria Field Epidemiology and Laboratory Training Program, Abuja, Nigeria, <sup>2</sup>Federal Ministry of Health, Abuja, Abuja, Nigeria, <sup>3</sup>Nigeria Center for Disease Control and Prevention, Abuja, Nigeria

Lassa fever is an acute, highly infectious viral haemorrhagic illness caused by Lassa fever virus - a single stranded, RNA virus belonging to the virus family Arenaviridae. The reservoir is *Mastomys natalensis*. The disease is endemic in West African sub region causing 300,000-500,000 infections annually, with about 500 deaths. In March, 2012, we investigated a reported outbreak of Lassa fever in Taraba State, Nigeria to confirm the outbreak, determine its extent, characterize the outbreak, institute public health actions and make appropriate recommendations. We reviewed hospital records and used IDSR standard case definition for Lassa fever to identify and line-list cases. A suspected case was defined as "any person with severe febrile illness not responsive to the usual causes of fever in the area with or without sore-throat and at least one of the following: bloody stools, vomiting blood, bleeding into the skin, unexplained bleeding from the nose, vagina or eyes". A standardized line-listing form was developed to capture socio-demographic and clinical information of the cases. Various exposure factors including age, gender, occupation and contact history were examined. A total of 35 cases were recorded. Nine of 35 cases were laboratory confirmed (25.7%). Altogether, 14 deaths were recorded giving a case fatality rate of 40%. Majority of the cases belonged to the age group 25-34 years (40%) with females constituting 51%. Most of the cases were healthcare workers (22.9%). The commonest presenting features were fever (85.7%), cough (28.6%), bleeding from orifices or into skin (25.7%) and headache (20%). In addition, the State's Epidemic Management Committee was non-functional resulting in uncoordinated response to the outbreak. There were many exposure factors to Lassa fever such as over-crowding, drying of food items along high ways and bush burning and there was low index of suspicion of Lassa fever among health care workers. Community sensitization and sensitization of health workers in Taraba State on Lassa fever were carried out. There was a confirmed outbreak of Lassa fever in Taraba State mostly affecting healthcare workers. It was recommended that the State should reactivate its Emergency Management Committee, surveillance of Lassa fever should be strengthened, Public/Health workers sensitization activities should be scaled up and records keeping should be improved.

### 1376

### DIARRHEA INCIDENCE BEFORE AND AFTER ROTAVIRUS VACCINE INTRODUCTION IN NICARAGUA: A PROSPECTIVE, POPULATION-BASED STUDY

**Sylvia Becker-Dreps**<sup>1</sup>, Marlon Meléndez<sup>2</sup>, Luís Enrique Zambrana<sup>2</sup>, Félix Espinoza<sup>3</sup>, David J. Weber<sup>1</sup>, Michael G. Hudgens<sup>1</sup>, Douglas R. Morgan<sup>1</sup>, Mercedes Cáceres<sup>3</sup>, Rodolfo Peña<sup>4</sup>

<sup>1</sup>University of North Carolina, Chapel Hill, NC, United States, <sup>2</sup>Center for Epidemiology and Health (CIDS), Universidad Nacional Autónoma de Nicaragua, León, León, Nicaragua, <sup>3</sup>Universidad Nacional Autónoma de Nicaragua, León, León, Nicaragua, <sup>4</sup>Pan American Health Organization, San Salvador, El Salvador

Nicaragua was the first GAVI-eligible country to introduce the pentavalent rotavirus vaccine in 2006. Prior evaluations of the vaccine's effectiveness in developing countries have been performed in health facilities; however, the majority of rotavirus cases are treated in the community. The goal of this study was to examine changes in childhood diarrhea incidence in the community before and after vaccine introduction. We conducted active surveillance for diarrhea episodes using the Health and Demographic Surveillance Site, León to provide simple random population-based

samples. Two open cohorts of children were followed, one in the pre-vaccine period, 2001-2003, and the other in the post-vaccine period, 2010-2011. Home interviewers visited households to record each child's characteristics and returned every 2 weeks to record numbers of diarrhea episodes. Poisson regression models were used to compare the incidence rate of diarrhea in the pre- and post-vaccine periods, stratified by age. Because laboratory data were not available for comparison, a "rotavirus-specific" diarrhea surrogate definition was used, based on the literature: greater than 4 stools per 24 hr period with either vomiting or fever or both. We anticipated a decline in rotavirus-specific diarrhea incidence in the post-vaccine period. A total of 726 children were enrolled in the pre-vaccine cohort and were followed for 249 person-years (py); 826 children were enrolled in the post-vaccine cohort and were followed for 563 py. Overall unadjusted diarrhea incidence was lower in the post-vaccine period than in the pre-vaccine period. Rotavirus-specific diarrhea incidence showed a greater decline from the pre-vaccine to the post-vaccine periods: among infants from 0.38 to 0.14 cases per py ( $p=0.026$ ), among 12-23 month old children from 0.35 to 0.07 cases per py ( $p=0.001$ ), and among 24-59 month old children from 0.10 to 0.02 cases per py ( $p=0.002$ ). In conclusion, substantial declines in the incidence of rotavirus-specific diarrhea were observed in the post-vaccine period in this community setting.

### 1377

### MOLECULAR DETERMINANTS OF MOUSE NEUROVIRULENCE AND MOSQUITO INFECTION FOR WESTERN EQUINE ENCEPHALITIS VIRUS

Eric C. Mossel<sup>1</sup>, Jeremy P. Ledermann<sup>2</sup>, Aaron T. Phillips<sup>1</sup>, Erin M. Borland<sup>2</sup>, Ann M. Powers<sup>2</sup>, **Ken E. Olson**<sup>1</sup>

<sup>1</sup>Colorado State University, Fort Collins, CO, United States, <sup>2</sup>Division of Vector-Borne Infectious Diseases, Centers for Disease Control and Prevention, Fort Collins, CO, United States

Western equine encephalitis virus (WEEV) is a naturally occurring recombinant virus derived from ancestral Sindbis and eastern equine encephalitis viruses. We previously showed that infection of CD-1 mice with WEEV McMullan (McM) and IMP-181 (IMP) isolates resulted in high (~90-100%) and low (0%) mortality, respectively, when virus was delivered by either subcutaneous or aerosol routes. However, relatively little is known about specific virulence determinants of WEEV. We additionally observed that IMP infected *Culex tarsalis* mosquitoes at a high rate (app. 80%) following ingestion of an infected bloodmeal but these mosquitoes were infected by McM at a much lower rate (10%). To understand the viral determinants generating these phenotypic differences, we characterized the pathogenic phenotypes of McM/IMP chimeras. Exchanging the arginine present at IMP E2 glycoprotein position 214 for the glutamine present at the same position in McM ablated mouse mortality. However, the reciprocal exchange did not confer mouse virulence to the IMP virus. Mosquito infectivity was determined by multiple loci one of which was the same E2-214 amino acid identified above as the mouse virulence determinant. Replacing either IMP E2 amino acid 181 or 214 with the corresponding McM amino acid lowered mosquito infection rates to McM-like levels. As observed during our study of mouse neurovirulence, neither reciprocal exchange conferred mosquito infectivity. The identification of WEEV E2 amino acid 214 as necessary for both IMP mosquito infectivity and McM mouse neurovirulence indicated that they are mutually exclusive phenotypes and suggests an explanation for the lack of human or equine WEEV cases even in the presence of active transmission.

## 1378

### PROBING THE ROLE OF CD4+ AND CD8+ T-CELLS IN CONTROLLING EARLY INFECTION WITH THE CHIKUNGUNYA CHIKV/IRES CANDIDATE VACCINE AND PROTECTING AGAINST CHIKV CHALLENGE

Haiyan Chu<sup>1</sup>, Subash Das<sup>1</sup>, James Weger<sup>2</sup>, Charalambos Partidos<sup>1</sup>, Scott Weaver<sup>3</sup>, Dan Stinchcomb<sup>4</sup>, Jorge Osorio<sup>1</sup>

<sup>1</sup>Inviragen, Madison, WI, United States, <sup>2</sup>University of Wisconsin, Madison, WI, United States, <sup>3</sup>University of Texas Medical Branch, Galveston, TX, United States, <sup>4</sup>Inviragen, Fort Collins, CO, United States

Recently, Chikungunya virus (CHIKV), a mosquito-borne alphavirus, re-emerged in Africa and spread to islands in the Indian Ocean, Indian subcontinent, SE Asia and Italy. Viremic travelers have also imported CHIKV to the Western hemisphere, which highlights the risk of CHIKV in naïve populations. In addition to the great burden of arthralgic disease, which can persist for months or years, epidemiologic studies estimated case-fatality rates of ~0.1%, principally from neurologic disease in older patients. There are no licensed vaccines or effective therapies. Using the La Reunion strain as the genetic backbone we inserted a picornavirus internal ribosome entry site (IRES) that functions poorly in insect cells, and inactivated the subgenomic promoter which drives overexpression of the structural proteins, to develop a live-attenuated CHIKV vaccine (CHIKV/IRES). This vaccine is highly attenuated yet immunogenic in mouse models and non-human primates, and is incapable of replicating in mosquito cells. In an effort to understand better the contribution of host response to CHIKV/IRES replication at the initial stages of virus infection we are currently conducting a series of studies to determine whether CD4+ and/or CD8+ T cells control virus replication in the A129 mice (deficient in the IFN  $\alpha/\beta$  response). Prior to CHIKV/IRES infection, T cell subsets are depleted and the replication of the virus in the serum and various tissues (brain, spleen, muscles, liver) are monitored over a period of 12 days. In addition, isolated T cell subsets collected on days 0, 3, 6, 9 and 12 are characterized by intracellular cytokine staining using flow cytometry. Furthermore, we are conducting a series of adoptive transfer studies to determine which T cell subset is contributing to the protection afforded by the vaccine against wt CHIKV challenge. Understanding the role of T cell immunity in controlling infection and its contribution to protection will assist our efforts in designing an effective vaccination strategy against CHIKV.

## 1379

### VACCINE SAFETY AND THE DEVELOPMENT OF A RODENT MODEL OF PERSISTENT CHIKUNGUNYA VIRUS INFECTION

Robert L. Seymour, Alison P. Adams, Scott C. Weaver

University of Texas Medical Branch, Galveston, TX, United States

Chikungunya virus (CHIKV) is a positive sense single stranded RNA virus in the genus Alphavirus and the etiologic agent of several epidemics in Africa, and recently, the Indian subcontinent and Southeast Asia. CHIKV causes a syndrome characterized by rash, fever, and debilitating arthritis. In the more recent outbreaks, CHIKV has begun to manifest more neurologic signs of illness in the elderly and those with co-morbidities. The syndrome is often self-limited; however, many patients develop persistent arthralgia that can last months or years. These characteristics make CHIKV not only important from a human health standpoint, but also from an economic standpoint. Currently, there is no licensed vaccine. Many studies have begun to elucidate the pathogenesis of CHIKV, the mechanism of arthralgia persistence and the role of the adaptive immune response that is poorly understood. In this study, Rag1 KO (Recombination activation gene 1 knockout) mice were inoculated subcutaneously or in the foot pad with 3 log<sub>10</sub> PFU of the La Réunion strain of CHIKV (CHIKV-LR) or varying doses of our vaccine candidate CHIKV/IRES (1, 3, or 5 log<sub>10</sub> PFU) or the U.S. Army vaccine strain 181/clone25 (3 or 5 log<sub>10</sub> PFU). Mice were bled on days 1-8, 14, 28, 42, 56 and 70 after infection and weighed on days 1-14. Tissues were harvested on days 2, 4, 7, 14, 28, 42, 56 and 70. None of the subcutaneously inoculated mice demonstrated clinical

signs of illness (e.g., weight loss, lethargy, or scruffy fur). Mice inoculated with CHIKV-LR developed persistent infection. Viremia reached a peak of 4 log<sub>10</sub> PFU on day 6 after infection, gradually decreasing to 2 log<sub>10</sub> on day 28; no viremia was detected after day 28 post infection. CHIKV-LR also persisted in several organs up to day 42 after infection, but no virus was detected by plaque assay in the organs after day 42 post infection. The brain had inflammation 28 days post infection. These findings are in contrast to both vaccine strains, which never produced detectable viremia or viral persistence in the organs. This study has two key findings: 1) the adaptive immune system is critical for clearance of CHIKV, and 2) the newly developed CHIKV/IRES vaccine strain does not persist even in the absence of T/B cells. The latter point is very important when considering vaccine safety, because many people in developing countries that are exposed to CHIKV are also immunosuppressed due to various conditions (e.g., HIV, malnourishment).

## 1380

### DEVELOPMENT, VALIDATION, AND FIELD PERFORMANCE OF A FIVE-PLEX REAL-TIME QPCR ASSAY TO DETECT DIARRHEAGENIC RNA VIRUSES

Darwin J. Operario<sup>1</sup>, Jie Liu<sup>1</sup>, Mami Taniuchi<sup>1</sup>, Stephen Becker<sup>1</sup>, Shihab Uddin Sobuz<sup>2</sup>, Sharmin Begum<sup>2</sup>, Rashidul Haque<sup>2</sup>, Michel Dione<sup>3</sup>, Jainaba Manneh<sup>3</sup>, Martin Antonio<sup>3</sup>, Senyael Swai Ndealilia<sup>4</sup>, Athanasia Maro<sup>4</sup>, Jean Gratz<sup>1</sup>, Tayyab Un Nissa<sup>5</sup>, Adil Kalam<sup>5</sup>, Shahida Qureshi<sup>5</sup>, Anita Zaidi<sup>5</sup>, Pimnapar Neesanant<sup>6</sup>, Sasikorn Silapong<sup>6</sup>, Lertsethakarn Paphavee<sup>6</sup>, Ladaporn Bohidatta<sup>6</sup>, Carl Mason<sup>6</sup>, Eric Houpt<sup>1</sup>

<sup>1</sup>University of Virginia Health System, Charlottesville, VA, United States, <sup>2</sup>International Centre for Diarrhoeal Disease Research, Bangladesh, Dhaka, Bangladesh, <sup>3</sup>Medical Research Council, Banjul, Gambia, <sup>4</sup>Kilimanjaro Christian Medical Centre, Moshi, United Republic of Tanzania, <sup>5</sup>Aga Khan University, Karachi, Pakistan, <sup>6</sup>Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand

Several viruses and bacteria are known to cause diarrheal disease in the developing world. Traditional methods such as microscopy or culture are either inappropriate or impossible when dealing with these pathogens. In addition, ELISA-based tests may not possess the sensitivity required to detect these pathogens from stool samples. PCR-based methods are generally more sensitive compared to both traditional and ELISA-based methods. In this work, we developed and validated a 5-plex TaqMan-based real-time qPCR assay targeting diarrheagenic RNA viruses including: Astrovirus, Norovirus GII, Rotavirus, and Sapovirus (types 1, 2, 4, and 5), and includes an extraction/amplification control based on a non-coding region of MS2 phage. In addition, we also developed a 4-plex TaqMan-based real-time qPCR panel targeting *Campylobacter*, *Salmonella*, and *Vibrio* bacterial species with the Glycoprotein B gene from Phocine Herpes Virus as the extraction/amplification control. The validation process revealed at least five logs of linear range for each viral target, as well as low CV values (range 0.500-1.855%) for within-run precision and moderate CV values (range 2.8%-28.9%) for between-run precision depending on the target. In addition, the assay appears to perform well in stool matrices having varying degrees of inhibition. After validation, the assays were evaluated at five international field sites each using one of three different real-time PCR platforms including the BioRad CFX96, Corbett/Qiagen RotorGene, and the Applied Biosystems ViiA 7. The field evaluations were based upon measures of linearity, limit of detection, within- and between-run precision ("repeatability" and "reproducibility", respectively), as well as accuracy and carry-over studies. Similar to the results from the validation, the field performance evaluation revealed low CV values (range 0.08-7.52%) for within-run precision and moderate CV values (range 2.36-11.06%) for between-run precision analyses. While there were site-to-site and target-to-target differences, overall, the assays performed similarly over the five field sites and similarly between the three real-time PCR platforms.



## 1381

**SEVERE HEMORRHAGIC FEVER IN STRAIN 13/N GUINEA PIGS INFECTED WITH LUJO VIRUS**

**Brian H. Bird**, Kimberly A. Dodd, Stuart T. Nichol, Christina F. Spiropoulou

*Centers for Disease Control and Prevention, Atlanta, GA, United States*

Lujo virus (LUJV) is a novel member of the *Arenaviridae* family that was first identified in 2008 after an outbreak of severe hemorrhagic fever (HF). In what was a small but rapidly progressing outbreak, this previously unknown virus was transmitted from the critically ill index patient to 4 attending healthcare workers. Four persons died during the outbreak, for a total case fatality of 80% (4/5). The suspected rodent source of the initial exposure to LUJV remains a mystery. Because of the ease of transmission, high case fatality, and novel nature of LUJV, we sought to establish an animal model of LUJV HF. Initial attempts in mice failed, but infection of inbred strain 13/N guinea pigs resulted in lethal disease. A total of 41 adult strain 13/N guinea pigs were infected with either wild-type LUJV or a full-length recombinant LUJV. Results demonstrated that strain 13/N guinea pigs provide an excellent model of severe and lethal LUJV HF that closely resembles what is known of the human disease. All infected animals experienced consistent weight loss (3-5% per day) and clinical illness characterized by ocular discharge, ruffled fur, hunched posture, and lethargy. Uniform lethality occurred by 11-16 days post-infection. All animals developed disseminated LUJV infection in various organs (liver, spleen, lung, and kidney), and leukopenia, lymphopenia, thrombocytopenia, coagulopathy, and elevated transaminase levels. Serial euthanasia studies revealed a temporal pattern of virus dissemination and increasing severity of disease, primarily targeting the liver, spleen, lungs, and lower gastrointestinal tract. Establishing an animal LUJV model is an important first step towards understanding the high pathogenicity of LUJV and developing vaccines and antiviral therapeutic drugs for this highly transmissible and lethal emerging pathogen.

## 1382

**ORAL ROTAVIRUS IMMUNIZATION PROTECTS UNDERNOURISHED WEANLING MICE AGAINST INFECTION DESPITE REDUCED VACCINE SHEDDING AND MODULATED ANTIBODY RESPONSES**

Elizabeth A. Maier, Monica M. Mcneal, **Sean R. Moore**

*Cincinnati Children's Hospital Medical Center, Cincinnati, OH, United States*

Oral rotavirus vaccines protect against the most common cause of severe childhood diarrhea worldwide, but are less effective in low-income countries. A higher prevalence of undernutrition, reducing both innate and adaptive immunity, may partially explain this disparity. Therefore, we designed mouse experiments to test the hypothesis that undernutrition impairs immune responses to rotavirus vaccine and infection. Wild type BALB/c dams with 10-day-old sucklings were randomized to a standard diet or an isocaloric, multideficient "regional basic diet" (RBD) we have previously shown produces moderate malnutrition and phenocopies key features of human environmental enteropathy, including villous blunting and reduced gut integrity (Ueno et al. *AJP* 2011). We immunized RBD mice and controls at 6 weeks of age with a live oral rotavirus vaccine (RRV) or a vehicle control. We then challenged immunized mice and unimmunized controls with murine rotavirus (EDIM  $10^4$  SD<sub>50</sub>) 4 weeks later. Stool and blood were collected after RRV or EDIM challenges to determine viral shedding and antibody responses. RRV shedding in stool following immunization was decreased by 50% in RBD mice vs. controls (15.1 ng/mL vs. 30.8 ng/mL,  $P < 0.03$ ), however protection against EDIM was undiminished. Following immunization, RBD mice had 2-fold higher anti-rotavirus serum IgA levels vs. controls. Following infection, unimmunized RBD mice produced 50% lower levels of anti-rotavirus IgG vs. well-nourished controls ( $P = 0.16$ ). This was not significant after correcting for marked decreases in total IgG levels in RBD mice). In conclusion, weanling

undernutrition alters host immune responses to rotavirus vaccination and infection, but does not mitigate vaccine efficacy. Further research defining the role of malnutrition and other host factors is needed to improve vaccination outcomes in children who bear the greatest risk of disease.

## 1383

**IRES-BEARING VENEZUELAN EQUINE ENCEPHALITIS VIRUSES ARE POTENTIAL VACCINE CANDIDATES**

**Shannan L. Rossi**, Mathilde Guerbois, Rodion Gorchakov, Kenneth Plante, Naomi A. Forrester, Scott C. Weaver

*University of Texas Medical Branch, Galveston, TX, United States*

Venezuelan equine encephalitis virus (VEEV) is an arbovirus associated with morbidity and mortality in equines and humans across Central and South America. Despite its success in curbing the severity and range of epidemics in the past, the current VEE vaccine, TC-83 is a suboptimal vaccine for the following reasons: (i) unstable attenuation; (ii) high reactogenicity and poor long-term immunogenicity (in humans); and (iii) transmissibility in nature. Previously, we reported that when the EMCV IRES was placed in lieu of the virus' subgenomic promoter, the resulting virus exhibited an attenuated phenotype and inability to replicate in mosquito cells. Here, we describe the use of IRES-based attenuation strategy for VEEV vaccine (subtypes ID and IE) construction and characterization. *In vitro*, VEEV/IRES vaccines produce small plaques and replicate to lower titers than the parental 68U201 (IE) or ZPC738 (ID) viruses. Mice injected subcutaneously with  $1 \times 10^5$  pfu of VEEV/IRES show no signs of illness or changes in weight, produce neutralizing antibodies and are fully protected against their respective wild-type lethal challenge. Moreover, VEEV/IRES viruses are unable to propagate in C6/36 cells, implying that these viruses would be unable to be transmitted by mosquitoes in nature. These results, as well as those obtained from studies on chikungunya and eastern equine encephalitis viruses, demonstrate that the IRES-based method of alphavirus vaccine generation provides a predictable method for alphavirus attenuation while maintaining a host-restricted range of replication.

## 1384

**HANTAVIRUS-DAF/CD55 ENGAGEMENT INITIATES RHOGTPASE ACTIVITY AND PARACELLULAR PERMEABILITY IN EPITHELIAL CELLS**

Tione Buranda, Scarlett Swanson, Dominique Perez, Jacob Agola, Elsa G. Romero, Chunyan Ye, Larry Sklar, Angela Wandinger-Ness, **Brian Hjelle**

*University of New Mexico Health Science Center, Albuquerque, NM, United States*

Pathogenic Hantaviruses cause hemorrhagic fever with renal syndrome (HFRS) and hantavirus cardiopulmonary syndrome (HCPS). Hantaviruses have profound tropism for microvascular endothelial cells, and capillary leak at sites of infection is important in pathogenesis. Hantaviruses are hypothesized to target the decay accelerating factor (DAF/CD55), a ubiquitous molecule expressed on the apical surface of polarized epithelia, as a co-receptor for accessing  $\alpha_v\beta_3$  integrin, the entry receptor, expressed basolaterally. Initial engagement of DAF by UV-killed Sin Nombre virus results in upregulation of GTP-bound Rho GTPases (Rac1, Cdc42, RhoA), which is measured by confocal microscopy and G-LISA assays. The Rac1 inhibitor, NSC23766 and a novel Cdc42 inhibitor, ML 141 are used to establish the role of signal cross-talk among Rac1, Cdc42, and RhoA, during the induction of paracellular permeability in epithelial cells. These results are important for understanding the pathogenesis of hantavirus disease.

## 1385

**EVIDENCE OF OUTDOOR BLOOD FEEDING IN THE HIGHLAND ANOPHELES OF WESTERN KENYA: A NEW CHALLENGE FOR MALARIA CONTROL?**

Mary Cooke<sup>1</sup>, Jennifer C. Stevenson<sup>1</sup>, Samuel Kahindi<sup>2</sup>, Chrispin Owaga<sup>2</sup>, Elizabeth Ayoma<sup>2</sup>, Robin Oriango<sup>2</sup>, Chris Drakeley<sup>1</sup>, Jonathan Cox<sup>1</sup>

<sup>1</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>2</sup>Centre for Global Health Research, Kenya Medical Research Institute/Centers for Disease Control and Prevention, Kisumu, Kenya

Indoor residual spraying (IRS) and long-lasting insecticide treated nets (LLINs) are core elements in most malaria control programmes. The effectiveness of these methods relies on the assumption that the majority of *Anopheles* vectors feed indoors and at times when people would be under a net. It is therefore vital to establish whether this assumption is true and determine the time and location that these mosquitoes bite. In addition to divergent behaviors, vector control methods may be undermined by development of insecticide resistance which will affect the success of both IRS and LLINs and may lead to the persistence of malaria transmission. This study aimed to compare the proportion and age of vector species biting at different hours of the night inside and outside houses in an area of seasonal low malaria transmission in Rachuonyo South district, Nyanza Province, western Kenya. This study also aimed to calculate the risk of infected bites with respect to the time that local residents entered their houses and used LLINs. The study took place between June 2011 and July 2012. Collections occurred each month for 6 nights, in 24 houses per night which were randomly allocated to indoor or outdoor trapping. CDC light-traps were hung adjacent to occupied LLINs, located either within houses or in rain shelters set outdoors. Hourly collections were made between 17:30 and 22:30 and then 05:30-06:30 the next morning. Questionnaires were used to capture the time that the local population entered houses and used LLINs. Seasonal fluctuations in vector species were recorded and more *Anopheles* were caught in outdoor traps. The morphological identification of vectors was confirmed by rDNA and mtDNA sequencing and exposure to each vector is discussed. There was evidence that the local population were at risk of infected bites both outdoors and indoors at a time when LLINs were not protecting a sizeable proportion of the population. Exposure to such bites may be responsible for maintaining transmission in the area. This work provides data on vector dynamics that can inform future malaria control programmes.

## 1386

**EVALUATION OF AN ATTRACTIVE LETHAL OVI-TRAP (ALOT) AGAINST Aedes aegypti FOR DENGUE CONTROL IN IQUITOS, PERU**

Dawn M. Wesson<sup>1</sup>, Amy C. Morrison<sup>2</sup>, Valerie A. Paz Soldan<sup>1</sup>, Robin M. Moudy<sup>1</sup>, Kanya Long<sup>2</sup>, Loganathan Ponnusamy<sup>3</sup>, James P. Mohler<sup>1</sup>, Helvio Astete<sup>4</sup>, Luma Kennedy<sup>3</sup>, Eric S. Halsey<sup>4</sup>, Coby Schal<sup>3</sup>, Thomas W. Scott<sup>2</sup>, Charles S. Apperson<sup>3</sup>

<sup>1</sup>Tulane University, New Orleans, LA, United States, <sup>2</sup>University of California, Davis, CA, United States, <sup>3</sup>North Carolina State University, Raleigh, NC, United States, <sup>4</sup>United States Naval Medical Research Unit Six, Lima, Peru

Dengue, the most important mosquito-borne virus world-wide, is primarily transmitted by the container-inhabiting mosquito *Aedes aegypti*. Without a vaccine to prevent new human infections, vector control remains the only method of preventing transmission. Female mosquitoes acquire the virus by taking blood from an infected human, then use a variety of cues to identify potential oviposition sites, where they must deposit eggs before taking another bloodmeal. We hypothesize that by specifically targeting older gravid females, we can most efficiently reduce dengue virus transmission. Toward that end, we have worked to develop an effective lethal ovitrap (Attractive Lethal OviTrap = ALOT) for *Ae. aegypti* control, with concentration on identification of oviposition attractants

and stimulants. Starting in June 2011, we tested the ALOT in a large scale field trial in Iquitos, Peru, where dengue is endemic. The study design was a prospective nonrandomized controlled trial in two cohorts of Iquitos residents from two comparable city neighborhoods each of 2500 houses selected as either intervention or control zones. Traps were placed in houses at a density of ~3 per residence, with ~85% participation in the intervention area. Local ministry of health fumigation to control adult mosquitoes was ongoing in both areas during the study. Entomological indices were monitored in participating households at 3 month intervals, and individuals were monitored serologically, both through a longitudinal survey (at months 0, 12, 18) and through 3X weekly febrile surveillance. Nine months into the trial, dengue incidence as measured by febrile surveillance was 78% lower (0.3% vs. 1.34%) in the intervention area compared to the control area ( $p < 0.0001$ ). Confirmation of these results through separate longitudinal surveillance is pending. We also observed a difference in adult mosquito indices of approximately 50% (e.g. 65 to 30 females/100 houses) between the two areas. These preliminary results suggest that area-wide application with the ALOT could significantly lower dengue transmission.

## 1387

**CHANGING BEHAVIORAL PATTERNS OF ARBOVIRAL VECTOR Aedes africanus: A CONCERN FOR EMERGING AND REEMERGING DISEASES**

Martin Lukindu<sup>1</sup>, Louis G. Mukwaya<sup>2</sup>, Charles Masembe<sup>1</sup>, Josephine Birungi<sup>2</sup>

<sup>1</sup>Makerere University Kampala, Kampala, Uganda, <sup>2</sup>Uganda Virus Research Institute, Entebbe, Uganda

*Aedes (Stegomyia) africanus* Theobald is a key arboviral vector to humans. It is a highly competent vector for several viruses that cause hemorrhagic fevers including; Yellow fever (YF), Rift Valley fever, dengue fever, and other arboviral vectors, most of which are widely distributed in Africa. There are no vaccines for these arboviral diseases except YF which has a safe and effective vaccine, yet YF outbreaks are still reported in Africa. Vector control is therefore crucial yet little is known about the biology of *Ae. africanus* to enable effective vector targeted control and management of hemorrhagic fevers. *Aedes africanus* has specific behavioral preferences, some of which facilitate their spread within the rapidly changing landscape of Africa. *Ae. africanus* is reportedly confined to forests. However, it was implicated in the peridomestic transmission of YF to humans during the 1987 Nigerian YF epidemic. This study aims to understand the behavior of *Ae. africanus*. Bamboo pots containing water were placed on a 120 feet steel tower in Zika forest, Entebbe. The pots were placed at ground level, platforms at 20, 40, 60, 80, 100 feet above the ground and at shaded spots of the encroached forest buffer zone. Immature samples were collected weekly, reared to maturity and morphologically identified. After 32 weeks, a total of 734 mosquitoes were collected inside the forest, 89% of which were collected at 60 feet and below. A total of 642 *Ae. africanus* mosquitoes were collected at 200 and 400 feet from the forest boundary. These results indicate that *Ae. africanus* prefers to oviposit at levels below the tree canopy. These are shaded areas in the forest and heights at which the host, primates, are found. There is also a tendency for a change from a sylvatic (forest confinement) to a peridomestic behavior. This is probably due to the increased human activities in the forest buffer zone. Encroachment on the forest buffer zone must be strongly discouraged given previous isolations of several arboviruses from the forest, most of which have been isolated in *Ae. africanus*.

## 1388

**SUMILARV 0.5G, A PROMISING INSECTICIDE FOR THE CONTROL OF *ANOPHELES GAMBIAE* S.L.?**Oscar O. Mbare<sup>1</sup>, Steve Lindsay<sup>2</sup>, Ulrike Fillinger<sup>3</sup><sup>1</sup>International Center for Insect Physiology and Ecology, Mbita, Kenya, <sup>2</sup>Durham University, Durham, United Kingdom, <sup>3</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom

Malaria vector control with long-lasting insecticidal nets (LLINs) and indoor residual spraying (IRS) has resulted in a significant decline of malaria in Africa. However, recent reports have shown both behavioural avoidance and physiological resistance to insecticides by vectors. Thus, the need to explore and integrate other tools for malaria vector control. Larval source management is a proven tool for malaria vector control. Difficulties with larviciding are (1) interventions are based at targeting all aquatic habitats and (2) current larvicides have short residual activity requiring weekly application which necessitate large labour and large amounts of larvicides which is not cost effective especially in Africa. Thus the need to evaluate persistent larvicides and study sound application strategies of the persistent larvicides. Sumilarv is a persistent larvicide with great potential for mosquito control. Bioassays showed that Sumilarv was ten times more effective than microbials for *Anopheles* control. Sumilarv application at 0.05 ppm a.i. resulted in 80% emergence inhibition for up to 6 weeks under standardized field conditions. Evaluations of the optimum dose of Sumilarv identified in the standardized field tests are on-going in an area of focal malaria transmission in Western Kenya. Preliminary results from the first three months of field testing indicate that the three week application results on average in 71% emergence inhibition of malaria vectors from treated sites. The use of residual larvicides has a risk of vector production from untreated habitats created or filled with water after larvicide application. Intensive monitoring and sampling of sites is ongoing to estimate this risk in the dry and rainy seasons.

## 1389

**DECLINE IN FREQUENCY OF THE 2LA CHROMOSOMAL INVERSION IN AN *ANOPHELES GAMBIAE* S.S. POPULATION WITH INCREASING USE OF INSECTICIDE TREATED BED NETS IN WESTERN KENYA**Damaris Matoke<sup>1</sup>, Luna Kamau<sup>1</sup>, M. Nabie Bayoh<sup>2</sup>, John Gimnig<sup>3</sup>, Edward Walker<sup>4</sup><sup>1</sup>Centre for Biotechnology Research and Development, KEMRI, Nairobi, Kenya, <sup>2</sup>Centre for Global Health Research, Centers for Disease Control and Prevention/KEMRI, Kisumu, Kenya, <sup>3</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>4</sup>Michigan State University, East Lansing, MI, United States

The 2La chromosomal inversion is polymorphic in populations of *Anopheles gambiae* s.s. and has been positively associated with indoor resting behavior. Although the genotype/phenotype relationship is not precisely known, it is likely adaptive for microclimatic conditions related to humidity. Specifically, reports from West Africa indicate that the 2La arrangement is more common in mosquitoes found resting indoors where a nocturnal saturation deficit exists. Ownership of insecticide treated bed nets (ITNs) has risen rapidly in western Kenya in the last decade, with subsequent declines in malaria transmission and malaria-related mortality and altered vector population genetic structure, with an increase to fixation of the East African kdr allele in *An. gambiae* s.s. Our study focused on the frequency of the 2La chromosomal inversion of *An. gambiae* s.s. in that setting. Adult *An. gambiae* mosquitoes were sampled from 1996 to 2011 in Asembo, an area with high ITN coverage since 1999, and from the adjacent community of Seme, where ITN ownership was <5% in 1999 but increased to over 60% by 2006. The 2La analysis was done using a PCR assay with primers designed for 2La and 2La+ proximal breakpoints and visualization of amplicons by electrophoresis on agarose gels. In Asembo, the frequency of the 2La chromosomal inversion declined from 93% in 1996 to 15% in 2005 and remained low through 2011 (21%). Similarly

in Seme, the frequency declined from 55% in 2000 to 19% in 2005 and remained low in 2008 (17%). These results suggest that high coverage of ITNs may have selected for the 2La+ chromosomal arrangement in *An. gambiae* s.s., a genotype not associated with indoor resting. A possible explanation is that ITNs are effective against indoor resting *An. gambiae* s.s., which are more likely to have the 2La inversion karyotype. Further studies are proposed to determine if populations with the 2La+ karyotype successfully avoid ITNs, and are responsible for maintaining residual malaria transmission in areas with high ITN coverage.

## 1390

**AN EXAMPLE FROM ZAMBIA OF USING NOVEL APPROACHES TO MONITORING AND MANAGE INSECTICIDE RESISTANCE FOR EFFECTIVE VECTOR CONTROL**Michael Coleman<sup>1</sup>, Emmanuel Chanda<sup>2</sup>, Musapa Mulenga<sup>3</sup>, Janet Hemingway<sup>1</sup>, Clare Strode<sup>1</sup><sup>1</sup>Liverpool School of Tropical Medicine, Liverpool, United Kingdom, <sup>2</sup>National Malaria Control Centre, Lusaka, Zambia, <sup>3</sup>Zambia Integrated Systems Strengthening Programme, Lusaka, Zambia

Increased coverage with insecticide treated nets (ITNs) and indoor residual spraying (IRS) with DDT and pyrethroids, have led to impressive decreases in malaria transmission in Zambia. However, the detection of high levels of insecticide resistance in both *Anopheles gambiae* and *An. funestus* is a serious risk to vector control efforts. In 2011 an Insecticide Resistance Management Technical Working Group was established to develop a plan to sustain current control levels and conserve insecticides for malaria control in the country. Here we report on results from bioassays and molecular analysis of resistance mechanisms for two regions, the Copperbelt and Eastern Provinces of Zambia. A high prevalence of resistance to deltamethrin (27% Mortality), permethrin (34%M), etofenprox (5%M) and DDT (6%M) was detected in *An. gambiae* from the Copperbelt; the same populations were susceptible to bendiocarb and malathion. Resistance to the pyrethroids and DDT was due to kdr (the 1014F mutation is fixed in this population) and over expression of several p450's including *CYP6Z3* and *CYP6M3*. *An. funestus* from Eastern Province also exhibited resistance to diagnostic doses of deltamethrin (45% M), permethrin (81.5% M), etofenprox (18%M) and bendiocarb (77% M), but was susceptible to DDT. This population has elevated *CYP6P9a*, *CYP6Z1* and *CYP6M3*. A more susceptible population of *An. funestus* was found in the Copperbelt and only had elevated *CYP6M3*. As well as a different resistance profile in these regions the collections indicated very different malaria vector species abundance patterns that will impact vector control decisions. The impact of this information has allowed the Zambian malaria control programme to move away from ineffective insecticides used in the Copperbelt (DDT) and Eastern (etofenprox) to effective insecticides and to put an insecticide resistance management programme in place with the aim of prolonging the successes already gained. We examine the entomological M&E in Zambia and how lessons learnt here can be applied to other vector control programmes in the region.

## 1391

**A LONG-LASTING *BACILLUS SPHAERICUS* (BS) AND *BACILLUS THURIGIENSIS* VAR *ISRAELENSIS* (BTI) FOR CONTROLLING MALARIA VECTORS: TRIALS FROM KENYA**Yaw A. Afrane<sup>1</sup>, Guofa Zhou<sup>2</sup>, Andrew Githeko<sup>1</sup>, Guiyun Yan<sup>1</sup><sup>1</sup>Kenya Medical Research Institute, Kisumu, Kenya, <sup>2</sup>University of California, Irvine, Irvine, CA, United States

Bio-larvicides are alternatives for larval mosquito control as they are benign to the environment instead of synthetic insecticides. However, the currently available bio-larvicide formulations have a short effective duration, and consequently larval control incurs a high operation expense due to requirement for frequent re-treatment of larval habitats. Therefore, formulation of biological larvicides that has long-lasting effects is highly desired. A recently developed fourStar™ Single Brood Granules (SBG)

of *Bacillus thuringiensis israelensis* (Bti) was evaluated under semi-natural and natural conditions to test its effectiveness in reducing mosquito population in western Kenya. This formulation is designed to be effective against mosquito larvae for up to 6 months. In semi-natural habitats containing soil and rain water, second-instar larvae of *Anopheles gambiae* were introduced and FourStar™ Bti granules dissolved in rain water with appropriate concentrations were added. The number of pupae produced from the larvae was recorded daily as the outcome. Formulation was also tested in natural productive habitats. Formulation was then tested for its efficiency to reduce mosquito population during the transmission season, when it is applied earlier in sentinel sites. Larval control was undertaken in field trials in three sites and with three other sites taken as control. We found 100% mortality rate within 48 hrs after introduction of 2nd instars larvae in semi-natural habitats. The Bs/Bti formulation killed larval mosquitoes for 6 months. Formulation killed larvae for 5 months in natural habitats despite the effects of rain. In larval control field trials the formulation reduced density of mosquitoes in houses from between 60-80% in the intervention sites during the transmission season. Larval control has the potential to reduce the population of malaria mosquitoes. The Bs/Bti briquets present a promising biological formulation to use for larval control. This formulation is recommended to the National Malaria Control programme.

### 1392

#### RE-ASSESSMENT OF DENGUE NEUTRALIZING ANTIBODY AND VIREMIA TITERS IN DENGUE PATIENTS USING FCγR-EXPRESSING CELLS

**Meng Ling Moi**, Chang-kweng Lim, Masayuki Saijo, Tomohiko Takasaki, Ichiro Kurane

*National Institute of Infectious Diseases, Japan, Tokyo, Japan*

One of the major obstacles in dengue vaccine development is the potential infection-enhancement activity induced by vaccination. Sub-neutralizing levels of antibody against dengue virus (DENV) is speculated to enhance infection, and play a central role in the pathogenesis of severe and life-threatening illness, dengue hemorrhagic fever (DHF). General understanding on the biological properties of antibody in protection against dengue infection is based on the titers determined by the use of FcγR-negative cells in conventional neutralizing antibody. Additionally, conventional viremia titration assays do not consider infectious immune complex which may be infectious only through FcγR. Using FcγR-expressing BHK cells and FcγR-negative BHK cells, we examined the infection-enhancement activity and neutralizing activity in serum samples from patients with secondary and primary DENV infection. Serum samples with low neutralizing activity demonstrated infection-enhancing activity and those with high neutralizing activity demonstrated low or no infection-enhancement activity in FcγR-expressing cells. Additionally, neutralizing activity to the infecting DENV serotype detected by using FcγR-negative was absent in FcγR-expressing cells. Higher levels of viremia were detected using FcγR-expressing cells as compared to FcγR-negative cells in serum samples obtained from patients and a dengue non-human primate (NHP) model during secondary dengue infection. The results suggest that DENV-antibody complexes which are incapable of infecting FcγR-negative cells retain infectivity in FcγR-expressing cells due to infection mechanism through FcγR. Our findings suggest that in comparison to FcγR-negative cells, FcγR-expressing cells may better reflect the biological properties of antibodies *in vivo*. In summary, we established an assay which possesses the ability to detect the sum of infection-enhancement and neutralizing activities. The newly developed assay provides a platform to define dengue virus infectivity and viremia titers in the presence of neutralizing and enhancing antibody activities and offer insights into the role of antibodies in protection in natural infection and vaccination.

### 1393

#### DISSECTING HUMAN ANTIBODY RESPONSES TO SILENT AND CLINICALLY-APPARENT DENGUE VIRUS INFECTION

**Kizzmekia S. Corbett**<sup>1</sup>, Hasitha Tissera<sup>2</sup>, Aravinda de Silva<sup>1</sup>, Dharshan de Silva<sup>3</sup>

<sup>1</sup>*University of North Carolina at Chapel Hill, Chapel Hill, NC, United States*, <sup>2</sup>*Sri Lanka Ministry of Health, Colombo, Sri Lanka*, <sup>3</sup>*Genetech Research Institute, Colombo, Sri Lanka*

Dengue is the most significant vector-borne viral disease of humans. The dengue virus (DENV) complex consists of 4 serotypes. Following primary DENV infection people develop immunity to the infecting serotype, but remain susceptible to a second infection with a new serotype. Secondary DENV infections are more likely to result in severe disease than primary infections. Antibody dependent enhancement is proposed to explain this phenomenon. Using prospectively collected samples from a cohort of children from Colombo, Sri Lanka, we explored the quantity and quality of pre-infection antibodies in children who experienced secondary silent and apparent DENV infections. Quantity of DENV-specific IgG was determined by ELISA, and antibody quality was determined by performing virus neutralization or enhancement assays. Children who acquired secondary silent and apparent DENV infections had similar pre-existing DENV-specific IgG levels. However, children who acquired secondary silent DENV infections had pre-existing antibodies that were more broadly neutralizing than children who acquired secondary apparent DENV infections. In this presentation, we will also discuss the ability of pre-infection antibodies from silent and apparent cases to enhance DENV infection of Fc-receptor bearing cell lines and primary human cells. Together, our findings demonstrate how neutralization capacity and enhancement ability of pre-existing antibodies influences disease presentation in secondary dengue infections.

### 1394

#### LONGITUDINAL ANALYSIS OF THE LEVELS OF CROSS-REACTIVE ANTIBODIES RECOGNIZING THE FUSION LOOP OF DENGUE VIRUS AND CORRELATION WITH NEUTRALIZING ANTIBODY TITERS IN NICARAGUAN DENGUE CASES

Chih-Yun Lai<sup>1</sup>, Katherine L. Williams<sup>2</sup>, Yi-Chieh Wu<sup>1</sup>, Angel Balmaseda<sup>3</sup>, Eva Harris<sup>2</sup>, **Wei-Kung Wang**<sup>1</sup>

<sup>1</sup>*Department of Tropical Medicine, University of Hawaii at Manoa, Honolulu, HI, United States*, <sup>2</sup>*Division of Infectious Diseases and Vaccinology, School of Public Health, University of California, Berkeley, Berkeley, CA, United States*, <sup>3</sup>*National Virology Laboratory, National Center for Diagnosis and Reference, Ministry of Health, Managua, Nicaragua*

The envelope (E) protein of dengue virus (DENV) is the major target of neutralizing antibodies (Abs). Previous studies of human convalescent sera after DENV infection revealed that a significant proportion of anti-E Abs recognized the highly conserved fusion loop (FL) of domain II of E protein (FL Abs), whereas a minor proportion recognized domain III. The role of FL Abs in dengue pathogenesis remains unclear. In this study, we tested the hypothesis that cross-reactive FL Abs, though not contributing to the monotypic neutralization profile after primary DENV infection, may play a role in protection against heterologous serotypes after secondary DENV infection. A quantitative virion-capture ELISA was established by using known concentrations of a human anti-E monoclonal Ab as a standard to measure the concentration of anti-E Abs, [anti-E Abs], in sera of dengue patients from Nicaragua. The proportion of FL Abs was determined by a previously described capture ELISA using virus-like particles, and the concentrations of FL Abs, [FL Abs], were calculated. Neutralization titers were determined using a flow cytometry-based neutralization assay with reporter viral particles of the different DENV serotypes. Analysis of sequentially collected serum samples (3M, 6M, 12M and 18M) from 10 cases of primary or secondary DENV infection revealed that [anti-E Abs] and [FL Abs] stabilized at 12 M after infection and were higher in secondary DENV infection cases than in primary infection cases. The [FL

Abs], while not correlated with neutralization titers in primary infection cases, increased as the neutralization titers against heterologous serotypes increased in secondary infection cases. These findings are being verified in sera from 26 additional secondary DENV infection cases. Our results demonstrate the kinetics of FL Abs over time after DENV infection and suggest that FL Abs might play a protective role against heterologous serotypes after secondary DENV infection.

## 1395

### CORRELATION BETWEEN DENGUE VIRUS-SPECIFIC NEUTRALIZATION, SERUM AVIDITY AND ANTIBODY TITERS IN PRIMARY AND SECONDARY DENV-3 NATURAL HUMAN INFECTIONS

Andreas Puschnik<sup>1</sup>, Louis Lau<sup>1</sup>, Angel Balmaseda<sup>2</sup>, **Simona Zompi**<sup>1</sup>, Eva Harris<sup>1</sup>

<sup>1</sup>Division of Infectious Diseases and Vaccinology, School of Public Health, University of California, Berkeley, Berkeley, CA, United States, <sup>2</sup>Laboratorio Nacional de Virología, Centro Nacional de Diagnóstico y Referencia, Ministerio de Salud, Managua, Nicaragua

The 4 serotypes of dengue virus (DENV1-4) infect ~100 million people annually. While heterotypic secondary (2) DENV infection has been associated with severe disease, the vast majority of 2 infections are mild or asymptomatic, suggesting protective cross-reactive immunity in addition to long-lasting homotypic immunity. The mechanism of antibody (Ab)-mediated protection is not well defined. We are analyzing DENV-specific neutralization titer, IgG avidity and Ab titer in well-characterized serum samples from a pediatric dengue hospital-based study in Managua, Nicaragua. In 2010, 130 DENV-positive cases were enrolled (primary (1) n=75; 2 n=55), with DENV3 as the dominant serotype (83.1%). The 50% neutralization titer (NT<sub>50</sub>) was measured by flow cytometry. Avidity and Ab titer were measured by a modified ELISA with urea washes and by Inhibition ELISA, respectively. We observed a significant increase in avidity vs. DENV3 between the convalescent and 3-month (3m) timepoints (% IgG bound = 45.8 vs. 82.6, p<0.0001) in 1 infections, reflecting affinity maturation. We also noted a significant increase in avidity between the acute and convalescent phase in 2 infections (69.2% vs 79.7, p=0.0015), without further increase over time (3-6m), attributable to newly formed Ab against the current infecting serotype. The NT<sub>50</sub> peaked at convalescence in both 1 and 2 cases, with significantly higher titer detected in 2 cases (5284 ± 683 vs. 11476 ± 1183, p<0.0001). In the convalescent phase and 3m after 1 infection, neither DENV3-specific avidity nor DENV-specific Ab titer correlated with DENV3-specific NT<sub>50</sub>, implying that either innate immune and/or naïve T cell responses and/or low-avidity Abs control 1 infections. In acute 2 infections, we observed a correlation between avidity and NT<sub>50</sub> vs. DENV3 (Spearman r=0.50, p=0.002) and a correlation with DENV-specific Ab titers (Spearman r=0.61, p<0.0001), most likely reflecting an expansion of cross-reactive DENV-specific memory B cells formed during the previous infection. We are currently processing these samples against DENV2, the most likely 1 infecting serotype, to confirm this hypothesis. Lastly, we find that at the 3m timepoint, DENV3-specific avidity correlates positively with DENV3-specific NT<sub>50</sub> (Spearman r=0.49, p=0.0015). A better understanding of the protective immune response in natural infections is critical for the development of safe and effective vaccines.

## 1396

### MAPPING ENHANCING ANTIBODIES PRODUCED BY THE HUMAN IMMUNE RESPONSE AFTER PRIMARY DENGUE VIRUS INFECTIONS

**Ruklanthi de Alwis**<sup>1</sup>, Katherine L. Williams<sup>2</sup>, Eva Harris<sup>2</sup>, Aravinda M. de Silva<sup>1</sup>

<sup>1</sup>University of North Carolina at Chapel Hill, Chapel Hill, NC, United States,

<sup>2</sup>University of California, Berkeley, Berkeley, CA, United States

Dengue virus (DENV) is a mosquito-borne flavivirus of global significance. DENV exists as four serotypes, named DENV1 through DENV4. Following a primary infection, individuals produce a mixture of type-specific and cross-reactive antibodies (Abs). Pre-existing immunity is sufficient to protect against re-infection with the same serotype, but may enhance infection and increase disease severity during a secondary infection with one of the other three DENV serotypes. A leading theory to explain the higher frequency of severe disease is the antibody-enhancement (ADE) theory, where a fraction of pre-existing DENV-specific Abs are thought to bind viral particles and aid infection of host cells through Fcγ receptors. Due to the complexity of the human humoral immune response, the enhancing anti-DENV Abs within human polyclonal sera have not been well characterized. Previously, Abs in DENV-immune human sera were fractionated using DENV virions, and the role of specific antibody populations in DENV enhancement was investigated in cell culture and in the AG129 mouse model of DENV infection and disease. We demonstrated that people exposed to primary DENV infections have serotype-specific and serotype cross-reactive populations of circulating Abs. The serotype-specific Abs were responsible for neutralization of the homologous serotype, whereas the serotype cross-reactive Abs were responsible for ADE of heterologous serotypes. The ability of the serotype cross-reactive Abs to enhance DENV was observed both *in vitro* and *in vivo*. Further studies were then performed to identify the antigens and epitopes engaged by enhancing Abs in human serum by fractionating DENV-immune sera using recombinant viral proteins and assaying the depleted sera in *in vitro* ADE assays and in the AG129 mouse model. Our studies demonstrate that enhancing Abs in DENV-immune sera recognize epitopes on E protein as well as prM. Further studies are in progress to quantify the relative contribution of Abs against different antigens to ADE and to map specific epitopes responsible for ADE.

## 1397

### ANTIBODY RESPONSES TO THE DENGUE VIRUS PROTEOME DURING SEASONAL OUTBREAKS OF INFECTION

Stefan Fernandez<sup>1</sup>, Emily D. Cisney<sup>2</sup>, Sarah L. Keasey<sup>2</sup>, Stephen J. Thomas<sup>3</sup>, Jorge Munoz<sup>4</sup>, **Robert G. Ulrich**<sup>2</sup>

<sup>1</sup>Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand,

<sup>2</sup>United States Army Medical Research Institute of Infectious Diseases, Frederick, MD, United States, <sup>3</sup>Walter Reed Army Institute of Research, Silver Spring, MD, United States, <sup>4</sup>Centers for Disease Control and

Prevention, Dengue Branch, San Juan, PR, United States

Dengue is a mosquito-borne infection caused by four distinct serotypes of dengue virus, each appearing cyclically in the tropics and subtropics along the equator. The viral proteome is comprised of capsid, membrane, envelope and the non-structural (NS) proteins NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5. Though each of these proteins synthesized during infection are potential targets of host defenses, current knowledge of the immune response to the DENV proteome is limited. Here we describe a protein microarray approach for measuring antibody responses to the complete viral proteome of dengue virus serotypes 1-4. Using this microarray, we examined humoral immunity to dengue occurring during seasonal outbreaks in Puerto Rico, and identified unique immunological profiles resulting from pediatric and adult infections. Our results demonstrate discriminating details concerning the nature of antibody responses to dengue virus at the proteomic level and suggest the usefulness of this information for vaccine development.

## 1398

**CONSIDERING THE ROLE OF ANTIBODY IN DENGUE VIRUS CLEARANCE: DATA ANALYSIS AND MODELLING**

Hannah E. Clapham<sup>1</sup>, Than Ha Quyen<sup>2</sup>, Duong Thi Hue Kien<sup>2</sup>, Cameron P. Simmons<sup>2</sup>, Neil M. Ferguson<sup>1</sup>

<sup>1</sup>Imperial College, London, United Kingdom, <sup>2</sup>OUCRU, HCMC, Vietnam

Antibodies in dengue infection are thought to play a critical role in controlling infection, but also may enhance viral replication in secondary infection via the phenomenon of antibody-dependent enhancement. Here, we consider mainly the former role, using sequentially sampled measurements of virus and antibody titres (IgM, IgG, anti-E IgG and anti-D3 IgG) from patients hospitalised with dengue infection in Vietnam. Analysis of such data is not straightforward, due to differences in timing of measurements relative to virus peak and symptoms onset, however using multiple sequential measurements from throughout natural infections is an excellent way to consider the interaction between virus and the immune response. In addition to descriptive statistical analyses, we fitted a mechanistic mathematical model of dengue pathogenesis within the human host to these data to investigate whether the observed kinetics were compatible with antibody playing the dominant role in controlling viral replication. A model variant which assumes clearance of virus or infected cells is proportional to overall IgM titres is able to fit data from both primary and secondary infections, and the same model with clearance proportional to overall IgG titres is able to fit data from secondary infections. However, this fit relies on variation in how much measured antibody is useful, and in some individuals there are issues in timing of virus peaks and antibody increase. A model for secondary infections in which viral clearance rates were proportional to anti-E IgG titres gives, in most cases, the best model fit, overcoming some of these issues. We will also present extensions to this work to include mechanistically the interactions between the different antibody measures. Interestingly, for all model fits, we estimate that the level of antibody required to control viral replication is low, and over an order of magnitude below the peak titres reached by the time infection is cleared. In our presentation we will consider the implications of this result for measurement of antibody kinetics.

## 1399

**INNOVATIVE IMMUNOLOGICAL ASSAYS FOR DIAGNOSIS OF SCHISTOSOMA MANSONI FOR CLINICAL ACUTE AND/OR CHRONIC FORMS**

Rafaella F. Queiroz<sup>1</sup>, Donald A. Harn<sup>2</sup>, Paulo Marcos Z. Coelho<sup>1</sup>

<sup>1</sup>Oswaldo Cruz Foundation, Belo Horizonte, Brazil, <sup>2</sup>University of Georgia, Veterinary Medicine School, Department of Infectious Diseases, Athens, GA, United States

Control constraints of schistosomiasis include the lack of diagnostic methods with high sensitivity. We initiated a prospective study in southeast Brazil in order to develop sensitive diagnostic methods for *Schistosoma mansoni* infection. Residents on 3 endemic areas in Minas Gerais state, together with 84 travelers infected in a freshwater pool on a country house located on a new focus of the disease, participate of this survey. Sera samples from all those patients are used for the standardization of innovative methods for schistosomiasis mansoni. Comparisons are performed with the presence of eggs in faecal samples, IgG antibody titers, presence of eggs in liver after biopsy, encephalomyelitis by magnetic resonance imaging, and/or clinical symptoms. The first assay using schistosomula antigen is capable of properly diagnosing all the 84 travelers with clinical acute form as soon as 10 days post-infection, including patients with severe hepatic form and encephalomyelitis. Two other assays using egg and adult worm antigens are capable of detecting more than 95% of positive cases from chronic and low parasite load patients (1-36epg). A forth method called Immunomagnetic separation (IMS) was developed in order to concentrate sera samples. We used several antigens, in separate, for IgG titers detection, as purified glycoprotein

Circulating Cathodic Antigen (CCA), CCA recombinant protein (CCAr), and five different types of peptides (10 amino acids each) of CCA. Data showed that IMS is superior to ELISA ( $p=0.001$ ) since it is capable of detecting a higher number of positive patients. The purified CCA was not a good candidate due to its susceptibility for cross reaction. On the contrary, peptides and especially CCAr, are excellent tools for the differential diagnosis with 100% of sensitivity. Furthermore, IMS method was standardized for a direct detection of CCA in sera. For that matter, monoclonal antibodies against the protein portion of the native CCA (MAb-CCA) were produced. Using only 0.05ml of concentrated sera, we were able to detect 100% of chronic patients and 98% of patients with acute form of the disease. Finally, a last methodology were developed, a qualitative method using magnetic beads and CCA-MAb conjugated to Alexa Fluor for the direct visualization of fluorescent CCA in sera samples. A double-blinded study showed that 3 slides of each sample are sufficient to achieve a sensitivity of 98% and a specificity of 95%.

## 1400

**DIAGNOSTIC APPROACHES FOR PEDIATRIC TUBERCULOSIS AMONG HIV-INFECTED AND HIV-UNINFECTED CHILDREN IN PERU**

Richard A. Oberhelman<sup>1</sup>, Giselle Soto-Castellares<sup>2</sup>, Robert H. Gilman<sup>3</sup>, Luz Caviedes<sup>4</sup>, Maria Castillo<sup>5</sup>, Lenka Kolevic<sup>5</sup>, Mayuko Saito<sup>6</sup>, Eduardo Salazar-Lindo<sup>7</sup>, Sonia Montenegro<sup>8</sup>, V. Alberto Laguna-Torres<sup>9</sup>, Carlton A. Evans<sup>9</sup>

<sup>1</sup>Tulane School of Public Health and Tropical Medicine, New Orleans, LA, United States, <sup>2</sup>U.S. Naval Medical Research Unit Six, Lima, Peru, <sup>3</sup>Department of International Health, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, United States, <sup>4</sup>Department of Microbiology, Universidad Peruana Cayetano Heredia, Lima, Peru, <sup>5</sup>Infectious Diseases Service; Instituto Nacional de Salud del Niño, Lima, Peru, <sup>6</sup>Asociación Benéfica Proyectos en Informática, Salud, Medicina y Agricultura (PRISMA), Lima, Peru, <sup>7</sup>Department of Pediatrics, Hospital Nacional Cayetano Heredia, Lima, Peru, <sup>8</sup>Universidad de Concepción, Concepción, Chile, <sup>9</sup>Wellcome Trust Centre for Clinical Tropical Medicine and Department of Infectious Diseases and Immunity, Imperial College, London, United Kingdom

Children with pulmonary tuberculosis (PTB) usually present with paucibacillary disease and without sputum, and HIV co-infection may further complicate diagnostic testing. We evaluated HIV-infected Peruvian children with suspected PTB with a series of culture and PCR-based techniques, and compared results from these subjects with similar results from HIV-infected controls and from HIV-negative cases and controls. TB culture and a heminested IS 6110 polymerase chain reaction (PCR) assay were performed on specimens from children with symptoms of PTB and well controls. Two specimens of each type (gastric aspirates [GA], nasopharyngeal aspirates [NPA], and stools) from each case were examined by 1) auramine smear, 2) broth culture by Microscopic-Observation Drug-Susceptibility (MODS) technique, 3) standard culture on Lowenstein Jensen (LJ) agar, and 4) PCR. Specimens from controls included one NPA and 2 stools. The study included 209 HIV-negative cases, 81 HIV-positive cases, 200 HIV-negative controls, and 35 HIV-positive controls. Overall, 22 HIV-negative case subjects (10%) had at least one positive TB culture. In contrast, TB was only isolated from one HIV-positive case (1.2%), from both GA specimens only ( $p<0.01$ ). In contrast to the difference in TB isolation between HIV-positive and HIV-negative cases, the proportions of subjects in these groups with at least one positive PCR result were similar, and both case groups had more positive PCR results than the HIV-negative controls ( $p<0.001$ ). Rates of PCR positive specimens were similar for HIV-positive cases and controls. In contrast to reports from Africa, TB recovery from HIV-positive patients with suspected PTB in our Peruvian pediatric population is less common. In spite of the differences in culture-based MTB recovery, HIV-positive cases had similar rates of PCR-positive specimens as compared to HIV-negative case subjects. These PCR-positive, culture-negative specimens may reflect paucibacillary disease, or in HIV-positive controls they may indicate latent or subclinical infection.

### PEPTIDE YY, GHRELIN, LEPTIN AND IL-10 AS MEDIATORS OF APPETITE AND RESPONSE TO TREATMENT IN PERUVIAN ADULTS WITH TUBERCULOSIS

**Nancy Vu**<sup>1</sup>, Daniela E. Kirwan<sup>2</sup>, Jose Lopez<sup>3</sup>, Raul Montalvo<sup>4</sup>, Robert Gilman<sup>5</sup>, Eduardo Ticona<sup>6</sup>, Lilia Cabrera<sup>7</sup>, Jose Cabrera<sup>8</sup>, Nancy Chile<sup>9</sup>, Luz Caviedes<sup>10</sup>

<sup>1</sup>Department of Internal Medicine, University of Utah, Salt Lake City, UT, United States, <sup>2</sup>Imperial College London, London, United Kingdom, <sup>3</sup>CRONICAS-Center of Excellence in Chronic Diseases, Lima, Peru, <sup>4</sup>Committee of Infections, Hospital Nacional Dos de Mayo, Lima, Peru, <sup>5</sup>Johns Hopkins University, Bloomberg School of Public Health, Baltimore, MD, United States, <sup>6</sup>Service of Infectious and Tropical Diseases, Hospital Nacional Dos de Mayo, Lima, Peru, <sup>7</sup>Asociacion Benefica PRISMA, Lima, Peru, <sup>8</sup>Department of Pulmonology, Hospital Daniel A. Carrion, Lima, Peru, <sup>9</sup>Department of Cellular and Molecular Sciences, School of Sciences and Philosophy, Universidad Peruana Cayetano Heredia, Lima, Peru, <sup>10</sup>Department of Microbiology, Cayetano Heredia University, Lima, Peru

Cachexia is one of the sentinel symptoms of pulmonary tuberculosis (TB). TB causes an inflammatory response that leads to alterations of appetite hormones affecting appetite and satiety. Yet the relationship of TB disease severity and appetite hormone levels has not been well studied, despite its potential utility as an indication of treatment failure. 23 adult patients with sputum positive TB were evaluated on days 0, 14, and 28 days of treatment by Simplified Nutritional Appetite Questionnaire (SNAQ), body mass index (BMI), and appetite and inflammatory markers. Peptide YY, ghrelin, leptin, and IL-10 levels were determined using Luminex and ELISA kits. We also administered a questionnaire to qualitatively determine appetite. Appetite questionnaire results trended towards a gain in appetite with treatment, displaying a significant difference between day 0 vs.14 ( $p=0.004$ ) and day 28 ( $p=0.0095$ ). Peptide YY levels dropped 14.6% by Day 14 of treatment (not significant), while ghrelin levels dropped 54% by Day 14 ( $p<0.05$ ). Leptin levels increased 67.36% by day 28 of treatment ( $p<0.05$ ), and the anti-inflammatory cytokine IL-10 decreased 12.5% by Day 14 (not significant). Subjective appetite improved with treatment as early as day 14, while BMI was slower to respond and still had not increased significantly by day 30. Delayed recovery of weight gain suggests that the increase in leptin is secondary to TB infection. Wasting in TB patients may partly be mediated by upregulation of anorexigenic PYY with resulting appetite suppression. Decrease in IL-10 levels may indicate intact immunity with normal response to treatment. Deviation from improving appetite status, clinical factors and appetite hormone levels may be used to detect treatment failure in cases such as multi-drug-resistant TB. While loss of appetite is a well-known symptom of TB, little work has been done in utilizing measurements of appetite in the characterization of the disease, and this work suggests that it may be a useful indicator of treatment success.

### BRUCellosIS AMONG HOSPITALIZED FEBRILE PATIENTS IN NORTHERN TANZANIA

**Andrew J. Bouley**<sup>1</sup>, Holly M. Biggs<sup>1</sup>, Robyn A. Stoddard<sup>2</sup>, Anne B. Morrissey<sup>1</sup>, John A. Bartlett<sup>1</sup>, Isaac A. Afwamba<sup>3</sup>, Venance P. Maro<sup>4</sup>, Grace D. Kinabo<sup>4</sup>, Wilbrod Saganda<sup>5</sup>, Sarah Cleaveland<sup>6</sup>, John A. Crump<sup>1</sup>

<sup>1</sup>Division of Infectious Diseases and International Health, Department of Medicine, Duke University Medical Center, Durham, NC, United States, <sup>2</sup>Bacterial Special Pathogens Branch, Division of High Consequence Pathogens and Pathology, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>3</sup>Kilimanjaro Christian Medical Centre, Moshi, United Republic of Tanzania, <sup>4</sup>Kilimanjaro Christian Medical College, Tumaini University, Moshi, United Republic of Tanzania, <sup>5</sup>Mawenzi Regional Hospital, Moshi, United Republic of Tanzania, <sup>6</sup>College of Medicine, Veterinary Medicine and Life Sciences, University of Glasgow, Glasgow, United Kingdom

Brucellosis is an important cause of zoonotic disease worldwide. However, non-specific clinical features, low clinical suspicion, and lack of access to adequate diagnostic services result in brucellosis being underdiagnosed and untreated in many low-resource countries. Human clinical data are scarce in sub-Saharan Africa. Acute and convalescent serum samples were collected from febrile inpatients admitted to two hospitals in Moshi, Tanzania serving a catchment area dominated by smallholder farming communities. Confirmed brucellosis was defined as a positive blood culture for *Brucella* spp or a  $\geq 4$ -fold increase in microagglutination test (MAT) titer, and probable brucellosis was defined as a single reciprocal titer  $\geq 160$ . A total of 870 patients were enrolled in the study, 403 (46.3%) adults and adolescents and 467 (53.7%) infants and children. Of 455 participants with paired sera tested for brucellosis, 16 (3.5%) met criteria for confirmed brucellosis. Of 830 participants with  $\geq 1$  serum sample, 4 (0.5%) met criteria for probable brucellosis. Five (31.3%) of the participants with confirmed brucellosis were female. The median (range) age of participants with confirmed brucellosis was 28.4 (1.1, 68.5) years. Brucellosis was associated with increased median age ( $p = 0.024$ ), leukopenia (odds ratio [OR] 7.8,  $p = 0.005$ ), thrombocytopenia (OR 3.9,  $p = 0.018$ ), and evidence of other zoonoses (OR 3.2,  $p = 0.026$ ). There was no association between brucellosis and rural residence, hepato- or splenomegaly, lymphadenopathy, anemia, pleural effusion, or HIV. Brucellosis was never diagnosed clinically. Although all participants with brucellosis received antibacterials or antimalarials in the hospital, none received standard brucellosis treatment. Brucellosis is an underdiagnosed and untreated cause of febrile disease among hospitalized adult and pediatric patients in northern Tanzania. Increased clinician awareness, access to reliable diagnostic tests, and additional research on risk factors are needed to identify, appropriately manage, and prevent brucellosis in this area.

### INFECTIOUS DISEASES ARE A LARGER CONTRIBUTOR THAN OBSTETRIC CAUSES TO MATERNAL MORTALITY IN RURAL WESTERN KENYA

**Meghna Desai**<sup>1</sup>, Penelope A. Phillips Howard<sup>2</sup>, Frank O. Odhiambo<sup>1</sup>, Abraham Katana<sup>1</sup>, Peter Ouma<sup>1</sup>, Mary Hamel<sup>3</sup>, Annemieke van Eijk<sup>2</sup>, Kayla F. Laserson<sup>1</sup>

<sup>1</sup>Kenya Medical Research Institute/Centers for Disease Control and Prevention, Kisumu, Kenya, <sup>2</sup>Liverpool School of Tropical Medicine, Liverpool, United Kingdom, <sup>3</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States

Improving maternal health is a high priority for the United Nations' development agenda where it is targeted as the fifth Millennium Development Goal. In Kenya, the maternal mortality ratio remains high, at 488 per 100,000 live births per the 2008/09 Demographic Health Survey.

It is commonly assumed that maternal deaths are primarily a result of direct obstetric complications that occur around the time of childbirth. We conducted descriptive analyses of data from a Health and Demographic Surveillance System encompassing a population of approximately 220,000 individuals in rural western Kenya, an area that bears a disproportionate share of infectious diseases. Standard WHO methodology for verbal autopsy (VA) was implemented to determine contributors to maternal mortality (defined as the death of a woman while pregnant or within 42 days of the termination of pregnancy). The maternal mortality ratio for the six year period between 2003 and 2008 was 740 per 100,000 live births, with no evidence for a linear trend over time. Of 249 maternal deaths, one-third (n=85) were due to directly ascribed causes, predominantly by postpartum hemorrhage (n=22), complications from abortion/miscarriage (n=14), and puerperal sepsis (n=13). However, the majority of maternal deaths (n=164) were classified through VA as deaths from infectious diseases, predominantly from HIV (n=74), malaria (n=22) and TB (n=16). While the impact of HIV on maternal mortality has been previously recognized, in this area with high levels of malaria transmission, malaria was also a significant factor among deaths of pregnant or recently delivered women (65 maternal deaths associated with malaria per 100,000 live births). This was equal to the number of directly attributed obstetrical deaths due to documented postpartum hemorrhage. These data add to our awareness of the relationship between infectious diseases and poor maternal outcomes in Africa. Our data suggest that improved access to, and increased uptake of, emergency obstetric care, as well as preventive measures against HIV, malaria and TB among all women of childbearing age, will result in measurable impact on maternal health outcomes.

#### 1404

##### SCABIES COMMUNITY PREVALENCE AND MASS TREATMENT IN TWO FIJIAN VILLAGES

Karin Haar<sup>1</sup>, Lucia Romani<sup>2</sup>, Raikanidoda Filimone<sup>3</sup>, Kamal Kishore<sup>3</sup>, Meciusela Tuicakau<sup>3</sup>, Josefa Koroivueta<sup>3</sup>, Handan Wand<sup>2</sup>, John M. Kaldor<sup>2</sup>, Andrew Steer<sup>2</sup>, **Margot J. Whitfeld<sup>4</sup>**

<sup>1</sup>Robert Koch Institute, Berlin, Germany, <sup>2</sup>Kirby Institute, Sydney, Australia, <sup>3</sup>Ministry of Health, Suva, Fiji, <sup>4</sup>St. Vincents Hospital, Sydney, Australia

Scabies is a major public health problem with complications caused by bacterial secondary infection. A community mass treatment study in two Fijian villages was undertaken to compare the efficacy and tolerability of topical benzyl benzoate and oral ivermectin. Two research sites with approximately 600 inhabitants each were chosen, and study participants enrolled, completed questionnaires and examined to assess for scabies. In one village participants received benzyl benzoate and in the other either oral ivermectin or, for children under 2 years, permethrin cream. At follow-up, participants were re-examined and possible adverse events documented. Pre and post-treatment questionnaires included questions regarding history, itch, adverse events and satisfaction with treatment. Although ethnic and age demographics were similar in the two villages, scabies prevalence rates differed significantly, 38% and 24%. Prevalences in both villages were particularly high in children, with superinfection of scabies lesions common. Only 43% of those treated returned for follow-up overall. The scabies prevalence rate in those who returned for follow-up dropped from 37.9% to 19.9% after treatment with benzyl benzoate, compared to 23.7% and 9.5% following ivermectin treatment. Thus scabies prevalence was reduced by 53% following therapy with benzyl benzoate, and by 52% in those who received ivermectin. People treated with benzyl benzoate more commonly reported initial worsening of itch and of pre-existing dermatologic conditions after application than those treated with ivermectin. No serious side effects occurred with either treatment, and patient satisfaction did not differ between the treatments. In conclusion, mass treatment with oral or topical therapy in a village setting with high prevalence of scabies is feasible. Despite the difficulties in assessing ongoing active scabies infestation when the papules persist, a reduction in scabies prevalence of 53% and 52% was recorded.

#### 1405

##### FACTORS INFLUENCING ATTENDANCE AT TREATMENT AND PREVENTION CLINICS BY PATIENTS WITH PODOCONIOSIS IN SOUTHERN ETHIOPIA: A QUALITATIVE STUDY

**Ababayehu Tora<sup>1</sup>**, Gail Davey<sup>2</sup>, Getnet Tadele<sup>3</sup>

<sup>1</sup>Wolaita Sodo University, Wolaita Sodo, Ethiopia, <sup>2</sup>Brighton and Sussex Medical School, Brighton, United Kingdom, <sup>3</sup>Addis Ababa University, Addis Ababa, Ethiopia

Podoconiosis is a lymphoedema of non-infectious cause which results in long-term ill health in affected individuals. Simple, effective treatment is available in certain parts of Ethiopia, but anecdotally, not all patients continue collecting treatment supplies from clinic sites once started. We used qualitative techniques to explore factors affecting continued collection of treatment supplies from outreach clinics of a non-government organization in southern Ethiopia. A cross-sectional qualitative study was conducted in four clinic sites through unstructured in-depth individual interviews, key informant interviews and focus group discussions with the involvement of 88 study subjects. Sub-optimal continuation with clinic visits is common among podoconiosis patients. The reasons were: remoteness from the clinic sites, unrealistic expectation of 'special' aid, worry about increasing stigma, illness, misconceptions about treatment, and being too busy. Several of these factors are remediable through community and individual information and education. Appropriate routes to deliver this information must be identified. Certain factors (such as distance to clinic sites and stigma) require substantial expansion of services or liaison with village-level government health services.

#### 1406

##### PREVENTION OF TUNGIASIS AND TUNGIASIS-ASSOCIATED MORBIDITY USING A HERBAL REPELLENT: A RANDOMIZED CONTROLLED FIELD STUDY IN RURAL MADAGASCAR

**Hermann Feldmeier<sup>1</sup>**, Marlene Thieleck<sup>1</sup>, Vaomalala Raharimanga<sup>2</sup>, Charles-Emile Ramarakoto<sup>2</sup>, Angela Schuster<sup>1</sup>, Fanomezantsoa Randriamanantena<sup>3</sup>, Christophe Rogier<sup>2</sup>, Vincent Richard<sup>2</sup>

<sup>1</sup>Institute of Microbiology and Hygiene, Charité University Medicine, Berlin, Germany, <sup>2</sup>Institut Pasteur de Madagascar, Antananarivo, Madagascar, <sup>3</sup>Ministère de la Santé de Madagascar, Antananarivo, Madagascar

Tungiasis (sand flea disease) is a neglected tropical disease. It is endemic in many resource poor populations in South America, the Caribbean and in sub-Saharan Africa and is associated with significant morbidity. Since there is no effective drug treatment, prophylaxis is the only means to prevent sand flea disease. In a randomized, controlled field study in rural Madagascar, two preventive measures were compared: the twice-daily application of Zanzarin (a repellent based on coconut oil) on the feet and the free distribution of closed shoes. A control group was left without any intervention. Over a period of 10 weeks, study participants were examined every two weeks and the number of newly penetrated sand fleas, the total number of lesions, the proportion of different developmental stages, and tungiasis-associated morbidity were determined quantitatively. Compared to the control group, the total number of penetrated sand fleas decreased only by 5% after the distribution of shoes. The regular application of Zanzarin reduced the parasite load by 85%. In the shoe group, the median attack rate fell by 22%, in the Zanzarin group by 95%. The distribution of shoes reduced tungiasis-associated morbidity only marginally. The protective effect of shoes was related to the regularity with which shoes were worn. After 10 weeks of application of the repellent tungiasis-associated morbidity had disappeared almost completely. The study shows that twice-daily application of a repellent based on coconut oil provided an excellent protection against the development of sand flea disease. The free distribution of shoes had only a minimal protective effect, mainly because shoes were not worn regularly.



### IMPACT OF INTRODUCTION OF THE *HAEMOPHILUS INFLUENZAE* TYPE B CONJUGATE VACCINE INTO CHILDHOOD IMMUNIZATION ON MENINGITIS IN BANGLADESHI INFANTS

Nadira S. Kakoly<sup>1</sup>, Samir K. Saha<sup>2</sup>, Hassan M. Al-Emran<sup>2</sup>, Joyanta K. Modak<sup>2</sup>, Yushuf Sharker<sup>1</sup>, Shams El Arifeen<sup>1</sup>, Adam L. Cohen<sup>3</sup>, Abdullah H. Baqui<sup>4</sup>, Stephen P. Luby<sup>1</sup>

<sup>1</sup>International Centre for Diarrhoeal Disease Research, Bangladesh, Dhaka, Bangladesh, <sup>2</sup>Dhaka Shishu Hospital, Dhaka, Bangladesh, <sup>3</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>4</sup>Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, United States

Some Asian countries have been reluctant to adopt Hib vaccination because of uncertainty over disease burden. We assessed the impact of introduction of Hib conjugate vaccine into the Expanded Program on Immunization (EPI) in Bangladesh on purulent and laboratory confirmed *Haemophilus influenzae* meningitis. Within a well-defined catchment area around two surveillance hospitals in Dhaka, Bangladesh, we compared the incidence of Hib meningitis confirmed by culture, latex agglutination and polymerase chain reaction (PCR) assay among infants one year before and one year after introduction of Hib vaccine. We adjusted the incidence rate for the proportion of children who sought care at the surveillance hospitals. Among infants, the incidence of confirmed Hib meningitis decreased from 92 to 16 cases per 100 thousand within 1 year of vaccine introduction [Vaccine preventable incidence (VPI) =76; 95% CI: 18, 135/ 100 thousand]. The incidence of purulent meningitis decreased from 1659 to 1159 per 100 thousand [VPI=500; 95% CI: 203, 799/ 100 thousand]. During the same time period, there was no significant difference in the incidence of meningitis due to *Streptococcus pneumoniae*. Introduction of conjugate Hib vaccine into Bangladesh EPI markedly reduced the burden of Hib and purulent meningitis.

### IMMUNOGENICITY, SAFETY, DOSE AND SCHEDULE RESPONSE OF A MENINGOCOCCAL GROUP A CONJUGATE VACCINE IN INFANCY: A HOPE FOR ROUTINE IMMUNIZATION IN THE AFRICAN MENINGITIS BELT

Abraham Hodgson<sup>1</sup>, Patrick Ansah<sup>1</sup>, Godwin Enwere<sup>2</sup>, Julie Chaumont<sup>2</sup>, Helen Findlow<sup>3</sup>, Cheryl Elie<sup>4</sup>, Emanuele Montomoli<sup>5</sup>, Nana Akosua Ansah<sup>1</sup>, Philip Ayivor<sup>1</sup>, Oscar Bangre<sup>1</sup>, Valerio Stanzani<sup>5</sup>, Gandhali Paranjape<sup>6</sup>, Amber Randall<sup>7</sup>, Fred Binka<sup>1</sup>, Elisa Marchetti<sup>2</sup>, Marc LaForce<sup>2</sup>, Ray Borrow<sup>3</sup>, George Carlone<sup>4</sup>, Prasad Kulkarni<sup>8</sup>, Brian Plikaytis<sup>4</sup>, Simonetta Viviani<sup>2</sup>, Yuxiao Tang<sup>9</sup>, Marie-Pierre Preziosi<sup>10</sup>

<sup>1</sup>Navrongo Health Research Center, Navrongo, Ghana, <sup>2</sup>Meningitis Vaccine Project (MVP), PATH, Ferney-Voltaire, France, <sup>3</sup>Health Protection Agency, Manchester, United Kingdom, <sup>4</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>5</sup>University of Siena, Siena, Italy, <sup>6</sup>DiagnoSearch Life Sciences, Mumbai, India, <sup>7</sup>Axio Research, Seattle, WA, United States, <sup>8</sup>Serum Institute of India, Pune, India, <sup>9</sup>MVP, PATH, Seattle, WA, United States, <sup>10</sup>MVP, World Health Organization, Geneva, Switzerland

Meningitis epidemics remain a major plague in countries in the African meningitis belt, with group A meningococcus being the predominant causal agent. An affordable meningococcal group A conjugate vaccine was developed through the Meningitis Vaccine Project, and introduced at public health scale in 2010-11, using single dose mass campaigns among 1 to 29 year-olds in 6 out of 26 target countries of the meningitis belt, with extremely promising results. Roll-out in all countries is ongoing. To maintain population immunity level after initial campaigns, protection of new birth cohorts should be achieved early in life. We conducted a dose ranging study of the newly developed MenA conjugate vaccine in infants to evaluate the safety and immunogenicity of three different doses administered in a two dose schedule at 14 weeks and 9 months, or in one dose schedules at 9 or 12 months concomitantly with the EPI vaccines. Starting in 2008, 1198 infants were recruited in the Kassena

Nankana districts of Northern Ghana and followed up till 2012. Results confirmed noninferiority of the alternate dosages to the licensed dosage. No significant interferences with co-administered EPI vaccines were found. The proportions of subjects with seroconversion at Day 28 post 9 months vaccination were high and similar in all MenA vaccine groups (1 or 2 doses regimens), but the magnitude of the responses was higher in subjects previously primed with MenA vaccine (2 doses regimens vs. 1 dose regimen), nonetheless administration of a single dose at 9 months of age induced a high immune response. No significant safety concerns were identified. The majority of adverse events were due to infections consistent with background morbidity in the area. Sustainable protection from MenA disease among new birth cohorts could be achieved through immunization starting in late infancy at 9 months. This could be a powerful strategy for sub-Saharan countries, leveraging on vaccine herd protection effect, preventing overcrowding early infancy schedules, and allowing paired administration of the MenA with that of the measles vaccine.

### PERSISTENT, WIDESPREAD OUTBREAK OF TYPHOID FEVER ASSOCIATED WITH INTESTINAL PERFORATIONS - BUNDIRUGYO AND KASESE DISTRICTS, UGANDA, 2009-2011

Maroya S. Walters<sup>1</sup>, Janell Routh<sup>1</sup>, Matthew Mikoleit<sup>1</sup>, Samuel Kadivane<sup>2</sup>, Caroline Ouma<sup>3</sup>, Denis Mubiru<sup>4</sup>, Ben Mbusa<sup>5</sup>, Amos Murangi<sup>6</sup>, Emmanuel Ejoku<sup>7</sup>, Absalom Rwantangle<sup>8</sup>, John Lule<sup>9</sup>, Richard Wod-Ongom<sup>9</sup>, Nancy Garrett<sup>1</sup>, Jessica Halpin<sup>1</sup>, Nikki Maxwell<sup>1</sup>, Fred Mulabya<sup>10</sup>, Molly Freeman<sup>1</sup>, Kevin Joyce<sup>1</sup>, Vince Hill<sup>1</sup>, Robert Downing<sup>9</sup>, Eric Mintz<sup>1</sup>

<sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>2</sup>Kenya Field Epidemiology Training Program, Kisumu, Kenya, <sup>3</sup>Centers for Disease Control and Prevention-Kenya, Kisumu, Kenya, <sup>4</sup>Uganda Central Public Health Laboratory, Kampala, Uganda, <sup>5</sup>Bundibugyo District Health Office, Bundibugyo, Uganda, <sup>6</sup>Kasese District Health Office, Kasese, Uganda, <sup>7</sup>Bundibugyo Hospital, Bundibugyo, Uganda, <sup>8</sup>Kagando Hospital, Kagando, Uganda, <sup>9</sup>Centers for Disease Control and Prevention-Uganda, Entebbe, Uganda, <sup>10</sup>Uganda Ministry of Health, Kampala, Uganda

*Salmonella enterica* serovar Typhi causes approximately 22 million typhoid fever infections worldwide each year; among these, 1-3% of patients develop intestinal perforation (IP). In 2008, an outbreak of typhoid fever with a high rate of IP was reported in Kasese, a rural district in western Uganda. A 2009 investigation of this outbreak identified 577 cases through July 15, 2009; 249 had IP. A high rate of IP was sustained in Kasese through 2011 and the neighboring district of Bundibugyo reported a typhoid fever outbreak in August 2011. We gathered information about cases through enhanced surveillance and hospital and district health office (DHO) records. A suspected typhoid case was defined as diagnosis of IP or symptoms of fever, abdominal pain, and one or more of the following: vomiting, diarrhea, constipation, joint pain, headache, general body weakness, clinical suspicion of IP, or failure to respond to antimalarials in a Kasese resident from July 16, 2009-December 31, 2011 or in a Bundibugyo resident in 2011. Among Kasese residents, 658 suspected cases were identified; 519 were diagnosed with IP. Among Bundibugyo residents, 330 suspected cases were identified and 56 were diagnosed with IP. Laboratory surveillance from October -December 2011 isolated *Salmonella* Typhi by blood or stool culture from 9 Kasese and 15 Bundibugyo patients. Among 19 isolates tested for antimicrobial sensitivity, 1 had intermediate susceptibility to ciprofloxacin, 15 were multidrug resistant but sensitive to ciprofloxacin, and 3 were pan-susceptible to all antimicrobials tested. Several pulsed field gel electrophoresis patterns were shared by isolates from both districts, suggesting that the outbreak spread from Kasese to Bundibugyo. Untreated drinking water was suspected as the chief transmission route. Drinking water sources in areas of high typhoid incidence in both districts yielded *Escherichia coli*, an indicator of fecal contamination. Recommended control measures included emergency point-of-use water treatment interventions and community education about sanitation and hygiene.

## 1410

### IDENTIFICATION OF ANTI-SALMONELLA ENTERICA SEROVAR TYPHI IMMUNE RESPONSES IN CHRONIC CARRIERS OF S. TYPHI IN KATHMANDU, NEPAL

Richelle C. Charles<sup>1</sup>, Tania Sultana<sup>1</sup>, Mohammad Murshid Alam<sup>2</sup>, Yanan Yu<sup>1</sup>, Meagan Bufano<sup>1</sup>, Sean Rollins<sup>1</sup>, Lillian Tsai<sup>1</sup>, Jason B. Harris<sup>1</sup>, Regina C. LaRocque<sup>1</sup>, Daniel Leung<sup>1</sup>, Stephen B. Calderwood<sup>1</sup>, Sabina Dongol<sup>3</sup>, Buddha Basnyat<sup>3</sup>, Jeremy Farrar<sup>4</sup>, Farhana Khanam<sup>2</sup>, Firdausi Qadri<sup>2</sup>, Stephen Baker<sup>4</sup>, Edward T. Ryan<sup>1</sup>

<sup>1</sup>Massachusetts General Hospital, Boston, MA, United States,

<sup>2</sup>International Centre for Diarrhoeal Disease Research, Bangladesh, Dhaka, Bangladesh, <sup>3</sup>Oxford University Clinical Research Unit, Kathmandu, Nepal,

<sup>4</sup>Oxford University Clinical Research Unit, Ho Chi Minh City, Vietnam

*Salmonella enterica* serotype Typhi can colonize and persist in the gallbladder of infected individuals. This can result in an asymptomatic chronic carrier state and chronic carriers can act as persistent reservoir of infection within a community. Unfortunately, little is known about host-pathogen interactions in the biliary tract of chronic carriers, and there is currently no reliable diagnostic assay to identify asymptomatic *S. Typhi* carriage. To address this, we applied an immunoscreening technique, *in vivo*-induced antigen technology (IVIAT), to identify potential biomarkers unique to *S. Typhi* chronic carriers. IVIAT identifies humorally immunogenic antigens expressed uniquely *in vivo*, and we hypothesized that *S. Typhi* surviving in the biliary tract of humans may express a unique proteomic profile. In brief, we generated a 120,000 clone genomic inducible expression library of *S. Typhi* CT18 (500-1500 bp fragments) in *E. coli* BL21DE3 and screened the library against pooled sera of patients (pre-adsorbed with *in vitro* grown *S. Typhi* and *E. coli* BL21DE3) who had bile cultures positive for *S. Typhi* at the time of elective cholecystectomy in Kathmandu. We identified 268 genes of interest from our primary screen, and subsequently sub-cloned each identified gene. Thus far, we have identified 50 proteins that are immunoreactive in *S. Typhi* carriers; these include a number of putative membrane proteins, lipoproteins, and hemolysin-related proteins. We are comparing these responses to those in patients with acute *S. Typhi* infection (typhoid fever) and patients from *S. Typhi* endemic zones with bile cultures negative for *S. Typhi* to identify uniquely immunoreactive antigens in *Typhi* carriers.

## 1411

### IMPACT ASSESSMENT OF A MASS TYPHOID FEVER VACCINATION CAMPAIGN - FIJI, 2011

Heather M. Scobie<sup>1</sup>, Eric Nilles<sup>2</sup>, Jacob Kool<sup>2</sup>, Terri Hyde<sup>1</sup>, Eric Mintz<sup>1</sup>, Akanisi Dawainavesi<sup>2</sup>, Sheetalpreet Singh<sup>3</sup>, Mike Kama<sup>3</sup>, Samuel Korovou<sup>4</sup>, Kylie Jenkins<sup>3</sup>, Kathleen Wannemuehler<sup>1</sup>, Kashmira Date<sup>1</sup>

<sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States,

<sup>2</sup>World Health Organization, Suva, Fiji, <sup>3</sup>Fiji Ministry of Health, Suva, Fiji,

<sup>4</sup>Fiji Ministry of Health, Labasa, Fiji

Typhoid fever, a life-threatening disease, is endemic in Fiji. During June-December 2010, a mass typhoid vaccination campaign was conducted in Fiji targeting 65,000 persons  $\geq 2$  years old in cyclone and outbreak-affected areas. Considering limited use of typhoid vaccine in post-disaster or outbreak settings, we evaluated the campaign impact. We calculated confirmed typhoid incidence rates for 2008-11 using Fiji's national laboratory surveillance data. For all reporting subdivisions, we calculated risk ratios (RR) and 95% confidence intervals (CIs) for incidence in years post- (2011) versus pre-campaign (2008-9 annual average). The percentage of the population vaccinated was determined from campaign doses administered and medical area census populations; subdivision populations  $>20\%$  vaccinated were called "vaccinated." In subdivisions with high pre-campaign incidence ( $\geq 100/100,000/\text{year}$ ), we used log-binomial regression to estimate RRs and 95% CIs for the proportion of positive blood cultures in the high season months (January-August) post-

(2011) versus pre-campaign (2008-10). Nationwide, 7% of the population was vaccinated, and confirmed typhoid was unchanged at 44/100,000/year between 2008-9 and 2011. In 11 unvaccinated subdivisions, post-campaign incidence was either unchanged, or significantly increased in 6 subdivisions (individual RRs ranged 2.2-7.8). In the 3 vaccinated subdivisions, post-campaign incidence was significantly decreased (individual RRs ranged 0.2-0.6). In the 2 high-incidence, unvaccinated subdivisions, the post-campaign proportion of positive-cultures increased (RR=1.8, CI=1.2-2.7; RR=1.6, CI=1.1-2.2). In three high-incidence, vaccinated subdivisions, the post-campaign proportion of positive-cultures decreased (RR=0.3, CI=0.1-0.6; RR=0.5, CI=0.3-0.9) or was unchanged (RR=1.4, CI=0.9-2.0). Post-campaign, confirmed TF cases in Fiji decreased in vaccinated areas and increased in unvaccinated areas. Typhoid vaccination can be considered in other high-incidence areas in Fiji and similar settings along with comprehensive typhoid control measures.

## 1412

### ORIENTIA TSUTSUGAMUSHI, RICKETTSIA AND LEPTOSPIRA SPECIES AS CAUSES OF MENINGOENCEPHALITIS IN LAOS

Sabine Dittrich, Phonepasith Panyanivong, Daniel H. Paris, Paul N. Newton

Lao-Oxford-Mahosot Hospital Wellcome Trust Research Unit, Microbiology Laboratory, Mahosot Hospital, Lao PDR and Centre for Clinical Vaccinology and Tropical Medicine, Churchill Hospital, University of Oxford, United Kingdom

Rickettsial and leptospiral diseases have been recorded as rare causes of meningoencephalitis. We see such patients in the Lao PDR (Laos) where *Leptospira* spp., *Orientia tsutsugamushi* (scrub typhus), *R. typhi* (murine typhus), *Rickettsia* spp. (Spotted Fever Group) are important causes of fevers. There have been no prospective studies to determine the clinical importance and the epidemiology of rickettsial and leptospiral CNS infections in endemic countries using modern techniques. We therefore investigated the incidence of *Leptospira*, *Rickettsia* spp and *O. tsutsugamushi* among patients presenting with CNS infections to Mahosot Hospital in Vientiane, between 2003 and 2011. We performed paired MAT serology for anti-IgM/G *Leptospira*, paired IFA anti-IgM serology for rickettsial pathogens and cerebrospinal fluid (CSF) and blood PCR for *Leptospira* spp., *Rickettsia* spp. and *O. tsutsugamushi*, by qPCR using 47kDa, 17kDa and *rrs* targets, respectively. We found evidence, using CSF PCR assays, for *O. tsutsugamushi*, *Leptospira* and *Rickettsia* spp. in 17/1030 (1.7%), 16/994 (1.6%) and 14/ 975 (1.4%) consecutive patients, respectively. In comparison to these 47 positive patients, CSF PCR for *S. pneumoniae*, *N. meningitis* and *H. influenzae* b identified 38 patients in the same series with 'conventional' meningitis pathogens in CSF. These data suggest that scrub typhus, leptospirosis and murine typhus are important causes of CNS disease in Laos. The data underline the need for timely testing of patients with meningoencephalitis for these 'atypical' pathogens. Such tests would be clinically important as rickettsial CNS disease would not be expected to respond to third generation cephalosporins that are commonly used for the empirical therapy of meningitis.

## 1413

### LEPTOSPIROSIS IN MAMMALIAN RESERVOIRS AND SURFACE WATER IN ALTO MAYO VALLEY, SAN MARTIN, PERU

Marieke Rosenbaum<sup>1</sup>, Bruno Ghersi<sup>1</sup>, Enrique Canal<sup>1</sup>, Romina Tejada<sup>2</sup>, Jenell Stewart<sup>1</sup>, Silvia Montano<sup>1</sup>, Joseph Zunt<sup>3</sup>, Giovanna Galarza Silva<sup>4</sup>, Matthew R. Kasper<sup>5</sup>, Jorge Alarcon<sup>2</sup>

<sup>1</sup>U.S. Naval Medical Research Unit Six, Lima, Peru, <sup>2</sup>Universidad Nacional Mayor de San Marcos, Lima, Peru, <sup>3</sup>University of Washington, Seattle, WA, United States, <sup>4</sup>DIRESA, Lima, Peru, <sup>5</sup>U.S. Naval Medical Research Unit Six, Lima, Peru

Leptospirosis is caused by bacterial spirochetes of the genus *Leptospira*. All mammals can chronically shed *Leptospira* in their urine and humans

can become infected following contact with contaminated water or soil. In 2010, the Institute of Tropical Medicine of the Universidad Nacional Mayor de San Marcos found that 64.75% (CI 95%: 58.76-70.74) of rice field workers (n=261) in Alto Mayo Valley, Peru were seropositive for pathogenic leptospirosis by microagglutination test (MAT). The present study aimed to identify mammalian reservoirs and water sources of pathogenic leptospirosis in this region. In October 2011, at the start of the rainy season, serum and urine samples were collected from 179 domestic animals, including 57 dogs, 56 cows, 49 pigs, and 17 sheep from three rural settlements in the Alto Mayo Valley. In addition, 217 rodents, primarily *Mus musculus*, were trapped from rice fields and houses, and serum and kidneys were collected. Water samples were collected from 146 locations including rice fields (n=28), canals (n=47), standing water sources (n=45), and tap water (n=26). Epidemiological surveys were conducted (n=114) to identify risk factors associated with leptospirosis-positive households. MAT analysis of domestic animal and rodent sera is currently underway, as well as PCR of urine samples. To date, 14.29% (31/217) of kidney samples and one water sample (1/146) were positive by PCR for *Leptospira* spp. Genetic sequencing revealed that 2 of 31 rodent kidney samples were colonized by pathogenic *Leptospira interrogans*, while the remaining were colonized by the non-pathogenic species *Leptospira biflexa*. Water sources did not appear to be a significant source of leptospirosis prior to the rainy season. Preliminary results indicate that *Mus musculus* in rice fields may be a significant reservoir for leptospirosis in this region. Upon completion of all sample processing, this data will complement our understanding of the site-specific epidemiology of this disease and will provide information necessary for public health interventions in the Alto Mayo Valley.

#### 1414

##### IMPACT OF A RURAL BANGLADESH SCHOOL WATER SANITATION AND HYGIENE INTERVENTION WITH AND WITHOUT ADDING HARDWARE

**Tania Bulbul**<sup>1</sup>, Probir Kumar Ghosh<sup>1</sup>, Leanne Unicomb<sup>1</sup>, Tarique M. n. Huda<sup>2</sup>, Mohammad Tarikul Islam<sup>1</sup>, Jade Benjamin-Chung<sup>3</sup>, Stephen P. Luby<sup>1</sup>

<sup>1</sup>International Centre for Diarrhoeal Disease Research, Bangladesh, Dhaka, Bangladesh, <sup>2</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>3</sup>University of California Berkeley School of Public Health, Berkeley, CA, United States

To improve hygienic practices in Bangladesh, a countrywide school-based behavior change communication (BCC) intervention was implemented for 18 months that included hygiene promotion sessions taught by trained teachers; formation of student brigades engaged in maintaining clean school compound; and quarterly hand hygiene demonstration through street shows, fairs and rallies. In a subset of these schools the intervention added to or improved existing water, sanitation and hygiene (WASH) facilities along with the BCC. We evaluated whether BCC alone was sufficient, or if provision of WASH facilities combined with BCC was necessary to improve hygiene practices. We selected 800 intervention schools, 200 of which received combined interventions, and 600 control schools, each from 50 similar clusters, where the probability of selection was proportional to the size of the cluster. We interviewed 1400 headmasters and 5600 students. We calculated the risk difference (RD) adjusted for clustering for facilities and practices between combined and control schools and also between schools receiving only BCC and controls. We calculated difference in difference to estimate the effect of WASH facilities in addition to BCC. Fifty-six percent of combined intervention schools had clean water points with proper drainage compared with 42% of BCC only schools (p=0.004) and 35% of control schools (RD= 20; 95% CI= 11, 29). Of combined intervention schools, 64% had soap available inside/ near the toilet compared with 62% of BCC only schools (p=0.62) and 49% of control schools (RD= 16; 95% CI= 7, 25). Of combined intervention schools, 66% had clean toilets compared with 65% of BCC only schools (p=0.80) and 56% of control schools (RD=10; 95% CI=0.3, 20). When we asked students to demonstrate how they usually washed

their hands, 52% of students from combined intervention schools washed both hands with soap compared with 54% of students from BCC only schools (p=0.32) and 42% of students from control schools (RD= 10; 95% CI=8, 18). Levels of hygiene practice and WASH facilities among all intervention schools were significantly better than the schools that did not receive any intervention. Behavior was no better in schools that received combined interventions compared with those that received only behavioral communication interventions. Behavioral communication messages may be a particularly cost effective approach to improving hand washing in schools.

#### 1415

##### THE IMPACT OF IMPROVED SCHOOL WATER, SANITATION AND HYGIENE ACCESS ON PUPIL DIARRHEA: A CLUSTER-RANDOMIZED TRIAL

**Matthew Freeman**<sup>1</sup>, Thomas Clasen<sup>2</sup>, Robert Dreifelbis<sup>1</sup>, Leslie Greene<sup>1</sup>, Shadi Saboori<sup>1</sup>, Richard Rheingans<sup>3</sup>

<sup>1</sup>Emory University, Atlanta, GA, United States, <sup>2</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>3</sup>University of Florida, Gainesville, FL, United States

Numerous studies have assessed the impact of improved access to water, sanitation, and hygiene (WASH) at the household level in reducing diarrheal disease, but few have rigorously assessed the impact of WASH in the school setting. Lack of access to improved WASH facilities and behaviors at school may increase risk of diseases due to the vulnerable age of children, increased opportunity for transmission of infectious agents, and lack of an immune response to organisms circulating in the public domain. We conducted a cluster-randomized trial to assess the impact of a school-based WASH intervention on diarrheal disease among primary school pupils. The study was carried out among 4,665 pupils in 185 public primary schools in Nyanza Province, Kenya. Two study populations were used: schools with a dry season water source within 1KM and those without. Schools with water nearby were randomly assigned to receive hygiene promotion and water treatment (HP&WT), HP&WT + sanitation, or no intervention (control). Schools without a nearby water source were randomly assigned to receive HP&WT, sanitation, and water supply improvements or no intervention (control). Our primary outcome was pupil-reported seven-day recall of diarrheal symptoms. At endline, pupils in schools with nearby dry-season water sources that received improvements in HP&WT and sanitation demonstrated similar measures of diarrhea period prevalence (RR 0.88, 95% CI 0.60-1.28) and diarrhea illness duration (IRR 0.85, 95% CI 0.57-1.24) compared to pupils attending associated control schools. Similar results were noted for pupils attending schools with HP&WT interventions only. Pupils attending schools without a water source in the dry season that received a water supply improvement followed by HP&WT and sanitation showed a 66% reduction in diarrheal disease (RR 0.34, 95% CI 0.17-0.64) and 70% reduction in days of illness (IRR 0.30, 95% CI 0.15-0.60) compared to associated controls. In settings with no water supplies in the dry season, an integrated school-based intervention to improve water supply, water quality, sanitation, and handwashing can reduce diarrheal illness among pupils. Since many schools in low-income settings function without year-round water supplies, these should be a priority for implementing WASH interventions.

## 1416

### EVALUATION OF EDUCATION THROUGH LISTENING, A COMMUNITY ENGAGEMENT METHODOLOGY, TO PROMOTE THE ADOPTION OF SAFE HOUSEHOLD WATER TREATMENT BEHAVIORS IN COMMUNITIES IN WESTERN KENYA

Christine Stauber<sup>1</sup>, Bobbie Person<sup>2</sup>, Katherine Schilling<sup>2</sup>, Ronald Otieno<sup>3</sup>, Ibrahim Sadumah<sup>3</sup>, Jared Oremo<sup>3</sup>, Ben Nygren<sup>2</sup>, Robert Quick<sup>2</sup>

<sup>1</sup>Georgia State University, Atlanta, GA, United States, <sup>2</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>3</sup>Safe Water and Aids Project, Kisumu, Kenya

Household water treatment has been shown to reduce diarrhea risk by nearly 40%, but relatively low rates of adoption of these interventions have limited the scale at which they are being used. New behavior change approaches are needed to accelerate adoption. In 2010, we evaluated the impact of Education through Listening (ETL), a behavior change methodology, on the adoption of household chlorination. ETL is a community engagement technique that is a person-centered way of communicating and giving feedback to promote behavior change. We randomized 12 villages in Vihiga District, Kenya into an intervention group in which ETL was used to motivate home water chlorination and a comparison group that used the standard village-based social marketing approach promoted by the Safe Water and Aids Project, a local Kenyan non-governmental organization. Over a 6-month period, during biweekly home visits mothers were interviewed about reported water treatment and diarrheal disease in children <2yo; water treatment was confirmed by testing stored water for residual chlorine. A higher percentage of households in ETL villages than comparison households had reported (14% versus 11%, Pearson's chi-square,  $p = 0.03$ ) and confirmed (7.5% versus 3.6%, Pearson's chi-square,  $p < 0.0001$ ) household water treatment with chlorine products. There was no difference in the proportion of children <2yo reported to have diarrheal disease between the intervention (6%) and comparison (6%) groups. However, the percentage of children with reported diarrheal disease was significantly lower in households that reported treating drinking water by any method than non-treating households (4% vs 7%, Pearson's chi-square,  $p = 0.027$ ). Although use of ETL appeared to increase the reported and observed use of chlorine products, adoption was modest. Further study of barriers to water treatment is needed.

## 1417

### SOAPY WATER: A LOW-COST SOLUTION FOR HAND WASHING PROMOTION

Sania Ashraf<sup>1</sup>, Mahfuza Islam<sup>1</sup>, Mahbub-Ul Alam<sup>1</sup>, Bimal K. Das<sup>1</sup>, Aasma Afroz<sup>1</sup>, Fosiul Nizame<sup>1</sup>, Pavani Ram<sup>2</sup>, Leanne Unicomb<sup>1</sup>, Stephen P. Luby<sup>3</sup>

<sup>1</sup>International Centre for Diarrhoeal Disease Research, Bangladesh, Dhaka, Bangladesh, <sup>2</sup>University at Buffalo, Buffalo, NY, United States, <sup>3</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States

Cost, theft and difficulty in sharing are barriers to keeping soap at a hand washing station that hinder regular hand washing in low income communities. Soapy water, a solution of water and locally available detergent, contained in plastic soda bottles is a low cost alternative to bar soap. We piloted soapy water in rural communities and measured uptake. We enrolled rural Bangladeshi households with children age <3 years in 12 villages, for four study arms: promotion only ( $n=148$ ), promotion plus handwashing stations with soapy water bottles ( $n=118$ ), promotion plus handwashing stations with bottles plus detergent refills ( $n=107$ ) and control (no products no promotion;  $n=73$ ). Our hand washing stations (wholesale cost per unit USD 6.5) included a bucket fitted with a tap, a stool, a basin and a soapy water bottle. Health workers promoted hand washing, the convenience of having soap and water together and the utility of making and using soapy water in all study arms except the control. We collected data on handwashing resources and

practices through observations and survey questions 3-4 months after commencement of the intervention. Soapy water or soap together with water was observed in 6% of (4/72) control households, 23% (26/116) of households with promotion only, 63% (65/103) of households with handwashing station plus bottles, and 75% (68/90) of households with station, bottles plus detergent. Intervention arms had significantly higher proportions of handwashing stations stocked with soap or soapy water compared to controls ( $p < 0.001$  in all three arms). Additional intervention components were associated with significant increase in uptake: 40% ( $p < 0.001$ ) higher with stations plus bottles versus promotion only and 12% ( $p < 0.04$ ) higher with stations, bottles and detergent compared with stations plus bottles. Soapy water was an acceptable low cost hand washing agent alternative to bar soap in rural low income communities. Providing hand washing stations increased uptake of soapy water, but even in the absence of project provided detergent and hardware, households prepared this easily and kept it at the handwashing station. Soapy water may increase habitual handwashing by addressing key barriers such as cost, sharing and availability near water sources. This uptake should be further evaluated to assess its longer term impact on habits and health.

## 1418

### MICROBIOLOGICAL EVALUATION OF THE EFFICACY OF SOAPY WATER TO CLEAN HANDS

M. Nuhu Amin<sup>1</sup>, Amy J. Pickering<sup>2</sup>, Pavani K. Ram<sup>3</sup>, Leanne Unicomb<sup>1</sup>, Nusrat Najnin<sup>1</sup>, Nusrat Homaira<sup>1</sup>, Sania Ashraf<sup>1</sup>, Jaynal Abedin<sup>1</sup>, M. Sirajul Islam<sup>1</sup>, Stephen P. Luby<sup>1</sup>

<sup>1</sup>International Centre for Diarrhoeal Disease Research, Bangladesh, Dhaka, Bangladesh, <sup>2</sup>Stanford University, Stanford, CA, United States, <sup>3</sup>University at Buffalo, Buffalo, NY, United States

The high cost of bar soap relative to household income is an important barrier to handwashing in low-income communities. Soapy water made from powdered detergent is a low-cost alternative that could overcome these barriers. Among low-income households in Dhaka, Bangladesh, we compared the efficacy of handwashing with soapy water to washing with bar soap or water alone for removal of fecal indicator organisms from hands. We enrolled 84 mothers with at least one child < 5 and randomly assigned 28 mothers to each of three handwashing agents: water alone, bar soap and soapy water (30g of powdered detergent mixed with 1.5 liters of water). For each mother, field workers randomly selected the right or left hand to collect a hand rinse sample before handwashing and then collected a hand rinse sample from the opposite hand after washing. An unwashed hand rinse sample and a washed hand rinse sample were collected in each of 5 different visits: two after 15 seconds of washing with soapy water, two after washing with bar soap at two rubbing times (15s and 30s), and one after 15s rinsing with water alone. We assessed the concentration of thermotolerant coliforms in hand rinse samples (log CFU per hand) by membrane filtration, and used paired t-tests to compare these concentrations before and after handwashing with each agent. We collected 168 hand rinses each for soapy water and bar soap, and 84 hand rinses for water alone. Soapy water and bar soap removed thermotolerant coliforms effectively after 15s of rubbing (log mean reduction=0.66,  $p < 0.001$  for soapy water; and 0.58,  $p = 0.001$  for bar soap). Increasing rubbing time from 15s to 30s did not significantly alter the microbiological efficacy of soapy water or bar soap (log mean reduction of 15s minus log mean reduction of 30s = 0.04,  $p = 0.48$  for soapy water; and 0.08,  $p = 0.53$  for bar soap). Washing hands with water alone also reduced thermotolerant coliforms (log mean difference=0.30,  $p = 0.029$ ). Washing hands with soapy water was more effective than washing hands with water alone in reducing thermotolerant coliforms (difference in log mean reduction = 0.35,  $p = 0.048$ ). Soapy water is more effective than water alone and as effective as bar soap in removing indicator organisms from hands. Washing for 15s is sufficient to remove bacteria from hands with bar soap and soapy water. In low-income communities, washing hands with soapy water can be promoted as an effective, low-cost alternative to bar soap.

## 1419

**CHRYSOMYA PUTORIA, A PUTATIVE VECTOR OF DIARRHEAL DISEASES**

Steven W. Lindsay<sup>1</sup>, Thomas Lindsay<sup>2</sup>, Jessica Duprez<sup>2</sup>, Martin Hall<sup>3</sup>, Brenda Kwambana<sup>4</sup>, Musa S. Juwara<sup>4</sup>, Ikumapayi U. Nurudeen<sup>4</sup>, Neneh Sallah<sup>4</sup>, Nigel Wyatt<sup>3</sup>, Umberto D'Alessandro<sup>4</sup>, Margaret Pinder<sup>4</sup>, Martin Antonio<sup>4</sup>

<sup>1</sup>Durham University, Durham, United Kingdom, <sup>2</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>3</sup>Natural History Museum, London, United Kingdom, <sup>4</sup>MRC Unit, The Gambia, Banjul, Gambia

*Chrysomya* spp are common blowflies in Africa, Asia and parts of South America and some species are generated in prodigious numbers from pit latrines. Because of their strong association with human faeces and their synanthropic nature, we examined whether these flies are likely to be vectors of diarrhoeal pathogens. Flies were sampled using exit traps placed over the drop hole of latrines in Gambian villages. A median of 12.5 flies/latrine/day (IQR=0.0-86.0) was collected, of which 95% were *Chrysomya* spp, nearly all *C. putoria*. Odour-baited traps were used to determine the relative attractiveness of different breeding media and foods to these flies. More flies were collected from traps with faeces from young children (median=2.5, IQR=1.0-8.5) and dogs (median=1.0, IQR=0.0-12.0) than from herbivores (median=0.0, IQR=0.0-0.0; calf, cow, goat and horse; p<0.001). Flies were strongly attracted to raw meat (median=44.5, IQR=26.2-143.0) and fish (median=0.0, IQR=0.0-19.8) compared with cooked and uncooked rice, and mangoes (median=0.0, IQR=0.0-0.0; p<0.001). The presence of bacteria in wild caught flies was confirmed by culture and bacterial DNA was identified using PCR. *Escherichia coli* were cultured from the surface of 21% of *Chrysomya* and 10% were enterotoxigenic (ETEC). Enteroaggregative *E. coli* (EAEC) were identified by PCR in 2% of homogenized *Chrysomya* spp, *Shigella* spp in 1.4% and *Salmonella* spp in 0.6% of samples. The large numbers of *Chrysomya* that can be produced from pit latrines, the presence of enteric pathogens on flies, and their strong attraction to raw meat and fish suggests these flies may be important vectors of diarrhoeal diseases in Africa.

## 1420

**QUANTITATIVE PCR-BASED DETECTION OF PATHOGENIC LEPTOSPIRA IN SLUM WATER**

Federico Costa<sup>1</sup>, Irina N. Riediger<sup>2</sup>, Daiana Santos<sup>1</sup>, Erica Sousa<sup>1</sup>, Diogenes C. Mota<sup>1</sup>, Vladimir A. Querino<sup>1</sup>, Guilherme S. Ribeiro<sup>3</sup>, Mitermayer G. Reis<sup>1</sup>, Peter J. Diggle<sup>4</sup>, Albert I. Ko<sup>5</sup>

<sup>1</sup>Oswaldo Cruz Foundation, Brazilian Ministry of Health, Salvador, Brazil, <sup>2</sup>Central Laboratory of the State of Paraná, Curitiba, Paraná, Brazil, <sup>3</sup>Institute of Collective Health, Salvador, Brazil, Salvador, Brazil, <sup>4</sup>Lancaster University, Lancaster, United Kingdom, <sup>5</sup>Yale University, New Haven, CT, United States

Leptospirosis has emerged as a major public health problem in urban slum settlements worldwide. Environmental surface water is an important reservoir for disease transmission in this setting. Pathogenic *Leptospira* have been detected in surface water from slum communities. However the ecological factors which influence the spatial and temporal dynamics of leptospires in this reservoir remain poorly understood. We performed a one-year longitudinal survey of leptospires in environmental surface water in an urban slum community, which was situated in a valley of 0.1 km<sup>2</sup> in the city of Salvador, Brazil. Pooled water and sewage samples were systematically collected from study households during a two-week period in the months of July, October and January. A lipL32-based qPCR assay was used to determine genome equivalents of leptospires in DNA extracted from 50ml samples. We detected leptospires in 12% (61) from 498 surface water samples collected during two survey periods of July and October. The proportion of qPCR positive samples (18% vs. 9%, P<0.05) and leptospiral concentration (10.1 vs. 6.6/ml, P<0.05) were significantly increased for the month where rainfall was greater (October vs. July; 230

vs. 81mm). Samples collected in the morning were significantly more frequently positive (17% vs. 6%) and had higher leptospiral concentration (9.3 vs. 5.8/ml) than those collected in the afternoon samples. The proportion of qPCR positive samples and leptospiral concentrations were also significantly higher in sewage (18%; 8.8/ml) than pooled water (6%; 6.2/ml). These findings indicate that the diurnal and seasonal variations influence the dynamics of leptospires in the environment. Furthermore they also suggest sewage may be a key transmission source in slum communities, and interventions targeting this reservoir will be necessary for effective prevention.

## 1421

**APPLICATION OF NANOTRING™ TECHNOLOGY TO MEASURE CHANGES IN GENE EXPRESSION IN PLASMODIUM FALCIPARUM**

Daria Van Tyne<sup>1</sup>, Chris Williams<sup>2</sup>, Supriya Gupta<sup>2</sup>, Jill Mesirov<sup>2</sup>, Dyann Wirth<sup>1</sup>, Danny Milner<sup>3</sup>

<sup>1</sup>Harvard School of Public Health, Boston, MA, United States, <sup>2</sup>Broad Institute, Cambridge, MA, United States, <sup>3</sup>Brigham and Women's Hospital, Boston, MA, United States

Experiments that investigate differential gene expression have traditionally taken a gene-by-gene approach (using quantitative real-time PCR) or a genome-scale approach (using microarrays). Nanotring™ technology is based on direct multiplex measurement of gene expression, effectively "counting" transcripts using barcoded probes and single molecule imaging. This approach offers a middle-level throughput to assay hundreds of transcripts simultaneously, using much less material than a microarray. We sought to apply Nanotring™ to measure gene expression in *Plasmodium falciparum* culture-adapted parasites and patient samples. We designed a custom codeset of 328 genes that distinguish between stages of the malaria asexual life cycle as well as between distinct transcriptional profiles previously observed in parasites isolated directly from infected patients. Using this subset of genes we were able to distinguish between asexual life cycle stages using small volumes (10µl parasitized red blood cells) of cell lysate. Life cycle stage correlations between Nanotring™ and microarray data were maintained with as few as 10,000 parasites. Direct patient samples, containing an abundance of human RNA, showed good correlation with microarray data gathered from the same samples. Even at parasitemia levels relevant to human infection, life cycle correlations were very strong. Whole genome imputation from the codeset for direct patient samples was also performed. Overall, Nanotring™ performs well with very small amounts of both cell lysate and extracted RNA, and constitutes a highly sensitive, enzyme-free approach to measuring gene expression in the malaria parasite. This tool could be ideal for screening patient samples prior to performing in-depth RNA sequencing, or as independent data for studies of parasite physiology during drug treatment or other experiments.

## 1422

**COPY NUMBER VARIATION WITHIN A NATURAL POPULATION OF PLASMODIUM FALCIPARUM**

Derrick K. DeConti<sup>1</sup>, Nicholas Blouin<sup>1</sup>, Kate M. Fernandez<sup>2</sup>, Sarah K. Volkman<sup>2</sup>, Dyann F. Wirth<sup>2</sup>, Daniel E. Neafsey<sup>3</sup>, Jeffrey A. Bailey<sup>1</sup>

<sup>1</sup>University of Massachusetts Medical School, Worcester, MA, United States, <sup>2</sup>Harvard School of Public Health, Department of Immunology and Infectious Disease, Cambridge, MA, United States, <sup>3</sup>The Broad Institute, Cambridge, MA, United States

Copy number variation is a key evolutionary mechanism for gene evolution and diversification. In *Plasmodium falciparum*, it is known to play important roles in virulence and drug resistance. Copy number variants (CNVs) have been extensively studied in culture-adapted laboratory strains. However, the genome-wide extent of CNVs in natural populations is not well understood. In order to address this we have analyzed over 30 short-term cultured field isolates from Senegal. Using whole-genome next-generation sequencing, using our novel correction algorithms for

sequencing biases and a mean shift approach to delineate CNVs allows the precise demarcation of CNVs, often to the base pair resolution. We find that on average the number of CNVs > 1kb in a strain was 158 of which 38 were duplications and 122 deletions. The vast majority of CNVs fall within the virulence genome compartment (e.g. var, rifin and stevor gene families and subtelomeric regions) highlighting their important role in host evasion. The higher proportion of deletion CNVs is mainly due to inadequate remapping of highly polymorphic var genes and as such do not strictly represent a deletion at the given var nor a reduced var complement. The core genome is relatively invariant compared to the virulence regions. It also appears less variant relative to culture-adapted strains suggesting variation may be selected for or more tolerated in such settings. Many of the core CNVs detected are shared within the Senegalese population, indicating either regional selection or the 3D7 reference genome being the rare variant. Interestingly several isolates demonstrated extensive and markedly-elevated read depth within the subtelomeric var regions - over three times the CNV content - suggesting that the virulence compartment may vary more extensively than previously appreciated. Together with our ongoing experimental validation we will present a detailed picture of the pattern and nature of copy number variation within this important pathogen.

### 1423

#### **PLASMODIUM COATNEYI CAUSES SEVERE ANEMIA AND INFLAMMATION IN BONE MARROW AND OTHER ORGANS OF RHESUS MACAQUES**

Jessica E. Taaffe<sup>1</sup>, Lynn Lambert<sup>1</sup>, Anthony Johnson<sup>2</sup>, Sachy Orr-Gonzalez<sup>1</sup>, Marlene Orandle<sup>2</sup>, Marvin Thomas<sup>3</sup>, Michal Fried<sup>1</sup>, Patrick E. Duffy<sup>1</sup>

<sup>1</sup>Laboratory of Malaria Immunology and Vaccinology/National Institute of Allergy and Infectious Diseases/National Institutes of Health, Rockville, MD, United States, <sup>2</sup>Comparative Medicine Branch/National Institute of Allergy and Infectious Disease/National Institutes of Health, Rockville, MD, United States, <sup>3</sup>Office of Research Services/National Institutes of Health, Bethesda, MD, United States

*Plasmodium coatneyi* infection in rhesus macaques has been considered a relevant animal model of *P. falciparum* infection in humans, due to its tertian periodicity, tissue sequestration features, and severe disease outcomes. In particular, *P. coatneyi* infection in rhesus macaques has been proposed for studies of cerebral malaria, with sequestration in the brains of infected rhesus macaques and associated clinical sequelae. However, the clinical features of this infection, including neurological syndromes, have not been recently evaluated for their similarity to severe human malaria disease. We conducted a pilot infection of six rhesus macaques with blood-stage *P. coatneyi* (frozen stabilate obtained at 7.05% parasitemia; strain deposited in MR4 by Dr. W. Collins) and obtained clinical, immunological, pathological, and parasitological data longitudinally. The infection was allowed to progress in individual monkeys until pre-determined clinical endpoints appeared, including any features of severe malaria. All monkeys developed severe anemia with a >60% drop from baseline hematocrit (final hemoglobin levels 3.2 - 5.6 g/dL) twelve to fourteen days post-infection and displayed peak parasitemias between 6.5 and 12.45%. Animals demonstrated lassitude and withdrawal at higher parasitemias, but not convulsions, unresponsiveness, or focal neurologic signs. Phagocytic cells and red blood cells containing pigment were observed in several organs without prominent parenchymal changes, including cerebral vessels without evidence of ischemia. T cell activation and proliferation, together with pigment-laden macrophages, were evident during in peripheral blood and tissues, including bone marrow. *P. coatneyi* infection in rhesus macaques routinely causes acute severe anemia, which may be useful for future mechanistic studies of this common severe malaria manifestation in humans.

### 1424

#### **IMPAIRED SKELETAL MUSCLE MICROVASCULAR FUNCTION AND INCREASED SKELETAL MUSCLE OXYGEN CONSUMPTION IN SEVERE *FALCIPARUM* MALARIA**

Tsin W. Yeo<sup>1</sup>, Daniel A. Lampah<sup>2</sup>, Enny Kenangalem<sup>3</sup>, Emiliana Tjitra<sup>4</sup>, Richard N. Price<sup>1</sup>, Nicholas M. Anstey<sup>1</sup>

<sup>1</sup>Menzies School of Health Research, Darwin, Australia, <sup>2</sup>Menzies School of Health Research-National Institute of Health Research and Development Research Program, and District Ministry of Health, Timika, Papua, Timika, Indonesia, <sup>3</sup>Menzies School of Health Research-National Institute of Health Research and Development Research Program, and District Ministry of Health, Timika, Indonesia, <sup>4</sup>National Institute of Health Research and Development, Jakarta, Indonesia

Organ dysfunction in severe *falciparum* malaria (SM) is associated with tissue hypoxia, which results from an imbalance between oxygen supply and demand. In SM, microvascular obstruction from parasite sequestration results in impaired oxygen delivery. However, microvascular function (capacity to increase oxygen delivery in response to ischemia) and oxygen consumption have not been assessed in host tissue. We used near-infrared resonance spectroscopy (NIRS) to measure tissue oxygen saturation (StO<sub>2</sub>), combined with an ischemic stress to compare microvascular function (StO<sub>2</sub>recov) and oxygen consumption (VO<sub>2</sub>) in the forearm muscles among adults in Papua, Indonesia with SM (n=36), moderately-severe malaria (MSM; n=33), severe sepsis (n=24) and healthy controls (HC; n=36). Mean StO<sub>2</sub>recov (skeletal muscle reoxygenation rates) was 16% and 22% lower in SM (2.7%/s) compared to MSM (3.1%/s) and HC (3.5%/s) (p<0.001), and comparable to severe sepsis (2.5%/s). In SM, StO<sub>2</sub>recov inversely correlated with venous lactate (r=-0.63; p<0.001) after adjustment for disease severity. StO<sub>2</sub>recov was a significant predictor of death (ROC: 0.71 [95%CI: 0.51-0.92]), with each percentage decrease associated with an increased risk of death (OR 2.49 (95%CI 1.05-6.2)). In contrast, VO<sub>2</sub> was increased in SM by 8% compared to MSM and 18% with HC and sepsis (p<0.001), and associated with parasite biomass (plasma HRP2); r=0.49, p=0.04. Microvascular function is impaired in SM and associated with increased mortality, while oxygen consumption is increased. Tissue hypoxia and organ dysfunction may arise not only from parasite sequestration and heterogeneous microvascular obstruction, but also from impaired functional ability of the microvasculature to match oxygen delivery to increased oxygen demand.

### 1425

#### **USING LABORATORY AND SEASONAL DIFFERENCES IN RETINOPATHY NEGATIVE VERSUS POSITIVE CEREBRAL MALARIA TO IMPROVE UNDERSTANDING OF DISEASE PATHOPHYSIOLOGY**

Douglas Postels<sup>1</sup>, Gretchen Birbeck<sup>1</sup>, Clarissa Valim<sup>2</sup>, Kara Mannor<sup>1</sup>, Terrie Taylor<sup>3</sup>

<sup>1</sup>Michigan State University, East Lansing, MI, United States, <sup>2</sup>Harvard School of Public Health, Boston, MA, United States, <sup>3</sup>Blantyre Malaria Project, Blantyre, Malawi

Children with cerebral malaria (CM) can be categorized by the presence or absence of malaria retinopathy. We compared admission laboratory, demographic, and seasonal data between children admitted with retinopathy positive versus negative and used these comparisons to gain insight into the underlying pathophysiology of retinopathy negative CM. We retrospectively reviewed admission laboratory and clinical parameters and the seasonal pattern of disease presentation in patients admitted with CM in Blantyre, Malawi from 1997-2010 and compared these data across retinopathy status. Patients with retinopathy negative CM had higher glucose concentrations, hematocrits, platelet counts, and lower lactate concentrations and peripheral parasite counts than those with retinopathy positive CM. Children with retinopathy negative CM were more likely to be in deeper coma upon admission than those with malaria retinopathy. The seasonal pattern of disease presentation also varied by retinopathy

status. Taken together, these findings support the hypothesis that these conditions have different underlying etiologies. Acute *Plasmodium falciparum* infection is likely not sufficient to produce the retinopathy negative CM syndrome.

## 1426

### MOLECULAR PATHOLOGICAL INVESTIGATIONS OF FATAL *PLASMODIUM FALCIPARUM* MALARIA

Panote Prapansilp<sup>1</sup>, Josefo Ferro<sup>2</sup>, Robert J. Marshall<sup>3</sup>, Carlos B. Ventura<sup>2</sup>, Ilse C. Hendriksen<sup>1</sup>, Arjen M. Dondorp<sup>1</sup>, Nicholas J. White<sup>1</sup>, Nicholas P. Day<sup>1</sup>, **Gareth D. Turner<sup>1</sup>**

<sup>1</sup>Mahidol-Oxford Research Unit, Bangkok, Thailand, <sup>2</sup>Department of Pathology, Hospital Central de Beira, Beira, Mozambique, <sup>3</sup>Peninsular College of Medicine, Truro, United Kingdom

To investigate the pathophysiology of fatal human malaria using molecular pathology techniques, we are conducting an autopsy study in Beira, Mozambique, examining malaria and control deaths in children and adults. Full clinical and autopsy based clinicopathological correlation determined the spectrum of clinical complications of severe malaria and cause of death. Tissues from different organs were used to extract total mRNA and microRNA. Whole genome and miRNA expression profiles were generated using the Illumina Human-12 V4 BeadChip array and Affymetrix GeneChip miRNA array v2 respectively. An initial screening analysed total mRNA and microRNA transcriptomes from the brain of patients dying of fatal malaria and non-malaria control deaths (both n=3, 3 separate brain regions, samples = 9 per group). Clustering analysis showed no significant differences between three brain regions. A total of 223 mRNAs and 54 miRNAs were significantly differentially expressed in malaria (using cutoffs of fold difference x1.5, and p<0.05). The network, functional and canonical pathway analyses were generated using Ingenuity software pathway analysis. Integration of the putative mRNA targets of differentially regulated miRNAs with mRNA expression data from the same specimens revealed a wide number of enriched functions and pathways, mainly associated with host immune responses, cellular morphological changes and cell death regulation. Gene families which were significantly upregulated included pathways of cell signalling and transmigration, inflammation and cellular homeostasis. Transcripts encoding markers of neuronal damage, such as S100 and APP, were highly increased, as were the chemokine MCP-1, cytokines Ang-4, IL-6 and IL-17 (but not TNF or IFN- $\gamma$ ). Hypoxic inducible molecules such as C7orf68 were increased, and mediators of cerebral oedema formation, such as aquaporin 4 and fibrinogen. There was downregulation of several genes stimulating cell death and neuronal apoptosis. Neurotransmitters and proteins involved in synaptic function and stabilization or microtubule formation were downregulated, such as PENK (proenkephalin precursor A). This study, the first integrated analysis of miRNA and mRNA expression profiling in fatal *P.falciparum* malaria, represents a proof of concept for using molecular techniques on autopsy tissues to understand the pathology and pathogenesis of human malaria.

## 1427

### SURROGATE MRI MEASURE (SAMKAM RATIO) PREDICTS OUTCOME IN PEDIATRIC CEREBRAL MALARIA

**Samuel Kampondeni<sup>1</sup>**, Cowles Chilingulo<sup>2</sup>, Karl B. Seydel<sup>3</sup>, Michael J. Potchen<sup>3</sup>, Kevin J. DeMarco<sup>3</sup>, William G. Bradley, Jr.<sup>4</sup>, Matthew Latourette<sup>3</sup>, Gretchen L. Birbeck<sup>3</sup>, James Siebert<sup>3</sup>, Terrie E. Taylor<sup>3</sup>

<sup>1</sup>Queen Elizabeth Central Hospital, Blantyre, Malawi, <sup>2</sup>Blantyre Malaria Project, Blantyre, Malawi, <sup>3</sup>Michigan State University, East Lansing, MI, United States, <sup>4</sup>University of California, San Francisco, CA, United States

Pediatric cerebral malaria (CM) increases both brain volume and intracranial pressure (ICP). The mortality from CM is 15-25% even with highly attentive care. Massive increases in brain volume, assessed by magnetic resonance imaging (MRI) and interpreted by radiologists, are

strongly associated with fatal outcomes in Malawian children with cerebral malaria. We developed a surrogate measure of brain volume for use by non-radiologists, and evaluated its utility, using images generated by 0.35T GE Signa Ovation scanner. The SamKam ratio is calculated using the height of the right parietal lobe on the first coronal T2 slice behind the splenium divided by the peri-brainstem CSF. The latter is the sum of the measurements of the CSF anterior and posterior to the brainstem at the level of the 4<sup>th</sup> ventricle apex, measured on the midsagittal section (T1). Three independent observers calculated the ratio on the same 20 scans. Pearson's correlation coefficients were calculated and were greater than 0.86 for all combinations. When SamKam ratio is used to predict severe brain swelling as measured by two independent radiologists the AUROC is 0.75. During the 2009 and 2010 seasons, 120 Malawian children with retinopathy-positive CM underwent brain MRI scanning on admission and daily thereafter until death or discharge (Age 9-168mo, mean 48mo; 45.8% male). There were twenty fatalities, and in 85%, the admission SamKam ratio was > 6.5. SamKam ratios declined over time in survivors with serial scans (n=8). The SamKam ratio may be used to identify CM patients increased brain volumes when radiologists are not available.

## 1428

### USE OF GEOSPATIAL MAPPING MODELS TO ACCURATELY PREDICT *SCHISTOSOMA MANSONI* PREVALENCE IN NYANZA PROVINCE, KENYA

**Dana Woodhall<sup>1</sup>**, Ryan E. Wiegand<sup>1</sup>, Michael Wellman<sup>1</sup>, Pauline N. Mwinzi<sup>2</sup>, Diana M. Karanja<sup>2</sup>, Elizabeth J. Mately<sup>2</sup>, Elizabeth A. Ocholla<sup>2</sup>, Susan P. Montgomery<sup>1</sup>, W. Evan Secor<sup>1</sup>

<sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States,

<sup>2</sup>Kenya Medical Research Institute, Kisumu, Kenya

Schistosomiasis, a parasitic disease that affects over 200 million people, can lead to significant morbidity and mortality; distribution of single dose preventative chemotherapy significantly reduces disease burden. Implementation of control programs is dictated by disease prevalence rates. For *Schistosoma mansoni*, infection prevalence is determined by costly and labor intensive screening of stool samples. Because ecological and human factors are known to contribute to the focal distribution of schistosomiasis, we sought to determine if specific environmental and socioeconomic factors could be used to accurately predict *S. mansoni* prevalence. We designed a mixed model to assess associations with *S. mansoni* rates in schools and controlled for spatial autocorrelation. Data on *S. mansoni* prevalence, school name, and GPS location of the school were obtained from 457 primary schools in Nyanza province in western Kenya. *S. mansoni* rates were calculated through examination of stool samples from children in the selected school; the median number of children tested per school was 42 (range 9-80). Geographic layers for environmental and population features, such as water source proximity, poverty rates, land elevation, and soil type, were obtained from publicly available sources. Mapping models were constructed using ArcGIS 10 and R 2.13.0. Higher *S. mansoni* rates were associated with closer distance (km) to Lake Victoria (prevalence ratio = 0.75, 95% CI = 0.73-0.77), increasing soil pH (0.83, 0.79-0.86), and increasing monthly rainfall (mm; 0.991, 0.989-0.993). Distance to health facility, human influence index, poverty rate, and agricultural land use were not significantly associated with *S. mansoni* rate. Our mapping model suggests that easily assessable geographic data can be used by schistosomiasis control programs to accurately predict schistosomiasis prevalence. Development and use of these prevalence maps will allow control programs to plan and prioritize efficient control campaigns to decrease schistosomiasis burden.

## 1429

### EVALUATION OF A NOVEL RAPID DIAGNOSTIC TEST FOR SCHISTOSOMIASIS HAEMATOBIIUM (RDT-SH) BASED ON THE DETECTION OF HUMAN IMMUNOGLOBULINS BOUND TO FILTERED *SCHISTOSOMA HAEMATOBIIUM* EGGS

Johnathan M. Sheele<sup>1</sup>, Jimmy Kihara<sup>2</sup>, Sarah Baddorf<sup>1</sup>, Jonathan Byrne<sup>1</sup>

<sup>1</sup>Eastern Virginia Medical School, Norfolk, VA, United States, <sup>2</sup>Kenya Medical Research Institute, Nairobi, Kenya

Schistosomiasis haematobium is a major cause of morbidity in Africa and the Middle East. A rapid diagnostic test for *Schistosoma haematobium* is needed to facilitate diagnosis and treatment, assist with disease surveillance and guide public health interventions. We evaluated a rapid diagnostic test for *S. haematobium* (RDT-Sh), a novel method for diagnosing *S. haematobium* infection. *S. haematobium* eggs are highly immunogenic and excreted into the urine coated in human IgG. We filtered 160 urine samples from children in the Kwale district of Kenya to isolate eggs and used anti-human IgG antibody conjugated to horseradish peroxidase to bind to the human IgG attached to the eggs. We then added 3,3',5,5'-tetramethylbenzidine base (TMB) which turns blue in the presence of horseradish peroxidase to detect the presence of *S. haematobium* eggs. The RDT-Sh was compared in a double-blinded manner to the gold-standard method of diagnosing infection by urine microscopy. The RDT-Sh was positive in 89% of urine samples containing >1 egg/10mL (58/65 samples) and 97% of urine samples containing >11 eggs/10mL urine (35/36 samples) seen by microscopy. The RDT-Sh was negative 79% of the time when no eggs were seen on urine microscopy, but because up to three times more urine was used for the RDT-Sh, there were likely cases in which eggs were on the RDT-Sh filter but not detected by microscopy. We used latent class analysis incorporating urine microscopy, hematuria, proteinuria, and RDT-Sh results to determine an overall 97% sensitivity and 78% specificity for RDT-Sh, 96% and 81% for urine microscopy, 71% and 98% for microscopic hematuria, and 46% and 89% for proteinuria, respectively. The RDT-Sh is quick, inexpensive and easy to perform in the field for the diagnosis of *S. haematobium*. The RDT-Sh is able to detect all but the lightest of *S. haematobium* infections with a high degree of accuracy.

## 1430

### URINE FOAM AS A MARKER FOR INFECTION WITH SCHISTOSOMIASIS HAEMATOBIIUM

Sarah Baddorf<sup>1</sup>, Johnathan Sheele<sup>1</sup>, Jimmy Kihara<sup>2</sup>

<sup>1</sup>Eastern Virginia Medical School, Norfolk, VA, United States, <sup>2</sup>Kenya Medical Research Institute, Nairobi, Kenya

The Baddorf-Sheele (BS) shake test measures urine foam to help diagnose Schistosomiasis haematobium in the field. The BS-shake test was performed by shaking 20mL of urine in a 50mL test tube as vigorously as possible by hand for approximately five seconds. Immediately after shaking, the height of the foam inside the test tube was recorded and these results compared to urine microscopy counts of *Schistosoma haematobium* eggs. The average height of the urine foam for study subjects with 17 to >1000 eggs/10mL urine was at the 36.4mL (SD 1.35) mark on the test tube, and for subjects with 0 eggs/10mL urine was at the 32.2mL (SD 2.36) mark. The sensitivity and specificity of the BS-shake test (positive when foam was measured at or above 34mL) was 74% and 72%, for microscopic hematuria 61% and 97%, and for proteinuria 43% and 83%, respectively, compared to microscopy. When >17 eggs/10mL urine were present, the BS-shake test, microscopic hematuria, and proteinuria were positive in 100%, 90%, and 80% of cases, respectively. Combining hematuria and the BS-shake test results detected 87% of samples with eggs seen on microscopy. The current gold standard test requires slide preparation, a trained technician, access to a microscope, and significant time and resource costs. A more easily performed and cost

effective, though still reliable test is needed, especially for field studies and large public health screenings. The BS-shake test is an inexpensive, quick, and easy way to diagnose *S. haematobium* in endemic areas.

## 1431

### TOWARDS THE DEVELOPMENT OF A RAPID DIAGNOSTIC TEST (RDT) FOR DETECTION OF ANTI-SCHISTOSOME ANTIBODIES

Emily M. Dawson, Michael J. Doenhoff

University of Nottingham, Nottingham, United Kingdom

Mass drug administration (MDA) of praziquantel is widely used in control programmes for both *Schistosoma mansoni* and *S. haematobium* infections. Different MDA strategies are used depending on how prevalent infection is in a given area. The Kato-Katz method is used for mapping *S. mansoni* infections, and questionnaires, detection of macrohaematuria and/or urine filtration methods for *S. haematobium*. Parasitological methods of diagnosis are however relatively insensitive, often misdiagnosing the infected as uninfected, and so prevalence is often underestimated. This can lead to the implementation of an inappropriate treatment strategy for a given community. The problem of underestimating prevalence is likely to become exacerbated in areas where praziquantel treatment has taken place, since the number of lighter infections which parasitology cannot detect is likely to increase. The need for more sensitive diagnostic assays is therefore greater than ever and it is envisaged that antibody-detection methods are likely to become increasingly useful. Indeed, they are already widely used in travellers' medicine clinics and have been integrated into the Chinese national control programme for *S. japonicum*. To be useful in schistosome-endemic areas however, a diagnostic test needs to meet the ASSURED criteria (particularly with regard to Affordability and User-friendliness), and so we are developing a rapid diagnostic test (RDT) that works by detection of anti-schistosome antibodies in human blood. Preliminary results indicate that this RDT could be useful for diagnosis of both *S. mansoni* and *S. haematobium* infections, and its low cost could make it useful not only for mapping purposes but also for diagnosis at the individual patient level.

## 1432

### EVALUATION OF POINT-OF-CONTACT CIRCULATING CATHODIC ANTIGEN ASSAYS FOR THE DETECTION OF *SCHISTOSOMA MANSONI* INFECTION IN LOW AND MODERATE PREVALENCE SCHOOLS IN WESTERN KENYA

Karen T. Foo<sup>1</sup>, Anna J. Blackstock<sup>2</sup>, Elizabeth A. Ochola<sup>3</sup>, Daniel O. Matete<sup>3</sup>, Pauline N. Mwinzi<sup>3</sup>, Susan P. Montgomery<sup>2</sup>, Diana M. Karanja<sup>3</sup>, W. Evan Secor<sup>2</sup>

<sup>1</sup>Karolinska Institute, Solna, Sweden, <sup>2</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>3</sup>Kenya Medical Research Institute, Kisumu, Kenya

Increased attention to schistosomiasis control efforts has highlighted the need for improved field diagnostics where rapid screening and mapping of *Schistosoma mansoni* infection guide control efforts. A urine point-of-contact circulating cathodic antigen (POC/CCA) assay manufactured by Rapid Medical Diagnostics (Pretoria, South Africa) has shown promise in areas where prevalence of schistosomiasis is high, but the assay has not been evaluated extensively in areas where prevalence is low. To evaluate the performance of the POC/CCA assay in areas of low to moderate prevalence, we tested primary school children for schistosomiasis in the Asembo region of western Kenya, using two versions of the POC/CCA assay—one commercially available and one experimental formulation—as well as duplicate Kato-Katz stool examinations and an anti-schistosome IgG ELISA. Latent class analysis was used to estimate sensitivities and specificities of the individual tests at each of three school prevalence levels: <10%, 10-25%, and >25%. Respective sensitivities and specificities of the POC/CCA assays among all participants (n=1798) were 93.9% and 57.8% for the commercial test and 76.9% and 89.8% for the experimental test.



The commercial POC/CCA assay was found to be most sensitive overall, but the experimental POC/CCA assay offered the best combination of sensitivity and specificity (82.0% and 91.4%, respectively) in the lowest prevalence zone. Both POC/CCA assays demonstrated positive correlation with infection intensity (as measured by egg count). The commercial POC/CCA assay was also evaluated for consistency and for measurement of treatment outcome, demonstrating substantial agreement across three daily administrations and reductions in POC/CCA band intensity one week after treatment. As intervention programs move toward sustained control and elimination, a diagnostic assay's abilities to perform in areas of low prevalence becomes paramount. Our findings suggest that the experimental POC/CCA assay may be a field-friendly alternative to the Kato-Katz exam in low prevalence settings.

### 1433

#### COMPARING HIGH-THROUGHPUT QUANTITATIVE DETECTION OF *SCHISTOSOMA*-DNA USING REAL-TIME PCR AND EXTENSIVE MICROSCOPY IN URINE SAMPLES FROM PRIMARY SCHOOL GIRLS IN COASTAL KWAZULU NATAL

**Pavitra Pillay**<sup>1</sup>, Myra Taylor<sup>2</sup>, Jaco J. Verweij<sup>3</sup>, Govert G. van Dam<sup>3</sup>, Svein G. Gundersen<sup>4</sup>, Eric A. Brienen<sup>3</sup>, Siphon Zulu<sup>2</sup>, Elisabeth Klepp<sup>5</sup>, Eyrun F. Kjetland<sup>5</sup>, Lisette van Lieshout<sup>3</sup>

<sup>1</sup>Durban University of Technology, Durban, South Africa, <sup>2</sup>University of KwaZulu Natal, Durban, South Africa, <sup>3</sup>Leiden University Medical Center, Leiden, The Netherlands, <sup>4</sup>University of Agder, Kristiansand, Norway, <sup>5</sup>Oslo University Hospital, Oslo, Norway

Of 300 million women and girls in Africa at risk of schistosomiasis, those most vulnerable to infection are pre-school and primary school children, adolescent girls and women of childbearing age. Genital schistosomiasis is reported as a complication among children. Since the diagnosis of female genital schistosomiasis (FGS) is difficult among children, diagnosing urinary schistosomiasis may help identify endemic areas for mass treatment where young girls are at risk for FGS. The diagnosis of schistosomiasis from urine may be challenging since haematuria and egg excretion are variable particularly in adults and in children with light infections with low levels of egg excretion. The aim was to compare two diagnostic tests using urine samples: real-time PCR for detection of *Schistosoma*-genus DNA and extensive microscopy as a practical tool for multiple exploration. Urine samples were collected on three consecutive days from 688 girls, aged 10-12 years, during a cross-sectional study in 18 primary schools. Quantification of *Schistosoma*-specific DNA was performed on a 200 µL aliquot of the first day urine, using a custom-made automated handling system for high through-put DNA isolation and PCR set-up. Full microscopy (3 days 2x10mL urines) was done on 621 (90.3%) and day 1 microscopy (2x10 mL urines) was done on 677 (98.4%) of the participants. Only 250 (36.3%) showed eggs in all 10 mL examinations collected over 3 days, while 210 (30.5%) were positive in only one out of six screenings collected on day 1. In addition, the number of eggs counted varied highly from day-to-day. *Schistosoma* DNA was detected using 200 µL of urine in 197 (28.6%) urine samples and DNA loads corresponded significantly with the average intensity of infection determined by microscopy. Also at school level, PCR determined *Schistosoma* infection reflected the focal distribution of disease transmission seen after extensive microscopy. The automated system facilitated high throughput quantification of *Schistosoma*-specific DNA loads in urine. In addition only 200 µL urine samples were required to achieve a sensitivity similar to extensive and labour intensive microscopy on consecutively collected large volume samples. The described PCR set-up could be used as a relatively straightforward laboratory-based procedure to assess the distribution of schistosomiasis in one urine only for large study populations, identifying communities at risk.

### 1434

#### COMPARISON OF DIAGNOSTIC METHODS AGAINST PCR FOR THE DETECTION OF *SCHISTOSOMA MANSONI* AMONG SCHOOL CHILDREN IN WESTERN KENYA

**Elizabeth A. Ochola**<sup>1</sup>, L. Van Lieshout<sup>2</sup>, Karen T. Foo<sup>3</sup>, John M. Williamson<sup>1</sup>, Eric Brienen<sup>2</sup>, Daniel O. Matete<sup>1</sup>, Pauline N. Mwinzi<sup>1</sup>, Susan P. Montgomery<sup>3</sup>, Jaco J. Verweij<sup>2</sup>, W. Evan Secor<sup>3</sup>, Diana M. Karanja<sup>1</sup>

<sup>1</sup>Center for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya, <sup>2</sup>Leiden University Medical Center, Department of Parasitology, Leiden, The Netherlands, <sup>3</sup>Division of Parasitic Diseases and Malaria, Centers for Disease Control and Prevention, Atlanta, GA, United States

The most widely used tools for detection of *Schistosoma mansoni* infection, stool examination and serology, are limited by low sensitivity or inability to distinguish between current from former infections, respectively. As a result, there is not an accepted "gold standard" for *S. mansoni* diagnosis for evaluation of new diagnostic assays. However, recent development of a semi-quantitative PCR that detects schistosome DNA in stool provides a tool for this purpose. We utilized the PCR method to evaluate a point of contact (POC) test designed to detect circulating cathodic antigen (CCA) in urine of persons infected with *S. mansoni*. School children (n = 1898) aged between 8-12 years from villages in western Kenya provided 3 stool and 3 urine samples on consecutive days for testing by Kato-Katz and a commercially available POC-CCA cassette. A portion of the first day's stool was preserved in ethanol and subsequently tested for presence of schistosome DNA by PCR (n=950). In addition, serum from a single blood sample was tested by ELISA for adult worm antigen-specific IgG. Children who were infected with *S. mansoni* were treated using praziquantel. A single urine sample was collected 1 week later for post-treatment POC-CCA testing. Compared to PCR, the single day POC-CCA urine test had an average sensitivity of 81.7% and an average specificity of 54.4%. Average single day Kato-Katz sensitivity was 58.2% and average specificity was 91.5%. When testing from the 3 days was combined, the POC-CCA sensitivity was 92.1%, and the Kato-Katz sensitivity was 70.4%; 3 day specificities of these tests were 68.7% and 92.1%, respectively. The ELISA was 52.6% sensitive and 85.1% specific. There were 675 children that were initially positive by POC-CCA and provided a urine sample 1 week after treatment with praziquantel; 461 (68.3%) of these children demonstrated decreased POC-CCA band intensity following treatment. Comparison of *S. mansoni* diagnostic tools demonstrates attributes and limitations of each test. Further development to optimize detection methods for *S. mansoni* is needed.

### 1435

#### MALARIA PREVENTION IN PREGNANCY IS ASSOCIATED WITH REDUCTIONS IN LOW BIRTH WEIGHT AND NEONATAL MORTALITY: A META-ANALYSIS OF 32 NATIONAL CROSS-SECTIONAL DATASETS IN AFRICA

**Thomas P. Eisele**<sup>1</sup>, David A. Larsen<sup>1</sup>, Philip A. Anglewicz<sup>1</sup>, Joseph Keating<sup>1</sup>, Josh Yukich<sup>1</sup>, Adam Bennett<sup>1</sup>, Paul Hutchinson<sup>1</sup>, Richard W. Steketee<sup>2</sup>

<sup>1</sup>Tulane University, New Orleans, LA, United States, <sup>2</sup>PATH-MACEPA, Atlanta, GA, United States

Low birth weight (LBW) is a significant risk factor for neonatal death. A prominent cause of LBW is *Plasmodium falciparum* infection during pregnancy. Intermittent preventive therapy (IPTp) and insecticide-treated mosquito nets (ITNs) have been shown by randomized trials to significantly reduce the risk of LBW in areas of stable transmission. We created a retrospective birth cohort from 32 national cross-sectional datasets in 25 African countries from 2000-2010 to examine the association of malaria prevention in pregnancy (IPTp and/or ITNs) with LBW and neonatal mortality under routine program conditions. An important innovation in this meta-analysis is the substantial effort made to limit potential selection

bias through exact matching on confounding factors associated with both exposure to malaria prevention in pregnancy and birth outcomes. A logistic regression model was used for assessing the association of malaria prevention in pregnancy on LBW, while a Poisson model was used for the outcome of neonatal mortality. Both models incorporated the matched strata as a random effect, while accounting for additional confounding factors with fixed effect covariates. Exposure of women in their first or second pregnancy to malaria prevention with IPTp and/or ITNs was significantly associated with decreased risk of neonatal mortality [Incident rate ratio = 0.820; 95% Confidence interval (CI): 0.698-0.962], compared to women with no protection. Compared to no protection, exposure of pregnant women during their first 2 pregnancies to malaria prevention in pregnancy through IPTp and/or ITNs was significantly associated with reduced odds of LBW, as measured by a combination of weight and perceived birth size [adjusted odds ratio = 0.792; 95% CI: 0.732-0.857]. These data show malaria prevention in pregnancy to be associated with substantial reductions in neonatal mortality and LBW under routine malaria control program conditions, and for the most part are consistent with the efficacy results from controlled trials.

### 1436

#### A TRIAL OF INTERMITTENT SCREENING AND TREATMENT AS AN ALTERNATIVE TO INTERMITTENT PREVENTIVE TREATMENT WITH SULFADOXINE-PYRIMETHAMINE FOR THE CONTROL OF MALARIA IN PREGNANCY

Harry Tagbor<sup>1</sup>, Kassoum Kayentao<sup>2</sup>, Sheick O. Coulibaly<sup>3</sup>, Khalifa Mohammed<sup>4</sup>, Kalifa Bojang<sup>4</sup>, John Williams<sup>5</sup>, Fanta Njie<sup>4</sup>, Matthew Cairns<sup>6</sup>, Paul Milligan<sup>6</sup>, Feiko Ter Kuile<sup>7</sup>, Daniel Chandramohan<sup>6</sup>, Brian Greenwood<sup>6</sup>

<sup>1</sup>Kwame Nkrumah University of Science and Technology, Kumasi, Ghana, <sup>2</sup>Medical Research and Training Centre, Bamako, Mali, <sup>3</sup>Université de Ouagadougou, Ouagadougou, Burkina Faso, <sup>4</sup>Medical Research Council Laboratories, Fajara, Gambia, <sup>5</sup>Navrongo Health Research Centre, Navrongo, Ghana, <sup>6</sup>London School of Hygiene & Tropical Medicine, London, United Kingdom, <sup>7</sup>Liverpool School of Tropical Medicine, Liverpool, United Kingdom

The incidence of malaria, including the incidence in pregnant women, is declining in some African countries, and resistance to sulfadoxine-pyrimethamine (SP) is widespread. Thus, intermittent preventive treatment in pregnancy with SP (SP-IPTp) may no longer be appropriate in certain situations, and alternative strategies are needed. A randomised, multi-centre controlled trial has been undertaken in four west African countries, including 5000 pregnant women who slept under an insecticide treated bed net. The standard SP-IPTp regimen (two to three courses of SP in the second and third trimester) will be compared to intermittent screening and treatment (IST) of parasitaemia using a rapid diagnostic test at scheduled antenatal clinic visits in the second and third trimester. The primary end points of the trial are prevalence of low birth weight (LBW), mean maternal haemoglobin at 38 ± 2 weeks of gestation and prevalence of placental malaria. Other outcomes affecting mothers (anaemia, parasitaemia, clinical malaria) and children (still births, perinatal mortality) will also be analysed. The study was powered to show non-inferiority of IST compared to SP-IPTp with respect to prevalence of LBW. Recruitment of study participants is complete. Analyses will be finalised in the third quarter of 2012 and available to present at ASTMH in November. The study will provide information to national malaria control programmes in countries whether there are alternative, safe and effective methods to the WHO recommended SP-IPTp regimen for managing malaria in pregnancy. This could have particular important implications for the control of malaria in pregnancy in areas with high levels of SP resistance.

### 1437

#### EFFECTIVENESS OF INTERMITTENT PREVENTIVE TREATMENT WITH SULFADOXINE-PYRIMETHAMINE IN PREGNANT WOMEN IN WESTERN KENYA: RESULTS OF AN OBSERVATIONAL STUDY

Peter Ouma<sup>1</sup>, Florence Were<sup>1</sup>, Vincent Were<sup>1</sup>, Meghna Desai<sup>1</sup>, Kephias Otieno<sup>1</sup>, Simon Kariuki<sup>1</sup>, Laurence Slutsker<sup>2</sup>, Mary J. Hamel<sup>2</sup>

<sup>1</sup>KEMRI/Centers for Disease Control and Prevention Research and Public Health Collaboration, Kisumu, Kenya, <sup>2</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States

Intermittent preventive treatment with sulfadoxine pyrimethamine (IPTp) remains a key strategy for malaria prevention in pregnant women living in malaria endemic regions. However, increasing SP resistance threatens IPTp effectiveness. We assessed IPTp effectiveness in an area of western Kenya where *Plasmodium falciparum* malaria transmission is intense and resistance to SP is high. From August 2008 to June 2009, women delivering at two district hospitals were enrolled in a cross-sectional survey. We collected information on obstetric history, IPTp use (self-report or as recorded in the antenatal card), insecticide treated net use, and antimalarial treatment during pregnancy. At delivery, we measured the prevalence of maternal anemia (Hb < 8g/dL), peripheral parasitemia, placental parasitemia (impression smear) and low birth weight (LBW) (multivariate analysis pending). Overall, 977 HIV-negative women were enrolled and included in this analysis. Of these, 637 were gravida 1 or 2 and 340 were gravida 3+. Among women who were gravida 1 or 2, anemia prevalence by number of IPTp doses received was 14%, 11%, 7% and 2% for 0, 1, 2, and 3+ IPTp doses respectively ( $p < 0.01$ ); peripheral parasitemia prevalence was 19%, 12%, 12% and 7% for 0, 1, 2, and 3+ IPTp doses received respectively ( $p = 0.07$ ); placental parasitemia prevalence was 22%, 12%, 13% and 8% for 0, 1, 2, and 3+ IPTp doses received respectively ( $p = 0.04$ ); and LBW prevalence was 5%, 11%, 9% and 9% for 0, 1, 2, and 3+ IPTp doses received respectively ( $p = 0.73$ ). Among multigravidae, we found no significant reduction in the prevalence of anemia, or peripheral or placental parasitemia with increased number of IPTp doses; LBW prevalence was 11%, 6%, 3% and 0% for 0, 1, 2, and 3+ IPTp doses received respectively ( $p = 0.02$ ). Among gravida 1 or 2, IPTp was associated with a reduction in maternal anemia and placental parasitemia. In multigravidae, IPTp was associated with a reduction in LBW. During this time period, IPTp remained beneficial in this area of western Kenya, despite high SP resistance.

### 1438

#### ORIGIN OF PLACENTAL MALARIA INFECTION AND RESPONSE TO TREATMENT DURING PREGNANCY

Lauren M. Cohee<sup>1</sup>, Linda Kalilani-Phiri<sup>2</sup>, Mwayi Madanista<sup>2</sup>, Sudhaunshu Joshi<sup>1</sup>, Rabia Mukadham<sup>2</sup>, Sarah Boudova<sup>1</sup>, Karl B. Seydel<sup>3</sup>, Patricia Mawindo<sup>4</sup>, Phillip C. Thesing<sup>1</sup>, Gladys Membe<sup>2</sup>, Terrie E. Taylor<sup>3</sup>, Miriam K. Laufer<sup>1</sup>

<sup>1</sup>University of Maryland School of Medicine, Baltimore, MD, United States, <sup>2</sup>University of Malawi College of Medicine, Blantyre, Malawi, <sup>3</sup>Michigan State University School of Medicine, East Lansing, MI, United States, <sup>4</sup>Blantyre Malaria Project, University of Malawi College of Medicine, Blantyre, Malawi

Placental malaria is a significant cause of maternal anemia and infant low birth weight. Little is known about the characteristics of peripheral malaria infections during pregnancy that lead to placental infections. We sought to determine when during pregnancy peripheral infection leads to placental sequestration and whether sulfadoxine-pyrimethamine intermittent preventive treatment (SP-IPT) or lumefantrine-artemether (LA) treatment clear the parasites sequestered in the placenta. We screened 325 placentas from women enrolled in an observational study of malaria during pregnancy. We used 6 neutral microsatellite markers to genotype placental and peripheral parasites. Placental parasites from 17 women

were fully genotyped. Mean gestational age (GA) at enrollment was 18 weeks (range 13-24). Of 39 visits with any peripheral parasitemia, 25 (65%) were sub-microscopic. Four of 17 women with molecular evidence of placental malaria did not experience any peripheral parasitemia during follow-up. Among the 13 women with peripheral parasitemia during follow-up, 6 (46%) had peripheral genotypes matching placental genotypes. Matching genotypes occurred later in pregnancy than did non-matching (34 weeks vs. 25 weeks). SP-IPT cleared peripheral parasitemia in 4 of 8 (50%) cases and LA cleared peripheral parasitemia in 7 of 7 cases. Recrudescence after treatment with LA occurred after 3 of 7 doses at 25, 45, and 78 days after treatment. These data suggest the majority of women experience the peripheral infection leading to placental infection prior to 18 weeks GA and the majority of peripheral infections experienced by women who went on to have placental malaria were submicroscopic infections. LA, but not SP-IPT, cleared all peripheral infections. Both SP-IPT and LA treatment allowed for recrudescence of parasites during pregnancy, which likely reflects their failure to eliminate parasites sequestered in the placenta.

### 1439

#### ASSESSING MALARIA SURVEILLANCE DATA QUALITY: EXPERIENCE FROM BENIN, ETHIOPIA AND UGANDA

**Melody Miles**<sup>1</sup>, Jessica Butts<sup>1</sup>, Yemane Berhane<sup>2</sup>, Achuyt Bhattarai<sup>1</sup>, James Colborn<sup>1</sup>, Salam Gueye<sup>1</sup>, Daddi Jima<sup>3</sup>, Ruth Kigozi<sup>4</sup>, Joseph Malone<sup>1</sup>, Arthur Mpimbaza<sup>5</sup>, Sussann Nasr<sup>1</sup>, Carrie Nielsen<sup>1</sup>, Noel Paraiso<sup>6</sup>, Laura Steinhardt<sup>1</sup>, Steve Yoon<sup>1</sup>

<sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>2</sup>Addis Continental Institute of Public Health, Addis, Ethiopia, <sup>3</sup>Ethiopian Health and Nutrition Research Institute, Addis, Ethiopia, <sup>4</sup>Infectious Diseases Research Collaboration, Kampala, Uganda, <sup>5</sup>Child Health and Development Centre, Makerere University, Kampala, Uganda, <sup>6</sup>Institut Régional de Santé Publique, Cotonou, Benin

Health facility-based malaria surveillance in Africa presents challenges due to reporting based on clinical diagnosis but lacking diagnostic confirmation. However, the scale up of rapid diagnostic tests and shifting national policies to universal testing may alleviate many of these challenges. We evaluated three models of malaria sentinel surveillance in Benin, Ethiopia, and Uganda to identify the unique attributes of each system and evaluate standard metrics of data quality. Compared to routine health facility data, Benin's system provided complete and comprehensive malaria data and filled an important data gap for the national program. In Ethiopia, a multi-tiered reporting system leveraged an existing network of health extension workers for monitoring malaria cases in the community. This system provided epidemic detection for entire health facility catchment areas. In Uganda, ongoing supervision provided by the implementing partner resulted in strengthened malaria diagnostic capacity and a high testing proportion of suspect cases. In all three countries, key performance indicators were high: completeness of malaria indicators was >95%; accuracy was >75%; and the average proportion of suspect cases tested was >75%. Timeliness of monthly reporting was satisfactory for all systems but epidemic detection would be strengthened by more frequent reporting. Results of analyses in all three countries showed that system performance improved with frequent supervision, clear standard operating procedures, a laboratory quality control system, and simple data collection tools. Data use by health workers resulted in greater compliance to reporting procedures and better data quality. In all countries sentinel surveillance data was of superior quality compared to routine system data. Our results suggest that near universal testing and improved data quality exemplified by these three surveillance systems with distinctly different implementation have improved the usefulness and public health impact of malaria surveillance data.

### 1440

#### RELIABILITY OF SCHOOL SURVEYS IN ESTIMATING GEOGRAPHIC VARIATION IN MALARIA TRANSMISSION IN THE WESTERN KENYAN HIGHLANDS

**Jennifer C. Stevenson**<sup>1</sup>, Gillian Stresman<sup>1</sup>, Carol Gitonga<sup>2</sup>, Lynn Spencer<sup>1</sup>, Chrispin Owaga<sup>3</sup>, Elizabeth Marube<sup>3</sup>, Wycliffe Onyango<sup>3</sup>, Albert Oduor<sup>3</sup>, Robin Oriango<sup>3</sup>, Teun Bousema<sup>1</sup>, Simon Brooker<sup>1</sup>, Chris Drakeley<sup>1</sup>, Jonathan Cox<sup>1</sup>

<sup>1</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>2</sup>Kenya Medical Research Institute - Wellcome Trust Research Programme, Nairobi, Kenya, <sup>3</sup>Centre for Global Health Research, Kenya Medical Research Institute/Centers for Disease Control and Prevention, Kisumu, Kenya

To evaluate the effectiveness of control interventions against malaria, reliable estimates of malaria transmission within the community are essential. Cross-sectional surveys can be logistically demanding and prohibitively expensive for control programs if required repeatedly. Health facility data, whilst less expensive and logistically simpler, often rely on clinically diagnosed malaria so are therefore likely to miss asymptomatics and will be affected by health-seeking behavior. An alternative approach is to use school surveys, which are increasingly being used for estimating disease prevalence and may act as a focal point for rolling out interventions. Here we carried out surveys in primary schools in Rachuonyo South district in the highlands of western Kenya in July 2010 at the same time as cross-sectional surveys within the immediate community to compare prevalence of malaria by rapid diagnostic tests (RDT) and antibody responses to the *P.falciparum* merozoite antigen MSP-1<sub>19</sub> and AMA. All results obtained at the school were geolocated by following up children to their homes. Crude RDT prevalence from school data was 24% whilst that recorded from community surveys was 16%. Comparing RDT prevalences between school-level data and community surveys, resulted in a correlation coefficient of 0.74, with 42% of the community results being significantly different to those obtained at the school. This increased to a correlation coefficient of 0.81 when data within the community was restricted to school-age children. For this subset of data, only 13% of the paired school and community prevalence estimates were significantly different. Factors determining these differences focusing on altitude, distance of pupil households from the school and use of malaria control interventions will be presented. This data will be supplemented with age specific sero-prevalences and estimates of the sero-conversion rates. The utility of school-based sampling using RDT results and serology to discriminate areas of high and low transmission will be discussed.

### 1441

#### ASSESSMENT OF MALARIA CONTROL PROGRESS OVER A TWO-YEAR PERIOD USING A CONTINUOUS 'ROLLING' MALARIA INDICATOR SURVEY ACROSS AGE GROUPS IN CHIKHWAWA DISTRICT, MALAWI

**Arantxa Roca Feltrer**<sup>1</sup>, Sanie Sesay<sup>1</sup>, David Lalloo<sup>2</sup>, Kamija Phiri<sup>3</sup>, **Dianne J. Terlouw**<sup>2</sup>

<sup>1</sup>Malawi Liverpool Wellcome Trust Clinical Research Programme, Blantyre, Malawi, <sup>2</sup>Liverpool School of Tropical Medicine, Liverpool, United Kingdom, <sup>3</sup>College of Medicine, Blantyre, Malawi

Low cost, district-level monitoring and evaluation (M&E) tools that can provide real-time malaria control progress are urgently needed to guide and optimize control efforts and impact. From May 2011 we have conducted a continuous 'rolling' Malaria Indicator Survey (rMIS) in children aged 6-59 months in 51 villages within Chikhwawa district, Southern Malawi. In 2011, district wide indoor-residual spraying and the use of Rapid Diagnostic Tests were added to facility-based ACT case-management and the distribution of insecticide treated bednets. Monthly collection of standard malaria intervention coverage and burden indicators were conducted by a small team of 2 nurses and 2 field workers, sampling all villages twice a year, using PDAs for data capture. Findings from the first

year identified substantial temporal and spatial variation in intervention coverage and malaria transmission within the area. The continuous rMIS approach provided real-time feedback on coverage gaps and burden hotspots, suggesting that this type of M&E surveys would become an intervention in itself if could trigger specific local focused control action, and could strengthen our current arsenal of interventions. With the increasing focus on universal coverage and transmission reduction, the rMIS was expanded to include older children and adults in the second year (June 2011-May2012). Preliminary results of this second year rMIS will be presented, with a focus on the added value of including older age groups in MIS surveys and control progress over both years.

## 1442

### **BILHARZIA IN THE INFORMAL URBAN SETTLEMENTS OF WESTERN KENYA: PREVALENCE, DISTRIBUTION AND EVALUATION OF COMMUNITY AND SCHOOL-BASED APPROACHES FOR CONTROL**

**Glady O. Odhiambo**<sup>1</sup>, Maurice R. Odiere<sup>2</sup>, Selpha Opisa<sup>1</sup>, Ibrahim Shivwalo<sup>3</sup>, Diana M. Karanja<sup>2</sup>, Pauline N. Mwinzi<sup>2</sup>

<sup>1</sup>Kenya Medical Research Institution and Maseno University, Kisumu, Kenya, <sup>2</sup>Kenya Medical Research Institution, Kisumu, Kenya, <sup>3</sup>Ministry of Public Health and Sanitation, Kisumu, Kenya

Urban areas present unique challenges for primary health care, which have remained poorly researched, and urban bilharzia remains a neglected area when prioritizing intervention strategies. Control of schistosomiasis and soil-transmitted helminthiasis is hampered by poverty, inadequate clean water, occupational hazards and poor sanitation. The cross-sectional study determined the prevalence and distribution of schistosome and soil-transmitted helminth (STH) infections, among 1,308 children in 34 primary schools and in intermediate snail vectors in 8 informal urban settlements in Kisumu City. Schools, water bodies and snails were mapped and fecal contamination (presence of *Escherichia coli*) of public water sources determined. Community health workers, village elders, and teachers were sensitized on Bilharzia and trained on mass drug administration (praziquantel) to community members or school going children respectively. Prevalence of Bilharzia was 36% in one of the informal settlement areas (Nyalenda B) and over 10% in all other informal settlements. The overall prevalence for STHs was 16%. Of the snails collected, 1.8% shed schistosome cercariae and 95% of water sources sampled were contaminated with fecal matter. In the MDAs, about 60% of the target population was treated by CHWs in the community while the school-based treatment achieved over 90% coverage. This study observed that schistosomiasis and STH are important health priorities among schools in informal settlements of Kisumu City. The study confirmed that besides L. Victoria, schistosomiasis transmission exists within the informal settlements of Kisumu City. Snail control, treatment of public water sources and improvements in local sanitation and public health awareness are advocated for in such settings.

## 1443

### **PREDICTIVE VALUE OF SCHOOL AGE CHILDREN'S SCHISTOSOMIASIS PREVALENCE FOR PREVALENCE IN OTHER AGE GROUPS AND THE EFFECT OF ONE ROUND OF SCHOOL-BASED OR COMMUNITY-WIDE TREATMENT IN WESTERN KENYA - THE SCORE PROJECT**

**Pauline N. Mwinzi**<sup>1</sup>, Geoffrey Muchiri<sup>1</sup>, Elizabeth J. Matey<sup>1</sup>, Diana M. Karanja<sup>1</sup>, Susan P. Montgomery<sup>2</sup>, W. Evan Secor<sup>2</sup>

<sup>1</sup>Kenya Medical Research Institute, Kisumu, Kenya, <sup>2</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States

With increased global commitment to schistosomiasis control, mass drug administration (MDA) programs are being implemented in several settings. Depending on the prevalence of infection in school age children within a given community, WHO recommends that either school-based or community-wide MDA be employed. To test the assumption that school

prevalence reflects the underlying community prevalence, we evaluated how well infection prevalence and intensity in 9-12 year old school pupils correlated with infection levels in other children and adults within the same community. Cross-sectional surveys of pre-adolescents (9-12 years old) were compared to those of first year students (7-8 years old), adolescents (13-14 years old) and adults (20-55 years old) in 150 villages along the shores of Lake Victoria. Written informed consent was obtained from adults and both consent and assent were obtained for children. A single stool sample was collected from 50 adults, 50 adolescents and 100 first year students and three stools were collected from 100 pre-adolescents in each village. Two slides per stool were screened for *Schistosoma mansoni* using the Kato Katz method. Data were analyzed using Spearman's nonparametric correlation analysis; p values < 0.05 were considered significant. We surveyed 3900 first year students, 12037 pre-adolescents, 5417 adolescents and 7566 adults. Of these, 1098 (28.2%) first year students, 7390 (61.4%) pre-adolescents, 2207 (40.7%) adolescents, and 3185 (42.1%) adults were positive for *S. mansoni* infection. Initial evaluation suggested that a village's schistosomiasis prevalence for 9-12 years olds significantly correlated with prevalence for all other age groups, suggesting that this age group is in fact a good predictor. Preliminary analysis of infection levels in the 9-12 year old age group one year following MDA suggests that children in villages randomized to the school-based treatment arms had lower prevalence and intensity of infection than children in villages randomized to the community-wide treatment arms.

## 1444

### **COMPARING THE COST OF SCHOOL-BASED VERSUS COMMUNITY-WIDE PRAZIQUANTEL MASS DRUG ADMINISTRATION IN KENYA**

**Angela J. Keller**<sup>1</sup>, Martin O. Owino<sup>2</sup>, Emmy Kavare<sup>2</sup>, Elizabeth J. Matey<sup>2</sup>, Alphonse Awiti<sup>2</sup>, Edward Okoth<sup>2</sup>, Diana M. Karanja<sup>2</sup>, Pauline N. Mwinzi<sup>2</sup>, Susan P. Montgomery<sup>1</sup>, W. Evan Secor<sup>1</sup>

<sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>2</sup>Kenya Medical Research Institute, Kisumu, Kenya

In addition to impact on burden of schistosomiasis, cost can be an important factor in mass drug administration (MDA) program design. The Schistosomiasis Consortium for Operational Research and Evaluation (SCORE) is conducting studies in several African countries that analyze the benefits and costs of implementing either school-based or community-wide treatments over a 4-year intervention period. As part of the cost benefit analysis, cost estimates of the second year of MDA in SCORE projects in Kenya were calculated. Twenty-four out of 175 villages were selected for the study based on distance, school size, district, and initial schistosomiasis prevalence, including 8 villages with 10-25% initial prevalence and 16 with > 25% initial prevalence. Information about various inputs and resources used to conduct MDA were collected from the transportation department, human resources department, study coordinators, field coordinators, and project associates. Costs that varied across villages were identified and costs that were consistent across villages were determined a priori. Each cost was associated with an MDA activity such as advocacy, mobilization, drug distribution, coverage or feedback. Preliminary data analysis suggests that school based MDA costs less than community wide treatment. The major drivers of cost associated with community wide MDA were transportation and personnel costs. In contrast school based distribution of treatment was centralized and five days of salary for community distributors was not required. The final Kenya MDA cost effectiveness analysis will include impact of treatment, either school-based or community-wide, on disease prevalence after 4 years of intervention in order to describe the relationship between the cost of alternative MDA approaches and the benefits achieved in terms of decreases in prevalence and intensity of schistosomiasis.

### EVALUATION OF THE HEALTH-RELATED QUALITY OF LIFE (HRQOL) OF CHILDREN IN A *SCHISTOSOMA HAEMATOBIIUM*-ENDEMIC AREA IN KENYA

Charles H. King<sup>1</sup>, Carolyn C. Terer<sup>2</sup>, Amaya L. Bustinduy<sup>3</sup>, Ruth V. Magtanong<sup>1</sup>, Ng'ethe Muhoho<sup>2</sup>, Peter L. Mungai<sup>1</sup>, Eric M. Muchiri<sup>4</sup>, Uriel Kitron<sup>5</sup>, Francis M. Mutuku<sup>5</sup>

<sup>1</sup>Case Western Reserve University, Cleveland, OH, United States, <sup>2</sup>Kenyatta University, Nairobi, Kenya, <sup>3</sup>Great Ormond Street Hospital, London, United Kingdom, <sup>4</sup>Ministry of Public Health and Sanitation, Nairobi, Kenya, <sup>5</sup>Emory University, Atlanta, GA, United States

Schistosomiasis remains a public health challenge; 93% of the estimated 237 million infections occur in sub-Saharan Africa. Though rarely fatal, its recurring nature makes it a lifetime chronic disorder with significant health burden. Much of its negative health impact is due to subtle conditions such as anemia, undernutrition, pain, exercise intolerance, poor school performance, and decreased work capacity. This makes it difficult to estimate the disease burden specific to schistosomiasis using the current DALY metric. In our study, we used Pediatric Quality of Life Inventory (PedsQL), a modular instrument available for a wide range of ages (2-18 y), to assess Health-related Quality-of-Life (HrQoL) in children living in a *S. haematobium*-endemic area in coastal Kenya. The PedsQL questionnaires were administered by interview to children aged 5-18 y (and their parents) in 5 villages spread across three districts. HrQoL (total score) was significantly lower in villages with high prevalence of *S. haematobium* (-4.0 + 0.8%,  $p < 0.001$ ) and among the lower socioeconomic quintiles (-2.0 + 0.8%,  $p < 0.01$ ) after adjustment for age, sex, and undernutrition. A greater effect was seen in the psychosocial scales as compared to physical function scale. Individual *S. haematobium* egg output was not associated with PedsQL score within the subset of three high-prevalence villages, whereas, in low prevalence villages, detection of any eggs in the urine were associated with a significant -2.1 + 0.9% ( $p = 0.025$ ) reduction in total score. The PedsQL reliabilities were high (Cronbach alphas generally  $\geq 0.70$ ), floor effects were acceptable, and identification of children from low socioeconomic status was valid. We conclude that urogenital schistosomiasis is specifically associated with at least a 2-4% reduction in HrQoL. Further research is needed on reproducibility and responsiveness properties of QoL testing in relation to schistosomiasis; we expect that a case definition based on more sensitive diagnosis will better define the immediate and long-term QoL impact of *S. haematobium* infection.

### COMMUNITY PERCEPTIONS OF SCHISTOSOMIASIS RISK AMONG SCHOOL CHILDREN IN ZANZIBAR

Bobbie Person<sup>1</sup>, Khalfan Mohammed<sup>2</sup>, Said Ali<sup>3</sup>, David Rollinson<sup>4</sup>, Stefanie Knopp<sup>5</sup>

<sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>2</sup>Helminth Control Laboratory Unguja, Zanzibar Ministry of Health, Stonetown, United Republic of Tanzania, <sup>3</sup>Public Health Laboratory Ivo de Carneri, Pemba, Chake-Chake, United Republic of Tanzania, <sup>4</sup>Natural History Museum, London, United Kingdom, <sup>5</sup>Department of Public Health and Epidemiology, Swiss Tropical and Public Health Institute, Basel, Switzerland

School-aged children on Unguja and Pemba Islands (Zanzibar) are at particular risk of infection by *Schistosoma haematobium*, a schistosome species that causes urinary schistosomiasis, a neglected tropical disease common throughout much of Africa. Despite the high prevalence of schistosomiasis (locally called Kichocho) in some communities, little is known about the community's perspectives on the disease among school children. In 2011, as part of a larger study aiming for schistosomiasis elimination, qualitative data were collected in Zanzibar from 39 groups of children, 45 community leaders, 21 teachers and 16 parents to better understand their knowledge, perceptions and practices associated with preventing, controlling, and treating Kichocho in children. Using a

grounded theory approach, we transcribed, coded, and analyzed the data. Kichocho was not seen as a disease of females. People typically acquired their knowledge through informal social networks and characterized the disease as one of young boys spending time in a dirty pond or stream. Identification of the parasite and mode of transmission was lacking. People often failed to seek treatment for children due to anticipated costs and home treated with plant-based teas and water. Schools lacked Kichocho education curriculums. People recognized the need for prevention and suggested organizing educational trainings for public and religious schools and the community; developing interactive teaching tools; partnering with student clubs to educate students; working with the community to build latrines, urinals, wells, and washing platforms near the river and at home; building play areas and offering play opportunities for children; and providing free local drugs. Our findings illuminated major gaps in local knowledge as well as practical, structural, educational, cultural and medical issues to consider when preparing for mass drug distribution and school-based interventions as well as the need to collaborate with the community on future prevention efforts.

### MEFLOQUINE-PRAZIQUANTEL FOR THE TREATMENT OF *SCHISTOSOMA HAEMATOBIIUM* INFECTIONS IN SCHOOL-AGED CHILDREN IN CÔTE D'IVOIRE

Jennifer Keiser<sup>1</sup>, Kigbafori D. Silué<sup>2</sup>, Lukas K. Adiossan<sup>3</sup>, Jürg Utzinger<sup>1</sup>, Eliézer K. N'Goran<sup>2</sup>

<sup>1</sup>Swiss Tropical and Public Health Institute, Basel, Switzerland, <sup>2</sup>UFR Biosciences, Université de Cocody, Abidjan, Côte D'Ivoire, <sup>3</sup>Hôpital Général de Taabo, Taabo, Côte D'Ivoire

The global strategy for schistosomiasis control is morbidity control, relying on a single drug, praziquantel. Although no clinically relevant resistance to praziquantel has been described to date, development of drug resistance is of growing concern as control efforts are going to scale. We have recently shown that mefloquine possesses promising antischistosomal properties *in vitro*, *in vivo*, and in proof-of concept clinical trials. In contrast to praziquantel, high worm burden reductions were observed following mefloquine treatment in the juvenile *Schistosoma mansoni* infection mouse model. Additionally, synergistic interactions were observed *in vitro* and in the *S. mansoni*-mouse model, when praziquantel was combined with mefloquine. We present results from the first exploratory randomized trial in school-aged children in southern Côte d'Ivoire evaluating the efficacy and safety of mefloquine (25 mg/kg) combined with praziquantel (40 mg/kg), and mefloquine/artesunate (3 x (100 mg artesunate + 250 mg mefloquine) combined with praziquantel (40 mg/kg) compared to standard praziquantel treatment (40 mg/kg) against *S. haematobium*. In the absence of prior drug interaction studies, drugs were administered on subsequent days. Two urine samples were collected before and on days 21-22 and 78-79 after the first dosing. Sixty children were present on all examination time points. No significant difference in efficacy was observed between the three treatment groups on the first treatment follow-up (mefloquine-praziquantel: cure rate (CR), 32%, egg reduction rate (ERR), 95%; mefloquine-artesunate-praziquantel: CR, 32%, ERR 95%; praziquantel: CR, 30%, ERR, 93%) and on days 78-79 posttreatment (mefloquine-praziquantel: CR, 32%, ERR, 94%; mefloquine-artesunate-praziquantel: CR, 33%, ERR, 92%; praziquantel: CR, 19%, ERR, 93%). Adverse events were mostly mild in all treatment groups. In conclusion, the addition of mefloquine or mefloquine-artesunate does not enhance the efficacy of praziquantel in the treatment of *S. haematobium*.

## 1448

**PREDICTIVE MAPPING VS. EMPIRIC ASSESSMENT OF SCHISTOSOMIASIS: IMPLICATIONS FOR TREATMENT PROJECTIONS IN GHANA**

**Philip W. Downs<sup>1</sup>**, Achille Kabore<sup>1</sup>, Nana-Kwadwo Biritwum<sup>2</sup>, Ricardo J. Magalhaes<sup>3</sup>, Yaobi Zhang<sup>4</sup>, Eric A. Ottesen<sup>1</sup>

<sup>1</sup>RTI International, Washington, DC, United States, <sup>2</sup>Neglected Tropical Diseases Control Programme, Ghana Health Services, Accra, Ghana, <sup>3</sup>University of Queensland, Infectious Disease Epidemiology Unit, School of Population Health, Brisbane, Australia, <sup>4</sup>Helen Keller International, Regional Office for Africa, Dakar, Senegal

Mapping the distribution of schistosomiasis is essential to determine where control programs should operate, but because it is impractical to assess infection prevalence in every potentially endemic community, model-based geostatistics (MBG) is increasingly being used to predict prevalence and determine intervention strategies. To assess the accuracy of MBG predictions for *Schistosoma hematobium* infection in Ghana, school surveys were evaluated at 79 sites to yield empiric prevalence values that could be compared with values derived from recently published MBG predictions. Based on these findings schools were categorized according to WHO guidelines so that practical implications of any differences could be determined. Using the predicted values alone, 21 of the 25 empirically determined 'high-risk' schools requiring yearly praziquantel would have been undertreated and almost 20% of the remaining schools would have been treated despite empirically-determined absence of infection - translating into 28% of the children in the 79 schools being undertreated and 12% receiving treatment in the absence of any demonstrated need. Using the current predictive map for Ghana by aggregating prevalence estimates to the district level was clearly not adequate for guiding the national program, but the alternative of assessing each school in potentially endemic areas of Ghana or elsewhere is not at all feasible; modelling must be a tool complementary to empiric assessments. We conclude that for practical usefulness, predictive risk mapping should not be thought of as a one-time exercise but must, as in the current study, be an iterative process that incorporates empiric testing and model refining to create updated versions with increasingly accurate predictions.

## 1449

**INTERVENTIONS TO STABILIZE ENDOTHELIUM IMPROVE SURVIVAL IN EXPERIMENTAL CEREBRAL MALARIA**

**Sarah J. Higgins<sup>1</sup>**, Karlee L. Silver<sup>2</sup>, John G. Hay<sup>3</sup>, Lisa A. Robinson<sup>4</sup>, W. Conrad Liles<sup>5</sup>, Kevin C. Kain<sup>5</sup>

<sup>1</sup>Department of Laboratory Medicine and Pathobiology, University of Toronto; SAR Labs, Sandra Rotman Centre for Global Health, University Health Network, Toronto, ON, Canada, <sup>2</sup>SAR Labs, Sandra Rotman Centre for Global Health; University Health Network, Toronto, ON, Canada, <sup>3</sup>Division of Pulmonary and Critical Care Medicine, New York University School of Medicine, New York, NY, United States, <sup>4</sup>The Hospital for Sick Children Research Institute; Institute of Medical Science, University of Toronto, Toronto, ON, Canada, <sup>5</sup>SAR Labs, Sandra Rotman Centre for Global Health, University Health Network; Toronto General Hospital, Division of Infectious Diseases; Department of Medicine, University of Toronto, Toronto, ON, Canada

Cerebral malaria (CM) pathogenesis is associated with endothelial activation and perturbation of the blood brain barrier (BBB). Endothelial specific signalling pathways, including the Angiopoietin (Ang)-Tie-2 and Slit/ Roundabout (Robo)-4 systems, are key regulators of endothelial integrity and vascular leakage. Our lab and others have reported that adult and pediatric CM is associated with increased circulating levels of biomarkers of endothelial activation and dysfunction (e.g. Ang-2, sTie-2, sICAM-1). We hypothesize that interventions to promote endothelial stability will prevent deleterious alterations to the BBB and improve outcome following *Plasmodium* infection. Using the murine model of *Plasmodium berghei* ANKA (PbA)-induced experimental CM (ECM), we

show that alterations in protein and mRNA levels of angiopoietins are associated with disease severity in the ECM, similar to observations in human populations. Time course experiments established a temporal relationship where PbA-associated alterations in endothelial regulators directly precede the loss of BBB integrity and the onset of neurological symptoms of ECM, such as seizures and paralysis. Pro-Ang-1 treatment strategies (e.g. Adenoviral mediated expression of Ang-1) significantly improved survival in PbA-infected ECM-susceptible C57Bl/6 mice compared to empty adenoviral vector and vehicle controls ( $p=0.001$ ). Pharmacological activation of the Slit-Robo pathway, using therapeutic administration of recombinant Slit2N, also significantly prolonged survival in PbA-infected C57Bl/6 mice compared to untreated controls ( $p=0.0007$ ). This benefit was further increased when Slit2N was used as adjunctive therapy in combination with a sub-curative dose of artesunate. To establish direct experimental evidence for a causal role of angiopoietins in ECM, the effect of Ang-1 genetic deletion on disease outcome is currently under investigation using a conditional Cre/loxP system. In summary, we show that adjunctive treatment strategies based on promoting endothelial quiescence and BBB integrity improve survival in ECM.

## 1450

**POSITRON EMISSION TOMOGRAPHY - AN *IN VIVO* IMAGING SYSTEM FOR FOLLOW UP ENCEPHALIC METABOLISM IN CEREBRAL MALARIA**

**Fernando Pereira Bruno**, Brandi D. Freeman, Wade R. Koba, Linda A. Jelicks, Eugene J. Fine, Mahalia S. Desruisseaux  
*Albert Einstein College of Medicine, Bronx, NY, United States*

Cerebral malaria (CM) is a neurological manifestation of *Plasmodium falciparum* infection which accounts for over 1 million deaths per year worldwide. About 25% of CM patients develop neurocognitive deficits, including memory loss and speech and learning impediments. As proper brain metabolism is critical to neurocognition, it may be altered in CM, but its role is poorly characterized. In addition, human CM studies are restricted to postmortem observations thus limiting our ability to characterize brain metabolic activity during disease. Non-invasive *in vivo* diagnostic tools are therefore needed to monitor the progression of CM. To investigate cerebral metabolic alterations in murine CM, we used positron emission tomography (PET) to monitor radioactive concentrations of fluorodeoxyglucose (FDG), a glucose analogue which reflects tissular metabolic activity. We examined encephalic metabolic activity in uninfected C57Bl/6 mice and mice infected with *Plasmodium berghei* ANKA (PbA), a mouse malarial strain which causes CM. Throughout the course of disease, glucose uptake was decreased in several brain regions in PbA-infected mice compared to controls, including the cerebral cortex, olfactory bulb, brainstem and cerebellum. There was also a significant effect of infection and time on mean expression of FDG in the eyes, indicating an ocular decrease of metabolism, which might be correlated to the known retinopathy of the disease. More importantly, decreased glucose uptake correlated temporally with increased CM pathology, thereby establishing a new tool to study disease. With FDG-PET, we have come up with a novel imaging tool to non-invasively study brain metabolism during CM. FDG-PET-CT will serve as an unprecedented translational technique to understand the brain metabolism in human CM patients.

### SCHISTOSOMA MANSONI POLO-LIKE KINASES : KEY REGULATORS OF REPRODUCTIVE ORGAN DEVELOPMENT

Thavy Long<sup>1</sup>, Mathieu Vanderstraete<sup>1</sup>, Katia Cailliau<sup>2</sup>, Svenja Beckmann<sup>3</sup>, Marion Morel<sup>1</sup>, Arlette Lescuyer<sup>2</sup>, Nadege Gouignard<sup>1</sup>, Christoph G. Grevelding<sup>3</sup>, Edith Browaeys<sup>2</sup>, Colette Dissous<sup>1</sup>

<sup>1</sup>Center for Infection and Immunity of Lille, Inserm U1019, Lille, France, <sup>2</sup>EA 4479, IFR 147, Université Lille 1 Sciences et Technologies, Villeneuve d'Ascq, France, <sup>3</sup>Institute for Parasitology, Justus-Liebig-University, Giessen, Germany

Polo-like kinases (Plks) constitute a family of conserved serine/threonine protein kinases known as important regulators of cell cycle progression and mitosis. Yeasts have only one Plk whereas vertebrate species possess five Plks (Plk1-5). Plk1, homolog to the *Drosophila* kinase Polo, is the best characterized member of the Plk family. Plk1 plays a major role in cell cycle progression by triggering G2/M transition and since it is overexpressed in various cancers, Plk1 constitutes a valuable target for anti-cancer therapy. Plk4/Sak (Snk akin kinase) is a divergent member of the family, structurally distinct from other Plk members, with essential functions in centriole duplication. The trematode parasite *Schistosoma mansoni*, responsible for schistosomiasis, has only, like *Drosophila*, two Plks, SmPlk1 and SmSak. Transmission and pathogenesis of schistosomiasis is due to the exceptional fecundity of schistosomes, for which Plks has been shown to play a decisive role. Both transcripts for schistosome Plks have been localized specifically in reproductive organs of female and male worms, with a majority of SmSak in ovary. Moreover, the treatment of worms with BI2536 (the anti-cancer drug inhibiting specifically Plk1 and SmPlk1) has shown a key role of SmPlk1 in gametogenesis and parasite reproduction, emphasizing its potential use as a novel therapeutic target against schistosomiasis. Studies in *Xenopus* oocyte, used as a protein expression system, have shown that the respective role of SmPlk1 and SmSak in G2/M transition triggering and centriole duplication during the cell cycle progression. Moreover, in these experiments, an unexpected interaction was demonstrated between SmPlk1 and SmSak, that could lead to Plk activation and spontaneous meiosis resumption in Plx1-depleted oocytes. These results suggest that Plk1 and Plk4 proteins are susceptible to interact and cross-activate in cells and thus attribute for the first time a potential role of Plk4 proteins in meiosis/mitosis entry. In addition to SmPlk1, this unexpected role of SmSak in meiosis could be relevant to further consider the function of this novel Plk in schistosome reproduction.

### UBIQUITIN FOLD MODIFIER (UFM-1) PROTEIN IS AN L. MEXICANA VIRULENCE FACTOR WHICH CONTRIBUTES TO PATHOGENESIS IN CL

Gayathri Natarajan<sup>1</sup>, Sreenivas Gannavaram<sup>2</sup>, Hira L. Nakhasi<sup>2</sup>, Abhay R. Satoskar<sup>1</sup>

<sup>1</sup>The Ohio State University, Columbus, OH, United States, <sup>2</sup>Center for Biologics Evaluation and Research, U.S. Food and Drug Administration, Bethesda, MD, United States

In this study, we generated *Leishmania mexicana* (Lm) lacking ubiquitin fold modifier (Ufm-1) gene, and examined *in vitro* parasite survival in dendritic cells and virulence *in vivo* using a murine model of CL. We found efficient internalization of both WT and Ufm-1-/- parasites by bone marrow derived dendritic cells (DCs), although Ufm-1-/- parasites were cleared significantly faster than WT parasites by DCs. We also found that Ufm-1-/- Lm-infected DCs produce significantly less IL-10 compared to WT Lm-infected DCs upon LPS stimulation *in vitro*. BALB/c mice infected with WT *L. mexicana* developed large non-healing lesions while Ufm-1-/- Lm-infected BALB/c mice had delayed lesion growth and developed smaller lesions by week 10 post-infection. Analysis of *Leishmania*-specific serum antibodies revealed that WT infected mice produced significantly higher titers of Lm-specific Th2-associated IgG1 than Ufm-1-/- Lm-infected mice, although Lm-specific IgG2a production was undetectable in both

groups. Upon *in vitro* stimulation with Lm antigen, draining lymph node cells from WT Lm-infected mice produced significantly more IL-4 compared to similarly stimulated cells from Ufm-1-/- Lm-infected mice although IFN- $\gamma$  production was comparable between the two groups. Taken together, our findings show that Ufm-1 is a *L. mexicana* virulence factor which contributes to establishment of infection and pathogenesis in CL. Furthermore, we demonstrate that Ufm-1 is not essential for parasite survival.

### THE EXISTENCE OF A G1 CELL CYCLE CHECKPOINT IN P. FALCIPARUM MEDIATED BY THE CYCLIN-DEPENDENT PROTEIN KINASE PFMRK; IMPLICATIONS FOR COMPOUND SELECTION AND INHIBITORY GROWTH ASSAY DEVELOPMENT

Norman C. Waters<sup>1</sup>, Veronica Zhang<sup>1</sup>, Marina Chavchich<sup>1</sup>, Kerry Rowcliffe<sup>1</sup>, Qin Cheng<sup>1</sup>, Peter O'Donoghue<sup>2</sup>, Dayadevi Jirage<sup>3</sup>

<sup>1</sup>Australian Army Malaria Institute, Enoggera, Australia, <sup>2</sup>University of Queensland, Brisbane, Australia, <sup>3</sup>Walter Reed Army Institute of Research, Silver Spring, MD, United States

Rapid growth and multiplication of *Plasmodium falciparum* during erythrocytic schizogony result in clinical symptoms and disease progression of malaria. Parasite growth is controlled by an unknown cell cycle regulatory mechanism, but believed to be similar to that of mammalian cells. However, there are many features of parasite schizogony that are unique. The ring stage of *P. falciparum* is representative of the G1 phase, while trophozoite and schizont stages are equivalent to S and M phases respectively. The regulation of how the parasite transits through these cell cycle phases and whether cell cycle checkpoints exist are unknown. Cyclin-dependent protein kinases (CDKs) are essential regulators for sequential growth and proliferation. Pfmrk, a sequence homologue of human CDK7 is suggested to play a role in both cell cycle control and DNA replication in *P. falciparum*. Transgenic parasites that over-express functional Pfmrk (HPG), non-functional Pfmrk (HKG), or control (empty vector control), revealed that HKG parasites exhibited a delay in the completion of the intraerythrocytic development cycle. To investigate the role of cell cycle regulators in *Plasmodium* growth and development, we assessed 41 mammalian cell cycle inhibitors, such as CDK inhibitors, DNA synthesis inhibitors and mitotic inhibitors, for growth inhibition. Of these compounds, 8 that significantly inhibited parasite growth ( $IC_{50} < 10 \mu M$ ) were shortlisted for further studies. FACS analysis demonstrated that control parasites treated with kenpaullone, a G1/S mammalian cell cycle inhibitor that inhibits Pfmrk kinase activity, "arrested" at trophozoite stages, whereas HPG parasites treated with the same inhibitor transitioned sooner from trophozoites to schizonts. In stage-specific growth inhibition studies, HPG parasites treated at trophozoite-stage were less sensitive to the growth inhibitory effects compared to early ring-staged treatment. Moreover, HPG parasites treated at early ring-stage development indicated a delay in the initiation of the next growth cycle by approximately five hours. The results suggest Pfmrk functions at the ring-trophozoite transition, reminiscent of a G1 checkpoint. The existence of a checkpoint would have a profound effect on the selectivity of compounds and warrant consideration for how and when compounds are tested in growth inhibition assays.

## 1454

### INVASION GENE HAPLOTYPES ASSOCIATE WITH PARASITEMIA IN HUMANS REPORTING WITH *PLASMODIUM KNOWLESI* MALARIA IN MALAYSIAN BORNEO

Mohammed Atique Ahmed<sup>1</sup>, Balbir Singh<sup>1</sup>, Ing Tien Wong<sup>2</sup>, Chan Woon Lu<sup>3</sup>, Ramlah bt Zainudin<sup>1</sup>, Paul C.S. Divis<sup>1</sup>, David J. Conway<sup>4</sup>, Sanjeev Krishna<sup>5</sup>, Janet Cox-Singh<sup>5</sup>

<sup>1</sup>Malaria Research Centre, UNIMAS, Kuching, Malaysia, <sup>2</sup>Hospital Sibul, Sibul, Malaysia, <sup>3</sup>Pathology Laboratory, Sarikei, Sarawak, Malaysia, <sup>4</sup>Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>5</sup>Infection and Immunity Research Centre, St George's University of London, London, United Kingdom

Human infections with *Plasmodium knowlesi*, a parasite of long and pig-tailed macaques, continue to be reported in most countries within Southeast Asia. Parasite invasion occurs daily in *P. knowlesi* infections and parasitemia is associated with disease severity. In this study we test the hypothesis that parasitemia is associated with particular alleles of two genes, *P. knowlesi* normocyte binding protein xa and xb (Pknbp<sub>xa</sub> and Pknbp<sub>xb</sub>), encoding invasion proteins on the merozoite apex. In the first instance a fragment 8500bp beginning at exon II of the Pknbp<sub>xa</sub> gene and a fragment 3500bp beginning at Exon I of the Pknbp<sub>xb</sub> gene were cloned and sequenced to high stringency using 5 reference isolates collected at geographically distinct locations. Sequence alignment indicated that most diversity occurred at the 5' region of exon II for both genes. Fragments with 37 non-synonymous and 7 synonymous substitutions with nucleotide diversity ( $\pi$ ) = 0.024 of Pknbp<sub>xa</sub> and 14 non-synonymous and 2 synonymous substitutions,  $\pi$  = 0.0056 of Pknbp<sub>xb</sub> were chosen to haplotype 147 *P. knowlesi* isolates from clinically well-characterised patients. Pknbp<sub>xa</sub> haplotypes were obtained for 138 isolates, 7 failed to amplify and 2 failed to sequence. Pknbp<sub>xb</sub> haplotypes were obtained for 134 isolates, 3 patients had multiple genotype infections and were excluded and 10 isolates failed to amplify. Within the Pknbp<sub>xa</sub> haplotyping fragment there were 82 polymorphic sites (56 non-synonymous, 26 synonymous substitutions)  $\pi$  = 0.02269 and 47 polymorphic sites (28 non-synonymous and 19 synonymous substitutions)  $\pi$  = 0.00642 within the Pknbp<sub>xb</sub> fragment. There were 75 Pknbp<sub>xa</sub> and 51 Pknbp<sub>xb</sub> haplotypes in the study population with haplotype diversity (h) of 0.9729 and 0.9216 respectively, suggesting high polymorphism among the isolates. Non-synonymous single nucleotide polymorphisms (SNPs), where the minor allele was represented in >10% of the isolates, were analysed for association with parasitemia. Preliminary analyses found significant associations between two Pknbp<sub>xa</sub> and one Pknbp<sub>xb</sub> SNPs and parasitemia suggesting that particular alleles may influence erythrocyte invasion efficiency in human infections. The results of this study will be presented within the context of parasitemia and disease severity in *P. knowlesi* malaria.

## 1454

### INVASION GENE HAPLOTYPES ASSOCIATE WITH PARASITEMIA IN HUMANS REPORTING WITH *PLASMODIUM KNOWLESI* MALARIA IN MALAYSIAN BORNEO

Mohammed Atique Ahmed<sup>1</sup>, Balbir Singh<sup>1</sup>, Ing Tien Wong<sup>2</sup>, Chan Woon Lu<sup>3</sup>, Ramlah bt Zainudin<sup>1</sup>, Paul C.S. Divis<sup>1</sup>, David J. Conway<sup>4</sup>, Sanjeev Krishna<sup>5</sup>, Janet Cox-Singh<sup>5</sup>

<sup>1</sup>Malaria Research Centre, UNIMAS, Kuching, Malaysia, <sup>2</sup>Hospital Sibul, Sibul, Malaysia, <sup>3</sup>Pathology Laboratory, Sarikei, Sarawak, Malaysia, <sup>4</sup>Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>5</sup>Infection and Immunity Research Centre, St George's University of London, London, United Kingdom

Human infections with *Plasmodium knowlesi*, a parasite of long and pig-tailed macaques, continue to be reported in most countries within Southeast Asia. Parasite invasion occurs daily in *P. knowlesi* infections and

parasitemia is associated with disease severity. In this study we test the hypothesis that parasitemia is associated with particular alleles of two genes, *P. knowlesi* normocyte binding protein xa and xb (Pknbp<sub>xa</sub> and Pknbp<sub>xb</sub>), encoding invasion proteins on the merozoite apex. In the first instance a fragment 8500bp beginning at exon II of the Pknbp<sub>xa</sub> gene and a fragment 3500bp beginning at Exon I of the Pknbp<sub>xb</sub> gene were cloned and sequenced to high stringency using 5 reference isolates collected at geographically distinct locations. Sequence alignment indicated that most diversity occurred at the 5' region of exon II for both genes. Fragments with 37 non-synonymous and 7 synonymous substitutions with nucleotide diversity ( $\pi$ ) = 0.024 of Pknbp<sub>xa</sub> and 14 non-synonymous and 2 synonymous substitutions,  $\pi$  = 0.0056 of Pknbp<sub>xb</sub> were chosen to haplotype 147 *P. knowlesi* isolates from clinically well-characterised patients. Pknbp<sub>xa</sub> haplotypes were obtained for 138 isolates, 7 failed to amplify and 2 failed to sequence. Pknbp<sub>xb</sub> haplotypes were obtained for 134 isolates, 3 patients had multiple genotype infections and were excluded and 10 isolates failed to amplify. Within the Pknbp<sub>xa</sub> haplotyping fragment there were 82 polymorphic sites (56 non-synonymous, 26 synonymous substitutions)  $\pi$  = 0.02269 and 47 polymorphic sites (28 non-synonymous and 19 synonymous substitutions)  $\pi$  = 0.00642 within the Pknbp<sub>xb</sub> fragment. There were 75 Pknbp<sub>xa</sub> and 51 Pknbp<sub>xb</sub> haplotypes in the study population with haplotype diversity (h) of 0.9729 and 0.9216 respectively, suggesting high polymorphism among the isolates. Non-synonymous single nucleotide polymorphisms (SNPs), where the minor allele was represented in >10% of the isolates, were analysed for association with parasitemia. Preliminary analyses found significant associations between two Pknbp<sub>xa</sub> and one Pknbp<sub>xb</sub> SNPs and parasitemia suggesting that particular alleles may influence erythrocyte invasion efficiency in human infections. The results of this study will be presented within the context of parasitemia and disease severity in *P. knowlesi* malaria.

## 1455

### PHASE I TRIAL OF PFS25-EPA/ALHYDROGEL® A TRANSMISSION BLOCKING VACCINE AGAINST *FALCIPARUM* MALARIA IN HEALTHY MALARIA-NAÏVE ADULTS

Kawsar R. Talaat<sup>1</sup>, Ruth D. Ellis<sup>2</sup>, Anna P. Durbin<sup>1</sup>, David S. Jones<sup>2</sup>, David L. Narum<sup>2</sup>, Nicholas MacDonald<sup>2</sup>, Janet G. Hurd<sup>1</sup>, Daming Zhu<sup>2</sup>, Kelly Rausch<sup>2</sup>, Charles Anderson<sup>2</sup>, Joan Aebig<sup>2</sup>, Olga Muratova<sup>2</sup>, Michael P. Fay<sup>3</sup>, Patrick Duffy<sup>2</sup>, Yimin Wu<sup>2</sup>

<sup>1</sup>Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, United States, <sup>2</sup>Laboratory of Malaria Immunology and Vaccinology, National Institute of Allergy and Infectious Diseases/National Institutes of Health, Rockville, MD, United States, <sup>3</sup>Biostatistics Research Branch, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Rockville, MD, United States

We describe the results of a phase I dose-escalating clinical trial to assess the safety and immunogenicity of the transmission blocking vaccine Pfs25-EPA/Alhydrogel®. Pfs25 has previously been shown to induce antibody which inhibits parasite development in a standard membrane feeding assay (SMFA), but an immunogenic formulation safe for human use has been lacking. EPA as a conjugate has been shown to enhance immunogenicity and to be safe in humans. Pfs25 and EPA were chemically conjugated and adjuvanted with Alhydrogel. 30 subjects have received up to three doses of 8, 16 (at 0 and 2 months) or 47- $\mu$ g of Pfs25 at 0, 2 and 4 months. Vaccinations were generally well tolerated. The majority of solicited adverse events were mild in severity. No vaccine related serious adverse events occurred. The most common solicited adverse event was pain at the injection site, and the frequency of adverse events decreased with each successive dose of vaccine. A decrease in hemoglobin was seen in 8 of 30 subjects after the first vaccination, in 11 of 26 subjects after the second and 2 of 15 after the third vaccination. The majority of these were mild in nature, a few were moderate, and most were in subjects who had a previous history of low hemoglobins or anemia and were judged to be unrelated to vaccination. The vaccine was more immunogenic with each successive dose. Geometric mean antibody levels in the 47  $\mu$ g dose group



were 92 EU (95% CI 55, 155) and 228 EU (95% CI 151, 344) after the second and third vaccinations respectively. Sixteen of 17 subjects in the 47 µg dose group had detectable antibody response after 2 vaccinations; 15/15 had responses after 3 vaccinations. Transmission blocking activity correlates with antibody titer, as demonstrated by SMFA. The data to date demonstrate that Pfs25-EPA/Alhydrogel® is well tolerated, increasingly immunogenic with each dose, and induces antibodies which inhibit parasite development in the mosquito.

## 1456

### COMPARATIVE ASSESSMENT OF TRANSMISSION BLOCKING MALARIA VACCINE CANDIDATE ANTIGENS USING AN ADENOVIRUS-MVA PRIME-BOOST REGIME

**Melissa C. Kapulu**<sup>1</sup>, Dari F. Yannick<sup>2</sup>, Sumi Biswas<sup>1</sup>, Kazutoyo Miura<sup>3</sup>, Andrew M. Blagborough<sup>4</sup>, Andrew R. Williams<sup>1</sup>, Simon J. Draper<sup>1</sup>, Anna L. Goodman<sup>1</sup>, Alison V. Turner<sup>1</sup>, Alfredo Nicosia<sup>5</sup>, Takafumi Tsuboi<sup>6</sup>, Yimin Wu<sup>3</sup>, Sarah G. Gilbert<sup>1</sup>, Anna Cohuet<sup>2</sup>, Robert E. Sinden<sup>4</sup>, Adrian V. Hill<sup>1</sup>

<sup>1</sup>University of Oxford, Oxford, United Kingdom, <sup>2</sup>MIVEGEC, Bobo Dioulasso, Burkina Faso, <sup>3</sup>National Institutes of Health, Rockville, MD, United States, <sup>4</sup>Imperial College, London, United Kingdom, <sup>5</sup>Okairòs AG, Rome, Italy, <sup>6</sup>Cell-Free Science and Technology Research Centre, Ehime, Japan

Transmission blocking vaccines (TBVs) target *Plasmodium falciparum* sexual stages, aiming to block development within the mosquito. Different delivery systems, mainly protein-in-adjuvant formulations, have been previously employed giving varied transmission blocking activity (TBA). However, leading TBV candidate antigens have not been comparatively assessed to determine a rank order of their TBA. Simian adenovirus (ChAd63) and Modified Vaccinia Ankara (MVA) in a prime-boost regime were used to induce antibodies against five candidate antigens and assessed their TBA. Antigen sequences were codon optimised and cloned into ChAd63 and MVA to generate recombinant viral vectored vaccines. These were used to vaccinate Balb/c mice in a 70 day regimen comprising of a day 0 ChAd63 prime and MVA boost at day 56. Antibody responses were measured days 14, 55 post-prime and day 70 post-boost by ELISA. TBA against *P. falciparum* NF54 strain and African field isolates was assessed by SMFA using purified IgG from sera taken at day 70. Antibody responses measured provided evidence that the antigens were immunogenic with ChAd63 priming responses boosted following MVA vaccination. TBA exhibited against *P. falciparum* NF54 in *Anopheles stephensi* ranged between 16-100% giving a rank order of the antigen-specific antibody's ability to inhibit oocyst intensity. This rank order was replicated against field *P. falciparum* isolates from gametocyte carriers in *Anopheles gambiae*. Hence the antigens with the highest TBA (90-100%) were further tested at varying IgG concentrations giving 39-100% efficacy. Two out of the five antigens consistently showed 99-100% with 0-5% infectivity to the mosquito. Antibodies induced by viral vectors showed partial to complete blockade depending on the target antigen. This antigen delivery system provides a robust vaccine platform for inducing antibodies against target antigens and has enabled a head-to-head comparison of TBV candidates. This comparative analysis is essential to guide and inform future assessment of candidates for clinical development.

## 1457

### FUNCTIONAL COMPARISON OF LEADING *PLASMODIUM FALCIPARUM* TRANSMISSION BLOCKING VACCINE CANDIDATES BY STANDARD MEMBRANE FEEDING ASSAY

**Kazutoyo Miura**<sup>1</sup>, Eizo Takashima<sup>2</sup>, Bingbing Deng<sup>1</sup>, Gregory Tullo<sup>1</sup>, Ababacar Diouf<sup>1</sup>, Samuel E. Moretz<sup>1</sup>, Carole A. Long<sup>1</sup>, Takafumi Tsuboi<sup>2</sup>

<sup>1</sup>Laboratory of Malaria and Vector Research/National Institute of Allergy and Infectious Diseases/National Institutes of Health, Rockville, MD, United States, <sup>2</sup>Cell-Free Science and Technology Research Center/Ehime University, Matsuyama, Japan

Recently, there has been a renewed interest in the development of vaccines against the sexual stages of *P. falciparum* malaria. While several potential transmission blocking vaccine (TBV) candidates have been reported, studies directly comparing them in a functional assay are limited. To this end, recombinant proteins of 5 leading TBV candidates, Pfs25, Pfs48/45, Pfs230, PfHAP2, AnAPN1, and GST (as a control) were expressed in the wheat germ cell-free expression system. CD-1 outbred mice (n=10 per group) were immunized twice with the antigens adjuvanted with Montanide ISA720. Two weeks after the boost, antibody levels were measured by ELISA and the functionality of antibodies was assessed by a standard membrane feeding assay (SMFA) using cultured *P. falciparum* NF54 gametocytes and *Anopheles stephensi* mosquitoes. The levels of antibodies for all antigens were relatively similar (33,000 to 88,000 ELISA units as a median). For the functional analysis we prepared a pool of serum from each group and isolated IgGs from each by Protein G purification. The purified IgGs were tested at 0.75 mg/ml (the concentration at which mouse IgGs have shown minimum non-specific inhibition) by SMFA. Anti-Pfs25, anti-Pfs230 and anti-PfHAP2 antibodies showed 97-100% inhibition in oocyst density compared to anti-GST antibody, and these inhibitions were all statistically significant (p<0.01, Kruskal-Wallis test followed by Dunn's multiple comparison test). We confirmed the inhibitory activity of these three antibodies in an independent assay (93-100% inhibition in the second test), and the inhibition was dose-dependent. Alternatively, anti-Pfs48/45 (-48% inhibition) and anti-AnAPN1 (-11% inhibition) antibodies did not show any inhibition at 0.75 mg/ml. Of these 5 antigens expressed in the wheat germ cell-free expression system, antibodies to Pfs25, Pfs230 and PfHAP2 proteins showed superior functional activity in this study. Further studies of these 3 products are in progress and the current SMFA results support future TBV development of the candidates produced in this system.

## 1458

### EFFICACY OF TRANSMISSION BLOCKING VACCINE CANDIDATES IN BURKINA FASO

**Dari Da**<sup>1</sup>, Melissa Kapulu<sup>2</sup>, Jean Bosco Ouedraogo<sup>3</sup>, Robert Sinden<sup>4</sup>, Adrian Hill<sup>2</sup>, Sumi Biswas<sup>2</sup>, Anna Cohuet<sup>1</sup>

<sup>1</sup>Institut de Recherche en Sciences de la Santé (IRSS) et Institut de Recherche pour le Développement (IRD) - UMR MIVEGEC, Bobo-Dioulasso, Burkina Faso, <sup>2</sup>Jenner Institute, University of Oxford, United Kingdom, <sup>3</sup>Institut de Recherche en Sciences de la Santé, Bobo-Dioulasso, Burkina Faso, <sup>4</sup>Imperial College, London, United Kingdom

Malaria parasite transmission from humans to mosquitoes requires the ingestion of gametocytes that circulate in the human blood by *Anopheles* mosquito vector followed by several steps of parasite development in the mosquito. Transmission-blocking vaccines aim at impeding parasite development in the vectors and are nowadays viewed as a promising strategy for breaking this transmission and an important component for achieving malaria elimination and eradication. Antibodies specific for the vaccine candidate antigens Pfs25 and Pfs230 showed efficacy to limit *Plasmodium falciparum* transmission to mosquitoes in laboratory conditions. In the present study we aimed at assessing their efficacy against field isolates of parasites from Burkina Faso in semi natural conditions of transmission. Standard Membrane Feeding Assays (SMFA)

were carried out by exposing *An. gambiae* s.s females to gametocyte-infected blood from naturally infected patients. Pfs25 and Pfs230 antibodies, produced by mice immunization using recombinant viral vectors, were tested at different concentrations added to the blood, using different gametocytes densities. In parallel, an entomological study was performed in order to assess the natural parasite load in local mosquito vectors. SMFA revealed 100% transmission blocking activity (TBA) for both antibodies at titer from 62.5 to 500µg/ml, depending on infection intensity in the control mosquito group. Field collections showed that among the 2,293 wild mosquitoes dissected, 275 carried oocysts with an average of 8 oocysts per infected mosquito. For such a parasite load, we observed that a concentration of 250µg/ml of either Pfs25 or Pfs230 antibodies has a complete TBA activity. Our results demonstrated that Pfs25 and Pfs230 antibodies strongly limit human to mosquito *P. falciparum* transmission, suggesting that these antigens are valuable candidates for transmission blocking strategies against malaria if the required antibody titer can be obtained by immunization in human.

## 1459

### PASSIVELY TRANSFERRED *P. FALCIPARUM* MSP1P42-SPECIFIC ANTIBODIES MEDIATE PROTECTION AGAINST CHALLENGE WITH BLOOD STAGES OF PFMSP1P19-TRANSGENIC *P. BERGHEI* PARASITES

Elke Bergmann-Leitner<sup>1</sup>, Heather Hosie<sup>1</sup>, Franz Lichtner<sup>1</sup>, Lorraine Soisson<sup>2</sup>, Joe Cohen<sup>3</sup>, Brendan Crabb<sup>4</sup>, Christian Ockenhouse<sup>1</sup>, Carter Diggs<sup>5</sup>, Michele Spring<sup>1</sup>, Tania de Koning-Ward<sup>6</sup>, Evelina Angov<sup>1</sup>

<sup>1</sup>Walter Reed Army Institute of Research, Silver Spring, MD, United States,

<sup>2</sup>United States Agency for International Development, Washington, DC, United States, <sup>3</sup>GlaxoSmithKline Biologicals, Rixensart, Belgium,

<sup>4</sup>The Macfarlane Burnet Institute for Medical Research and Public Health, Melbourne, Australia, <sup>5</sup>United States Agency for International Development, Washington, DC, United States, <sup>6</sup>Deakin University, Melbourne, Australia

MSP1 is the major surface protein on merozoites and a prime candidate for a blood stage malaria vaccine. Preclinical and seroepidemiological studies implicate a role for anti-MSP1 antibodies in protection against malaria. These antibodies interfere with invasion or affect the growth of intra-erythrocytic parasites *in vitro*, depending on parasite strain. However, the biological activity of MSP1-specific antibodies is not fully captured by *in vitro* growth or invasion inhibition assays (GIA), which are frequently used to predict vaccine efficacy. GIA fail to address the potential role of cellular receptors that interact with antibodies and mediate anti-parasite activity through diverse antibody-dependent cellular mechanisms. Currently, this potentially cell-mediated functional activity of MSP1-specific antibodies can only be determined *in vivo*. Thus, we employed a PfmSP1p19-transgenic *P. berghei* parasite to test the ability of MSP1-specific antibodies to control parasitemia after challenge with infected erythrocytes. Various immune IgG preparations were tested in this model: a) IgG purified from rabbits immunized with MSP1p42 (FVO) using either complete Freund's adjuvant or an Adjuvant System, AS01<sub>B</sub> and b) Human IgG isolated from either high or low titer serum pools of malaria-naïve subjects immunized with MSP1p42 (FVO) adjuvanted with AS01<sub>B</sub>. Purified IgG was injected intraperitoneally thrice (Day -1, 0, 1) and blood parasitemia was measured daily by qRT-PCR (Day 1-5) and by flow cytometry (Day 5-10). Lack of parasitemia was confirmed by qRT-PCR at the end of the study. Anti-MSP1p42- rabbit IgG conferred 40-50% sterile protection. Human anti-MSP1p42 IgG derived from the low titer pool protected 40% of mice, while IgG derived from the high titer pool protected 80% of mice from developing parasitemia. These data suggest that the transgenic *P. berghei* mouse model could be useful in selection of candidate vaccines for future clinical studies.

## 1460

### PARTICLE DELIVERY OF MALARIAL PROTEINS USING AN ATTENUATED STRAIN OF *SHIGELLA FLEXNERI*

Heather E. Hosie<sup>1</sup>, Elke S. Bergmann-Leitner<sup>1</sup>, Ryan T. Ranallo<sup>1</sup>, Malabi M. Venkatesan<sup>1</sup>, Jessica Trichilo<sup>2</sup>, Paul Grewal<sup>2</sup>, Vito DelVecchio<sup>2</sup>, Evelina Angov<sup>1</sup>

<sup>1</sup>Walter Reed Army Institute of Research, Silver Spring, MD, United States,

<sup>2</sup>Vital Probes, Inc., Mayfield, PA, United States

Particle-presentation of malarial antigens can significantly improve vaccine efficacy as show-cased by the RTS,S vaccine in which the circumsporozoite protein (CSP) is expressed as a fusion with hepatitis B surface antigen. While soluble CSP antigen plus adjuvant has not induced sterile protection, the RTS,S vaccine sterilely protects about 50% of malaria-naïve individuals. The advantages of particle delivery are that they can directly target antigen-presenting cells, contain immunostimulatory signals and provide increased epitope density thus assuring a potent immune stimulation. Our previous work using *E. coli* as particulate delivery platform has demonstrated that expression of malarial antigens at different cellular localizations (i.e., periplasmic space and outer membrane) modulates the type of immune response and can induce sterile protection against sporozoite challenge in murine models. In the present study, we use *Shigella*, a gram-negative bacterium, for particle presentations of malaria antigens and in the process potentially develop a dual-disease vaccination approach. Two malarial antigens were expressed in different compartments of strain 15G, an attenuated strain of *Shigella flexneri* 2a, to evaluate their immune responses in mice. The cell-traversal protein for ookinetes and sporozoites (CelTOS) was fused with the maltose binding protein, targeting it to the periplasmic space and the CSP was fused with the peptidoglycan associated lipoprotein in the outer membrane. We will report the results of bacterial dose selection, immunogenicity (humoral and cellular responses) and the protective efficacy against sporozoite challenge with either *P. berghei* or PfcSP transgenic *P. berghei* sporozoites.

## 1461

### A NOVEL GLYCOLIPID ADJUVANT STRONGLY ENHANCING THE CELLULAR IMMUNOGENICITY OF ADENOVIRUS-BASED MALARIA VACCINES IS ATTRIBUTABLE TO ITS LOCALIZED BIO-DISTRIBUTION

Xiangming Li<sup>1</sup>, Neal Padte<sup>1</sup>, Mar Boente-Carrera<sup>1</sup>, Chasity Andrews<sup>1</sup>, Akira Kawamura<sup>2</sup>, Douglass Wu<sup>3</sup>, Noelle Patterson<sup>4</sup>, Deena Oren<sup>5</sup>, Joe Bruder<sup>6</sup>, Martha Sedegah<sup>4</sup>, Thomas Richie<sup>4</sup>, David D. Ho<sup>1</sup>, Chi-Huey Wong<sup>3</sup>, Moriya Tsuji<sup>1</sup>

<sup>1</sup>Aaron Diamond AIDS Research Center, Affiliate of the Rockefeller University, New York, NY, United States, <sup>2</sup>Hunter College of the City University of New York, New York, NY, United States, <sup>3</sup>Scripps Research Institute, La Jolla, CA, United States, <sup>4</sup>Naval Medical Research Center, Silver Spring, MD, United States, <sup>5</sup>Structural Biology Resource Center, Rockefeller University, New York, NY, United States, <sup>6</sup>GenVec, Inc., Gaithersburg, MD, United States

A key strategy to a successful vaccine against malaria is to identify and develop new adjuvants that can enhance T cell responses elicited by a malaria vaccine.  $\alpha$ -galactocylceramide ( $\alpha$ -GalCer), a glycolipid that has been extensively investigated, is known to display a significant biological activity, including an adjuvant effect, by binding CD1d molecules and stimulating invariant NKT (iNKT) cells. Recently, we identified a novel synthetic  $\alpha$ -GalCer analog, 7DW8-5, which can display a stronger adjuvant effect on the immunogenicity and efficacy of malaria vaccines in mice. Most recently, we have co-injected increasing doses of 7DW8-5 intramuscularly (i.m.) to rhesus macaques with an AdPfCA vaccine that consists of two Ad5-based vaccines each expressing the CS or AMA-1 antigen of *Plasmodium falciparum*, and found that 7DW8-5 could significantly enhance the level of malaria antigen-specific T cell responses without showing a significant side effect. Very surprisingly, we discovered that upon i.m. injection,  $\alpha$ -GalCer, but not 7DW8-5, induced a systemic

production of cytokines including IFN- $\gamma$  and IL-12 in the sera, whereas both glycolipids induced a similar level of systemic cytokine production upon their intravenous (i.v.) administration. Using labeled glycolipids with fluorophores, we found that the two glycolipids exhibited a distinctly different bio-distribution upon i.m. but not i.v. administration, resulting in only 7DW8-5 got trapped by DCs residing in the draining lymph nodes. The localized 7DW8-5 seems to facilitate the activation and maturation of lymph node DCs, thus improving the capability of DCs to prime malaria antigen-specific T cells and ultimately leading to its super adjuvant activity. Taken together, our study demonstrates a uniquely localized bio-distribution of our novel  $\alpha$ NKT-activating glycolipid, 7DW8-5, upon its i.m. injection, which could lead to a potent adjuvant effect on the cellular immunogenicity of an adenovirus-based malaria vaccine not only in rodents but also in non-human primates.

## 1462

### THE ROLE OF THE PROTEIN KINASE C SUPERFAMILY IN THE INNATE IMMUNE RESPONSE OF ANOPHELINE MOSQUITOES

**Nazzy Pakpour**<sup>1</sup>, Lauren Camp<sup>1</sup>, Hannah M. Smithers<sup>1</sup>, Bo Wang<sup>1</sup>, Zhijian Tu<sup>2</sup>, Steven A. Nadler<sup>1</sup>, Shirley Luckhart<sup>1</sup>

<sup>1</sup>University of California Davis, Davis, CA, United States, <sup>2</sup>Virginia Polytechnic Institute and State University, Blacksburg, VA, United States

Anopheline mosquitoes are the primary vectors of medically important parasites in the genus *Plasmodium*, the causative agents of malaria. Malaria parasites undergo a series of complicated developmental transformations upon ingestion by *Anopheles* mosquitoes and during this process innate immune defenses can reduce parasite numbers significantly. While some mosquito anti-parasite effectors have been well characterized, the regulatory factors that control the timing and magnitude of these responses are poorly understood. The protein kinase C (PKC) superfamily consists of serine/threonine kinases that serve as central signaling molecules and regulators of a broad spectrum of cellular processes including growth, reproduction, and immunity. PKCs are highly conserved, ranging from seven isoforms in *Drosophila* to 16 isoforms in mammals, yet none have been identified in mosquitoes. Additionally, PKC-dependent signaling is central to the regulation of mammalian immunity and has been targeted aggressively for drug development. Despite conservation of the PKC superfamily and their potential as targets for transmission-blocking strategies for malaria, no direct connections between PKCs and the mosquito immune response exist. Here, we present the identification and characterization of six PKC superfamily members – PKC $\beta$ , PKC $\delta$ , PKC $\epsilon$ , PKC $\zeta$ , PKD, PKN – in *Anopheles gambiae* and *Anopheles stephensi*. Phylogenetic analysis of the anopheline PKCs confirmed subfamily assignments. All six PKCs are expressed in the midguts of *A. gambiae* and *A. stephensi*, indicating availability for signaling in a tissue that is critical for malaria parasite development. Inhibition of PKC enzymatic activity *in vitro* decreased NF- $\kappa$ B-regulated anti-microbial peptide expression in response to bacterial and parasitic specific factors. Further, PKC inhibition significantly decreased development of *P. falciparum* oocysts in *A. stephensi*, suggesting that PKC-dependent signaling is a positive regulator of the mosquito immune response and a potential target for transmission-blocking strategies.

## 1462

### THE ROLE OF THE PROTEIN KINASE C SUPERFAMILY IN THE INNATE IMMUNE RESPONSE OF ANOPHELINE MOSQUITOES

**Nazzy Pakpour**<sup>1</sup>, Lauren Camp<sup>1</sup>, Hannah M. Smithers<sup>1</sup>, Bo Wang<sup>1</sup>, Zhijian Tu<sup>2</sup>, Steven A. Nadler<sup>1</sup>, Shirley Luckhart<sup>1</sup>

<sup>1</sup>University of California Davis, Davis, CA, United States, <sup>2</sup>Virginia Polytechnic Institute and State University, Blacksburg, VA, United States

Anopheline mosquitoes are the primary vectors of medically important parasites in the genus *Plasmodium*, the causative agents of malaria. Malaria parasites undergo a series of complicated developmental transformations upon ingestion by *Anopheles* mosquitoes and during this

process innate immune defenses can reduce parasite numbers significantly. While some mosquito anti-parasite effectors have been well characterized, the regulatory factors that control the timing and magnitude of these responses are poorly understood. The protein kinase C (PKC) superfamily consists of serine/threonine kinases that serve as central signaling molecules and regulators of a broad spectrum of cellular processes including growth, reproduction, and immunity. PKCs are highly conserved, ranging from seven isoforms in *Drosophila* to 16 isoforms in mammals, yet none have been identified in mosquitoes. Additionally, PKC-dependent signaling is central to the regulation of mammalian immunity and has been targeted aggressively for drug development. Despite conservation of the PKC superfamily and their potential as targets for transmission-blocking strategies for malaria, no direct connections between PKCs and the mosquito immune response exist. Here, we present the identification and characterization of six PKC superfamily members – PKC $\beta$ , PKC $\delta$ , PKC $\epsilon$ , PKC $\zeta$ , PKD, PKN – in *Anopheles gambiae* and *Anopheles stephensi*. Phylogenetic analysis of the anopheline PKCs confirmed subfamily assignments. All six PKCs are expressed in the midguts of *A. gambiae* and *A. stephensi*, indicating availability for signaling in a tissue that is critical for malaria parasite development. Inhibition of PKC enzymatic activity *in vitro* decreased NF- $\kappa$ B-regulated anti-microbial peptide expression in response to bacterial and parasitic specific factors. Further, PKC inhibition significantly decreased development of *P. falciparum* oocysts in *A. stephensi*, suggesting that PKC-dependent signaling is a positive regulator of the mosquito immune response and a potential target for transmission-blocking strategies.

## 1463

### ANTI-ADHESION MOLECULES INHIBIT PLASMODIUM INFECTION IN ANOPHELES MOSQUITOES

**Clara Brando**<sup>1</sup>, Tatyana Savranskaya<sup>1</sup>, Dipali Patel<sup>1</sup>, Alejandra Zapata<sup>1</sup>, Cezary Marcinkiewicz<sup>2</sup>, Megan Dowler<sup>1</sup>, Jittawadee Murphy<sup>1</sup>

<sup>1</sup>Walter Reed Army Institute of Research, Silver Spring, MD, United States,

<sup>2</sup>Temple University, Philadelphia, PA, United States

*Plasmodium* gametocytes ingested by mosquitoes with blood meal undergo gametocytogenesis and fertilization in mosquito midgut and develop to ookinetes. Ookinetes penetrate through mosquito gut wall to reach the gut epithelia where they attach themselves to the underlying basal lamina and develop to oocysts. Oocysts mature, develop thousands of sporozoites, and eventually rupture and release sporozoites into the mosquito haemolymph. Sporozoites then invade mosquito salivary glands. All these steps are governed by a series of adhesion phenomena made possible by interaction between receptors on the parasites and ligands expressed on mosquito tissues. Sporozoite invasion of salivary glands is also controlled by receptor-ligand interaction. Here we investigated the effect of several disintegrins and a c-lectin, which are proteins that interfere with adhesion phenomena mediated by integrins, on the *P. berghei* development in *Anopheles stephensi*. After mosquitoes were infected with *P. berghei*, they were fed daily with either 1  $\mu$ g/ml of seven different disintegrins, c-lectin, or sugar (control). The mosquitoes were then examined for oocyst infection at Day 11 post infection and for sporozoite infection at Day 16. Mosquitoes treated with echistatin and VP12 showed decreased numbers of oocysts averaging 20/msq as opposed to averaged 50/msq in the controls. Only 30-40 % of mosquitoes treated with echistatin or VP12 showed at least 10 sporozoites in their salivary glands, while 90 % of mosquitoes fed on sugar (control) did. The results show that these disintegrins interfered with the adhesion phenomena leading to a decrease in oocyst attachment to mosquito midgut and sporozoite invasion of salivary glands.

## 1464

### SELECTION FOR CHLOROQUINE-SENSITIVE *PLASMODIUM FALCIPARUM* BY *ANOPHELES ARABIENSIS* IN SOUTHERN ZAMBIA

Sungano Mharakurwa<sup>1</sup>, Mavis Sialumano<sup>1</sup>, Kun Liu<sup>1</sup>, Phil Thuma<sup>1</sup>, Peter Agre<sup>2</sup>

<sup>1</sup>The Malaria Institute at Macha, Choma, Zambia, <sup>2</sup>Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, United States

The emergence of *Plasmodium falciparum* drug resistance poses a major obstacle for malaria control and elimination. Public health strategies are needed to delay or minimize escalation. Field observations point to a link between mosquito control and the prevalence of *P. falciparum* drug resistance, the origin of which has remained unclear. Here we show field evidence for natural selection of wild type chloroquine-sensitive malaria parasites by *An. arabiensis* in southern Zambia. We screened 753 *An. arabiensis* by PCR, of which 8% and 10% were positive for salivary gland and mid-gut *P. falciparum* infections, respectively. We typed *P. falciparum* in humans and mosquitoes at the chloroquine resistance conferring amino acid codon 76 of the *PfCRT* gene. Our data showed that despite being acquired from humans within a few weeks, *P. falciparum* infections in mosquitoes were up to 10X more likely to bear wild type *PfCRT* K76 than in humans (OR [95%CI]: 10 [4.3 - 25.3],  $p < 0.001$ ,  $n = 370$ ). We concluded that a sporogonic selection occurs against mutated *PfCRT* 76T-bearing *P. falciparum* in mosquitoes, presumably owing to altered biological fitness. This strong selection would seem to explain the association seen in the field between mosquito control and prevalence of drug resistance. We hypothesize that through this sporogonic selection, mosquitoes contribute to restoration of chloroquine-sensitive K76 parasites after suspension of drug use in humans. Understanding the nature and direction of the sporogonic selection could be instrumental in rational curtailment of drug resistance in integrated malaria control or elimination programmes.

## 1465

### DEVELOPMENT OF A NEW BIOMARKER OF EXPOSURE TO *ANOPHELES* BITES BASED ON HUMAN ANTIBODY RESPONSES TO SALIVARY PROTEINS: FROM THE CONCEPT TO THE APPLICATIONS

Franck J. Remoue

IRD, Cotonou, Benin

The study of human-vector immune relationships could allow several applications for the control of vector-borne diseases. Indeed, some salivary proteins from blood-feeding arthropods could induced a specific immune responses in human populations exposed to arthropod vectors bites. One hypothesis is that human immune response and especially antibody (Ab) response to whole saliva of mosquito could be an epidemiological biomarker of human exposure to vector bites. In the objective to increase the specificity to vector exposure, the second step was to identify salivary proteins i) specific to *Anopheles* genus and ii) antigenic in individuals exposed to malaria. First, the identification of antigenic salivary proteins of mosquito by an immuno-proteomic approach was assessed. The second step was to design peptide sequences, from one selected mosquito salivary protein using a bioinformatic approach, taking into consideration i) their potential antigenic properties and ii) the absence of cross-reactivity with other arthropods/organisms. For malaria, the specific IgG Ab levels were then evaluated in African children in different context of malaria. From five peptides, only one peptide (gSG6-P1) presented all criteria to be an optimal candidate biomarker for evaluating human exposure to *An. gambiae* and *An. funestus* bites and interestingly for evaluating the efficacy of vector control. This new "salivary" biomarker of *Anopheles* exposure could be used as a geographic indicator for mapping the risk of malaria transmission and especially in low *Anopheles* density conditions,

where entomological methods are limited in sensitivity (dry season, altitude or urban malaria). It also represents a direct criterion of efficacy in the evaluation of anti-vector strategies.

## 1466

### MALARIA IN SCHOOL CHILDREN UNDER A NEW POLICY OF UNIVERSAL COVERAGE OF NETS: RECENT DATA FROM MALI AND SENEGAL

Sian E. Clarke<sup>1</sup>, Natalie Roschnik<sup>2</sup>, Saba Rouhani<sup>1</sup>, Seybou Diarra<sup>3</sup>, Modibo Bamadio<sup>3</sup>, Moussa Sacko<sup>4</sup>, Diahara Traore<sup>5</sup>, Alioune B. Ly<sup>6</sup>, Oumar Gaye<sup>6</sup>, Malick Sembene<sup>7</sup>, Fatou Ba Fall<sup>8</sup>

<sup>1</sup>London School of Hygiene & Tropical Medicine, London, United Kingdom, <sup>2</sup>Department of Education and Child Development, Save the Children, Washington, WA, United States, <sup>3</sup>Save the Children, Bamako, Mali, <sup>4</sup>Institut National de Recherche en Santé Publique, Bamako, Mali, <sup>5</sup>Programme National de Lutte contre le Paludisme, Ministry of Health, Bamako, Mali, <sup>6</sup>Universite Cheikh Anta Diop, Dakar, Senegal, <sup>7</sup>Division Contrôle Médical Scolaire, Ministry of Education, Dakar, Senegal, <sup>8</sup>Programme National de Lutte contre le Paludisme, Ministry of Health, Dakar, Senegal

Malaria control has traditionally focused on pregnant women and children under five years, in whom the risk of malaria-related mortality is greatest. Yet studies have shown that older school-age children can also benefit from malaria control, with potential gains for both health and education. Insecticide-treated nets are a cornerstone of malaria prevention efforts, but in many countries net usage is lowest in school-age children compared with younger children and adults. Universal coverage of nets will help address this gap, and is increasingly being adopted into policy by national control programmes in malaria-endemic countries. Senegal and Mali recently introduced universal coverage of nets, with national roll-out of community-wide distributions of long-lasting insecticidal nets (LLINs) starting in 2010 and 2011 respectively. The coverage of LLINs amongst schoolchildren in these two countries was examined through school surveys 6-12 months after the net distributions, and the prevalence of malaria parasitaemia and anaemia measured at the end of the transmission season. Data was collected in 38 primary schools (1900 children) in Sikasso, Mali and 6 primary schools (865 children) in Kedougou, Senegal. Our data provide evidence that the new strategy was successful in achieving coverage in this previously neglected age group: reported and observed use of nets was high in both countries, with over 80% of schoolchildren (age 7-14 years) using nets. Yet paradoxically, levels of malaria infection remained high. Overall 83% of primary schoolchildren in Mali (range: 46-98%), and 54% of schoolchildren in Senegal (range: 20-81%) had asymptomatic parasitaemia in December 2011. Factors which may account for this apparent paradox will be discussed, and data presented on patterns of net use by child and household characteristics, including time of going to bed and discontinued use of nets in later months. We shall also present findings from an alternative malaria control strategy in schools, intermittent parasite clearance, which is currently being trialed in these two sites.

### THE EFFECT OF LIMITED RESIDUAL LIFE OF INSECTICIDE AND OUTDOOR BITING ON MALARIA INFECTION IN CHILDREN ON BIOKO ISLAND, EQUATORIAL GUINEA: AN EXAMINATION OF TWO KEY ASSUMPTIONS OF INDOOR RESIDUAL SPRAYING

John Bradley<sup>1</sup>, Abrahan Matias<sup>2</sup>, Christopher Schwabe<sup>3</sup>, Daniel Vargas<sup>2</sup>, Feliciano Monti<sup>2</sup>, Gloria Nseng<sup>4</sup>, Immo Kleinschmidt<sup>1</sup>

<sup>1</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>2</sup>Medical Care Development International, Malabo, Equatorial Guinea, <sup>3</sup>Medical Care Development International, Silver Spring, MD, United States, <sup>4</sup>Ministry of Health and Social Welfare, Malabo, Equatorial Guinea

Malaria is endemic on Bioko Island, Equatorial Guinea, with year round transmission. In 2004 an intensive malaria control strategy primarily based on Indoor Residual Spraying (IRS) was launched. The limited residual life of IRS poses particular challenges in a setting with year round transmission such as Bioko. Recent reports of outdoor biting by *An. gambiae* are a further cause for concern. In this study the effect of the short residual life of bendiocarb insecticide and of children spending time outdoors at night on malaria infection prevalence was examined. Data from the 2011 annual malaria indicator survey and from standard WHO cone bioassays were used to examine the relationship between time since IRS, mosquito mortality and prevalence of infection in children. Children spending time outside at night and the association of this behavior with malaria infection were also examined. Prevalence of malaria infection in 2 to 14 year-olds was 18.4%, 21.0% and 28.1% in communities with median time since IRS of three, four and five months respectively. After adjusting for confounders, each extra month since IRS corresponded to an odds ratio (OR) of 1.44 (95% CI 1.15 - 1.81) for infection prevalence in 2 to 14 year-olds. Mosquito mortality was 100%, 96%, 81% and 78%, at month two, three, four and five respectively after spraying. Only 4.1% of children spent time outside the night before the survey between the hours of 10pm and 6am and were not at a higher risk of infection (OR 0.87, 95% CI 0.50 - 1.54). Sleeping under a mosquito net provided additive protection (OR 0.68, 95% CI 0.54 - 0.86). The results demonstrate the epidemiological impact of reduced mosquito mortality with time since IRS. The study underscores that in settings of year round transmission there is a compelling need for longer lasting IRS insecticides, but that in the interim high coverage of long lasting insecticidal nets (LLINs) may ameliorate the protective effect conferred by current shorter lasting IRS insecticides.

### EARLY MORNING BITING BY ANOPHELES VECTORS: A POTENTIAL RISK PERIOD FOR MALARIA INFECTION IN AN AREA WITH HIGH AND SUSTAINED USE OF INSECTICIDE TREATED BED NETS IN WESTERN KENYA

M. Nabie Bayoh<sup>1</sup>, Edward Walker<sup>2</sup>, Meghna Desai<sup>1</sup>, Jacklyn Kosgei<sup>1</sup>, Chris Odero<sup>1</sup>, George Olang<sup>1</sup>, Peter Otieno<sup>1</sup>, Maurice Ombok<sup>1</sup>, Vincent Were<sup>1</sup>, Simon Kariuki<sup>1</sup>, John Vulule<sup>1</sup>, John Gimnig<sup>3</sup>

<sup>1</sup>Centre for Global Health Research, Centers for Disease Control and Prevention/KEMRI, Kisumu, Kenya, <sup>2</sup>Michigan State University, East Lansing, MI, United States, <sup>3</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States

As malaria vector control activities using insecticide-based interventions such as indoor residual spraying and insecticide treated nets (ITNs) expand, the question emerges as to how these activities shape the distribution, population and behavior of the vectors; as these processes will influence the effectiveness of each intervention. Outdoor and early evening biting have been suggested as possible vector behavior changes resulting from indoor vector control interventions. Therefore, we conducted a study during the peak malaria season in an area of high ITN ownership in western Kenya to quantify the biting behavior of the local malaria vectors, and related results to the behavior of people in the community. A total of

150 adult men were recruited as human landing catchers who collected and stored mosquitoes hourly at indoor and outdoor fixed positions, from 5 PM to 7 AM, for 4 nights per week, in a total of 75 villages for a period of 6 weeks. The main malaria vectors were *Anopheles arabiensis* (n=153, sporozoite rate SR=0.04); *A. gambiae* s.s (n=241, SR=0.12) and *A. funestus* (n=1169; SR=0.09). More than a third of bites by each of the main vectors occurred outdoors. However, by 9 PM, 88% of the human population was indoors and were presumably not at risk for malaria infection by outdoor biting mosquitoes. Indoors, the peak biting for all three species occurred after midnight, and biting continued to 7 AM. Net use was high with 77% of the population reporting the use of a net the previous night. By 11 PM, 96% of the population reported going to bed and those who reported using a net were likely at a low risk of mosquito bites and malaria infection. In the morning hours, about 52% of the population was awake before 6 AM, a time when vector mosquitoes, particularly *An. funestus* were still active, suggesting a window of risk for malaria infection. The temporal distribution of risk of infectious bites among the population and implications for vector control will be discussed.

### CLUSTER-RANDOMIZED TRIAL OF TEXT MESSAGE REMINDERS TO RETAIL STAFF OF APPROPRIATE PRACTICES FOR DISPENSING ARTEMETHER-LUMEFANTRINE IN DRUG SHOPS IN TANZANIA: EFFECT ON DISPENSER KNOWLEDGE AND PATIENT ADHERENCE

Katia Bruxvoort<sup>1</sup>, Admirabilis Kaloella<sup>2</sup>, Charles Festo<sup>2</sup>, Matthew Cairns<sup>1</sup>, S. Patrick Kachur<sup>3</sup>, Catherine Goodman<sup>1</sup>, David Schellenberg<sup>1</sup>

<sup>1</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>2</sup>Ifakara Health Institute, Dar es Salaam, United Republic of Tanzania, <sup>3</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States

Patient adherence, the extent to which patients promptly and correctly take the full course of a drug, is a key component in ensuring drug effectiveness. As artemisinin-based combination therapies (ACTs) for malaria become more widely available in the private sector, there are concerns that patient adherence might be low due to insufficient or incorrect advice provided by dispensers with limited training. In this cluster-randomized trial in drug shops in southern Tanzania, we assess the effect of text message reminders to retail staff on advice to provide when dispensing artemether-lumefantrine (AL) on dispenser knowledge and patient adherence. Of 72 randomly selected drug shops in Mtwara region, 36 were randomized for dispensers to receive text message reminders once per day five days per week beginning a month prior to the study. No intervention was delivered in the control arm. Patients desiring to purchase ACT at study drug stores were eligible to receive AL from a mixed supply of regular blister packs and identical-looking blister packs containing devices to record the date and time each blister was opened to remove pills. From each arm, 468 patients receiving study AL were followed up at home a minimum of 75 hours after drug purchase; consenting patients or their caregivers were administered a detailed questionnaire about when and how each dose of AL was taken. Patients were asked to present their blister packs for a pill count and extraction of timestamp data. Following patient data collection, dispensers were interviewed regarding their knowledge of AL dispensing practices, and mobile phone usage and receipt of malaria-related messages. Using data from questionnaires, pill-counts, and timestamps, we will report the effects of the intervention on dispensers' knowledge, the proportion of patients completing all doses within 75 hours of purchase and those adhering to the correct timing of each dose, and the advice patients received from the dispenser. These data will be useful for designing strategies to enhance the effectiveness of ACTs in the private sector.

## 1470

**ANALYSIS OF FACILITY-LEVEL STOCKOUTS OF ACTS IN ZAMBIA: THE IMPACT OF INVENTORY MANAGEMENT**Jeremie Gallien<sup>1</sup>, Zachary Leung<sup>2</sup>, Prashant Yadav<sup>3</sup><sup>1</sup>London Business School, London, United Kingdom, <sup>2</sup>Massachusetts Institute of Technology, Cambridge, MA, United States, <sup>3</sup>University of Michigan, Ann Arbor, MI, United States

Despite remarkable and successful recent improvements efforts by the government and its partners, the current public distribution system of essential medical drugs in Zambia still results in low availability to patients relative to private sector standards. Many possible causes have been cited, including procurement financing and processes, supply capacity, communication and road infrastructure, distribution resources and planning methods, personnel staffing and training, coordination among stakeholders. A field experiment in Zambia's public distribution system conducted from Q3 2009 to Q2 2010 involved a high adherence to recommended inventory control policies and offers an opportunity to isolate their impact. To do so we collected daily clinic storeroom stock levels of Artemether-Lumefantrine (AL) antimalarial products in up to 90 facilities through photography and manual transcription, then used that data to estimate demand patterns and service levels. Delivery lead-times and estimates of monthly facility accessibility were obtained through survey of health workers. Monthly national warehouse stock levels were extracted from a software database. A simulation model was constructed to reproduce and interpret observations of stock-out patterns. We found that up to 30% of surveyed facilities stocked out of all AL products at certain times of the year despite ample inventory being available at the national warehouse. The simulation model closely reproduced these results and linked them to the use of average past monthly issues and failure to capture lead-time variability in current inventory control policies. These results suggest that inventory control policies widely recommended and used for distributing medicines in Sub-Saharan Africa directly account for some of the stockouts observed in situations involving demand seasonality and/or clinic access interruptions. They also suggest specific improvement opportunities for pharmaceutical inventory control systems that include digital transmission of inventory transactions through mobile wireless devices, standard forecasting algorithms and mathematical optimization.

## 1471

**A REVIEW OF THE CAUSES OF ACT STOCK-OUTS IN BURUNDI**Rima Shretta<sup>1</sup>, Aline Mukerabirori<sup>2</sup>, Patrick Garapayi<sup>3</sup>, Diane Ndayiragije<sup>2</sup>, Emmanuel Maregeya<sup>2</sup>, Lidwine Baradahana<sup>4</sup>, Liévin Mizero<sup>5</sup>, Eleonore Rabelahasa<sup>6</sup><sup>1</sup>Management Sciences for Health, Arlington, VA, United States, <sup>2</sup>Management Sciences for Health, Bujumbura, Burundi, <sup>3</sup>Management Sciences for Health, Kigali, Rwanda, <sup>4</sup>Programme National Intégré de Lutte contre le Paludisme, Bujumbura, Burundi, <sup>5</sup>Ministry of Health, Bujumbura, Burundi, <sup>6</sup>United States Agency for International Development, Bujumbura, Burundi

Prompt treatment of malaria cases with an effective antimalarial is a key global strategy for malaria control. Despite global efforts to scale up the use of artemisinin-based combination therapies (ACTs), coverage across Africa remains poor, with public sector health facilities frequently plagued by stock-outs. The causes of stock-outs vary, but often reflect poor planning and weak supply chain management systems. Data from public health facilities in 6 African countries illustrated that in some cases up to 90% of health facilities lacked the full range of weight-specific packs of the recommended ACT treatments in stock. Stock-outs often last several weeks, leaving malaria patients dangerously vulnerable. We analyzed the root causes of these stock-outs in Burundi using both record reviews and in-depth interviews with providers at the national, district, and facility levels between June and December 2011. Results indicated that districts required five signatures with their monthly requisition for ACTs, which led

to delays and a resignation to use other treatment options or split blister packs of other age groups, which skewed consumption data. The districts did not receive sufficient stock to cover their health facilities, and little provision was made for safety stock or emergencies, resulting in partially filled orders. As soon as districts receive monthly orders, they repeat the process without allowing time to monitor stock sent to the facilities. The time between preparing an order and distribution to the facilities is long, and emergency procurements are frequent and expensive. The formulas used to forecast needs at the multiple levels are inconsistent; in addition, data are sometimes "created" in reports to place an order and to meet performance targets. Staff also appeared to be complacent regarding the effect of stock-outs on patient outcomes. While interventions to avert some challenges are being implemented, more efforts are needed to ensure uninterrupted availability of ACTs and to promote the importance of these efforts at all levels.

## 1472

**QUALITY OF UNCOMPLICATED MALARIA CASE MANAGEMENT IN MALAWI-FINDINGS FROM A NATIONAL HEALTH FACILITY SURVEY**Laura C. Steinhardt<sup>1</sup>, Jobiba Chinkhumba<sup>2</sup>, Adam Wolkon<sup>1</sup>, Madalitso Luka<sup>2</sup>, Misheck Luhanga<sup>3</sup>, John Sande<sup>3</sup>, Jessica Oyugi<sup>4</sup>, Doreen Ali<sup>3</sup>, Don Mathanga<sup>2</sup>, Jacek Skarbinski<sup>1</sup><sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States, <sup>2</sup>Malaria Alert Centre, Blantyre, Malawi, <sup>3</sup>National Malaria Control Programme, Lilongwe, Malawi, <sup>4</sup>Centers for Disease Control and Prevention, Lilongwe, Malawi

Quality malaria case management is dependent on patients being appropriately assessed, diagnosed, and treated with artemisinin-based combination therapy (ACT) for uncomplicated malaria. We conducted a nationally representative cross-sectional health facility survey in Malawi to examine malaria case management quality and assess factors related to correct treatment. We sampled 107 public health centers and hospitals in all 29 districts of Malawi in April-May 2011, during peak malaria transmission. In all, 2,019 patients seeking curative care at outpatient departments were interviewed after their consultation, and blood smears were taken. Malaria was defined as fever or history of fever and malaria parasitemia on exit interview blood smear. Logistic regression was used to examine factors associated with correct treatment, defined as ACT prescription for patients with malaria. Thirty-four percent of all patients presenting to facilities in Malawi had malaria, including 46% of children <5 years and 27% of patients ≥5 years ( $p < 0.001$ ). Among patients with malaria, 67% received correct treatment; the most common reason for incorrect treatment was missed diagnosis (27%). Clinicians did not assess fever/history of fever in 27% of all patients. Only 21% of patients were tested for malaria using microscopy, and rapid diagnostic tests were not yet available. Overtreatment was common with 31% of patients without malaria prescribed an ACT. Patient-level factors, including high temperature (adjusted odds ratio (aOR) = 3.3; 95% confidence interval (CI) 3.3-5.5), spontaneous complaint of fever (aOR = 4.0; 95% CI 3.3-7.2), and complaint of cough (aOR = 0.3; 95% CI 0.2-0.5) were significantly associated with correct treatment. Health worker- or facility-level factors were not. Malawi has a high burden of uncomplicated malaria, but both failure to deliver correct treatment and overtreatment are common. Improved assessment of fever and increased parasitological confirmation of malaria diagnosis are critical to improve malaria case management.

### ADVERSE DRUG EVENTS RESULTING FROM USE OF DRUGS WITH SULFONAMIDE AND ARTEMISININ-BASED ANTIMALARIALS: FINDINGS ON INCIDENCE AND HOUSEHOLD COSTS FROM THREE DISTRICTS WITH ROUTINE DEMOGRAPHIC SURVEILLANCE SYSTEMS IN RURAL TANZANIA

Joseph D. Njau<sup>1</sup>, Abdulnoor M. Kabanywany<sup>2</sup>, Catherine Goodman<sup>3</sup>, John R. MacArthur<sup>1</sup>, B.k. Kapella<sup>1</sup>, John E. Gimning<sup>1</sup>, Elizeus A. Kahigwa<sup>4</sup>, Peter B. Bloland<sup>1</sup>, Salim M.k. Abdulla<sup>2</sup>, Patrick S. Kachur<sup>1</sup>

<sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States,

<sup>2</sup>Ifakara Health Institute, Dar es Salaam, United Republic of Tanzania,

<sup>3</sup>London School of Hygiene and Tropical Medicine, London, United Kingdom, <sup>4</sup>Swiss Development Cooperation (SDC), Dar es Salaam, United Republic of Tanzania

Antimalarial regimens including sulfonamide and artemisinin derivatives have been deployed in many parts of the world in an effort to halt the acceleration of antimalarial drug resistance problem. Access to these drugs has faced multiple obstacles including availability, acceptability, and adherence. Meanwhile, weak public health infrastructures and drug regulatory authorities prevalent in most malaria endemic countries, particularly in sub-Saharan Africa, are partly responsible for poor post-marketing surveillance and have enhanced the proliferation of fake antimalarials. We used active and passive surveillance to identify and document antimalarial-associated adverse drug reactions (ADR) in three rural districts of Tanzania with high malaria transmission. Clinicians were trained to identify, categorize and report ADR cases linked to sulfadoxine/pyrimethamine (SP) and artemisinin (AS) use. Additional questions relating to demographics, care-seeking and treatment costs were asked. A total of 95 suspected ADR cases were identified. 79 were traced and successfully classified. 67 (85%) of the 79 cases were related to use of SP and/or AS antimalarial drugs. 51% of the 67 cases were classified as 'probable' and 49% were classified as 'possible' ADR events. Annual ADR incidence per 100,000 was calculated at 5.6 for AS/SP and 25.0 for SP monotherapy. Treatment costs per episode ranged from a median of US \$2.00 for those making a single visit to US \$21.13 for patients with 4 visits to healthcare providers. Drug costs constituted 43% of the treatment costs. Faith-based and NGO facilities were the most expensive source of care. 85% of the patients used out-of-pocket funds to pay their bills. 21% of the patients had to sell assets or borrow from relatives to settle their bills. Costs of treatment of ADR episodes were substantially catastrophic.

### PROVIDER AND COMMUNITY RESPONSES TO THE NEW MALARIA TREATMENT REGIME IN SOLOMON ISLANDS

Rushika S. Wijesinghe<sup>1</sup>, Jo-An M. Atkinson<sup>1</sup>, Albino Bobogare<sup>2</sup>, Lyndes Wini<sup>2</sup>, Maxine Whittaker<sup>1</sup>

<sup>1</sup>University of Queensland, Herston, Australia, <sup>2</sup>National Vector Borne Disease Control Programme, Ministry of Health, Honiara, Solomon Islands

Improvements in availability and accessibility of artemisinin-based combination therapy (ACT) for malaria treatment and the emergence of multi-drug-resistant parasites have prompted many countries to adopt ACT as the first-line drug. In 2009, Solomon Islands (SI) likewise implemented new national treatment guidelines for malaria. The ACT, artemether-lumefantrine is now the primary pharmacotherapy in SI for *Plasmodium falciparum* malaria, *Plasmodium vivax* malaria and mixed infections. Targeted treatment is also recommended in the new treatment regime through maintenance of quality microscopy services and the introduction of Rapid Diagnostic Tests (RDTs). Ascertaining the factors that influence community and provider acceptance of and adherence to the new treatment regime will be vital to improving the effectiveness of this intervention and reducing the risk of development of drug resistance. To understand community and prescriber perceptions and acceptability

of the new diagnostic and treatment regime, 12 focus group discussions and 12 key informant interviews were carried out in rural and urban villages of Malaita Province, Solomon Islands, four months subsequent to roll out of these interventions. Lack of access to microscopy or distrust in the accuracy of diagnostic tools were reported by some participants as reasons for the ongoing practice of presumptive treatment of malaria. Lack of confidence in RDT accuracy negatively impacted its acceptability. Artemether-lumefantrine had good acceptability among most participants; however, some rural participants questioned its effectiveness due to lack of side effects and the larger quantity of tablets required to be taken. Storing of left over medication for subsequent fever episodes was reported as common. To address these issues, further training and supportive supervision of healthcare workers will be essential, as will the engagement of influential community members in health promotion activities to improve acceptability of RDTs and adherence to the new treatment regime. Exploring the extent of these issues beyond the study population must be a priority for malaria programme managers. Practices such as presumptive treatment and the taking of sub-curative doses are of considerable concern for both the health of individuals and the increased risk it poses to the development of parasite resistance to this important first-line treatment against malaria.

### N-ACETYL TRANSFERASE GENE TYPE 2: PREDOMINANCE OF SLOW ACETYLATORS AND EFFECT ON RESPONSE TO ARTESUNATE AMODIAQUINE

Olivia A. Achonduh, Jean Paul Chedjou, Innocent A. Mbulli, Mercy Achu, Babara Atogho-Tiedeu, Eric Kamgue, Vera Veyee, Orise Karana, Akindeh M. Nji, Wilfred Mbacham

Laboratory for Public Health Research Biotechnologies, Biotechnology Center, University of Yaounde I, Yaounde, Cameroon

Inter individual differences in the metabolism of the antimalarials could be due to polymorphism of NAT2 gene. We determined the genotypic frequencies of single nucleotide polymorphism (SNP) of NAT2 gene and its implication in antimalarial treatment during a vitamin A and zinc supplementation intervention in children less than 5 years in Bangolan, Cameroon. A total of 100 children aged 6 to 24 months were recruited into the study after obtaining informed consent from parents or guardians. Participants were randomized to receive vitamin A +placebo or vitamin A+Zinc supplements. All participants received artesunate-amodiaquine(ASAQ) -toddler 50/135mg at baseline to clear any parasites, vitamin A administered and followed up for 30days. This was followed by daily administration of Zinc or placebo and follow up for 6 months for incidence of clinical malaria and other diseases. Blood was spotted on filter paper for DNA extraction by chelex method. RFLP-PCR was performed with restriction enzymes KpnI, TaqI, and BamHI for detection of NAT2\*5, NAT2\*6, NAT2\*7 SNPs respectively. Allelic frequencies and phenotypes were compared between participants with or without adverse reactions. A total of 55% of the participants had slow acetylator, 30% intermediate acetylator, 11% rapid acetylator and 4% an unknown genotype. NAT2 genotypes observed to be associated with susceptibility to develop anorexia were NAT2\*5/5 (OR=13,000) and NAT2\*4/6 (OR=6,538). Those likely to develop fever were NAT2\*4/7 (OR=5,082), NAT2\*5/6 (OR=2,389), NAT2\*6/7 (OR=1,481) and NAT2\*5/7 (OR=1,156). Those likely to develop fever of unknown etiology were NAT2\*6/6 (OR=23,467), NAT2\*4/5 (OR=2,933), NAT2\*5/5 (OR=2,048) and NAT2\*4/6 (OR=1,026). Those likely to develop skin rash were NAT2\*4/5 (OR=2,857), NAT2\*5/7 (OR=2,483), NAT2\*6/7 (OR=1,385), and NAT2\*4/7 (OR=1,357). Those likely to develop cough, catarrh (common cold) and fever were NAT2\*4/6 (OR=2,255), NAT2\*6/6 (OR=1,895), NAT2\*4/5 (OR=1,850), NAT2\*5/5 (OR=1,200) and NAT2\*5/5 (OR=1,016). The slow acetylator genotype NAT2 gene was the most predominant in the study population. Both slow and intermediate acetylators were more likely to the develop adverse reactions to ASAQ, vitamin A and Zinc supplements.

## 1476

### EXPLORING HOW LARGE-SCALE IMPLEMENTATION OF MALARIA CONTROL PROGRAMS MEDIATES THE RELATIONSHIP BETWEEN HOUSEHOLD SOCIOECONOMIC STATUS AND VARIOUS CHILDHOOD MALARIA CONTROL INDICATORS: EXPERIENCE FROM THREE PRESIDENT'S MALARIA INITIATIVE COUNTRIES IN SUB-SAHARAN AFRICA

Joseph D. Njau<sup>1</sup>, Rob Stephenson<sup>2</sup>, Patrick S. Kachur<sup>1</sup>

<sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States,

<sup>2</sup>Rollins School of Public Health, Emory University, Atlanta, GA, United States

Following the first Global Malaria Eradication Program in the 1950's malaria was confined almost exclusively in the poorest nations of the world, particularly in sub-Saharan Africa and Southeast Asia. While macroeconomic studies consistently show a strong and stable relationship between malaria and poverty, most microeconomic studies have largely been inconclusive. This study explores how variations in implementation of large scale malaria control programs may explain the reason why microeconomic studies remain inconclusive. It sets out to explain the critical role played by large scale implementation of malaria control strategies such as those financed by Global Fund and the President's Malaria Initiative (PMI) in mediating the relationship between households' socioeconomic status (wealth, education and place of domicile) and key malaria control indicators. The study focuses on malaria parasitemia, bed-net ownership and bed-net use among children aged less than five years as key outcome variables of interest. We analyzed Malaria Indicator Survey data for the first three PMI countries: Angola, Tanzania and Uganda. A multilevel-hierarchical cluster analysis restricted to malaria program implementation regions was used. SES interaction terms with malaria program implementation were found to have significant bearing across the three countries. In Angola, programs were more likely to benefit households headed by individuals or mothers with higher education levels whereas household wealth status was less important. In Tanzania, wealth, education and living in urban or rural settings were all significant determinants of which households benefited more from the programs while in Uganda programs were more likely to benefit poorer households. Following these findings, policy relevant conclusions are drawn to help design more pro-poor malaria control policies in light of the renaissance of malaria eradication policy debates.

## 1477

### PREVENTION OF NEONATAL HYPOTHERMIA IN SOUTHERN PROVINCE, ZAMBIA

Davidson H. Hamer<sup>1</sup>, Karsten Lunze<sup>2</sup>, Julie Herlihy<sup>2</sup>, Arthur Mazimba<sup>3</sup>, Caroline Grogan<sup>4</sup>, Manka Nkimberg<sup>4</sup>, Lauren Owens<sup>4</sup>, Kojo Yeboah-Antwi<sup>4</sup>, Katherine Semrau<sup>2</sup>

<sup>1</sup>Zambia Centre for Applied Health Research and Development, Lusaka, Zambia, <sup>2</sup>Center for Global Health and Development, Boston University, Boston, MA, United States, <sup>3</sup>Zambia Chlorhexidine Application Trial (ZamCAT), ZCAHRD, Choma, Zambia, <sup>4</sup>Center for Global Health and Development, Boston, MA, United States

Newborn hypothermia is associated with increased neonatal mortality. Zambian guidelines recommend facility-based delivery by skilled birth attendants and immediate postpartum skin-to-skin care to provide thermoprotection of the neonate. This study assessed institutional capacity to prevent neonatal hypothermia in Zambia. We conducted comprehensive health center (HC) surveys in Southern Province, Zambia, and pregnant women were recruited at the same HCs during routine antenatal care to participate in a neonatal study (ZamCAT). Enrollees were interviewed 4 days post-delivery about the delivery and immediate postpartum care. Of the 90 primary HCs surveyed, only 8.8% had a neonatal warmer and 6.7% had heat control for the delivery room. When HC directors were asked about delivery practices, 36.7% said the newborn was placed the mother's abdomen after delivery, 46.7% put

the baby next to the mom and 15.6% placed the baby in a cot. Nearly all HCs (94.4%) reported drying and wrapping the baby in a new cloth, and, in the last month, 92.2% recommended skin-to-skin contact to new mothers. Among 9,816 deliveries [63% at a facility, 36% at home], the baby was placed on mother's skin after delivery 49.9% of the time; this was significantly higher in facility compared to home deliveries ( $p < 0.001$ ). Women delivered by a nurse/midwife or trained TBA were more likely to have the baby put on the mother's skin afterwards compared to those delivered by family members, self or untrained TBAs (61.8% vs. 21.5%,  $p < 0.001$ ). In 98% of deliveries, the baby was wrapped in a dry cloth; this did not differ by delivery location. Southern Province health centers are not well equipped to prevent neonatal hypothermia although evaluation of actual practices suggests that efforts are made to warm the newborn and recommend skin-to-skin care. These practices are less common in home deliveries, thus increasing risk of hypothermia in newborns delivered by unskilled birth attendants.

## 1478

### USING CURRENT AND EXTENDED ROUTINE PREVENTION VISITS TO HEALTH FACILITIES ACHIEVE HIGHER COVERAGE WITH CHILD-SURVIVAL INTERVENTIONS IN SUB-SAHARAN AFRICA

Kristen M. Little<sup>1</sup>, Asia Miller<sup>2</sup>, Michael S. Deming<sup>1</sup>

<sup>1</sup>Centers for Disease Control and Prevention, Atlanta, GA, United States,

<sup>2</sup>Research Triangle Institute, Atlanta, GA, United States

Interventions to improve child survival in sub-Saharan Africa are frequently administered during mass campaigns (MCs), particularly for interventions targeting children 1-4 years old. Integrated delivery of interventions in MCs, including Vitamin A supplementation, insecticide-treated bednets, supplemental immunizations, and deworming, has been promoted to decrease program costs and to expand coverage. However, integrated preventive services have long been provided during routine preventive visits (RPVs) to health facilities by pregnant women and mothers and their children during the child's first year of life. While the interventions offered during RPVs are currently limited, they could be expanded and offered as well as new RPVs scheduled up to the age of five. To assess RPVs as a platform for expanded service delivery and compare them to MCs, we analyzed data from Demographic and Health Surveys in 12 sub-Saharan African countries in which mothers were asked about receipt of services for themselves or their children in one or more MCs (median number of MCs: 4.5; range: 2-11). RPV coverage demonstrating access (the percentage of mothers seen at least once for an RPV) was high in all countries (range: 80.6 [Nigeria]-99.9% [Swaziland]; median: 96.7), typically exceeding the percentage of eligible 1-4 year-old children receiving an intervention in at least one MC (range: 36.3 [Sierra Leone]-89.5% [Eritrea], median difference: 28.1 percentage points). The median number of RPVs among mothers of 1-4 year-old children ranged from 4.5 in Niger, to 12.9 in Swaziland. The percentage of children aged 1-4 years missed by all MCs but whose mothers made at least one RPV ranged from 62.7% in Nigeria to 99.5% in Sao Tome & Principe. The median number of RPVs among these children ranged from 2.3 in Niger to 11.0 in Ghana. Among 1-4 year-olds whose mother made no RPV, the percentage receiving at least one MC intervention for which they were eligible was lower (range: 0.0 [Sao Tome & Principe]-35.5% [Niger]; median 4.8%). Current and extended RPVs may reach children missed by MCs, and are potentially an effective alternative to MCs for delivering some child-survival interventions, particularly to 1-4 year-old children.



### IMPACT OF A BRIEF IN-HOME NEONATAL HEALTH PROMOTION ON SELF-REPORTED BIRTH AND NEONATAL CARE PRACTICES AMONG PRIMIPAROUS WOMEN IN THE THIRD TRIMESTER IN RURAL BANGLADESH

Kelly B. Kamm<sup>1</sup>, Sharifa Nasreen<sup>2</sup>, Jelena Vujcic<sup>1</sup>, Shams el Arifeen<sup>2</sup>, K. Zaman<sup>2</sup>, Stephen P. Luby<sup>3</sup>, Pavani K. Ram<sup>1</sup>

<sup>1</sup>University at Buffalo, SUNY, Buffalo, NY, United States, <sup>2</sup>International Centre for Diarrhoeal Disease Research, Bangladesh, Dhaka, Bangladesh, <sup>3</sup>Division of Global Disease Detection and Emergency Response, Centers for Disease Control and Prevention, Atlanta, GA, United States

Over 75% of neonatal deaths occur in the first week of life. Community-based promotion programs that have promoted safe birthing and early infant care practices have decreased neonatal mortality; but they included prolonged staff training and antenatal visits as early as 12-16 weeks gestation. Although desirable, reaching women early in pregnancy with highly trained staff is difficult and expensive, potentially limiting the scale of these programs. We sought to describe the behavioral impact of safe birthing and neonatal care messages delivered to primiparous women in the third trimester as part of a randomized controlled trial of handwashing promotion in rural Bangladesh. We promoted delivery at a medical facility, use of a clean delivery kit for a home delivery, recognition of maternal and neonatal danger signs, and essential neonatal care to all participants and their families. Field workers received four days of training and delivered the messages during one home visit between 33 and 35 weeks gestation and two visits within one week after birth. We compared self-reported changes in knowledge and beliefs of these practices before and after the intervention. Of 250 women in the study, 212 completed interviews before and after the intervention. Prior to the intervention, 57% of the women had  $\geq 1$  prenatal visit to a health care provider, which increased to 94% after the intervention ( $p < 0.01$ ). Only 2% planned to deliver at a medical facility but 41% reported delivering at a medical facility ( $p < 0.01$ ). Before the intervention, 32% of women reported a foreign substance (such as oil or dung) should be placed on the umbilical cord after cutting, and 72% agreed a baby should be bathed immediately after birth. However, only 6% reported placing anything on the cord after it was cut ( $p < 0.01$ ) and 2% of neonates were reportedly bathed  $< 5$  hours after birth ( $p < 0.01$ ). This program requiring minimal training of field staff resulted in reports of improved birth and neonatal care practices compared to reported prior beliefs. Neonatal care and birthing practices can be improved, even when women are identified late in pregnancy. A brief training of community health workers may be feasible and effective for reducing risky health behaviors in the antenatal and neonatal period, and may be scalable.

### THE ASSOCIATION BETWEEN COGNITION AND ACADEMIC ACHIEVEMENT IN UGANDA CHILDREN SURVIVING MALARIA WITH NEUROLOGICAL INVOLVEMENT

Paul Bangirana<sup>1</sup>, James S. Hodges<sup>2</sup>, Jeremiah Menk<sup>2</sup>, Chandy C. John<sup>2</sup>

<sup>1</sup>Makerere University, Kampala, Uganda, <sup>2</sup>University of Minnesota, Minneapolis, MN, United States

An understanding of the contribution of different cognitive abilities to academic achievement in children surviving cerebral injury can guide the choice of interventions to improve cognitive and academic outcomes. This study's objective was to identify which cognitive abilities are associated with academic achievement in children after an episode of malaria with neurological involvement (MNI). 62 children with a history of MNI were assessed for cognitive ability (working memory, reasoning, learning, visual spatial skills, attention) and academic achievement (arithmetic, spelling, reading) three months after recovery from the illness. Linear regressions were run for each academic score with the five cognitive outcomes entered as predictors. Adjusters entered in the analysis were age, sex,

education level, nutritional status and quality of the home environment. Exploratory factor analysis (EFA) and structural equation models (SEM) were used to determine the nature of the association between cognition and academic achievement. In regression of a single academic score on all five cognitive outcomes and adjusters, only Working Memory was associated with Reading (coefficient estimate=0.36, 95% confidence interval=0.10 to 0.63,  $p < 0.01$ ) and Spelling (0.46, 0.13 to 0.78,  $p < 0.01$ ), Visual Spatial Skill was associated with Arithmetic (0.15, 0.03 to 0.26,  $p < 0.05$ ), and Learning was associated with Reading (0.06, 0.00 to 0.11,  $p < 0.05$ ). A single latent cognitive factor was identified using EFA. The SEM demonstrated a strong association between this latent cognitive ability and each academic achievement measure ( $P < 0.0001$ ). No additional association between the academic scores and the individual cognitive measures was found beyond the latent cognitive ability. Academic achievement is best predicted by a latent variable, cognitive ability, which captures most of the variation in the individual cognitive ability measures. EFA and SEM can help to define how cognitive testing outcomes relate to academic achievement in children with disease-associated brain injury.

### BELIEFS AND CULTURAL PRACTICES TOWARDS MEASLES AND MEASLES VACCINATION PROGRAMS IN A MULTI-ETHNIC URBAN NEIGHBORHOOD IN KENYA: A QUALITATIVE STUDY

Abdinoor H. Mohamed

Kenya Medical Research Institute, Nairobi, Kenya

A recent measles outbreak in Kenya began in late 2010 and by April 2011 had spread across the country, with the highest number of cases reported in Eastleigh, Nairobi, a community with a high proportion of refugees and migrants from neighbouring countries. To better understand cultural perspectives and community awareness of measles, and assess response to immunization activities, we conducted a series of focus group discussions (FGDs) in Eastleigh. Six FGDs were held (during April 23-29, 2011) before a supplementary immunization activity (SIA) for children  $< 5$  years and another 6 FGDs were held (during May 18-20, 2011) after the SIA. Between 6 and 10 individuals matched for primary language and gender participated in every session. Sessions were facilitated by persons with similar primary language and gender using facilitation guides with similar questions for all the groups. The sessions were recorded, transcribed and translated into English. Qualitative data were analyzed using NVivo 2.0. A total of 103 individuals (mean age, 30.5 years) representing three language groups (Oromo, Somali and Swahili) participated in the 12 discussions. Participants in all groups were able to identify measles and associated it with poverty, poor sanitation and dirty environment. The Oromo and Somali speakers mentioned home remedies as first-line therapy. Cost, long queues, distance to immunization sites, perceived discrimination by non-nationals, lack of understanding of health messages due to language barriers, belief that injections could cause death or exposure to disease, and belief that vaccinated children were not protected were some of the barriers to vaccination mentioned. Somali and Oromo participants recommended providing information through trusted community leaders and community health workers who speak their primary languages. Failure to provide linguistically and culturally appropriate health education materials may negatively impact disease prevention efforts in this setting with ethnically diverse populations.

## 1482

### PRACTICES OF ANTIBIOTIC USE IN CHILDREN LESS THAN FIVE OF MEDICAL PERSONNEL IN PRIMARY CARE CENTERS IN PERI-URBAN AREAS OF LIMA, PERU

Lucie Ecker<sup>1</sup>, Theresa J. Ochoa<sup>2</sup>, Martha Vargas<sup>3</sup>, Luis J. Del Valle<sup>4</sup>, Joaquin Ruiz<sup>5</sup>

<sup>1</sup>Instituto de Investigación Nutricional, Lima, Peru, <sup>2</sup>Universidad Peruana Cayetano Heredia, Lima, Peru, <sup>3</sup>CRESIB, Hospital Clínico/IDIBAPS, Barcelona, Spain, <sup>4</sup>Universitat Politècnica de Catalunya, Castelldefels, Spain, <sup>5</sup>Fundación Clinic para la Investigación Biomédica/CIBER Epidemiología y Salud Pública (CIBERESP), Barcelona, Spain

The increase of antibiotic resistant pathogens acquired in the community is a growing problem worldwide which requires prompt intervention. The overuse and misuse of antibiotics in children is a practice rooted in developing countries, and it has been assumed that the use of antibiotics without prescription is one of the main causes of this misuse. However, previous studies showed that physicians had prescribed more than 80% of the antibiotics used and have the main responsibility in the overuse of antibiotics. The objective of the study was to describe the practices of antibiotics use in children under 5 years by the medical staff of primary health care. A structured questionnaire was applied in 218 general practitioners of primary care facilities of three districts of peri-urban Lima. It consisted of 6 typical clinical cases that may occur in children less than 5 years. 75.6% of the doctors affirmed that of the total of patients attended, more than 25% were children under the age of 5 years. Only 3.2% doctors had received training in pediatric care. When asked if necessary the use of antibiotics in the case of common cold, 15.6 would use an antibiotic, mainly amoxicillin (76.5%). 78.9% of the physicians would use antibiotic in dysentery, mainly furazolidone (39.9%) and TMP-SMX (43.9). 84.2% of the doctors would recommend an antibiotic for pharyngitis and would use amoxicillin (54.3%) and amoxicillin-clavulanic acid (22.3%). 33.2% of the doctors responded that an antibiotic was needed for watery diarrhea treatment, they mainly used furazolidone (42.3%) and TMP-SMX (40.8%). 73.3% would recommend an antibiotic for bronchospasm. 28.3% would use amoxicillin-clavulanic acid and 28.9% amoxicillin. 98.1% would recommend an antibiotic in the case of pneumonia, mainly amoxicillin-clavulanic acid (30.7%) and cephalosporins (26.7%). Approximately half of patients treated in the study primary care establishments are children under five. However the doctors didn't receive training in pediatric care. An overuse of prescribed antibiotics in children less than 5 years was observed, especially in diagnoses as watery diarrhea, pharyngitis and bronchospasm. Misuse of antibiotics that are not considered first line of action on the pathogens or to which the pathogens are highly resistant show that training of medical personnel should be improved in order to reduce unnecessary antibiotic use.

## 1483

### RECONSTRUCTING THE POPULATION HISTORY OF WUCHERERIA BANCROFTI IN A POST-MDA REGION

Scott T. Small<sup>1</sup>, Akshaya Ramesh<sup>1</sup>, Moses Bockarie<sup>2</sup>, James Kazura<sup>1</sup>, Daniel Tisch<sup>1</sup>, Peter Siba<sup>3</sup>, David Serre<sup>4</sup>, Peter Zimmerman<sup>1</sup>

<sup>1</sup>Case Western Reserve University, Cleveland, OH, United States, <sup>2</sup>Liverpool School of Tropical Medicine, Liverpool, United Kingdom, <sup>3</sup>PNG IMR, Goroka, Papua New Guinea, <sup>4</sup>Cleveland Clinic Genomic Medicine Institute, Cleveland, OH, United States

Wuchereria bancrofti (Wb) is the primary causative agent of lymphatic filariasis (LF). Our studies of LF in Papua New Guinea have shown that it is possible to reduce the prevalence of Wb in human and mosquitoes through mass drug administration (MDA; diethylcarbamazine with/without ivermectin). While MDAs through 1998 significantly reduced prevalence of Wb infection, interruption has allowed parasite populations to recovering to pre-MDA levels. We collected genetic data with the

objectives to i) reconstruct Wb population dynamics post-MDA, ii) document contemporary levels of genetic diversity, and iii) differentiate mechanisms of population connectivity. We sequenced Wb infections from 17 patients across 8 villages encompassing both high and moderate annual transmission potentials (ATP). We confirmed the presence of a genetic bottleneck consistent with past MDA treatment with a successive period of exponential growth following treatment interruption. We characterized 175 unique maternal haplotypes currently segregating in the Wb population, with one common haplotype present in 75% of infections. Finally we describe the spread of haplotypes between villages corresponding to the period of population growth following interruption of MDA. We conclude that while the MDA was successful in reducing the Wb genetic diversity, it was not prolonged enough to eliminate all genetic diversity. Interruption of treatment allowed the parasite population to recover and consequently disperse across the landscape via host and vector migration. We hypothesize that through the combined use of long-lasting insecticide treated bed nets (LLINs) in conjunction with MDAs we can eliminate all but the most common haplotypes as well as prevent migration of drug resistant strains both among patients and among villages. Through examining genetic diversity, we have been able to make insights into the demographic history of the parasite population and estimate the most effective strategies to reduce genetic diversity.

## 1484

### COMPARATIVE PROTEOMICS OF WOLBACHIA STRAINS BETWEEN INSECTS AND NEMATODES

Stuart D. Armstrong, Catherine S. Hartley, Jonathan M. Wastling, Benjamin L. Makepeace

University of Liverpool, Liverpool, United Kingdom

The symbiont *Wolbachia* is of intense interest for tropical medicine, both as a drug target in filarial nematodes and as an inhibitor of pathogen transmission in insect vectors. Research on *Wolbachia* has been accelerated by genome sequencing from the major taxonomic "supergroups", including "A" (strain wMel from *Drosophila melanogaster*, 1.3 Mb), "C" (wOo from *Onchocerca ochengi*, 1.0 Mb) and "D" (wBm from *Brugia malayi*, 1.1 Mb). However, proteomic analysis of *Wolbachia* remains scant, despite its potential to illuminate the apparent divide between "parasitic" (group A) and "mutualistic" strains (C and D). Here, we present absolute abundance data for ~30% of the wMel proteome, compared with semi-quantitative estimates for wBm and wOo. Strikingly, the chaperonin GroEL represents 20% of wMel protein, and also dominates in wBm and wOo, alongside six other conserved proteins [*Wolbachia* surface protein, elongation factor (EF)-Tu, co-chaperonin GroES, chaperone DnaK, peptidoglycan-associated lipoprotein, and a porin]. Despite the larger genome of wMel, only two proteins absent from wBm and wOo (a hypothetical protein and a NAD-dependent epimerase) are highly expressed in wMel; although EF-G, heat-shock protein 90 and ribosomal protein L7/L12 are quantitatively elevated. Surprisingly, the profiles of proteins involved in the stress response, nucleotide salvage, transcription and DNA binding are more similar between wBm and wMel than wBm and wOo. The abundance of many proteins in wBm and wOo is not concordant, with increased representation of Zn peptidases, Lon protease and an ankyrin protein in wBm; in contrast with ClpB protease, the copper chaperone SCO1, and oxoglutarate dehydrogenase in wOo. However, shared overrepresentation of two proteins (ATP synthase and HtrA protease) may constitute a "mutualistic signature". Thus, proteome evolution in *Wolbachia* is shaped by compensatory mechanisms to maintain protein metabolism during genome reduction. However, that hypothesis that ATP is a key metabolite provisioned by the mutualistic strains is also supported.

## 1485

**WOLBACHIA-LIKE TRANSCRIPTS AND PROTEINS IN THE WOLBACHIA-FREE FILARIAL PARASITE *ONCHOCERCA FLEXUOSA***

Samantha N. McNulty<sup>1</sup>, Sahar Abubucker<sup>1</sup>, Gabriel Simon<sup>1</sup>, Makedonka Mitreva<sup>1</sup>, Nathan McNulty<sup>1</sup>, Kerstin Fischer<sup>1</sup>, Kurt Curtis<sup>1</sup>, Norbert Brattig<sup>2</sup>, Gary Weil<sup>1</sup>, Peter Fischer<sup>1</sup>

<sup>1</sup>Washington University School of Medicine, Saint Louis, MO, United States, <sup>2</sup>Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany

Most filarial parasites that infect humans require *Wolbachia* endobacteria for normal development and reproduction. It would be interesting to know how *Wolbachia*-free filarial worms function without an endosymbiont. We have previously reported that two *Wolbachia*-free filarial species contain *Wolbachia*-like sequences in their nuclear genomes and that some of these sequences are expressed at the RNA level in a tissue- and stage-specific manner. In the present study, we sequenced the transcriptome of adult *Onchocerca flexuosa* in order to further explore the phenomenon of horizontal gene transfer between *Wolbachia* and presently *Wolbachia*-free filarial species. We estimate that 40% of all *O. flexuosa* protein-coding genes are represented in our dataset, and we were able to detect regions with homology to 97 different *Wolbachia*-like genes. The transcriptome data facilitated a follow-up proteomic analysis in which 1,800 *O. flexuosa* proteins were identified, including two candidate *Wolbachia*-like proteins. Peptide antibodies raised against the two mass-spectroscopy identified and other computationally predicted *Wolbachia*-like proteins were used to further confirm their expression. Immunohistochemistry studies indicated that these proteins were present in many body regions in adult worms. However, *in situ* hybridization studies showed that the *Wolbachia*-like transcripts are expressed in the lateral chords, the tissues where *Wolbachia* are concentrated in species that harbor the *Wolbachia* endosymbiont. Future studies will attempt to demonstrate the functional significance of remnant *Wolbachia* genes and proteins in *Wolbachia*-negative filarial worms.

## 1486

**PROTEOMIC ANALYSIS OF EXCRETORY-SECRETORY PRODUCTS OF THE FILARIAL NEMATODE *LITOMOSOIDES SIGMODONTIS***

Stuart D. Armstrong<sup>1</sup>, Simon A. Babayan<sup>2</sup>, Gaganjot Kaur<sup>2</sup>, Mark L. Blaxter<sup>2</sup>, Jonathan M. Wastling<sup>1</sup>, Benjamin L. Makepeace<sup>1</sup>

<sup>1</sup>University of Liverpool, Liverpool, United Kingdom, <sup>2</sup>University of Edinburgh, Edinburgh, United Kingdom

The excretory-secretory (ES) products of a parasitic worm represent the 'frontline' in its interaction with the host. These products are known to have immunomodulatory roles in parasite invasion and long-term persistence of infection. The filarial nematode *Litomosoides sigmodontis* is a tractable experimental model for filariasis, as it can produce transmissible offspring in BALB/c mice. Proteomic analysis of adult female *L. sigmodontis* ES products was performed using shotgun LC-MS/MS, identifying several hundred proteins against a draft *L. sigmodontis* genome assembly. The protein abundance profile of the ES differed greatly to that of the somatic protein extract. The predominant ES protein families were protease inhibitors, proteases, lipid-binding proteins and antioxidants. The cysteine protease inhibitor Ls-cystatin, a key vaccine candidate, was the most abundant species present in the ES. Members of the transthyretin-like protein family were also well represented, consistent with earlier studies on the ES of *Ostertagia ostertagi* and *Brugia malayi*. Several previously characterised filarial antigens, including FAR1, leucyl aminopeptidase and RAL2 were also highly enriched in the ES material. In addition, a novel protein product highly expressed in the ES exhibited homology to an apolipoprotein from *Ascaris suum* (a lipid-binding protein). However, only three proteins from the *Wolbachia* endosymbiont of *L. sigmodontis* were detected and at low abundance. These initial proteomic

data from the adult females will be compared to the ES protein profiles of the adult male, microfilaria and L3 life stages of *L. sigmodontis* to obtain a comprehensive representation of the quantitative changes in the secretome during filarial development.

## 1487

**IDENTIFICATION OF GENES CONTAINING ECDYSONE RESPONSE ELEMENTS IN THE GENOME OF *BRUGIA MALAYI***

Tracy Enright<sup>1</sup>, Canhui Liu<sup>1</sup>, George Tzertzinis<sup>2</sup>, Thomas R. Unnasch<sup>1</sup>

<sup>1</sup>University of South Florida, Tampa, FL, United States, <sup>2</sup>New England Biolabs, Ipswich, MA, United States

Recent studies have demonstrated that filarial parasites contain a functional homologue of the insect ecdysone receptor (EcR). As a first step in deciphering the physiological role that ecdysteroids play in filarial parasites, adult female parasites cultured in the presence and absence of 20-OH ecdysone were metabolically labeled. Gel electrophoretic analysis of proteins extracted from the cultured parasites revealed changes in the level of expression of several proteins, indicating that adult female parasites contained an ecdysone-responsive gene network. A bioinformatic analysis was then conducted to identify putative ecdysone response elements (EcREs) in the *B. malayi* genome. A total of 18 genes were identified that contained putative EcREs located in the 4 kbp upstream from the start of their open reading frames. The most common functional classifications of the encoded proteins were factors involved in transcription and metabolism. These genes revealed a number of different developmental patterns of transcription. The promoter of one EcRE-containing gene was cloned into an luciferase reporter vector and transfected into *B. malayi* embryos. Reporter gene expression from embryos transfected with this construct was up-regulated by 20-OH ecdysone, a response which was dependent upon the putative EcRE. These results demonstrate the presence of endogenous functional EcREs in the *B. malayi* genome and provide insights into the role that ecdysteroids may play in the developmental processes of *B. malayi*.

## 1488

**STRUCTURAL ELUCIDATION OF *WUCHERERIA BANCROFTI* GLUTATHIONE-S-TRANSFERASE BY X-RAY CRYSTALLOGRAPHY TO EVALUATE ITS ROLE AS A THERAPEUTIC TARGET FOR HUMAN LYMPHATIC FILARIASIS**

Prince R. Prabhu<sup>1</sup>, Sakthi Devi<sup>1</sup>, Madhumathi Jeyaprakasam<sup>1</sup>, Kaliraj Perumal<sup>1</sup>, Christian Betzel<sup>2</sup>

<sup>1</sup>Centre for Biotechnology, Chennai, India, <sup>2</sup>University of Hamburg, Hamburg, Germany

Human lymphatic filariasis is an incapacitating vector borne disease and is the world's second leading cause of long-term disability. To worsen the condition there are no vaccines yet and vector control programs have limitations of insect resistance. The current drugs have limited ability in removing adult worms and do not remedy chronic morbidity and are suitable only for preliminary control measures. Further their broad use would increase the likelihood of accelerated drug resistance. With this distressing scenario there is a growing demand to identify new molecular targets for lymphatic filariasis towards development of drugs and prophylactics. The current study involved in structurally characterizing filarial glutathione-S-transferase (*Wb*-GST) as a drug target for lymphatic filariasis. Accordingly, the recombinant *Wb*-GST was expressed, purified and co-crystallised along with its native substrate glutathione. The structure was solved at a resolution of 2.3Å by X-ray crystallography. The structure resembles  $\alpha$ -class GSTs. The superimposed structures of *Wb*-GST and *Hu*-GST (human host) monomers showed an r.m.s. deviation of 1.2Å for all C $\alpha$  atoms. The G-site residues were highly conserved (differed by 8%), whereas the H-site residues revealed a significant difference (62%) between *Wb*-GST and *Hu*-GST. The H-site of *Wb*-GST showed greater accessibility for electrophilic substrates compared to *Hu*-GST. The electron

density map of *Wb*-GST showed that the catalytic residue Tyr<sup>7</sup> swings off and works as a proton shuttle for catalytic stabilization. The *Wb*-GST structure also revealed the presence of non-catalytic ligand binding sites (ligandin function) in the intersubunit cleft, which can serve as a binding site for hydrophobic ligands. These crucial insights from structural data could be exploited for developing parasite-specific inhibitors.

## 1489

### A VALIDATION STUDY FOR A MULTIPLEX QPCR ASSAY FOR THE DETECTION OF *WUCHERERIA BANCROFTI* AND *BRUGIA MALAYI*

Nils Pilotte<sup>1</sup>, Melissa Torres<sup>1</sup>, Francesca Tomaino<sup>1</sup>, Sandra J. Laney<sup>2</sup>, Steven A. Williams<sup>1</sup>

<sup>1</sup>Smith College, Northampton, MA, United States, <sup>2</sup>United States Department of State, Washington, DC, United States

Responsible for causing infection in more than 120 million individuals, *Wuchereria bancrofti* and *Brugia malayi* are the primary causative agents of lymphatic filariasis. As a number of Southeast Asian and South Pacific countries exist that are co-endemic for both parasite species, diagnostic tools capable of simultaneous detection of both filarial nematodes are an attractive option for infection monitoring and surveillance efforts. We previously described the development of a multiplex qPCR assay for the detection of both filarids within a single pool containing DNA extracted from larval worms of both species. However, the usefulness of this assay as a time and money-saving tool is dependent upon the assay's ability to accurately and repeatedly detect parasite DNA extracted from human bloodspots and from mosquito vectors. Here we describe a validation study using both vector mosquito DNA extracts and human bloodspot DNA extracts. This study demonstrates the sensitivity of this multiplex qPCR assay at the 1 pg level, which is as sensitive as the established singleplex assays for the detection of *W. bancrofti* and *B. malayi*.

## 1490

### HISTAMINE RELEASE DURING *LITOMOSIDES SIGMONDONTIS* INFECTION ENHANCES ADULT WORM BURDEN

Ellen C. Mueller, Marc P. Huebner, Paul Morris, Edward Mitre  
Uniformed Services University, Bethesda, MD, United States

Numerous studies have demonstrated that helminth antigens induce release of histamine from basophils and mast cells of infected hosts. To date, however, the role histamine plays in the immune response against helminths has not been well characterized. In this study, we evaluated the role of histamine in mice infected with *Litomosoides sigmondontis*, a tissue-invasive filarial infection of rodents that lives for months in immunocompetent Balb/c mice. Extended time-course studies revealed that histamine in plasma peaked at 8 weeks of infection whereas expression of histidine decarboxylase mRNA in circulating blood cells increased throughout the course of infection. Mice vaccinated with irradiated L3 larvae demonstrated substantial increases in circulating histamine levels 30 minutes after challenge infection, but administration of HR1 and HR2 receptor blockers did not attenuate the protective efficacy of vaccination. Interestingly, short time course measurements demonstrated that primary infection of unvaccinated mice with L3s also causes histamine release into the bloodstream 30 minutes following infection indicating a non-specific mechanism of histamine release. To evaluate the role histamine may play during infection, mice were chronically administered HR1, HR2, and a combination of HR1 and HR2 blockers in their drinking water and assessed for adult worm survival after inoculation with 40 L3 larvae. Surprisingly, at 8 weeks post-infection all groups of mice treated with antihistamine antagonists had significantly reduced numbers of adult worms compared to untreated controls. Taken together, these data indicate that histamine, rather than being involved in vaccine-mediated protection, may be induced by filarial parasites for their growth and/or survival *in vivo*.

## 1491

### EOSINOPHILS AND STAT6 REGULATE *TRICHINELLA SPIRALIS* MUSCLE INFECTION BY CONTROLLING PARASITE GROWTH

Nebiat G. Gebreselassie<sup>1</sup>, Lu Huang<sup>1</sup>, Lucille F. Gagliardo<sup>1</sup>, Nancy A. Lee<sup>2</sup>, James J. Lee<sup>3</sup>, Judith A. Appleton<sup>1</sup>

<sup>1</sup>Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University, Ithaca, NY, United States, <sup>2</sup>Department of Hematology and Oncology, Mayo Clinic Arizona, Scottsdale, AZ, United States, <sup>3</sup>Department of Biochemistry and Molecular Biology, Mayo Clinic Arizona, Scottsdale, AZ, United States

The parasitic nematode *Trichinella spiralis* establishes chronic infection in skeletal muscle. The muscle phase of infection is characterized by tissue and blood eosinophilia. Using two models of eosinophil-ablated mice, we have previously shown that larval growth and survival are significantly compromised in the absence of eosinophils and that this correlates with reduced Th2 immunity. We show here that reduced Th2 cell accumulation at infection sites is caused by impaired Th2 cell production in draining lymph nodes. Defective Th2 cell accumulation did not correlate with the expression pattern of chemokines that direct the migration/activation of T cells, nor the ability of T cells to enter antigen-bearing tissue. Moreover, studies using STAT6<sup>-/-</sup> and IL-13<sup>-/-</sup> mice revealed that the IL-4/STAT6 axis regulated parasite growth. Impaired parasite growth in eosinophil-deficient mice correlated with increased expression of genes associated with nutrient deprivation (AMPK and INSR), but neither muscle nor larval glycogen content were affected. Our results support a pivotal immunoregulatory role for eosinophils in acquired immunity and nutrient acquisition during nematode infection.

## 1492

### EVIDENCE FOR THE SEQUESTRATION OF DEVELOPING *PLASMODIUM FALCIPARUM* GAMETOCYTES IN THE BONE MARROW

Regina Joice<sup>1</sup>, Jacqui Montgomery<sup>2</sup>, Danny A. Milner<sup>3</sup>, Belinda Morahan<sup>4</sup>, Karl B. Seydel<sup>5</sup>, Kim C. Williamson<sup>4</sup>, Terrie E. Taylor<sup>5</sup>, Matthias Marti<sup>1</sup>

<sup>1</sup>Harvard School of Public Health, Boston, MA, United States, <sup>2</sup>Malawi-Liverpool-Wellcome Trust Clinical Research Programme, Liverpool School of Tropical Medicine, Liverpool, United Kingdom, Blantyre, Malawi, <sup>3</sup>The Brigham and Women's Hospital, Boston, MA, United States, <sup>4</sup>Loyola University, Chicago, IL, United States, <sup>5</sup>Michigan State University, East Lansing, MI, United States

A hallmark of *Plasmodium falciparum* infection is the sequestration of asexual stages in deep tissue, which has been linked to cerebral malaria and other disease outcomes. Like late asexual stages, immature sexual stages are visibly absent from the bloodstream and are hypothesized to sequester. However, unlike asexual stages, their localization and mechanism for sequestration is largely unknown. In the current study, we systematically quantified gametocyte sequestration in autopsy cases from an ongoing study of fatal pediatric malaria in Blantyre, Malawi. An organ survey using immunohistochemistry (IHC) on tissue sections from nine body sites (brain, lung, heart, intestine, liver, kidney, subcutaneous fat, spleen, and bone marrow) suggested enrichment of gametocytes in the bone marrow. Quantitative real time RT-PCR supported this finding and revealed transcriptional signatures specific to young gametocytes, confirming that we are in fact observing gametocytes during development. Following up on these significant findings, we performed electron microscopy and observed the presence of knobless parasites in the bone marrow. We are currently performing detailed IHC studies on bone marrow samples using additional tissue markers, and complementary *in vitro* experiments to test alternative models of gametocyte development in the human bone marrow. The identification and characterization of a genuine bone marrow cycle of *P. falciparum* gametocytes is of

great relevance, in particular considering the field's renewed focus on understanding the dynamics of malaria transmission and the development of new strategies to interrupt it.

### 1493

#### A NOVEL *PLASMODIUM FALCIPARUM* SR PROTEIN IS AN ALTERNATIVE SPLICING FACTOR THAT IS REQUIRED FOR PARASITE PROLIFERATION IN HUMAN ERYTHROCYTES

Shiri Eshar<sup>1</sup>, Eric Alemand<sup>2</sup>, Ariel Sebag<sup>3</sup>, Fabian Glaser<sup>4</sup>, Yael Mandel-Gutfreund<sup>4</sup>, Rotem Karni<sup>3</sup>, Ron Dzikowski<sup>1</sup>

<sup>1</sup>IMRIC, The Kuvim Center for the Study of Infectious and Tropical Diseases, The Hebrew University of Jerusalem - Hadassah Medical School, Jerusalem, Israel, <sup>2</sup>Department of Developmental Biology, Institute Pasteur, Paris, France, <sup>3</sup>IMRIC, The Hebrew University of Jerusalem - Hadassah Medical School, Jerusalem, Israel, <sup>4</sup>Israel Institute of Technology - Technion, Haifa, Israel

The malaria parasites have a complex life cycle, during which it undergoes significant biological changes to adapt to different hosts and changing environments. *Plasmodium falciparum*, the deadliest form of human malaria, has adapted to its complex life cycle with relatively small number of genes. Alternative splicing (AS) is an important post-transcriptional mechanisms that enables eukaryotic organisms to expand their protein repertoire out of relatively small number of genes. SR proteins are major regulators of splicing in higher eukaryotes. Nevertheless, the splicing as well as the AS machinery in *Plasmodium spp.* are still elusive. We show that PfSR1 is a putative SR protein that can mediate RNA splicing *in vitro*. In addition, we demonstrate that PfSR1 functions as an alternative splicing factor in a mini-gene system similar to the mammalian SRSF1. Expression of PfSR1-*myc* in *P. falciparum* shows distinct patterns of cellular localization during intra erythrocytic development. Furthermore, we determine that the predicted RS domain of PfSR1 is essential for its localization to the nucleus. Finally, we demonstrate that proper regulation of *pfsr1* is required for parasite proliferation in human RBCs, and affect the splicing pattern of endogenous genes.

### 1494

#### A CELL INTRINSIC ROLE FOR MUC5AC IN MEDIATING THE TH2-RESPONSE TO HELMINTHES AND ALLERGIC ASTHMA

Kristen Kindrachuk<sup>1</sup>, Thirumalai R. Ramalingam<sup>1</sup>, Margaret M. Mentink-Kane<sup>1</sup>, Luke Barron<sup>1</sup>, Kevin M. Vannella<sup>1</sup>, Jason Kindrachuk<sup>2</sup>, Sandra White<sup>1</sup>, Allen Cheever<sup>3</sup>, Christopher M. Evans<sup>4</sup>, Thomas A. Wynn<sup>1</sup>

<sup>1</sup>National Institutes of Health/National Institute of Allergy and Infectious Diseases/Laboratory of Parasitic Diseases, Bethesda, MD, United States, <sup>2</sup>Emerging Viral Pathogens Section, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD, United States, <sup>3</sup>Biomedical Research Institute, Rockville, MD, United States, <sup>4</sup>Department of Pulmonary Medicine, University of Texas M.D. Anderson Cancer Center, Houston, TX, United States

MUC5AC is a secreted mucin known to be upregulated in response to IL-13 as part of the Th2-mediated response that occurs during helminth infection, fibrotic disease and allergic asthma. IL-13 signals through the Type II IL-4 receptor by binding the IL-13Ra1 chain to drive complex formation and phosphorylation of STAT6, thus mediating downstream effects such as upregulation Fizz1, Ym1 and Arg1, as well as increased eosinophilia, tissue remodeling and mucus hypersecretion. The purpose of this study was to investigate the role of Muc5ac in mouse models of helminth infection, fibrosis and allergic asthma using wildtype C57BL/6 (WT) and Muc5ac knockout (KO) mice. The three models used included a model of *Nippostrongylus brasiliensis* infection, a pulmonary granuloma model using *Schistosoma mansoni* eggs, and a model of allergic asthma using house dust mite. In all three models, a significant reduction in airway eosinophilia in conjunction with reduced expression of Fizz1, Ym1 and Arg1 was observed in KO compared to WT mice; however, no

differences in the expression or production of IL-4, IL-5 and IL-13 were observed. To determine if the KO mice were capable of responding to IL-13, rIL-13 was delivered i.t. to WT and KO mice. No tissue inflammation, airway eosinophilia or increase in IL-13 regulated genes was observed in the KO mice in response to rIL-13. Alveolar macrophages and lung fibroblasts isolated from naïve WT and KO mice were grown in culture and treated with either IL-4 or IL-13. Isolated cells from KO mice had reduced expression of Fizz1 and Ym1 compared to WT in response to IL-13, however did not have reduced expression levels of these genes in response to IL-4. Phosphorylation of STAT6 in response to IL-13 but not IL-4 was ablated in KO macrophages, and phosphorylation of STAT6 in response to IL-4 was also ablated after pretreatment with a blocking antibody against the Type I IL-4 receptor. These data identify Muc5ac as a novel component of the Type II IL-4 receptor and thus a novel target to disrupt IL-4/IL-13-mediated inflammation.

### 1495

#### TLR3-DEPENDENT RECOGNITION OF A PROTOZOAN PARASITE

Daniel Beiting<sup>1</sup>, L. Peixoto<sup>1</sup>, I. E. Brodsky<sup>2</sup>, E. J. Wherry<sup>2</sup>, D. S. Roos<sup>1</sup>

<sup>1</sup>Department of Biology, University of Pennsylvania, Philadelphia, PA, United States, <sup>2</sup>Department of Microbiology, University of Pennsylvania School of Medicine, Philadelphia, PA, United States

Despite striking similarities in invasion, intracellular growth and cellular ultrastructure between *Toxoplasma gondii* and its close relative *Neospora caninum*, these two protozoan parasite species exhibit different host ranges and are associated with distinct disease pathogenesis. The molecular mechanisms underlying these differences have not been well characterized. To address this, we utilized comparative genomics of the host response to these parasites in order to identify host pathways induced during *Neospora*, but not *Toxoplasma* infection. Our results revealed that *Neospora* is a potent activator of innate immune signaling and canonical antiviral responses, whereas representative members of the three archetypal strains of *Toxoplasma* failed to trigger this host response. Recognition of *Neospora* by macrophages occurs via *Tlr3* and the adapter protein *Trif*, and is conserved across multiple species and cell types. RNA isolated from *Neospora*, but not *Toxoplasma*, is able to induce potent antiviral responses when targeted to the host endosomal system. Surprisingly, we found that although live *Toxoplasma* failed to trigger type I interferon production, heat-killed parasites were potent activators of this response. Direct competition experiments between *Toxoplasma* and *Neospora* revealed that *Toxoplasma* potentially suppresses innate immune signaling to prevent type I interferon production and that this is the dominant phenotype, suggesting that *Toxoplasma* acquired and retained a suppressive factor after divergence from *Neospora*.

### 1496

#### TOXOPLASMA SUBVERTS HOST CELL IMMUNE RESPONSE VIA ASSOCIATION WITH HOST MITOCHONDRIA

Lena Pernas<sup>1</sup>, Yaw Adomako-Ankomah<sup>2</sup>, Anjali Shastri<sup>1</sup>, Jon Boyle<sup>2</sup>, John Boothroyd<sup>1</sup>

<sup>1</sup>Department of Microbiology and Immunology, Stanford University, Stanford, CA, United States, <sup>2</sup>Department of Biological Sciences, University of Pittsburgh, Pittsburgh, PA, United States

As with some bacterial pathogens, the tachyzoite stage of the intracellular parasite *Toxoplasma gondii* is often found specifically and extensively associated with host mitochondria at the parasitophorous vacuole membrane (PVM) (Jones and Hirsch, 1972; Sinai et al., 1997). Although previously assumed to be metabolically beneficial for the parasite, the actual consequences of host mitochondrial association (HMA) and the molecules that mediate it have not been determined. We have observed

that HMA is substantially diminished in Type II parasites relative to Types I and III. This has enabled us to use genetic analysis of F1 progeny from a cross between Type II and Type III parasites to map the parasite locus involved. Through a candidate gene approach, we have identified the specific gene involved and dubbed it *Mitochondrial Association Factor 1 (MAF1)*. Introduction of a Type I allele of *MAF1* into Type II parasites is sufficient for conferring a strong HMA phenotype and this is associated with dramatic global changes in the host cell's transcriptional and induced cytokine response to parasitic infection. These results support a growing body of literature that mitochondria are a "hub" of innate immune responses. HMA may represent, therefore, an important adaptation by some strains of *Toxoplasma* to subvert host immunity, as well as a new mechanism by which an intracellular pathogen can interact with its host and manipulate this interaction.

## 1497

### CHew YOUR FOOD: "PARTIAL INGESTION" PLAYS A ROLE IN HUMAN CELL KILLING BY *ENTAMOEBIA HISTOLYTICA*

Katherine Ralston<sup>1</sup>, Michael Solga<sup>2</sup>, William Petri<sup>3</sup>

<sup>1</sup>Department of Medicine, Department of Medicine, University of Virginia Health Sciences Center, Charlottesville, VA, United States, <sup>2</sup>Department of Microbiology, University of Virginia Health Sciences Center, Charlottesville, VA, United States, <sup>3</sup>Department of Pathology, University of Virginia Health Sciences Center, Charlottesville, VA, United States

*Entamoeba histolytica* is the causative agent of amoebiasis, a diarrheal disease that is a major source of morbidity and mortality in the developing world. Pathogenesis is associated with profound tissue destruction, manifesting as ulceration of the intestinal epithelium or abscesses in extraintestinal sites. The cytotoxic activity of the parasite is central to tissue destruction, but the mechanism by which human cell death is induced is unknown. We sought to elucidate the mechanism by first employing live cell fluorescence video microscopy to observe host-parasite interactions in real time. Surprisingly, we found that within one minute, the amoebae internalize distinct "pieces" of the targeted human cell. These "pieces" contain target cell membrane and cytoplasm and organelles. "Partial ingestion" of the target cell precedes death, as assessed by irreversible calcium elevation and membrane permeabilization. We employed multiple independent strategies to inhibit amoebic phagocytosis in order to determine if ingestion is required for cell killing. By using Amnis ImageStream analysis to simultaneously quantify ingestion and killing, we find that the inhibition of partial ingestion prevents host cell killing. Live two-photon microscopy of amoebae with *ex vivo* mouse colon tissue demonstrates that the amoebae also partially ingest enterocytes, suggesting that partial ingestion is relevant to *in vivo* tissue destruction. Notably, we have rarely detected complete internalization of the human cells, and we find that once cells have been killed, they are not further ingested by the parasite. Therefore we speculate that complete ingestion of the killed cell may not be the "goal" and that rather partial ingestion represents an unusual, "offensive" mechanism to elicit cell killing. Thus, through these studies we have uncovered surprising host-parasite interactions and are beginning to get a clearer picture of how this parasite effects such devastating tissue destruction.

## 1498

### A MITOCHONDRIAL CATION/PROTON ANTIPOorter IS ESSENTIAL IN BOTH LIFE STAGES OF *TRYPANOSOMA BRUCEI BRUCEI* AND THE AKINETOPLASTIC *TRYPANOSOMA BRUCEI EVANSI*

Hassan Hashimi, Lindsay McDonald, Julius Lukes

Institute of Parasitology, Biology Center, Academy of Sciences of the Czech Republic and the University of South Bohemia, Ceske Budejovice, Czech Republic

The leucine zipper EF-hand-containing transmembrane protein (Letm1) is a ubiquitous mitochondrial (mt) protein that serves as a cation/proton

antiporter across the inner membrane. It remains controversial whether the cation in question is K<sup>+</sup> or Ca<sup>2+</sup>, as there are data supporting both scenarios. Furthermore, Letm1 is believed to anchor mitoribosomes to facilitate translation of mt genes in yeast. RNAi-silencing of Letm1 in PS and BS *Trypanosoma brucei brucei*, indicate this protein is essential in both life stages. Its ablation results in mitochondrial swelling, consistent with a role in cation efflux from the matrix. Furthermore, mitochondrial translation is indeed compromised in PS Letm1 knockdowns. However, treatment with ionophores that can mediate K<sup>+</sup>/H<sup>+</sup> exchange ameliorates these RNAi phenotypes. Letm1 is also essential in *T.b. evansi*, where translation is non-existent, not only supporting Letm1's role in K<sup>+</sup>/H<sup>+</sup> exchange but also indicating that the energy expenditure needed to maintain an active mitochondrion in the BS, which does not produce energy as in the PS, is cellular ion homeostasis.

## 1499

### INTERACTION AND COEVOLUTION BETWEEN POLYMORPHIC IRG PROTEIN FAMILY AND *T.GONDII* VIRULENCE FACTORS

Jingtao Lilue<sup>1</sup>, U. Benedikt Muller<sup>1</sup>, Martin A. Fleckenstein<sup>1</sup>, T. Steinfeldt<sup>1</sup>, Michael L. Reese<sup>2</sup>, John C. Boothroyd<sup>2</sup>, Jonathan C. Howard<sup>1</sup>

<sup>1</sup>Institute for Genetics, University of Cologne, Cologne, Germany, <sup>2</sup>Department of Microbiology and Immunology, Stanford University, Stanford, CA, United States

Immunity-related GTPases (IRGs) are important cell-autonomous resistant factors in mice against *Toxoplasma gondii* and *Chlamydia trachomatis*. We will report on significant polymorphism and copy number variation of IRG genes. In this study, the sequences of IRG genes were assembled from 18 strains of mouse from the Sanger Mouse Genomes Project and NIG. Further IRG genes were amplified and sequenced from genomic DNA samples of wild derived mouse strains and wild mice. The results reveal a gene family with haplotypic polymorphism apparently on the scale of the MHC in mouse populations. The *IRG* genes are essential for resistance against *T. gondii* and are the targets of virulence factors. Our experiments show an interaction between some IRG members and two polymorphic *T. gondii* virulence factors, the secreted kinase ROP18 and the secreted pseudokinase ROP5. Together these proteins inactivate IRG proteins by targeted phosphorylation of the switch I loop of the nucleotide binding domain. Certain *IRG* haplotypes may confer differential resistance of wild derived mouse strains against virulent *T. gondii* strains.



The number(s) following author name refers to the abstract number.

## A

- A, Gbessi E. 344  
 Aaskov, John 118  
 Ababio, William 333  
 Abaidoo, Robert C. 1256  
 Abassi, Ibrahim 814  
 Abbas, Ally K. 9  
 Abdallah, Joseph 552  
 Abdelhamid, Muzamil M. 172  
 Abdi, Abdirahman 137  
 Abdulla, Salim 179, 332, 458, 1473, 836  
 Abe, Mayumi 1212  
 Abebe, Yonas F. 982  
 Abecassis, Ana B. 119  
 Abedin, Jaynal 777, 1418  
 Abeles, Shira 689, 689, 885, 887  
 Abeyasinghe, Rabindra R. 687  
 Abeyasinghe, Nihal 410  
 Abilio, Ana Paula 404  
 Abiola, Annie 346, 349, 704  
 AboAly, Mustafa 1106  
 Aboellail, Tawfik A. 937  
 Aboonq, Moutasem S. 1066  
 Abot, Esteban 6  
 Aboualy, Mustafa A. 934  
 Aboudramane, Bathily 389  
 Aboulaye, Djimé 779  
 Aboutanos, Michel B. 286  
 Abraham, David 649, 1151  
 Abrão, Emiliana P. 1095  
 Abu Sayeed, Abdullah 886, 1269  
 Abubakari, Amina 1256  
 Abubucker, Sahar 1485  
 Abudho, Bernard 1033  
 Accrombessi, Manfred M. 374  
 Achan, Jane 316, 372, 1020  
 Achee, Nicole 733, 734, 737, 1224  
 Achidi, Eric 136, 318, 380  
 Achilla, Rachel 936  
 Achonduh, Olivia A. 337, 1475  
 Achtman, Ariel H. 1167  
 Achu, Mercy 1475  
 Ackers, Marta 453  
 Acosta, Luz Nereida 1097  
 Acosta, Monica 671, 1197  
 Adam, Elizabeth A. 1255  
 Adam, Ishag A. A. 139  
 Adams, Alison P. 1379  
 Adams, John H. 438  
 Adams, Mohammed 338  
 Adazu, Kubaje 453  
 Addiss, David 120  
 Addo, Kwasi 81  
 Adegnika, Ayola Akim 703  
 Adelani, Aanuoluwa 1171  
 Adeleke Adebayo, Monsuru 75  
 Adelli, Vijender 433, 682  
 Ademowo, George O. 673, 1202  
 Ademowo, Olusegun G. 1139  
 Adeniji, Johnson A. 408  
 Adéothy, Adicatou-laï 697  
 Adeotou-laï, Adicathy 711  
 Aderem, Alan 178  
 Ades, Veronica 462, 553, 880  
 Adesina-Adewole, Olubukola A. 1139  
 Adetifa, Jane U. 3  
 Adewole, Isaac F. 1139  
 Adhiambo, Christine 847  
 Adhin, Malti R. 1326  
 Adiku, Theophilus 414  
 Adiossan, Lukas K. 1447  
 Adjagba, Alex 402  
 Adjapong, Gloria 590  
 Adjei, Eunice A. 401, 1022  
 Adjei, George 653, 654  
 Adjei, Ohene 522  
 Adji, Eric 351  
 Adrianzen, Maria Paz 1156  
 Adu, Festus D. 408  
 Adu-Gyasi, Dennis 338, 653, 654  
 Aebig, Joan 1455  
 Aekplakorn, Wichai 284  
 Affara, Muna 369, 375  
 Afolabi, Muhammed O. 3  
 Afrane, Yaw 200, 865, 1391  
 Afroz, Aasma 1417  
 Afwamba, Isaac A. 1402  
 Agaba, Emmanuel I. 657  
 Agaba, Patience 657  
 Agbaje, Esther 1141  
 Agbaji, Oche O. 657  
 Agbenyega, Tsiri 802  
 Agbowai, Carine 696, 710  
 Agnandji, Selidji Todagbe 703, 179  
 Agola, Jacob 1384  
 Agorinya, Isaiah 1273  
 Agossa, Fiacre R. 966  
 Agre, Peter 1464  
 Aguayo, Nicolas 603, 1135  
 Aguiar, Anna C. C. 148  
 Aguiar, Joao 178, 495  
 Aguilar, Gloria 1135  
 Aguilar, Patricia 227, 422, 1102  
 Aguilar, Ruth 1167  
 Aguilar-Villalobos, Manuel 1248  
 Agwanda, Bernard 566  
 Ahadzie, Lawson 414  
 Ahasan, Ham Nazmul 1269  
 Ahemed, Abdi 567  
 Ahenda, Petronella 925  
 Ahmed, Dilruba 518, 1039  
 Ahmed, Gamal K. 320  
 Ahmed, Ishag A. 320  
 Ahmed, Kwaku B. 760  
 Ahmed, Mohammed Atique 1454  
 Ahmed, Saumu 836  
 Ahouidi, Ambroise 503  
 Aikins, Moses 571, 1250  
 Aime, Elena 978  
 Aina, Oluwagbemiga 1141  
 Ajaiyeoba, Edith O. 408  
 Ajayi, Jerry A. 1140  
 Ajisegiri, Simeon 1375  
 Ajjampur, Sitara 1031  
 Ajua, Anthony 318  
 Ajuik, Martin 571  
 Akaibe, Dudu 566  
 Akala, Hoseah 859, 860  
 Akame, Julie 298  
 Akao, Nobuaki 792  
 Akello, Miriam 875, 875  
 Akhter, Sadika N. N. 770  
 Akhund, Tauseef 1238  
 Akhvlediani, Tamar 1266  
 Akhwale, Willis 839  
 Akinpelu, Tolulope A. 673  
 Akintonwa, Alade 1141  
 Akinyede, Akinwumi A. 1141  
 Akinyemi-Omonijo, Gabriel 747  
 Akkin, Taner 331  
 Ako, Ako A. B. 344  
 Ako, Berenger A. A. 351  
 Akogbeto, Martin 213  
 Akoko, Daniel 1120  
 Akpakli, Jonas 571  
 Akpan, Henry 1375  
 Aksoy, Serap 475, 820  
 Aktar, Amena 42, 45  
 Akter, Jasmin 367  
 Akter, Shahinoor 774  
 Akurut, Helen 875, 875  
 Akweongo, Patricia 571  
 AL Dose Impact Study Group, on behalf of the WWARN 322  
 Al-Amin, H.m. 210  
 Al-Ani, Awsse Harith Hamed 1134  
 Al-Emran, Hassan M. 1407  
 al-joulany, Zahra Z. 232  
 Al-mafazy, Abdul-wahiyd 9, 695, 800, 890, 918  
 Al-Mekhlafi, Hesham H. 248  
 Al-Riyami, Lamyaa 1006  
 Al-Zahrani, Mohammed H. 390  
 AL/ASAQ Molecular Markers Study Group 352  
 Alabaster, Amy 997  
 Alam, Mohammad Murshid 42  
 Alam, Mohammad Shafiul 210  
 Alam, Md. Tauqeer 391  
 Alam, Masud 1026  
 Alam, Murshid 1041  
 Alam, M. Rajibul 1269  
 Alam, Mahbub-UI 1417  
 Alam, Mohammad M. 41, 45, 1410  
 Alam, Munir S. 632  
 Alarcon, Jorge O. 1055, 1094, 1373, 1413  
 Alaro, James R. 186  
 Albareda, Maria C. 1153  
 Albers, Anna 519  
 Albonico, Marco 35  
 Albrechtsen, Fritz 1280  
 Alegana, Victor 838  
 Alema-Mensah, Ernest A. 911  
 Alemayehu, Saba 1308  
 Alembo, Desta A. 285  
 Alexander, Neal 281, 1296  
 Alger, Jackeline 819  
 Alhakeem, Raafat F. 390  
 Alhassan, Andy 667  
 Ali, Asad 1238, 1245  
 Ali, Abdullah S. 9, 890, 901  
 Ali, Doreen 552, 830, 1472  
 Ali, Innocent M. 318  
 Ali, Raghib 297  
 Ali, Said M. 35, 1446  
 Alifrangis, Michael 346, 781  
 Alima, Hillary 656  
 Aliota, Matthew T. 425  
 Alisjahbana, Bachtu 430  
 Allan, Fiona E. 763  
 Allen, Denise Roth 332, 398  
 Allen, Henrietta 1021  
 Allen, Koya C. 1092  
 Alley, M.R.K 677  
 Allicock, Orchid M. 17  
 Almeida, Ericka L. 821  
 Almeida, Giulliana T. 529  
 Alokozai, Asif 461  
 Alomia, José 1054  
 Alonso, Pedro 188, 388, 990, 1167  
 Alphey, Luke 1208  
 Alphonsus, Kal 646  
 Alphs, Sarah 915, 1286  
 Alsheikh, Adel A. 390  
 Althabe, Fernando 819  
 Althouse, Benjamin M. 1229  
 Alva, Isaac E. 1373  
 Alvarado-Otegui, Julián 816, 822  
 Alvarez, Carlos 622  
 Alvarez, Celeste 1365  
 Alvarez, Dayra 253  
 Alvarez, Maria G. 1153  
 Alvarez, Natali 218  
 Amador, Manuel 230  
 Amajoh, Chioma N. 1140  
 Amalvict, Rémy 153  
 Amambua-Ngwa, Alfred 369, 503  
 Amankwah, Seth 333  
 Amany, Manfred 272  
 Amarasinghe, Ananda 1016  
 Amaratunga, Chanaki 985  
 Ambebila, Joel N. 337  
 Ambrose, Luke 560  
 Ambuel, Yuping 1013, 1014  
 Ame, Shaali M. 35  
 Amenga-Etego, Seeba 338  
 Amesiya, Robert 414  
 Amin, M. N. 1418  
 Amin, Ruhul 240



The number(s) following author name refers to the abstract number.

- Amin, Robed 886, **1269**  
 Aminata, Lo C. 1166  
 Aminu, Peace 528  
 Amnuaysirikul, Jack 434  
 Amoah, Abena S. **1109**  
 Amoako, Sabastina 338  
 Amolo, Asito S. 411  
 Amorim, Leila D. 1253  
 Ampuero, Julia S. 112, 415, 422, 1102, 1135  
 Amuasi, John H. 1314, 1360  
 Amza, Abdou 29  
 An, Chunju 1363  
 An, Huijuan 591  
 Anagnostou, Nicholas 3  
 Anaya-Izquierdo, Karim 388  
 Anchang-Kimbi, Judith 136  
 Andagalu, Ben 176, 859, 860  
 Anderreck, Jonathan W. **1127**  
 Anderson, Charles 1455  
 Anderson, Jillian 1130  
 Anderson, John F. 55  
 Anderson, Jennifer M. 712, 973, 985  
 Anderson, Kevin 797  
 Anderson, Kathryn B. **15**, 1087  
 Anderson, Matthew 1161  
 Anderson, Roy 307  
 Anderson, Timothy **700**  
 Anderson, Tim 992, 1169, 1324  
 Anderson, Tavis K. 745  
 Andersson, Bjorn 981  
 Andonova, Maya 924  
 Andrade, Christy C. 562  
 Andrade, Luiza F. 762  
 Andrade, Maria S. 821  
 Andrade, Zilton A. 765  
 Andreadis, Theodore G. **229**, 600  
 Andrews, Chasity 1461  
 Andrews, Emily 1002  
 Andrews, Katherine T. 147, **143**, 145  
 Andrews, Phyllis 487, 536, 1070  
 Andrews, Ross M. 489, 604  
 Añez, Germán **623**, **1107**  
 Angarita-Jaimes, Natalia 1212  
 Anges, Yadouleton 198  
 Anglewicz, Philip A. 1435  
 Angov, Evelina 4, 173, **174**, 176, 186, 1459, 1460  
 Angulo, Noelia 1080, **1157**  
 Angulo-Barturen, Iñigo **681**, **986**  
 Angutoko, Patrick 1307, 1309  
 Anh, Dang Duc 1017  
 Anh, Ngoc 1017  
 Annan, Zeinab 1002  
 Anoyna, Samuel 706  
 Ansah, Nana Akosua **842**, 1273, 1408  
 Ansah, Patrick 842, 1196, 1408, **1273**  
 Ansong, Daniel **802**, 1314  
 Anstey, Nicholas M. **155**, 946, **1424**  
 Anto, Francis 1332  
 Antonelli, Ls R. 38  
 Antonio, Martin 1380, 1419  
 Antonjaya, Ungke **409**  
 Antony, Andrew 1070  
 Antwi, Gifty D. **883**  
 Anyamba, Assaf 736  
 Anyangu, Samuel A. 49  
 Anyanwu, Greg I. 1140  
 Anye, Jules 389  
 Anyona, Samuel 705, **707**, 1191, 1192, 1193  
 Anyorigiya, Thomas 842, 1162, 1196  
 Apinjoh, Tobias **136**  
 Aponte, John J. 179, 188  
 Apperson, Charles S. 600, **725**, 1386, 609  
 Appiatse, Annshirley A. 571  
 Arabi, Mouhaman **960**  
 Aragam, Nagesh (Nash) R. **363**  
 Aramin, Samar 814  
 Arana, Yanina 89, 1080  
 Araujo, Ana I. F. 821  
 Arcà, Bruno 510  
 Arce, Maira **1065**  
 Archer, W. Roodly 47  
 Archuleta, Sophia 110  
 Arcia, Anlenys 599  
 Arcury-Quandt, Alice 1116  
 Aregawi, Maru 10  
 Arellano, Consuelo 725  
 Arenas, Diego 82  
 Arevalo, Jorge 1156  
 Arguello, Heather E. 851  
 Arguello, John 1083  
 Arguin, Paul M. 828  
 Arhin, Bernard 1314  
 Arias, Jorge R. 585  
 Arifeen, Shams E. 240, 1407  
 Arifin, S. M. Niaz **686**  
 Arifuzzaman, Mohammad 43, 41  
 Arinaitwe, Emmanuel 462, 540, **553**, 719  
 Ariti, Cono 950  
 Ariyoshi, Koya 246, 785  
 Arkedis, Jean 915  
 Armah, George 1327  
 Arman, Shaila **775**  
 Armero, Julio A. 1249  
 Armistead, Jennifer S. **167**  
 Armstrong, Stuart D. 1484, **1486**  
 Armstrong Schellenberg, Joanna 388  
 Arnold, Benjamin 1257  
 Arnold, Fred 290, 896, 1360  
 Arnquist, Sarah 293  
 Arogundade, Ekundayo 1300  
 Aroian, Raffi 1128  
 Arredondo, Jose L. 1012  
 Arrumm, Christopher 894  
 Arthur, Gilly 800  
 Artimovich, Elena M. **871**  
 Arumugam, Sridhar **649**, **1117**  
 Arunga, Geoffrey 1244  
 Arvelo, Wences 938, 1124, 1243  
 Aryati, A. 101  
 Asada, Masahito **974**  
 Asamene, Negga 567  
 Asante, Kwaku Poku 179, 338  
 ASAQ Dose Impact Study Group, on behalf of the WWARN 323  
 Asare, Simone Y. **276**  
 Ascough, Stephanie 524  
 Asgari, Sassan **506**  
 Ashine, Meskele I. 638  
 Ashley, Elizabeth A. 985, 1324  
 Ashraf, Sania 775, **965**, **1417**, 1418  
 Ashrafi, Kaveh 530  
 Ashton, Ruth **386**, **387**  
 Asimwe, Elizabeth M. **325**  
 Asimwe, Stephen B. **267**  
 Aslan, Hamide 472  
 Asmare, Kelemework A. Asmare. **238**  
 Asoala, Victor 276, 842, 1162  
 Assadou, Mahamadoun Hamady 1337, 184  
 Assefa, Ashenafi 386  
 Astete, Helvio 18, 220, 418, 724, **728**, 1222, 1386  
 Atashili, Julius **380**  
 Ateba Ngao, Ulysse 703  
 Ategeka, John 1307, 1309  
 Athrey, Giri 508, **1000**  
 Atia, Ehab **1237**  
 Atkinson, Jo-An M. 1474  
 Atogho Tiedeu, Barbara 318, 1475  
 Attaher, Oumar 664, 898  
 Attan-Adjetej, Apussi 590  
 Attout, Tarik 40  
 Atuguba, Frank 276, 842, 1162, 1196, 1332  
 Aubyn, Vivian A. 832  
 Audi, Allan 925, 943  
 Augagneur, Yoann 1025  
 Aumaung, Boonserm 907  
 Aug, Tin 1021  
 Auschwitz, Jennifer M. 683  
 Austin, Amy L. 594  
 Avery, Vicky M. 1145  
 Avila-Garcia, Miroslava 1152  
 Avilés, William **452**, **805**  
 Avula, Bharathi 679  
 Awad Elkarim, Mona 231  
 Awine, Timothy 842, 1162, 1196, 1273  
 Awini, Elizabeth 571, 1250  
 Awiti, Alphonse 1444  
 Awodele, Olufunsho 1141  
 Awolola, Adedapo 729  
 Awor, Phyllis **569**  
 Awuor, Alex O. 961  
 Aydin-Schmidt, Berit 901, **1306**  
 Ayele, Berhan 29  
 Ayele, Workenesh 567  
 Ayers, Tracy 513, 961  
 Ayi, Irene 256  
 Ayieko, Cyrus 698  
 Ayivor, Phillip K. 1273, 1408  
 Ayodo, George 698  
 Ayoma, Elizabeth 752, 1385  
 Ayvar, Viterbo 446, 1072, 1078  
 Azeez, Aderemi 1131  
 Azhari, Ala 1161  
 Aziz, Nabil 647, 1118  
 Azziz-Baumgartner, Eduardo 942, 944, 1249, 940
- 
- B**
- Ba, El Hadj 693, 1342  
 Ba, Mamadou S. 547, 1313  
 Ba Fall, Fatou 550, 1466  
 Baan, Robert 141  
 Baba, Coulibaly 351  
 Baba-Moussa, Lamine 780  
 Babacar, Faye **1166**  
 Babayan, Simon A. 1486  
 Baber, Ibrahimia 184, **223**  
 Babineau, Denise C. 721  
 Babu, Subash 39, 242  
 Bachelier, Françoise 40  
 Backenson, Bryon 564  
 Bacon, David J. 669  
 Bacon, Kristina M. **127**  
 Baddorf, Sarah 1429, **1430**  
 Badiane, Malick 324, 900  
 Bado, Aristide R. 956  
 Baffoe-Wilmot, Aba 401, 1354  
 Baguuya, Adama **956**  
 Bah, Mohamed S. 301  
 Bahashwan, Ahmed A. 1066  
 Bahia, Ana Cristina 1232  
 Bahia-Oliveira, Lillian M. 38  
 Baiden, Frank 338, 653, 654  
 Baidjoe, Amrish 685, 1186, 1203, **543**  
 Bailey, Jeffrey A. 363, 1422  
 Bailey, Kay 1130  
 Bain, Lisa 1024  
 Bain, Odile 40  
 Bakajika, Didier K. **639**  
 Baker, Bill 1091  
 Baker, Mark B. **437**, **1292**, 436  
 Baker, Stephen 1410  
 Bakhtash, Habib 461  
 Balakrishnan, Pachamuthu 16  
 Balazova, Miriama 793  
 Baldet, Thierry 213  
 Baldeviano, Geral C. 259, 1196  
 Baldwin, Susan 174

The number(s) following author name refers to the abstract number.

- Baliga, Priya 164, 894  
 Ballard, Jan P. 913  
 Ballesteros, Sebastien 933  
 Balliet, John W. 935  
 Ballou, Ripley 176  
 Balmaseda, Angel 113, 429, 625, 632, 633, 805, 1246, 1394, 1395  
 Balmer, Oliver 475  
 Balogun, Halima A. **699**  
 Balogun, Muhammad S. 1375  
 Balu, Bharath **438**  
 Bamadio, Modibo 1466  
 Bamani, Sanoussi 30, **84**, 1268, 1271  
 Bamba, Sanata 377  
 Bamiro, Jide 1141  
 Banania, Glenna 6, 995  
 Bancone, Germana 435  
 Banda, Bowen 574  
 Banda, Emmanuel 727  
 Bandara Herath, H M. T. 679  
 Bangiolo, Lois 997  
 Bangirana, Paul 1336, **1480**, 717  
 Bangre, Oscar 1408  
 Banic, Dalma M. 718  
 Banik, Gouri B. R. **263**  
 Bansal, Shweta **105**  
 Bao, Yuzhou **591**  
 Baqui, Abdullah H. 87, 240, 597, 1407  
 Baquilod, Mario 684  
 Baradahana, Lidwine 1471  
 Baraka, Vito 163  
 Barasa, Sheila O. **742**  
 Barbe, Valerie 1025  
 Barber, Bridget E. **946**  
 Barbosa, Lucio M. 528  
 Barbosa-Cabrera, Elizabeth 252  
 Barboza, Alma 1135  
 Bardaji, Azucena 990  
 Baret, Eric 153  
 Barfield, Cori A. **849**  
 Barford, Lea 170  
 Baric, Ralph S. 116  
 Barillas-Mury, Carolina 997  
 Barker, Christopher M. 1229  
 Barkhof, Frederik 1165  
 Barnes, Andres 754  
 Barnes, Kayla G. 969  
 Barnes, Trevor 926  
 Bärnighausen, Till 275  
 Barnor, Jacob S. 414  
 Barnwell, John 457  
 Barogui, Yves 780  
 Barongo, Aileen K. **78**  
 Barral, Aldina 471  
 Barrera, Roberto **230**  
 Barreto, Mauricio L. 1098, 1253  
 Barrett, Alan D. T. 1104, 1228  
 Barry, Amadou 664, 898  
 Barry, Binta 336  
 Bart-Plange, Constance 401, 832, 1022, 1327, 1354  
 Bartalesi, Filippo 1077  
 Bartlett, Alfred V. 1052  
 Bartlett, John A. 1402  
 Bartlett, Mackenzie 984  
 Bartlett, William C. **636**  
 Bartlett-Healy, Kristen 583, 584, 748  
 Bartoloni, Alessandro 1077  
 Bartsch, Sarah M. 127, 296  
 Bartz, Faith E. 1255  
 Barua, Milan K. 774  
 Basáñez, María-Gloria **479**, 481, 1355  
 Basher, Ariful 1269  
 Bashraheil, Mafudh 881  
 Basnyat, Buddha 1410  
 Bassene, Jonas 1330  
 Bassey, Edueno V. 1277, 1289  
 Bast, Joshua D. 224  
 Bastiaens, Guido J. H.. 180, 713  
 Bastos, Armanda D. S. 606  
 Batengana, Bernard 197, 226, 1204  
 Bates, Arturo 565  
 Bates, Imelda 801, 802, 883  
 Batisso, Esey 387  
 Batsa, Linda 519, 522  
 Bauleni, Andrew 857, 857  
 Baus, Esteban G. 824  
 Bausch, Daniel G. **48**, 237, 244, 929, 931, 942, 1247, 1275, 588  
 Bautista, Christian 1266  
 Bautista, Kim 733  
 Baveewo, Steven **319**  
 Bavia, Maria E. 812, 818  
 Baxter, Richard H. G. **28**, 1209  
 Baylis, Matthew 58  
 Bayoh, M. N. 1389, **1468**  
 Bayoh, Nabie 685, 1221, 200  
 Bazzone, Lindsey E. **1085**  
 Beach, Raymond 906, 906  
 Beadell, Jon S. 820  
 Beals, Aaron 293  
 Beattie, Jodi 311  
 Beatty, P. Robert 629  
 Beaudoin, Jennifer A. 675  
 Beaulieu, Ellen D. **1150**  
 Beaumier, Coreen M. 1034, 1087  
 Beauvais, Sophie 293  
 Beavogui, Abdoul Habib 348  
 Bebjak, Andrej 893  
 Beck, Andrew **1104**  
 Becker, Stephen 1380  
 Becker, Tim 519  
 Becker-Dreps, Sylvia **1376**  
 Becker-Ziaja, Beate 414  
 Beckmann, Anna M. 4  
 Beckmann, Svenja 980, 1451  
 Bediako, Isaac 1311  
 Bedu-Addo, George 802  
 Beebe, Nigel W. **560**  
 Beelen, Andrew P. 435  
 Beg, Mohammad A. 669  
 Begue, Sarah 110  
 Begum, Sharmin 512, 1380  
 Behrens, Ron **1296**  
 Bei, Amy 347  
 Beier, John C. 972  
 Beiting, Daniel 1495  
 Bejarano, Eduar E. **575**, **581**, **823**  
 Bejon, Philip 177, **179**, 874, **881**  
 Bekele, Abiyio 567  
 Bekusike, Godfrey 656  
 Béla, Samantha R. 38  
 Bélard, Sabine 703  
 Belay, Shewaye 814  
 Belem, Adrien M. Gaston. 811  
 Belem, Marie-Adrien 74  
 Belemsaga, Danielle 402  
 Belizan, Jose 819  
 Bell, David 457, 463, 1307, 1309  
 Bellis, Mark 453  
 Bellur, Adarsh 1161  
 Belmonte, Maria 6, 995  
 Belperron, Alexia A. 61  
 Beltran, Manuela 1097  
 Ben Mamoun, Choukri **1025**  
 Benante, John Paul **65**  
 Benavente, Luis 459, **848**, 1311  
 Benbrahim-Tallaa, Lamia 141  
 Benca, George 791  
 Bendick, Christoph 282  
 Benedict, Mark Q. 735, **1218**  
 Bengali, A M. 886  
 Bengaly, Zacharia 74  
 Bengaly, Zakaria 299  
 Benjamin, Sarah 619  
 Benjamin-Chung, Jade 1414  
 BenMarzouk-Hidalgo, Omar Jesus **1232**  
 Bennett, Adam **1340**, 1435, 903  
 Bennett, Andrew J. 48, 931  
 Bennett, Jason 176  
 Bennuru, Sasisekhar 36, 1008, **1010**  
 Benoit, Stephen 239, 626  
 Bent, Steven J. 61  
 Benzakri, Noelle 456  
 Berenger, Ako 864  
 Bergemann, Tracy L. 1336  
 Bergman, Lawrence W. 499, 1198  
 Bergmann-Leitner, Elke S. 4, 173, 174, 176, 1460, **1459**  
 Bergren, Nicholas A. **927**  
 Berhan, Meklit 120  
 Berhane, Yemane 903, 1439  
 Berhanu, Aklile 103  
 Berlanda Scorza, Francesco 1050  
 Bern, Caryn 825  
 Bernal, Maruja 1044  
 Bernardo, Roberto J 125  
 Bernart, Chris 239, 626, 938, 1243  
 Bernhards, Ogutu 859  
 Berry, Andrea A. 7, 1335  
 Berry, Neil 1115  
 Berté, Zana 30  
 Berthé, Zana 84  
 Beshir, Khalid B. **353**, 870  
 Bessoff, Kovi **1029**  
 Bestman, Hannan 459  
 Betancourt Cravioto, Miguel 634  
 Bethel, Delia 988, 1316  
 Bethony, Jeffrey 311, 1129, 127  
 Bett, Andrew J. **1015**  
 Bettger, Theresa 840  
 Betzel, Christian 1488  
 Beye, Ouleye T. 919  
 Beyenbach, Klaus W. 730, 1368  
 Beynon, Caryl 453  
 Bezekova, Maria 893  
 Bezuneh, Asrat 814  
 Bhagavan, Nadhipuram V. 1168  
 Bhagavatula, Lavanya 27  
 Bhatt, Samir 21  
 Bhattacharyya, Tapan **474**, 981  
 Bhattarai, Achuyt **9**, 879, 884, 1439  
 Bhuiyan, Md. Saruar 43, 44, 41  
 Bhuiyan, Taufiqur Rahman 43  
 Bhutta, Zulfiqar 1238, 1245  
 Bian, Guowu 505  
 Bichaud, Laurence 587  
 Biggerstaff, Brad 51  
 Biggs, Holly M. 1402  
 Biggs-Cicatelli, Susan 4  
 Bigira, Victor I. 316, **372**  
 Bigogo, Godfrey 271, 943  
 Bihary, Richard F. 1310  
 Bijker, Else M. **180**, 713  
 Billingsley, Peter F. 713  
 Bin Yunus, Emran 548, 886  
 Binagwaho, Agnes 10  
 Binopal, Yatinder 613  
 Bingawi, Haithem 1134  
 Bingham, Andrea M. **923**  
 Binka, Fred N. 842, 1327, 847, 1408  
 Biondo, Cheysa 850  
 Birbeck, Gretchen L. **1427**, 1425  
 Birch, Debra 263  
 Bird, Brian H. **1381**, 51  
 Biritwum, Nana-Kwadwo 1448  
 Birren, Bruce 1110  
 Birungi, Josephine 216, 400, 1387  
 Birungi, Krystal **216**  
 Biryukov, Sergei 1172  
 Bisanzio, Donal **563**  
 Bischof, John C. 331  
 Bishop, Henry S. 130, 1018  
 Bishop, Richard P. 1030  
 Biswas, Hope 633  
 Biswas, Subas C. 775  
 Biswas, Sumi 1456, 1458  
 Biukoto, Seini 270

The number(s) following author name refers to the abstract number.

- Bixler, Garvin 636  
 Björkman, Anders 9, 901, 988, 1306, 1316  
 Bjornson, Robert 475  
 Bjornstad, Ottar 933  
 Black, Robert E. 87, 516, 597  
 Black, IV, William C. 725  
 Blackstock, Anna J. 1432, 31  
 Blackwell, Jenefer M. 38  
 Blagborough, Andrew M. 1456  
 Blair, Silvia 1318  
 Blaise-Jean, Margarete 279  
 Blanas, Demetri 1330  
 Blanco, Natalia V. 1249  
 Blank, Walter A. 528  
 Blankenship, D'Arbra R. 1310  
 Blanton, Ronald E. 528, 1098  
 Blas, Magaly M. 1373  
 Blaxter, Mark L. 1486  
 Blay, Samuel 1360  
 Blaylock, Jason M. 922, 1089  
 Blish, Catherine 660  
 Bliss, Carly 3  
 Blitvich, Bradley 565, 1105  
 Bloink, Kristin 1050  
 Bloland, Peter B. 1473  
 Blom, Anna 602  
 Bloome, Jessica 987  
 Bloomquist, Jeffrey R. 24, 1213  
 Blouin, Nicholas 1422  
 Blum, Lauren S. 1052  
 Boadu, Nana Yaa A. 1314  
 Boakye, Daniel A. 306, 491, 760, 1109  
 Boamah, Daniel 526  
 Boaz, Mark 620, 636, 1086  
 Bobes, Raúl J. 98, 1076, 99  
 Bobogare, Albino 1024, 1474  
 Bock, Ronnie A. 315, 674  
 Bockarie, Moses 32, 300, 480, 642, 740, 1483, 302, 306, 484, 644  
 Bockenstedt, Linda K. 61  
 Bodeau-Livinec, Florence 371, 374  
 Bodhidatta, Ladaporn 1047  
 Boelaert, Marleen 534, 535, 826  
 Boente-Carrera, Mar 1461  
 Bogich, Tiffany L. 933  
 Bohidatta, Ladaporn 1380  
 Boisen, Matthew L. 1275  
 Boisson, Sophie 766  
 Bojang, Kalifa A. 3, 464, 179, 1436  
 Bolay, Fatorma 306  
 Bolton, Jessica 715  
 Boluwaji, Onabolu 1261  
 Bombelles, Thomas 1291  
 Bomfim, Teresa Cristina B. 265, 266  
 Bonano, Vivian I. 1142  
 Bonaparte, Matthew 1086  
 Boncy, Jacques 47, 1242  
 Bond, Nell 48  
 Bondá, Alexandre H. B. 1049  
 Bonhoeffer, Sebastian 872  
 Bonilla, Luis 944, 1249  
 Bonizzoni, Mariangela 204  
 Bonney, Joseph H. Kofi. 414  
 Bonsu, Frank 1250  
 Booker, Michael 1325  
 Boon-in, Patcharin 339  
 Boonpan, Peerayuth 877  
 Bopp, Cheryl 513, 514, 1045, 515  
 Borg, Natalie A. 167  
 Borge, P. Dayand 905, 905  
 Borgella, Sophie 696, 697, 710, 711  
 Borland, Erin 566, 930, 1377  
 Borrmann, Steffen 321, 988, 1316  
 Borrow, Ray 1408  
 Bosman, Andrea 457  
 Botchway, Felix A. 333  
 Bottazzi, Maria E. 649, 1034  
 Boubacar, Kadri 29, 1268, 1271  
 Bouchery, Tiffany 40  
 Boudova, Sarah 1438  
 Boudreaux, Carole 130  
 Bougma, Roland 34  
 Bougouma, Edith C. 1331  
 Boulanger, Lucy 567  
 Bouley, Andrew J. 1402  
 Boulware, David R. 331  
 Bourzac, Kevin 618  
 Bousema, Teun 156, 353, 466, 510, 543, 545, 685, 870, 1177, 1186, 1203, 1343, 1440  
 Boussard, Mathilde 444  
 Bouvard, Veronique 141  
 Bouyou Akotet, Marielle K. 852, 1344, 869  
 Bowen, Anna 514  
 Bowman, Leigh R. 747  
 Bowman, Natalie M. 368  
 Boyd, Alexis 39  
 Boyle, Glen 145  
 Boyle, Robert 867  
 Boyom, Fabrice F. 144  
 Bozdech, Zbynek 983  
 Bozo Gutierrez, Ricardo W. 825  
 Brackney, Doug E. 1108  
 Bradic, Martina 1028  
 Bradley, John 1467  
 Bradley, Mark 310  
 Bradley, Jr., William G. 1427  
 Brady, Oliver J. 21  
 Braga, Guilherme B. 250  
 Branco, Luis M. 1275  
 Brand, Nathan 542, 1276  
 Brandao, Adeilton 1160  
 Brandão Filho, Sinval P. 821  
 Brando, Clara 1463  
 Brant, Sara V. 527  
 Brasseur, Philippe 324, 864, 900, 1351  
 Brattig, Norbert 1485  
 Brault, Aaron C. 562  
 Bravo, Francisco 251  
 Brehm, Michael 427  
 Breiman, Robert F. 49, 456, 513, 515, 953, 961, 453, 514, 925, 943  
 Brelsfoard, Corey L. 203  
 Breña, Patricia 237, 244, 942  
 Brès, Virginie 1025  
 Bresee, Joseph 1249  
 Bretscher, Michael 903  
 Brett-Major, David M. 164, 790  
 Brewoo, Joseph 1014, 1083, 1013  
 Briand, Valérie 371  
 Briceno, Bertha 1257  
 Briceno, Ireneo 733, 734  
 Bridges, Daniel J. 73, 727, 165  
 Brieger, William R. 1277, 1289, 1350  
 Brienen, Eric A. T. 1433, 1434  
 Briët, Olivier 903, 914, 405  
 Briolant, Sébastien 153  
 Brito, Maria E. F. 821  
 Brittingham, Andrew 258  
 Britton, Sumudu 329  
 Brockschmidt, Felix 519  
 Broncano, Nely 488  
 Bronowski, Christina 1112  
 Brooker, Simon 307, 379, 386, 387, 596, 838, 1120, 1274, 1440, 544, 878  
 Brooks, W. Abdullah 940, 1041, 1241  
 Brotin, Emilie 40  
 Brouwer, Kimberly C. 885, 887  
 Browaey, Edith 980, 1451  
 Brown, Arianne 1084  
 Brown, Chris 1194  
 Brown, Graham 708, 708  
 Brown, Robert W. 1310  
 Brubaker, Scott 949  
 Bruce, Jane 1019  
 Bruder, Joseph T. 495, 1461  
 Brumeanu, Teodor D. 190, 264, 714, 715, 996  
 Brunetti, Enrico 448, 1067, 1239  
 Bruno, Antonella 448  
 Brutus, Laurent 696  
 Bruxvoort, Katia 11, 290, 334, 460, 833, 896, 1469  
 Bryant, Bart 26  
 bt Zainudin, Ramlah 1454  
 Bualombai, Pongwit 339, 358  
 Bucheton, Bruno 74, 299, 811  
 Budde, Julia 825  
 Buekens, Pierre 819  
 Bufano, Meagan 42, 45, 1041, 1410  
 Buffet, Pierre A. 1171  
 Buj, Valentina 1333  
 Bukovinova, Pavlina 791  
 Bulbul, Tania 1414  
 Bulimo, Wallace 936  
 Bull, Peter 137  
 Bulter, Elissa K. 331  
 Bunnell, Rebecca 953  
 Bunting, Sheida 286  
 Buranda, Tione 1384  
 Burgas, Rosa 1123  
 Burgeson, Jim 103  
 Burke, Donald 1082  
 Burke, Heather 953  
 Burke, Ronald L. 736  
 Burkett-Cadena, Nathan D. 75, 923  
 Burkot, Thomas R. 203, 222, 1231  
 Burns, Matthew 73, 165  
 Burns, Jr., James M. 186, 666  
 Burrows, Jeremy N. 681, 431  
 Burrus, Roxanne G. 588, 1223, 737  
 Burton, Matthew J. 1268  
 Burton, Samantha 991  
 Bush, David R. 1367  
 Bustamante, Juan M. 494  
 Bustinduy, Amaya L. 1445  
 Bustos, Javier A. 95, 445  
 Buteau, Josiane 1242  
 Butler, Noah 493, 874  
 Butterworth, Alice 853  
 Butts, Jessica 884, 1439  
 Buus, Soren 995  
 Buwembo, William 83  
 Buyungo, Peter 1300  
 Bwire, Godfrey 569, 894  
 Byaruhanga, Oswald 987  
 Byers, David 951  
 Byers, Peter A. 55  
 Byggbjerg, Ib C. 781  
 Byrd, Chelsea M. 103  
 Byrne, Jonathan 1429

## C

- Cabello de Quintana, Maritza 624  
 Cabral, Howard 1131  
 Cabrera, Jose 1401  
 Cabrera, Lilia 1401  
 Caccione, Adalgisa 475, 820  
 Caceda, Edna R. 416  
 Caceres, Mercedes 1376  
 Caci, Jennifer 1089  
 Cafferata, Maria-Luisa 819  
 Caffrey, Conor 530  
 Caillet, Catherine 110  
 Cailliau, Katia 980, 1451  
 Cairns, Matthew 11, 334, 460, 693, 1436, 1469, 897  
 Cairo, Hedley 1315, 1347, 1348, 1349

The number(s) following author name refers to the abstract number.

- Cajal, S. P. 825  
 Calcagno, Juan 19  
 Calderon, Celina 1249  
 Calderón, Félix 681  
 Calderon, Maritza 885  
 Calderon-Arguedas, Olger 607  
 Calderwood, Stephen B. 41, 42, 43, 45, 1048, 1410, 1041  
 Calegari-Silva, Teresa Cristina 476  
 Calisher, Charles 565  
 Calzada, Jose E. 63, 253, 815, 945, 1160  
 Cama, Vitaliano A. 1009, 1074, 1116, 249  
 Camacho, Daria 624, 627  
 Camara, Mamadou 74  
 Camara, Mamady 811  
 Camara, Papa Ibrahim 1342  
 Camargo Paredes, Yenny C. 1159  
 Cameron, Emilie 558  
 Camiña, M. 1044  
 Camp, Lauren 1462  
 Campbell, Corey L. 204, 1001  
 Campbell, Wesley R. 1272  
 Campos, Wesley R. 38  
 Campos-Rodriguez, Rafael 252, 254  
 Canal, Enrique 1413  
 Canales, Marco 125  
 Canan, Stacie 152, 1114, 1147  
 Canavati de la Torre, Sara E. 354  
 Cancino, Marcela 458  
 Candari, Christine 684  
 Cangalaya, Carla 1075  
 Cantey, Paul 1009, 1116  
 Cantilena, Louis 1303  
 Cao, Song 567  
 Capewell, Paul 811  
 Capobianco, Marcela P. 702  
 Cappello, Michael 491  
 Caputo, Beniamino 205, 998, 999  
 Carabali, Mabel 1016, 1017  
 Carabin, Hélène 447  
 Carapetis, Jonathan 604, 948  
 Cárdenas-Jaramillo, Luz M. 254  
 Cardim, Luciana L. 812, 818  
 Cardinal, Victoria 816, 822  
 Cardoso, Jédson F. 119, 1103, 932  
 Cardwell, Kara B. 103  
 Carey, Cristiam 418  
 Carlier, Paul R. 24, 1213  
 Carlier, Yves 819  
 Carlone, George 1408  
 Carlton, Elizabeth J. 1037  
 Carlton, Jane M. 1028, 1197  
 Carmoli, Marya 1011  
 Carneiro, Deborah D. M. T. 812, 818  
 Carneiro, Ilona 510  
 Carper, John 291  
 Carrasco, Hernan J. 981  
 Carreño, Numirin 598, 599  
 Carrero, Julio C. 98  
 Carriere, Yves 215  
 Carrillo-Tripp, Jimena 1105  
 Carrington, Christine V. F. 17, 1084  
 Carrington, Leslie 1084  
 Carrion, Gladys 415  
 Carrion, Jessica 1097  
 Carroll, Darin 455  
 Carter, Derek 4  
 Carter, Emily 1300  
 Carter, Mihaela 1070  
 Carter, Nick 435  
 Carter, Nicholas H. 279  
 Carvalho, Edgar M. 477, 813  
 Carvalho, Francisco G. 821  
 Carvalho, Lucas P. 477  
 Carvalho, Marília S. 451  
 Carvalho, Valéria L. 119, 932, 1103  
 Casandra, Debora 989  
 Casares, Sofia A. 190, 264, 714, 996, 715  
 Casimiro, Danilo R. 935  
 Cass, Quezia B. 93  
 Cassiano, Gustavo C. 702  
 Castelman, Moriah 1192  
 Castillo, Juan 1160  
 Castillo, Maria 1400  
 Castillo, Yesenia 91, 95, 443  
 Castro, Fanny 737  
 Castro, Rosario 795  
 Castro, Sheila 443  
 Castro, Yagahira 1157  
 Castro e Silva, Ana Alice M. C. 1095  
 Castro-Jorge, Luisa A. 1095  
 Cathers, Brian 1114  
 Catteruccia, Flaminia 554  
 Caturello, Gerson T. 1095  
 Cavazos, Nicole 1143, 1146  
 Caviedes, Luz 1400, 1401  
 Ccopa Aguilar, Fredy D. 1080  
 Ceballos, Leonardo 816  
 Ceesay, Serign J. 369, 375  
 Ceploova, Emilia 791, 793, 893  
 Cerami Hand, Carla 138, 661, 661  
 Cercone, Emily 940  
 Cerqueira, Gustavo 1110  
 Cevallos, William 1042  
 Cevini, Claudia 448  
 Chabot-Couture, Guillaume 1179  
 Chacon, Rafael 1249  
 Chadee, Dave D. 207  
 Chaki, Prosper 642  
 Chakkaravarthi, Arunkumar 1005  
 Chakma, Sumit 210  
 Chakraborty, Apurba 1056  
 Chalker, John 295  
 Chalmers, Iain W. 760  
 Chaluluka, Ebbie 365  
 Cham, Sulayman 375  
 Chambers, Eric W. 203  
 Champouillon, Nora 457  
 Chan, Adeline 404  
 Chan, Ernest R. 502, 559  
 Chan, Grace J. 87, 597  
 Chan, Warren C. W. 331  
 Chanda, Emmanuel 73, 1390  
 Chanda, Javan 738  
 Chandler, Clare 340, 341, 454, 549, 573, 803  
 Chandra, Venessa 1265  
 Chandramohan, Daniel 510, 545, 950, 1436  
 Chandrasekaran, V. 242  
 Chandrasekera, Ruvani 568  
 Chandre, Fabrice 213, 967, 1205  
 Chang, Aileen Y. 296  
 Chang, Hsiao-Han 504, 1201  
 Chang, Kyu Sik 1235, 1236  
 Chang, Michelle 892  
 Chann, Soklyda 720, 1303  
 Chanthavanich, Pornthep 1016, 1017, 1101  
 Chanty, Ny 241  
 Chao, Chien Chung 603, 610  
 Chao, Day-Yu 1099  
 Chaplin, Berth 657  
 Chareonviriyaphap, Theeraphap 786, 1224  
 Charlebois, Patrick 429  
 Charles, Richelle C. 41, 42, 43, 45, 1410, 1041  
 Charman, Susan 431, 837  
 Charras, Serge 153  
 Charrel, Rémi 587  
 Charunwatthana, Prakaykaew 548  
 Chase, Claire 1257  
 Chatterjee, Soumya 242, 492  
 Chau, Nguyen van Vinh 933  
 Chauhan, Virander S. 990  
 Chaumont, Julie 1285, 1408  
 Chaurasiya, Narayan D. 433, 679, 680, 680, 682  
 Chavchich, Marina 327, 356, 1453  
 Chaves, Luis F. 63, 378, 815  
 Chebu, Philipue 657  
 Checkley, William 516  
 Chedjou, Jean Paul 1475  
 Cheeseman, Ian 1169  
 Cheke, Robert A. 479  
 Chelbi, Ifhem 587  
 Chema, Mwajuma 388  
 Chen, Hua-Wei 593, 603, 610  
 Chen, I-Tzu 1119  
 Chen, Jingyang 184  
 Chen, Jing 223  
 Chen, Jun-hu 665  
 Chen, Joyce 1254  
 Chen, Nanhua 866  
 Chen, Ping 495  
 Chen, Qiao-Hong 24  
 Chen, Wei-June 66  
 Chen, Wei-Ju 240  
 Chen, Yao-Shen 1119  
 Chen, Yang 1366  
 Chenet, Stella 465, 1318  
 Cheng, Allen 604  
 Cheng, Qin 457, 866, 1024, 1453  
 Cheng, Weiqiang 1034  
 Cheng, Yang 665  
 Chepkorir, Edith 412, 421, 613  
 Cherif, Mahamoud S. 168  
 Cherni, Saifedine 587  
 Cheruiyot, Agnes 859  
 Chhun Ly, Kong 241  
 Chi-Johnston, Geoffrey L. 1293  
 Chiang, Serena 712  
 Chibale, Kelly 397  
 Chico, Martha 128, 488, 1253  
 Chico, R. Matthew 950  
 Chicucue, Silvia 1356  
 Chiduo, Sarah 844, 845, 846  
 Chien, Vu Huy 356  
 Chigusa, Yuichi 526  
 Chikawe, Maria J. 483, 642  
 Chile, Nancy 89, 1080, 1401  
 Chilingulo, Cowles 1427  
 Chimal-Monroy, Jesus 98  
 Chin, Wai-Hoe 983  
 China, Pauline 543  
 Chinchilli, Vernon M. 289  
 Ching, Wei-Mei 593, 603, 610  
 Chinkhumba, Jobiba 1472  
 Chinnawirotpisan, Piyawan 104  
 Chintala, Ramesh V. 1015  
 Chinula, Dingani 738  
 Chinwe, Godson K. 160  
 Chioccola, Vera L. Pereira. 1158  
 Chiodini, Peter 457  
 Chirambo, Petros 1311  
 Chirwa, Brian 727  
 Chirwa, Jacob 12, 165, 468, 694, 1180  
 Chisha, Zunda 165  
 Chitnis, Chetan E. 990  
 Chitnis, Nakul 405, 743, 914  
 Chizororo, Monica 1252  
 Chlikadze, Rusudan 1266  
 Choe, Se-eun 580  
 Chojnowski, Agnieszka N. 1114  
 Chokejindachai, Watcharee 1101  
 Chongsuvivatwong, Virasakdi 284  
 Chonzi, Prosper 1040, 1252  
 Chotivanich, Kesinee 983  
 Choudhary, Jyoti S. 440  
 Choudhary, Muhammad I. 408  
 Choudhury, Ehsan 1165  
 Chourasia, Ankita 534

The number(s) following author name refers to the abstract number.

- Chow, Angelia 115  
 Chowdhury, Fahima 42, 45, 46  
 Chowdhury, Fazlul K. 775  
 Chowdhury, Fahima **1048**  
 Chowdhury, Mohiul I. 44  
 Choy, Laurel 1130  
 Choy, Seow H. 248  
 Chrisanti, Andrea 716  
 Christanti, Sianny 1015  
 Christensen, Bruce 480  
 Christensen, Jessica A. **1008**  
 Christian, Elizabeth 635  
 Christofferson, Rebecca C. 426, **428**  
 Christophides, George K. 27  
 Christova, Iva 934, 1106  
 Chu, Brian 483  
 Chu, Haiyan 1083, **1378**  
 Chu, Nelson R. 636  
 Chuang, Shu-Fang 1099  
 Chuanxin, Yu 526  
 Chudy-Onwugaje, Kenechukwu O. **799**  
 Chung, Ida H. **594**  
 Chuquipiondo, Nahir 724  
 Chuquiyauri, Raul **885, 887**  
 Churcher, Thomas S. 481, 1355  
 Chuwa, Albina 800  
 Ciccone Miguel, Danilo 1142  
 Ciganda, Alvaro 819  
 Cimino, Ruben 825  
 Ciota, Alexander T. **561, 1217**  
 Cisney, Emily D. 1397  
 Cissé, Badara 294, 349, 547, **693, 1313, 1330, 1342**  
 Cisse, Kadidia 664, 898  
 Cisse, Moustafa 900  
 Cisse, Moustapha 919  
 Clapham, Hannah E. **1398**  
 Clara, Alexey W. **1249**  
 Clare, Rachel 524, 1115  
 Clark, Daniel D. 420, 928  
 Clark, Eva 825  
 Clark, Gary G. 583, 584, **1208, 748**  
 Clark, Jeffrey W. 224  
 Clark, Kristina B. **628**  
 Clark, Martha A. 138, **661, 661, 1164**  
 Clark, Megan E. 1148  
 Clark, Tamara 372  
 Clark, Taane 503  
 Clarke, Kevin R. **1045**  
 Clarke, Sian E. **340, 341, 550, 1466**  
 Clasen, Thomas **766, 774, 775, 1120, 1415**  
 Cleaveland, Sarah 1402  
 Clements, Archie C. A. 305, 118  
 Clements, John D. 43  
 Clemons, Anthony E. **62, 1002**  
 Coalson, Jenna 470  
 Coban, Cevayir 169  
 Cockrill, Jennifer A. 164  
 Coelho, Paulo Marcos Z. 1399  
 Coffeng, Luc E. **643**  
 Coffey, Lark L. **1374**  
 Cohee, Lauren M. **1438**  
 Cohen, Adam L. 1407  
 Cohen, Joe 176  
 Cohen, Jessica 915  
 Cohen, Justin 1345  
 Cohen, Joe 1459  
 Cohen, Justin M. **166, 469, 1298, 1301**  
 Cohen, Robert 958  
 Cohuet, Anna 1456, 1458  
 Coimbra, Roney S. 529  
 Colacicco-Mayhugh, Michelle 67  
 Colborn, James 1439  
 Cole, Donald **801**  
 Colebunders, Robert 235  
 Coleman, Marlice 390  
 Coleman, Michael **390, 1390**  
 Coles, Christian L. 592  
 Colford, John 1257  
 Colin, Sutherland 545  
 Collier, Beth-Ann 1015  
 Colley, Dan 35, 1033  
 Collier, Dami **1251**  
 Collins, Frank H. 1231  
 Collins, Mark O. 440  
 Colombo, Fabio A. 1158  
 Colon, Candimar 1097  
 Colucci, Anna Maria 1050  
 Comach, Guillermo 624, **627**  
 Combes, Valery 432  
 Comer, Eamon 675  
 Commodore, Adwoa 1248  
 Compaoré, Yves-Daniel 463, 1307  
 Comunale, Mary Ann 666  
 Concannon, Pat 1026  
 Conceicao, Luciana M. 702  
 Condit, William C. 1310  
 Condon, Curtis 939  
 Condon, Seth 368  
 Congpuong, Kanungnit 339, 358  
 Conn, Jan E. 218, 219  
 Connelly, Marie 293  
 Conrad, Melissa D. 1028  
 Conteh, Abdul 301  
 Conteh, Lesong 1342  
 Conteh, Michael L. 809  
 Contreras, Carmen L. **1243**  
 Conway, David J. 205, 464, 503, 1454  
 Cook, Alex 933  
 Cook, Darren A. 524, **1115, 977**  
 Cook, Joseph A. 53  
 Cook, Joselle M. **1130**  
 Cooke, Mary 752, 1385  
 Cooksey, Richard 868  
 Cooper, Ellen 1131  
 Cooper, Philip J. **128, 1253**  
 Cooper, Phil J. 488  
 Cooper, Roland A. 987  
 Cooper, Robert D. 560  
 Copenhagen, David J. 296  
 Coppellotti, Olimpia 1211  
 Corbel, Vincent 201, 213, 971, 1364  
 Corbett, Kizzmekia S. **1393**  
 Cordón-Rosales, Celia 626  
 Corliss, George 1358  
 Cornelle, Sylvie 74, 213, 299  
 Cornillot, Emmanuel 1025  
 Correa, Margarita M. 218, 219, **1233**  
 Correa-Oliveira, Rodrigo 1129  
 Cortés-Gil, Lorena 681, 986  
 Cortese, Joseph F. 1297  
 Cose, Stephen 759  
 Cosmas, Leonard 456, 486, 943, 953, 1259  
 Cosme, Luciano 508, 509, 1000  
 Costa, Federico 451, **1420**  
 Costa, Gustavo N. de Oliveira. 1098  
 Costa, Pietra L. 821  
 Costa, Rúbia 477  
 Cot, Michel 371, 374  
 Cotter, Chris 162, **1174, 1175**  
 Couillard, Michel 924  
 Coulibaly, Aristide A. M. 351  
 Coulibaly, Baba 344  
 Coulibaly, Brehima 1060  
 Coulibaly, Drissa 7, 1335  
 Coulibaly, Famolo 30, 84  
 Coulibaly, Flanon 236, 1288  
 Coulibaly, Mamadou 184, 223, 729  
 Coulibaly, M'Lhanhoro A. A. 344  
 Coulibaly, Sam 467, 920  
 Coulibaly, Sheick O. 1436  
 Coulibaly, Siaka Y. 782  
 Coulibaly, Yaya I. 478, 641, **740, 782**  
 Couret, Jannelle **735**  
 Courtright, Paul 1268, 1271  
 Cousin, Marc 467, 828, 920  
 Couto, Melissa C. Machado. Couto. 266  
 Cowan, Linda D. 447  
 Cowden, Jessica J. 4  
 Cox, John 693  
 Cox, Jonathan 752, 1343, 1385, 1440, 543, 685  
 Cox-Singh, Janet 1454  
 Coyle, Christina **487, 536, 1070**  
 Coyle, Peggy L. **807**  
 Coyle, Shawn 757  
 Crabb, Brendan 173, 1459  
 Crabtree, Mary 51, 566  
 Crabtree-Ide, Christina 1052, 1241, **1262**  
 Craig, Allen S. 165, 1045  
 Craik, Charles S. 1035  
 Cramer, Jakob P. **1294**  
 Cramer, Gary 413  
 Cranfield, Mike 930, 671  
 Cravioto, Alejandro 46  
 Cravo, Pedro 870  
 Crawford, Michael **311**  
 Crepeau, Taryn 748  
 Crevat, Denis 110  
 Crockett, Rebekah J. **51, 566, 930**  
 Croquet-Valdes, Patricia A. 88  
 Crompton, Peter D. 280, 389, 719, 874  
 Cromwell, Elizabeth A. 1268, 1271, 1346  
 Cros, Marion 570  
 Crosnier, Cecile 171  
 Cross, Anne 800  
 Cross, R. Matthew 431  
 Crump, John A. 1402  
 Crunkhorn, Bruce 731  
 Cruz, Jaqueline S. 19  
 Cruz, Maria 1156  
 Cruz-Hernandez, Teresita 254  
 Cuéllar, Victoria 485, 1124, 1125  
 Cui, Liwang 877  
 Culverwell, Lorna 752  
 Cummings, Derek A. T. 16, 1229, 15, 1082  
 Cummings, James F. 4, 176  
 Cummings, Richard D. 761  
 Cundill, Bonnie 341, 461  
 Cunningham, Andrew A. 228  
 Cunningham, Jane 463, 1307, 1309, **457**  
 Cuong, Hoang Quoc 933  
 Currie, Bart 57, 604, 612, 56  
 Currier, Jeffrey R. 1087  
 Cursino-Santos, Jeny R. **667**  
 Curti, Elena 495, **1034**  
 Curtis, Kurt 1485  
 Cysticercosis Working Group in Peru 91, 1078, 1080, 95, 443, 445, 1068, 1072, 1073, 1077  
 Cyubahiro, Beatus 906, 906

## D

- D'Alessandro, Umberto 464, 787, 870, 899, 1419, 369, 375  
 Da, Dari **1458**  
 da Silva, Alexandre J. **850, 1018, 1158**  
 da Silva, Daisy E. Andrade. 932  
 da Silva, Eliana V. P. 119  
 da Silva, Luiz J. 1016, 1017  
 da Silva, Simone D. 1305  
 Dabiré, Roch K. 746, 1211, 967  
 Dachraoui, Khalil 587  
 Dada, Nsa 786, 1263  
 Dadfarmia, Tahereh 88  
 Dagur, Pradeep K. 472

The number(s) following author name refers to the abstract number.

- Daher, André 1305  
 Dahir, Saidi 50, 423  
 Dahlström, Sabina 868, **1319**, 862  
 Dahourou, Georges 47  
 Dai, Bui 327, 356  
 Dai, Dongcheng 103  
 Dalal, Warren 953  
 Dalecha, Desalegn 287  
 Dalton, John 756  
 Daly, Thomas M. 499, 1198  
 Dama, Emilie T. H. **74**, 299  
 Damas, Deogratias **303**  
 Damien, Gorgia 213  
 Dang, Duc Anh 246  
 Dangoudoubiyam, Sriveny 129  
 Daniel-Ribeiro, Claudio T. 718  
 Daniels, Rachel 347, **504**  
 Daniyam, Comfort A. 657  
 Danner, Rebecca 190, 264, 714, 715, 996  
 Danquah, Daniel A. 1022  
 Dantas-Machado, Ricardo L. 669  
 Dao, Adama 782  
 Dao, Giang D. 807  
 Daouda, Ndiaye 1166  
 Dara, Antoine 348  
 Dara, Nianwanlou 898  
 Dardick, Kenneth 60  
 Darriet, Frédéric 1205  
 Das, Birendra K. 521  
 Das, Bimal K. 1417  
 Das, Subash 629, 1083  
 Das, Smita **1215**  
 Das, Subash 1378  
 Das, Sumon K. 518  
 Dasilva, Alexandre J. 854  
 Dassouli, Amina 1025  
 Daswani, Melissa 369  
 Daszak, Peter 1230  
 Dat, Tran V. 637  
 Data Santorino, Data 272  
 Date, Kashmira 1411  
 Datta, Dibyadyuti **169**  
 Daubenberger, Claudia A. 1030  
 Dauschies, Arwid 1064  
 Davalos, Maria 1069  
 Davé, Kirti 621  
 Davé, Sonia 621  
 Davenport, Gregory 706, 707, 1192  
 Daves, Gaylen 615  
 Davey, Gail 277, 285, 1405  
 David, Chella 714  
 David, Sullivan 367  
 Davies, Emmanuel 646  
 Davies, Tieren 771  
 Davis, Joe 731  
 Davis, Joshua 948  
 Davis, Stephanie M. **486**, 1259  
 Dawainavesi, Akanisi 1411  
 Dawson, Emily M. **758**, **1431**  
 Dawson-Hahn, Elizabeth E. 279  
 Day, Nicholas P. J. 548, 886, 983, 1165, 1426  
 Dayan, Gustavo H. **1012**  
 de Almeida, Marcos E. 1158  
 de Alwis, Ruklanthi **1396**  
 de Cózar, Cristina 1320  
 De Donato, Marcos 598, **599**  
 de Koning-Ward, Tania 173, 1459  
 De La Barrera, Rafael 1096  
 De La Cruz, Anna Y. **342**  
 De La Puente, Micaela 640  
 De Lamballerie, Xavier 587  
 de Lima, Clayton P. S. 119, 1103  
 de los Santos, Tala 304  
 de Mast, Quirijn 180, 430  
 De Meeüs, Thierry 811  
 de Oliveira, Camila 471  
 de Paula, Cláudio S. 1095  
 De Rissio, Ana M. 1153  
 de Silva, Aravinda 1393, 1396  
 de Silva, Dharshan 1393  
 de Souza, Dziejdom K. 306  
 de Vlas, Sake J. 33, 643  
 De Walque, Damien 956  
 Deal, Jeffery L. **778**  
 Debes, Jose **754**  
 Debrabant, Alain 539  
 Debrah, Alex 519  
 Debrah, Alexander Y. 522  
 deBruyn, Becky S. 557  
 deCock, Kevin 453  
 DeConti, Derrick K. **1422**  
 Deelder, André M. 976  
 DeGroot, Anne 650  
 Deissler, Robert J. 1310  
 Dek, Dalin 985  
 Del Valle, Luis J. 806, 1482  
 Delahoy, Miranda J. **515**  
 Delbecq, Stéphane 1025  
 della Torre, Alessandra **205**, **998**, 999  
 Dellicour, Stephanie **324**  
 Deloron, Philippe 696, 697, 710, 711  
 DelVecchio, Vito 1460  
 Delwart, Eric L. 1374  
 DeMarco, Kevin J. 1427  
 Demba, Sarr 344  
 Dembélé, Ahmadou 1335  
 Dembélé, Benoit 30, 84  
 Dembele, Demba 348  
 Dembélé, Mamadou 84  
 Dembele, Massitan 478  
 Dembele, Sinaly 236  
 Demetere-Verceil, Edith 299  
 Deming, Michael 482, 1478  
 Dénécé, Gaëlle 40  
 Deng, Bingbing 183, 1457  
 Dengue v2V Under-reporting Initiative 634  
 Denis, Emmanuelle **1317**  
 Dennis, Kyle 1321  
 Denny, Thomas 632  
 Dent, Arlene 700, 992, **497**  
 Dent, Jennifer **1291**  
 Denton, Jerod S. 730, 1368  
 Denys, Christiane 53  
 Derado, Gordana 485, 961, 1124, 1125  
 Deran, Tong Chor 647  
 Derbali, Mohamed 587  
 Deribe, Kebede **235**  
 Deribew, Amare 235  
 Derman, Alan 1128  
 Deroost, Katrien 978  
 Derrick, Steven C. 496  
 Desai, Aaloki 1103  
 Desai, Meghna **1403**, 1437, 1468  
 Desir, Luccene 482  
 Desjardins, Christopher **1110**  
 Desruisseaux, Mahalia S. 140, 1450  
 Devi, Sakthi 1488  
 Devine, Gregor 194, 737  
 Devine, Gregor J. **731**  
 Dey, Ranadhir **472**  
 Deye, Gregory 841  
 Dezee, Kent 1272  
 DHA-PQP Dose Impact Study Group, on behalf of The WWARN 551  
 Dhammika Nanayakkara, N P. 679  
 Dhar Chowdhury, Parnali **1090**, **1287**  
 Dhepaksorn, Panadda 339  
 Dhingra, Radhika **617**  
 Dhliwayo, Panganai 1040, 1252  
 Di Cioccio, Vito 1050  
 Di Pasquale, Aurelio **450**  
 Dia, Aliou 550  
 Dia, Ibrahima 722  
 Dia, Seydou 389  
 Diabate, Abdoulaye **746**, 1211  
 Diakate, Seidina 389  
 Diakite, Hamadoun 336  
 Diakite, Mahamadou 712, 973  
 Diakite, Seidina A. S. 712  
 Diallo, Aldiouma 1285  
 Diallo, Abdallah A. 641  
 Diallo, Abdoulbaki I. 898  
 Diallo, Dapa A. 1335  
 Diallo, Fatoumata 236, 1288  
 Diallo, Ibrahima 919  
 Diallo, Khady 550  
 Dialynas, Emmanuel 70  
 Diarra, Amidou 13, 467, 920, 1331  
 Diarra, Baba **641**  
 Diarra, Bakary 664, 898, 280  
 Diarra, Kounandji 1288  
 Diarra, Sadio 30  
 Diarra, Souleymane 664, 898  
 Diarra, Seybou 1466  
 Diatta, Beckenbauer 255  
 Diaw, Oumar T. 757  
 Diaz, Andre 1072, 1078  
 Díaz, Ana M. 1138  
 Diaz, James H. **601**  
 DiCicco, Beau A. 88  
 Dick, Edward 1143  
 Dick, Justin 675  
 Dickerson, Tobin J. **595**  
 Dickinson, Katie L. 776  
 Dickman, Lisa M. **1268**, 1271  
 Dicko, Alassane 280, 664, 898  
 Dicko, Ilo 641, 782  
 Dicko, Yahia 664, **898**  
 Dida, Gabriel O. 917  
 Dieckhaus, Kevin 656  
 Diemert, David 311, **1129**, 127  
 Dieng, Yemou 346  
 Dieye, Baba 255, **347**  
 Diggle, Peter J. 1420  
 Diggs, Carter 4, 6, 7, 176, 995, 1459  
 DiLiberto, Deborah 549, **573**, 803  
 Dilley, Katherine M. 570  
 Dimaano, Efren M. 785  
 Dimbu, Pedro Rafael 1018  
 Dimitrov, Hristo 934  
 Dimitrova, Kristina 924  
 Dimopoulos, George 1232, 1366, 1371, 1372  
 Dinglasan, Rhoel R. 167  
 Diniz, Renata 1129  
 Dinko, Bismarck 329  
 Dione, Michel 1380  
 Diop, Cheikh T. 919  
 Diouf, Ababacar 183, 185, 1457  
 Diouf, Mame B. 919  
 Diouf, Mamadou L. 919  
 Direny, Abdel Nasser **126**  
 Dirrigl, Frank 1225  
 Dissous, Colette 980, 1451  
 Dittrich, Sabine **1412**  
 Diuk-Wasser, Maria 20, **60**, 61  
 Divis, Paul C.S. 1454  
 DiVita, Margaret 940  
 Dixit, Amruta **939**, 1033  
 Dixon, Daniel P. **1362**  
 Djegbè, Innocent 971  
 Djenontin, Armel 213, 971  
 Djimde, Abdoulaye 348, 864, 1351, 988, 1316  
 Djimde, Moussa **336**  
 Djiteye, Mahamane 1288  
 Djogbénou, Luc S. **967**  
 Djombini, Desiré 298  
 Djuardi, Yenny 310  
 Dlamini, Sabelo 166, 469  
 Do, Tram A. 147  
 Dobaño, Carlota 188, 990  
 Dobson, Stephen L. 203  
 Dodd, Kimberly A. 1381  
 Dodoo, Alex 842  
 Doenhoff, Michael J. **758**, 1431

The number(s) following author name refers to the abstract number.

- Doggett, Joseph Stone 834, 834  
 Doggett, Stephen 1374  
 Dokladny, Karol 706  
 Dolan, Samantha B. **879**  
 Dolkart, Caitlin F. **1298**, 1301  
 Doll, Katherine **493**  
 Dolo, Housseini 740  
 Domi, Anisa 1162, 1196  
 Domingo, Gonzalo 304, 849  
 Domingue, Gil 1073  
 Dominguez, Samuel E. 53  
 Donadeu, Meritxell 1073  
 Dondorp, Arjen M. 548, 886, 983, 985, 988, 1165, 1316, 1426  
 Dong, Yuemei 1366  
 Dongol, Sabina 1410  
 Dongus, Stefan 194, 642, 732  
 Donn, Robert 523  
 Donnelly, Martin J. 193, 966, 998, 999, 1210, 226, 967, 1204  
 Doolan, Denise L. 495  
 Doorn, H. Rogier van 933  
 Dophu, Ugyen 158  
 Dor áková, Veronika **579**  
 Doranz, Ben **114**, 635, 926  
 Dorman, Karin 565  
 Dormoi, Jerome 153  
 Dorny, Pierre 91, 95, 96, 443, 447  
 Dorsey, Grant 316, 314, 372, 462, 540, 549, 553, 719, 779, 892, 1203, 1351  
 Dos Reis, Jonathan **1126**  
 dos Santos, Balbino L. 451  
 dos Santos, Guilherme Rodrigo R. 476  
 Dotson, Ellen M. 494, 735  
 Doucoure, Souleymane 213  
 Doudou, Sow 1166  
 Dougall, Annette M. **131**  
 Dougan, Gordon 128  
 Douglas, Alexander D. **171**  
 Douglas, Ian 388  
 Doumbia, Moussa **236**  
 Doumbia, Mory 712, 973  
 Doumbia, Moussa 1288  
 Doumbia, Saibou **132**, 712, 973  
 Doumbia, Seydou 782  
 Doumbia, Salif S. 478, 740  
 Doumbo, Ogobara 184  
 Doumbo, Ogobara K. 223, 336, 7, 389, 1335, 1337  
 Doumbo, Safiatou 389  
 Doumtabe, Didier 389  
 Dow, Geoffrey 676, **1100**  
 Dowler, Megan 1199, 1463  
 Downing, Robert 1409  
 Downs, Philip 1038, **1448**  
 Drakeley, Chris 156, 386, 510, 543, 545, 685, 693, 752, 882, 882, 1186, 1385, 1440, 466, 719, 1177  
 Drakeley, Chrispin 1343  
 Drame, Papa Makthar 213  
 Drammeh, Abdoulie 3  
 Draper, Simon J. 171, 1456  
 Drebot, Michael A. **924**, 1090  
 Dreibelbis, Robert **1264**, 1415  
 Drexler, Naomi **31**, 34, **645**  
 Dritsou, Vicky 70  
 Du, Zun-Wei 122  
 Du Preez, Charwan I. **315**  
 Duangdee, Chatnapa 343  
 Dube, Tina J. T. 1331  
 Dubec, Jan 895  
 Dubois, Marie-Claude 176  
 Duclos, Aurelie 1025  
 Duffull, Stephen B. 155  
 Duffy, Malia 291  
 Duffy, Patrick E. 184, 187, 280, 541, 664, 898, 1170, 1337, 1423, 223, 1455  
 Dugassa, Sisay **191**  
 Duggal, Priya 1026  
 Duman-Scheel, Molly 62  
 Dumonteil, Eric **533**, 819  
 Dumre, Shyam P. **104**, 158  
 Duncan, Christopher J. 5  
 Duncan, Elizabeth H. **173**  
 Duncan, Robert 472, **783**  
 Duncombe, Jennifer **118**  
 Dungu, Baptiste 1073  
 Dunn, William A. 204  
 Dunne, David W. 759, 1032  
 Dunning Hotopp, Julie 1110  
 Duparc, Stephan 150, 435, 436  
 Duplisis, Chris 790  
 Duprez, Jessica 1419  
 Dupuis, Alan P. 564  
 Dupuis, Kent 667  
 Duraisingh, Manoj T. 984  
 Durbin, Anna P. **1011**, 1455  
 Duri, Clement 1040, 1252  
 Durrani, Mohammad Haseeb 667  
 Durvasula, Ravi 582  
 Dussault, Patrick H. 531  
 Dutra, Miriam S. **38**  
 Dutra, Walderez O. 1150  
 Dutta, Notan C. 963  
 Dutta, Sheetij 7, **716**  
 Dwibedi, Bhagirathi 521  
 Dwivedi, Prabha 328
- E**
- Eagen, Sabrina 572  
 Earl, Long 1018  
 Eastwood, Gillian **228**  
 Ebel, Gregory D. 1001, 1108  
 Eberhard, Mark L. 130, 1009, 1116  
 Echebima, Adaku 1359  
 Echevarria, Juan 955  
 Echodu, Richard 475, **820**  
 Ecker, Lucie **806**, **1482**  
 Eckert, Erin 393  
 Eckhoff, Philip A. 1178, 1179, **1231**  
 Edgel, Kimberly A. 259, 640, 929, **1196**  
 Edinborough, Kevin A. 1162, 1196  
 Edstein, Michael D. **327**, 356  
 Eguiluz, Maria 1081  
 Egurrola, Jorge 1016, 1017  
 Egyir, Beverly **81**  
 Ehrbar, Dylan J. 561  
 Ehrhardt, Katharina 40  
 Eichinger, Daniel 1126  
 Eigege, Abel 1346  
 Eisele, Thomas P. 12, 468, 694, 1340, **1435**, 903  
 Eisenberg, Joseph N. S. 959, 1042, 1046, 1281  
 Eisenstein, Jana 41  
 Ejigiri, Ijeoma **272**  
 Ejoku, Emmanuel 1409  
 Ekawati, Lenny L. **159**  
 Ekberg, Greg 495  
 Ekenna, Uche 918  
 Eksborg, Staffan 835  
 el Arifeen, Shams 1479  
 El Bassuoni, Eman 278  
 El Ghissassi, Fatiha 141  
 El Kholy, Amani 245  
 El Mubarak, Wigdan 647  
 El-Asaad, Fatima 432  
 El-Hossary, Shabaan S. I.. 69  
 El-Karakasy, Hanaa 245  
 El-Minshawy, Osama **278**  
 El-Refaey, Samir 1237  
 Elahi, Rubayet 210  
 Elanga, Emmanuel 74, 971  
 Elanga Ndille, Emmanuel **213**  
 Elder, John P. 18  
 Eleveld, Alie 1260  
 Elie, Cheryl 1408  
 Elimelech, Menachem 962  
 Elizondo, Douglas 113  
 Elliott, Alison M. 759, 875, 875  
 Elliott, Suzanne 436  
 Ellis, Brett 1104  
 Ellis, Brian L. **1128**  
 Ellis, Esther M. 115  
 Ellis, John T. 263  
 Ellis, Ruth 1337  
 Ellis, Ruth D. 280, 1455, 223  
 Ellis, Ruth E. 184  
 Ellis, William 531, 537  
 Eloi, Silvana 539  
 Elrayah, Intisar **231**  
 Elsemore, David 311  
 Elsohly, Mahmoud A. 679  
 Embury, Paula 992  
 Emch, Michael 391  
 Emeje, Martins 146, **233**  
 Emerson, Ginny 455  
 Emerson, Paul M. 1268, 1271, 1359  
 Emery, Aidan M. **763**  
 Emidi, Basiliana 197  
 Emukah, Emmanuel 1346, 1359  
 Enato, Ehijie F. O. **326**  
 Endy, Timothy P. 15, 1087, 1082  
 Eng, Matthew W. **1369**  
 Engelman, Daniel **948**  
 Enger, Kyle S. **959**  
 Enogela, Jimmie 958  
 Enright, Tracy 1487  
 Enriquez, Gustavo 816, 822  
 Ensink, Jeroen 766  
 Enwere, Godwin 1273, 1285, 1408  
 Enyaru, John 475, 820  
 Enyioha, Chineme 820  
 Epstein, Judith E. 5, 178  
 Epstein, Jonathan H. 1039  
 Erazo, Silvia 1253  
 Erdman, Dean 943  
 Erickson, Bobbie Rae 51  
 Erickson, Sara 480  
 Ernst, Kacey 215  
 Escalante, Ananias A. 465, 669, 670, 671, 871, 1197, 1318  
 Escareño-Ramirez, Luis 252, 254  
 Eshar, Shiri 1493  
 Espina, Luz M. 623  
 Espinoza, Fabiola 487, 536  
 Espinoza, Félix 1376  
 Espinoza, Nereyda 1044  
 Espósito, Danilo L. 1095  
 Esquivel, Renata 1253  
 Essama, Josette 31  
 Estela, Abel 237, 244, 942  
 Esterhuizen, Johan 71, 76  
 Esteva, Mónica 1153  
 Estévez, Alejandra 626, 938  
 Eursitthichai, Veerachai 104  
 Evance, Illah 1300, 1360  
 Evangelista, Julio **418**  
 Evans, Benjamin 475  
 Evans, Brian P. 578  
 Evans, Carlton A. 1400  
 Evans, Darin **312**, **646**  
 Evans, Holly **1007**  
 Evehe, Marie Solange B. 318  
 Ewer, Katie 3  
 Existe, Alexandre 862  
 Eyase, Fredrick L. **859**, 860, 839  
 Eziefula, Alice C. **156**, **466**  
 Ezinmègnon, Sèm 696, 697, 710, 711
- F**
- Fabiszewski de Aceituno, Anna M. 1255

The number(s) following author name refers to the abstract number.

- Fabris, Clara 1211  
 Fair, Jeanne 797  
 Fairhurst, Rick M. 389, 669, 712, 973, 985, 988, 1316  
 Fairlie, David 147  
 Faiz, M. Abul 548, 886, 1165, 1269  
 Fakiola, Michaela 38  
 Falade, Catherine O. 673, **1139**, 1202  
 Falco, Richard 600  
 Falconi-Agapito, Francesca **1156**  
 Faldetta, Kimberly F. **776**  
 Falk, Hendrik 1167  
 Fall, Fatou B. 919  
 Fall, Ibrahim S. 10  
 Fanello, Caterina I. 653, 654  
 Farag, Tamer H. 513, 515, 961, 514  
 Faraja, Leah 994  
 Farajollahi, Ary 583, 584, 726, 748  
 Farfan-Ale, Jose 565  
 Faria, Nuno R. 119  
 Farias, C 1073  
 Farlow, Andrew 21  
 Färnert, Anna **902**, 994  
 Farooq, Fouzia 6  
 Farrar, Jeremy 933, 1410  
 Farrell, Margaret 1266  
 Faruque, A. S. G.. 518  
 Fasabi, Manuel 885  
 Fatty, Wandifa 375  
 Faulx, Dunia 304  
 Fay, Michael P. 183, 712, 973, 1455, 184, 242, 1337  
 Faye, Babacar 77, 255, 294, 346, 349, 547, 781  
 Faye, Djibril S. **757**  
 Faye, Ousmane 693, 722  
 Faye, Sylvain 1330  
 Fayed, Ahmed A. 1066  
 Feachem, Richard G. A. 687  
 Fedak, Kristen 395  
 Fegan, Gregory 838  
 Feghali, Karla C. 1308  
 Feikin, Daniel R. 953, 925, 943  
 Feitosa, Ana Luisa P. 1095  
 Feldmann, Heinz 54  
 Feldmeier, Hermann **608**, **792**, **1406**  
 Felgner, Phil 660, 719  
 Felices, Vidal 227  
 Felzemburgh, Ridalva D. M. 451  
 Feng, Carl 492  
 Feng, Gaoqian 365  
 Fennell, Sean 848, 1311  
 Fenwick, Alan 35  
 Ferdig, Michael T. 151, 154  
 Fergus, Cristin A. 694  
 Ferguson, Heather 739, 741  
 Ferguson, Neil 882, 1329, 1398  
 Fernandez, Facundo 328  
 Fernandez, Kate M. 1422  
 Fernandez, Roberto 588, 1223  
 Fernandez, Stefan 104, 1397  
 Fernandez-Robledo, Jose-Antonio 264  
 Fernández-Velando, Esther P. 681  
 Fernholz, Emily C. 851  
 Ferrari, Giovanfrancesco **1328**  
 Ferreira, Pedro 901  
 Ferreira-da-Cruz, Maria de Fatima **718**  
 Ferrer, Elizabeth 627  
 Ferrer, Santiago 681  
 Ferreras, Ana C. 627  
 Ferris, Robert 291, 572  
 Ferro, Josefo 1426  
 Ferro, Santiago 458  
 Ferrufino, Lisbeth 825  
 Festo, Charles **11**, 290, 334, 460, 896, 1469  
 Fichera, Laura 1153  
 Fidock, David A. 189, **439**, 1321, 867  
 Fields, Barry 271, 567, 943, 1244  
 Fienberg, Stephen 397  
 Fiestas, Victor 416, 422, 603, 1102  
 Fievet, Nadine 696, 697, 710, 711  
 Figueiredo, Camila A. 1253  
 Figueroa, Carlos A. 929  
 Filimone, Raikanidoda 1404  
 Filler, Scott 462, 553  
 Fillinger, Ulrike 191, 214, 217, 685, 1388  
 Fimmers, Rolf 522  
 Findlow, Helen 1408  
 Fine, Eugene J. 1450  
 Fink, Doran 1110  
 Fink, Guenther 359  
 Finlayson, Alexander E. T. **297**  
 Finnefrock, Adam C. 167  
 Fiore, Jacqueline 857, 857  
 Fiore, Nancy 411  
 Fischer, Anne 605, 613  
 Fischer, Katja 64, **68**, 602  
 Fischer, Kerstin 1485  
 Fischer, Peter U. 33, **310**, 639, 1485  
 Fish, Durland 60, 61  
 Fisher, Carolyn 783  
 Fisher, David 670  
 Fisher, Gillian **145**  
 Fitri, S. 1219  
 Fitter, David **1242**  
 Flaherty, Briana 991  
 Flanagan, Joseph 1332  
 Flandin, Jean-Frederic 789  
 Flegg, Jennifer A. 863, 863, 864, 868, 988, **1023**, 1195, **1316**  
 Fleming, Michael 296  
 Flippo, Lana Y. 270  
 Flora, Meerjady Sabrina 484  
 Flores, Ernesto 624  
 Flores, Martha 443  
 Flores Leon, Amilcar A. **1155**  
 Flores-Mendoza, Carmen 227  
 Flynn, Jessica A. 935  
 Flynn, Laurie 311  
 Fofana, Boubacar 782  
 Fofana, Mahamadou 236, 1060, 1288  
 Foley, Desmond H. **586**, 736, 1199  
 Foley, Michael 675  
 Folsom-O'Keefe, Corrine 60  
 Fong, Rachel 635, 926  
 Fonn, Sharon 801  
 Fonseca, Benedito A. L. **1095**  
 Fonseca, Dina 583, 584, 726, **558**, **748**  
 Foo, Karen T. **1432**, 1434  
 Foote, Andrew M. **964**  
 Ford, Louise **524**, 1115  
 Forey, Maggie 1143  
 Forgione, Michael A. 164  
 Forquer, Isaac 431  
 Forrester, Naomi A. 1383  
 Forshaw, Adam **582**  
 Forshey, Brett M. 18, 112, 418, 622, 416  
 Forson, Ivy 1354  
 Fortes de Araujo, Fernanda 539  
 Foster, James 1214  
 Fouché, Bernadette 47  
 Foulkes, Mary 297  
 Fox, LeAnne 486, 1259  
 Foxman, Betsy 1042  
 Foy, Brian D. 507  
 Fraga, Deborah 451  
 Fraga, Valeria D. 702  
 Fragoso, Gladis 99  
 Fragueiro Frías, Victoria **1151**  
 Frah, Ehab Frah 231  
 Fraile, María T. 681  
 Franco Muñoz, Carlos E. 1159  
 Frando, Andrew 631  
 Franke-Fayard, Blandine 978  
 Franzen, Oscar 981  
 Fredes, Fernando 964  
 Freeman, Brandi D. 140, 1450  
 Freeman, Matthew  
 Freeman, Molly 1409  
 Freeman, Matthew C. **1120**, 1264, 766, **1415**  
 Freeman, Nicole 47, 1242  
 Freire, Janaina 1129  
 Freund, Yvonne R. 677  
 Frey, Michèle C. 562  
 Friberg, Heather **1087**  
 Fridman, Arthur 167  
 Fried, Michal 280, 541, 664, 898, 1307, 1309, 1423  
 Frimpong, Augustina **170**  
 Frimpong, Eric H. 256  
 Fritz, Lee 48  
 Frosch, Anne E. P. **1336**  
 Fry, Alicia M. 940, 1241  
 Fryauff, David J. 69, **1162**, 1196, **1332**  
 Fu, Chi-Ling 975  
 Fu, Kasey Y. 20  
 Fuimaono, Saipale 270  
 Fukuda, Mark M. 164, 1063  
 Fuller, Claire **282**, **638**  
 Fuller, Kathleen 103  
 Fullman, Nancy 1174  
 Funkhouser, Sheana 609  
 Furini, Adriana A. C. 702  
 Furman, Barry D. 69  
 Furze, Julie M. 171
- ## G
- Gabriel, Sarah 91, 95, 443  
 Gadalla, Nahla 352  
 Gaidry, Alicia D. 683  
 Gakpey, Kwame 1354  
 Gakuya, Francis 605, 613  
 Galappaththy, Gawrie N. 687  
 Galdos-Cardenas, Gerson 825  
 Gale, Trevor V. 595  
 Galeano, Adolfo 1135  
 Galeano, Yadira 219, 1233  
 Galicia-Vega, Sindy 252, 254  
 Galindo-Sevilla, Norma **1152**  
 Galinski, Kevin 188  
 Galinski, Mary R. 1197  
 Galinsky, Kevin 675, 1201, 1297  
 Gallien, Jeremie **1470**  
 Gallo, Kerry **120**  
 Galzi, Jean Luc 40  
 Gamboa, Dionicia 1200  
 Gamboa-Leon, Rubi 819  
 Gamero, Maria E. 415  
 Gamo, Francisco-Javier 681, 986, **1320**  
 Gamo Benito, Francisco Javier 1325  
 Ganaba, Rasmané 447  
 Ganeshan, Harini 6, 995  
 Gannavaram, Sreenivas **979**, 1452  
 Gansané, Adama 467, 1331  
 Gansane, Zakaria 13  
 Gaona, Heather 840  
 Garabed, Rebecca 960  
 Garapayi, Patrick 1471  
 Garcia, Andres J. 1352  
 Garcia, Dan 239  
 Garcia, Hugo 1080  
 Garcia, Hector H. 446, 1068, 1069, 1072, **1073**, 91, 93, 94, 95, 96, **443**, 445, 1075, 1077, 1078, 1079, 1081  
 Garcia, J. Santos 1255



The number(s) following author name refers to the abstract number.

- Garcia, Maria P. 1094  
 García-Bustos, Jose F. 681  
 Garcia-Forey, Magdalena 1146  
 Garcia-Rejon, Julian 565  
 Gardiner, Don 143, 1194  
 Gardner, Malcolm 178  
 Garg, Seema 620  
 Garges, Eric 922  
 Garimo, Issa 890  
 Garley, Ashley 393  
 Garrett, Nancy 1409  
 Garry, Robert F. 1275  
 Garuti, Helena 681, 986  
 Garver, Lindsey 997  
 Garza-Hernandez, Javier Alfonso 75  
 Gasasira, Anne 314, 892  
 Gaspe, Maria Sol 816  
 Gatakaa, Hellen 1021, 1299, 1300, 1360  
 Gatti, Simona 448  
 Gattton, Michelle 457, 463, **853**, 1307  
 Gattton, Michelle L. 866  
 Gaugler, Randy 583, 584, 748  
 Gausi, Khoti 10  
 Gavidia, Cesar M. 1068, 1069, **1079**, 94, 1080, 1157  
 Gavotte, Laurent 40  
 Gaydon, Jane 436  
 Gaye, Oumar 294, 324, 346, 349, 547, 550, 693, 781, 864, 1313, 1330, 1342, 1466  
 Gaynor, Anne M. 245, 1237  
 Gaynor, Bruce D. 29  
 Gazos Lopes, Ulisses **476**  
 Gazzinelli, Andrea 38  
 Gazzinelli, Ricardo T. 38  
 Gbedande, Bienvenue 710  
 Gbedande, Komi **697**, **711**  
 Geary, Timothy 523  
 Gebreselassie, Nebiat 1491  
 Geertruyden, Jean-Pierre v. 899  
 Gendlina, Inessa 487, 536  
 Genedy, Mohamed 1237  
 Geng, Jinheng 311  
 Gentile A, Alex 271  
 George, Asha 233  
 George, Daniel R. 776  
 George, Jovvian 39  
 Gerke, Christiane **1050**  
 Gerns, Helen L. **660**  
 Gertler, Paul 1257  
 Gesase, Samwel 510  
 Getachew, Medhanit **908**  
 Gething, Peter W. 21  
 Getso, Kabiru I. **1051**, **1375**  
 Gettayacamin, Montip 837  
 Ghabra, Twafik 278  
 Ghani, Azra 177, 179, 856, 882, 882, 897, 1329  
 Ghansah, Anita 256, **383**  
 Gharbi, Myriam **862**, **863**, **863**, **864**, 1023  
 Gherzi, Bruno 588, 1413, **931**  
 Ghezehegn, Kahsay Huruy H. G. **419**  
 Ghose, Aniruddha 886, 1165, 1269  
 Ghosh, Probir K. 1414  
 Ghosh, Samir 774  
 Gibbons, Robert V. 15, 104, 1087, 102, 1082  
 Gibson, Wendy 475, 820  
 Gichangi, Anthony 925  
 Gichangi, Michael 596  
 Gicheru, Michael 957  
 Gichuki, Charity 707  
 Gidado, Saheed S. 1375  
 Gidwani, Kamlesh 534, 535  
 Giese, Russell 958  
 Gil, Ani 941  
 Gil, Ana I. 1248, **1258**  
 Gil, Jose 825  
 Gil, J. Pedro 901  
 Gilbert, Alexa 109  
 Gilbert, Amy 566  
 Gilbert, Clare 1274  
 Gilbert, Sarah G. 1456  
 Gilbreath, Thomas 202  
 Gilchrist, Carol 1027  
 Gillespie, Portia 1034  
 Gilman, Robert H. 95, 244, 446, 516, 825, 942, 1072, 1074, 1078, 1079, 1081, 1400, 1080, 89, 885, 887, 1157, 1401  
 Gimenez-Fourage, Sophie 110  
 Gimnig, John 200, 1389, 1468, 1473  
 Giordani, Maria T. **1239**  
 Girard, Jennifer 935  
 Gitawati, Retno 155  
 Githae, Elizabeth N. **366**  
 Githeko, Andrew K. 865, 1391  
 Gitonga, Carol 1440  
 Gizaw, Afework Kassu K. 419  
 Glaser, Kathleen 261  
 Glass, Gregory E. 210, 1334  
 Glenn, Travis 54  
 Goba, Augustine 1275  
 Goblirsch, Sam R. 448  
 Godeaux, Olivier 176  
 Goes, Viviane M. 850  
 Goethert, Heidi K. **59**  
 Goff, Tami 905, 905  
 Goh, Lucy M. L. **270**  
 Goita, Seydou 30, 84  
 Goldberg, Julia **359**  
 Goldberg, Jonathan 1110  
 Goldberg, Ronald 1114  
 Golden, Allison **304**  
 Golden, Frances V. 1208  
 Goldman, Ann S. 33  
 Golenbock, Douglas 795  
 Gollob, Kenneth J. 1150  
 Gomes, Ariane K. C. 38  
 Gomes, M. Gabriella M. 1281  
 Gómez, Gerardo 47  
 Gomez, Giovan F. **219**, 1233  
 Gomez, Jorge 237, 244, 415, 942, 1102  
 Gomez, Luis 1073  
 Gomez, Marinely B. 971  
 Gomez, Noe 1171  
 Gómez, Vanessa 681, 986  
 Gomez-Lorenzo, Maria G. 1320  
 Gomez-Puerta, Luis A. **94**, **249**, 1074  
 Gomis, Jules-Francois 1342  
 Goncalves, Bronner 184, 223, **541**, **1337**  
 Gonçalves, André H. O. 19  
 Gong, Bin 1058  
 Góngora Rivas, Ilse Maria 239  
 Gonzales, Armando E. 1075, 1080  
 Gonzales, Isidro 91, 443  
 Gonzales, I 445  
 Gonzales, Isidro 446, 1077  
 Gonzalez, Armando E. 95, 249, 446, 1072, 1073, 1074, 1078, 1079  
 Gonzalez, Armando E. for the Cysticercosis Working Group Peru, 94  
 Gonzalez, Demetrio 391  
 González, Elsa E. 420, 928  
 Gonzalez, Kadir 253  
 Gonzalez, Karla N. 425, 631  
 Gonzalez, Guillermo E. 446, 1072, 1078  
 Goodhew, Brook 949  
 Goodman, Anna L. 1456  
 Goodman, Catherine 11, 290, 332, 334, 460, 833, 838, 896, 1360, 1469, 1473, 878  
 Goodman, Christopher D. 147  
 Goodman, Simon J. 228  
 Goodson, David 724  
 Gopalakrishnan, Anusha M. **500**  
 Gope, Partha S. 777  
 Gopi, P G. 242  
 Gorchakov, Rodion V. 927, 1383  
 Gordon, Aubree 625, **633**, 805, **1246**  
 Gorenflot, Andre 1025  
 Gosi, Panita **1063**  
 Gosinary, Fabiola 262  
 Gosling, Roly 156, 510, 1174, 469, 545  
 Gosnell, William L. **1168**  
 Goswami, Doli 1241  
 Goto, Yasuyuki 974  
 Gottlieb, Eric R. 7  
 Gotuzzo, Eduardo E. 420, 251, 928, 955  
 Gougnard, Nadege 980, 1451  
 Gould, Sarah 630  
 Gourmelon, Gaelle J. A. 1255  
 Govella, Nicodem 741  
 Govindarajan, Dhanasekaran 1015  
 Govore, Emma 1040  
 Gracie, Alastair 1006  
 Grady, Caroline 645  
 Graf, Paul C. F. 259, 929  
 Graham, Sean P. 923  
 Grahek, Shannon 1129  
 Gramzinski, Robert 844, 845, 846  
 Grant, Donald S. **1275**  
 Grant, Fred 84  
 Grant, Richard 118  
 Graterol, Héctor 627  
 Gratz, Jean 1380  
 Grau, Georges E. 432  
 Grauer, Kristina 676  
 Graves, Patricia 312  
 Graves, Patricia M. 1346, 1359  
 Gray, Alyson M. **828**  
 Gray, Darren J. 305  
 Gray, Jennifer 626, 938  
 Gray, Karen-Ann 1024  
 Green, Justin A. **150**, 435  
 Green, Michael 906, 906, 328  
 Green, Sharone 15, 102  
 Greenbaum, Adena **241**  
 Greene, Leslie E. 1264, 1415  
 Greenhouse, Bryan 469, 540, 719, 1203  
 Greenwood, Brian 545, 1436  
 Greeson, Dana 1131  
 Gregory, Michael J. 259, 589, 1044  
 Gregory, Philip D. 439  
 Greiner, Dale 427  
 Grenfell, Bryan T. 933  
 Gresh, Lionel 113, 805, 1246  
 Gresty, Karryn 1024  
 Grevelding, Christoph G. 980, 1451  
 Grewal, Paul 1460  
 Grieco, John 733, 734, 736, 737, 1224  
 Griffin, Jamie 177, **1329**  
 Griffin, Paul 436  
 Grigg, Matthew J. 946  
 Grigorenko, Elena 783  
 Grijalva, Mario J. **824**  
 Grimberg, Brian T. **1310**  
 Grinev, Andriyan 1107  
 Groepe, Mary Anne 162, 1173, 1175  
 Grogan, Caroline 574, 1339, 1477  
 Grogl, Max 434, 537, 945, 1270  
 Grosenbach, Douglas W. 103  
 Grossman, Marissa **1042**  
 Groth, Janice 1137  
 Gu, Se Hun **53**  
 Guan, Liming 1015

The number(s) following author name refers to the abstract number.

- Guan, Yue 293  
 Guardabassi, Luca 81  
 Gubler, Duane J. 115, 424, 634  
 Guebey, Remy 444  
 Guedes, Marjorie M. G. **1049**  
 Guedes, Silas 792  
 Guelbeogo, Wamdaogo M. **912**  
 Guenther, Stephan 414  
 Guerbois, Mathilde 1383  
 Guérin, Philippe J. 862, 863, 863, 864, 868, **323**, 988, 1023, 1195, 1316  
 Guerra, Eduardo 624  
 Guerra-Giraldez, Cristina 93, 1075  
 Guerrant, Richard L. 516, 517  
 Guerrero-Jimenez, Darwin F. 824  
 Guevara, Carolina 112, 227, 244, 422, 603, **1102**  
 Guevara, Jose 589  
 Guevara Orozco, Jorge 239  
 Guevorkian, Mark **239**  
 Guéye, Aly 294  
 Gueye, Abdou S. 382  
 Gueye, Lamine 255  
 Gueye, Salam 1439  
 Guezala, Claudia 237, 588  
 Guha, Neela 141  
 Guiguemé, T. Robert 377  
 Guimarães, Luiz Henrique 813  
 Guindo, Agnes 184, 223, 1337  
 Guindo, Aldiouma 1335  
 Guindo, Boubacar 641  
 Guindo, Nouhoum 336  
 Guinovart, Caterina 1356  
 Guirou, Etienne 336, 336  
 Guis, Hélène 971  
 Guma, Victor 1357  
 Gumbo, Peter 1040  
 Gumo, Sussy K. 1183  
 Gundersen, Svein G. 1279, 1433  
 Guo, Denghui 677  
 Guo, Lizheng 1242  
 Guo, Shanchun 663  
 Gupta, Charu 539  
 Gupta, Pankaj 990  
 Gupta, Puneet 990  
 Gupta, Supriya 1421  
 Gurevitz, Juan 816  
 Gurley, Emily S. 413, 1056  
 Gürtler, Ricardo E. 816, 822  
 Gustafson, John 202  
 Gut, Jiri 677  
 Guthmann, Jean-Paul 1351  
 Gutierrez, Gamaliel **113**  
 Gutierrez, Mary 611  
 Gutman, Julie **830**, **880**, **552**  
 Gutteridge, Clare E. **683**  
 Guy, Bruno 110, 630  
 Guy, R. Kip 431  
 Guzmán, Diamelis 624  
 Guzman, Frank 1081  
 Guzman, Hilda 1104  
 Guzman, Militza 598, 599  
 Guzman, Maria G. 634  
 Guzman, Rene C. 1053, 1123  
 Gwadz, Robert W. 982  
 Gyapong, John 1327  
 Gyapong, Margaret 571, **1250**
- H**
- Ha, Kwon-soo 665  
 Ha, Sha 935  
 Ha, Tran T. N. 637  
 Haaland, Ane 803  
 Haaland, Benjamin 424  
 Haar, Karin 1404  
 Habimana, R.m. 655  
 Habluetzel, Annette 1211  
 Habomugisha, Peace 1118  
 Hachet-Haas, Muriel 40  
 Haddad, Danny 596  
 Hadj-Kaddour, Kamel 1025  
 Hafiz, Israt **484**  
 Hagan, Jose E. **451**  
 Haidara, Fadima C. 236, 1288  
 Haider, Najmul 1056  
 Haile, Ashley 997  
 Hailu, Asrat **814**  
 Hailu, Workagegnehu 814  
 Hajduck, Steve 86  
 Hakizimana, Emmanuel **906**, **906**  
 Halasa, Yara A. 583, 584, 1088, 748  
 Haldar, Kasturi 1171  
 Hales, Belinda J. 56  
 Hall, Eric 593  
 Hall, Eric R. 1053, 1123  
 Hall, Martin 1419  
 Halldin, Cara 559  
 Haller, Aurelia 1013, 1014  
 Hallett, Rachel 346, 349, 353, 870  
 Halliday, Katherine E. **544**  
 Halpin, Jessica 1409  
 Halsey, Eric S. 18, 112, 227, 415, 416, 418, **422**, 593, 622, 728, 603, 1222, 942, 1102, 1135, 1386  
 Halstead, Scott B. 634  
 Halton, Kate 305  
 Hamad, Amel 990  
 Hamado, Ouedraogo 1038  
 Hamainza, Busiku 12, 468, 694, **904**, 1180, 1340  
 Hamano, Shinjiro 526  
 Hamed, Kamal 467, 787, 828, 920  
 Hamel, Mary 453, 1403, 1437  
 Hamer, Davidson H. 574, 1339, **1477**  
 Hamer, Gabriel L. 745  
 Hamid, Mohammed 576  
 Hamisi, Yuna 388  
 Hamm, Tiffany 844, 845, 846  
 Han, Eun-taek 665  
 Hanafi, Hanafi A. H. **69**  
 Hand, Carla C. 1164  
 Handali, Sukwan 129  
 Hang, Jun 418  
 Haniotis, John 1374  
 Hanisch, Benjamin R. **717**  
 Hanley, Kathryn A. 116  
 Hanna, Refaat **894**  
 Hannaman, Drew 169  
 Hansen, Kristian S. 340, 341  
 Hanson, Josh 548  
 Hanson, Kara 290, 896, 1360  
 Hansson, Helle H. 781  
 Haq, Rouseli 484  
 Haque, C. Emdad 1090, 1287  
 Haque, Farhana **773**  
 Haque, Rashidul 210, 367, 512, 1026, 1027, 1380  
 Haque, Ubydul **1334**  
 Harb, Omar S. **672**  
 Harbach, Ralph 752  
 Hardie, Rochelle 1130  
 Harenberg, Anke **110**  
 Hariniaina, Elisoa 262  
 Harn, Donald A. 1399  
 Harnett, Margaret M. 1006  
 Harnett, William **1006**  
 Haroun, Yusuph 657  
 Harrell, Emma J. 150, 435  
 Harrington, Laura C. **555**  
 Harris, Caroline 194, 642, **732**  
 Harris, Eva 113, 425, 429, 625, 629, 631, 632, 633, 634, 805, 1246, 1394, 1395, 1396  
 Harris, Jason B. 41, 42, 43, 45, 1410, 1041, 1048  
 Harris, Tegan 489  
 Harrison, Genelle F. **1199**  
 Harrison, Lisa M. 491  
 Harrison, Thomas S. 1137  
 Hartgers, Franca C. 1109  
 Hartinger, Stella M. 941, 1258, **1248**  
 Hartl, Daniel L. 504, 1201  
 Hartley, Ashley N. 494  
 Hartley, Catherine S. 1484  
 Hartman, Fredrick **1357**  
 Hartsel, Joshua A. 24  
 Harty, John 493, 874  
 Hartzell, Joshua 1272, 951  
 Hasan, Hadura Abu 1207  
 Hasan, Mahtab U. 548, 886, 1165  
 Hasang, Wina 708, 708  
 Hasanzai, Anwar 461  
 Hashim, Kamal 647  
 Hashim, Rhamadhan 510, 545  
 Hashimi, Hassan 1498  
 Hashizume, M. 378  
 Hasker, Epcó **534**, 826  
 Hass, Meike 414  
 Hassan, Hassan 647  
 Hassan, Rohaizat 360  
 Hata, Nobuhide 792  
 Hatch, Steven 1087  
 Hattasingh, Weerawan 1101  
 Hattendorf, Jan 941, 1248  
 Haughey, David 678  
 Hauyon-La Torre, Yazmin 471  
 Hawela, Moonga 165, 1180  
 Hawley, William A. 1219  
 Hay, Bruce A. 1003  
 Hay, John G. 1449  
 Hay, Simon I. 21  
 Hayashi, Naoko 526  
 Haynes, Barton F. 632  
 He, Jian 935  
 Healy, Sara A. **187**  
 Healy, Sean 583, 584, 726, 748  
 Heidebrecht, Richard W. 675  
 Heimbürg-Molinario, Jamie 761  
 Heinke, Claudia 813  
 Heinze, Dar 577  
 Heisey, Daniel A. R. 623  
 Heitzinger, Kristen **1053**, **1123**  
 Helb, Danica A. **719**  
 Helegbe, Gideon K. 168  
 Helinski, Michelle E. H. 555  
 Heller, Tom 1239  
 Hemingway, Janet 390, 1390  
 Hemmat, Peggah 1143, 1146  
 Hemme, Ryan R. **482**  
 Hendler, Natalie 880  
 Hendriks, Ilse C. 1426  
 Heng Leang, Chhay 241  
 Henn, Matthew R. 429  
 Henning, Tyler C. **585**  
 Henrich, Philipp P. **1321**  
 Henriques, Gisela C. L. **870**  
 Henry, Christopher J. 1281  
 Henry, Marie C. 213  
 Henry, Noelie B. 1331  
 Henry-Halldin, Cara 208  
 Hepburn, Matthew 1266  
 Heppner, D. Gray 176, 7  
 Herdiana, Herdiana **161**  
 Heredia, Norma L. 1255  
 Herlihy, Julie 574, 1339, 1477  
 Herman, Jonathan D. **1297**  
 Hermance, Meghan 577  
 Hermsen, Cornelius C. 180  
 Hermsen, Rob 1186  
 Hernandez, Salvador 817  
 Hernandez-Luis, Francisco 1152  
 Herold, Christine 519  
 Herrera, Manuela **214**  
 Herrera, Raul 185  
 Herrera, Socrates 669  
 Herrera-Estrella, Luis 98  
 Herring, Belinda 1374  
 Hess, Ann 1001  
 Hesse, Elisabeth M. **1096**

The number(s) following author name refers to the abstract number.

- Hibbert, Jacqueline 663  
 Hickey, Bradley 178  
 Hickey, Patrick J. 361, 1295  
 Hickman, Mark 434, 537  
 Hickner, Paul V. 206, 207  
 Hien, Tran Tinh 933  
 Higazi, Tarig B. 647  
 Higgins, Sarah J. 1449  
 Higgs, Stephen 1228  
 Hightower, Allen 9, 49  
 Higinio-Rocha, Anna C. 38  
 Hildreth, Stephen W. 620, 1086, 636  
 Hill, Adrian V. S. 3, 171, 1456, 1458, 5  
 Hill, Vincent 854, 1409  
 Hill, Zelee 804, 1284  
 Hinrichs, David 834, 834  
 Hirayama, Kenji 168, 526, 637  
 Hirve, Siddhivinayak 1285  
 Hiscox, Alexandra 450  
 Hise, Amy G. 50, 423  
 Hittner, James 501, 705, 706, 707, 797, 957, 1191, 1192, 1193  
 Hjelle, Brian 1384  
 Ho, David D. 1461  
 Ho, Mae 548  
 Hochberg, Lisa P. 618, 1148  
 Hodges, James S. 1480  
 Hodges, Mary H. 300, 301  
 Hodges, Theresa K. 508, 1000  
 Hodgson, Abraham 842, 1162, 1196, 1273, 1285, 1332, 1408  
 Hoerauf, Achim 481, 519, 522, 523, 524  
 Hofer, Alexandra 948  
 Hoffman, Irving 363, 368  
 Hoffman, Stephen L. 189, 713, 982  
 Hoffmann, Karl F. 760  
 Hogrefe, Wayne 636  
 Hokke, Cornelis H. 760, 976, 1032  
 Holder, Anthony 1171  
 Holding, Penny 992  
 Holianjovony, Jeanine 262  
 Hollingdale, Michael R. 6, 995  
 Hollingsworth, Deirdre 307  
 Holloway, Kathleen A. 295  
 Holmen, Sigve D. 1279, 1280, 1278  
 Holmes, Chris 1195  
 Holmes, Eddie 933  
 Holmes, Kathryn V. 53  
 Holmes, Robert 894  
 Holmes, Randal K. 43  
 Holmes, Shanna M. 1148  
 Holt, Deborah 57, 604, 612, 489  
 Holte, Sarah 541  
 Homaira, Nusrat 1418  
 Honda, Stacey A. A. 1168  
 Hoogesteyn, Almira 797  
 Hooper, Craig 47  
 Hope, Louise K. 740  
 Hopkins, Adrian D. 643  
 Hopkins, Corey 730  
 Hopkins, Heidi 463, 1307, 1309  
 Hoque, M. Gofranul 548, 886  
 Horiuchi, Kalanthe 51  
 Hosen, Md. Ismail 43  
 Hosie, Heather E. 173, 1460, 1459  
 Hossain, M. Jahangir 413, 773, 1056, 1039  
 Hossain, Md. Amir 548, 886, 1165  
 Hossain, Zahid 240  
 Hostetler, Dana 328  
 Hotez, Peter J. 127, 1034, 1129  
 Hott, Amanda 989  
 Houghbegnon, Parfait 697, 711, 710  
 Houpt, Eric R. 512, 1380  
 House, Brent 176, 1266  
 Howard, Elizabeth 819  
 Howard, John 564  
 Howard, Randy 4, 174  
 Howe, Shiqin 115  
 Hruby, Dennis E. 103  
 Hsiang, Michelle 156, 469  
 Hsiao, Hui-Mien 628  
 Hsieh, Michael 975  
 Hu, Branda T. 1086  
 Hu, Yan 1128  
 Hu, Zhnghui 185  
 Huaman, Jose L. 415  
 Huang, Chiung-Yu 389, 541  
 Huang, Claire Y. H. 1014, 1013, 619  
 Huang, Jun 6, 995  
 Huang, Yuefang 1111  
 Huang, Yan-Jang S. 1228  
 Huayanay, Anibal 1223  
 Hubbard, Alan 1037  
 Hubert, Véronique 862, 863, 863, 864  
 Huda, Tarique M. 1414  
 Hudgens, Michael G. 1376  
 Hudson, Thomas 537  
 Hudson, Toni-Marie L. 728  
 Huffman, Ryan D. 258  
 Hughes, Angela 193  
 Hughes, Molly 1238, 1245  
 Humberstone, Andrew 436  
 Hume, Jen C. C. 187  
 Humphries, Debbie 276, 491  
 Hun, Laya 607  
 Hun, Lewis 1361  
 Hunsperger, Elizabeth 109, 1097  
 Hunt, Paul 870  
 Hunter, Shawn 949  
 Huong, Vu T. Q. 637  
 Hurd, Janet G. 1455  
 Hussain, Faruqe 774, 777, 965  
 Hussaini, Azra 150  
 Huston, Christopher D. 1029  
 Hutchinson, Paul 1435  
 Huttinger, Elisabeth 757  
 Hutton, Andra A. 562  
 Huy, Nguyen T. 637  
 Huynh, Bich-Tram 371  
 Huynh, Jeremy P. 116  
 Huynh, Uyen 1254  
 Hviid, Lars 170  
 Hwang, Jimee 156, 398  
 Hyacinthe, Toé K. 966  
 Hyde, Terri 1411  
 Ismayilov, Afrail 922  
 Isoe, Jun 22  
 Ithondeka, Peter 49  
 Ito, Daisuke 665  
 Iuliano, Danielle 241  
 Ivan, Scandale 523  
 Iwalewa, Ezekiel O. -. 149  
 Izugbara, Chimaraoko 801  
 Izumiya, Hidemasa 788  
 Jaal, Zairi 1207  
 Jaba, Hujo 737  
 Jabo, Aliyu M. 34  
 Jackson, Brendan R. 47, 1054  
 Jackson, Graham E. 397  
 Jacobs, David 41  
 Jacobs, Robert T. 1147  
 Jagannathan, Prasanna 540  
 Jagero, Geoffrey 1040  
 Jagne, Ya Jankey 3  
 Jagoe, George 569  
 Jahan, Nusrat 221  
 Jaiswal, Smitta 427  
 Jambou, Ronan 262, 432, 444  
 James, Anthony A. 204  
 James, Eric 713, 982  
 Jameson, Samuel B. 199  
 Jamonneau, Vincent 811  
 Jancovic, Mario 891  
 Jannat, Kaniz 940  
 Janse, Chris J. 978  
 Jara, Jorge 944, 1249  
 Jaramillo, Juan Felipe 281  
 Jaramillo, Luz M. 219, 1233  
 Jardim, Juliette G. 167  
 Jaribu, Jennie 1284  
 Jarillo-Luna, Adriana 252  
 Jarju, Lamin B. S. 464  
 Jarman, Richard G. 15, 1087, 1096, 1082  
 Jarnagin, Kurt 530  
 Jawara, Musa 375, 464  
 Jayabalasingham, Bamini 189  
 Jaykus, Lee-Ann 1255  
 Jean, Moliere 482  
 Jean, Ndiaye L. A. 1166  
 Jean-Luc, Nkurikiyimfura 651  
 Jeffrey, Eileen H. 215  
 Jeffries, David 464  
 Jelicks, Linda A. 1450  
 Jenkins, Adam M. 1216  
 Jenkins, Bethany J. 499  
 Jenkins, Kylie 1411  
 Jenkins, Miriam 766  
 Jenks, Mary H. 1009, 1074, 1116  
 Jensen, Beth 1240  
 Jeyaprakasam, Madhumathi 1488  
 Jhonston, Erik J. 422

The number(s) following author name refers to the abstract number.

- Jia, Hongwei 931  
 Jia, Wanzhong **1071**  
 Jiang, Hongmei 202  
 Jiang, Jinjin 25  
 Jiang, Ju 591  
 Jiang, Jinjin **1365**  
 Jiddawi, Mohammed 695  
 Jima, Daddi 567, 1439  
 Jiménez, Alfons 990  
 Jimenez, Juan A. 1069  
 Jimenez, Liliana 1135  
 Jiménez-Díaz, María B. 681, 986  
 Jin, Xiannu 840, 841  
 Jirage, Dayadevi 1453  
 Jitan, Jeetendra K. **1326**  
 Johanes, Boniface 11, 290, **896**  
 John, Chandy C. 331, 542, 698, 717, 1276, 1336, 1480  
 John-Stewart, Grace 660  
 Johnson, Anthony 1423  
 Johnson, Cynthia 611  
 Johnson, Christian 780  
 Johnson, Joey 615  
 Johnson, Jacob D. 164, 839, 859, 860, 847  
 Johnson, Kristin **291**  
 Johnson, Keith 1286  
 Johnson, Partrick **1091**  
 Johnson, Russell A. 42, **45**  
 Johnson, Tobias 459  
 Johnson, William L. 116  
 Johnston, Kelly L. 524, 1115  
 Joice, Regina 1492  
 Jones, Christopher M. **966**  
 Jones, David S. 1455  
 Jones, Franca R. 1053  
 Jones, Jason 1310  
 Jones, Joel J. **459**  
 Jones, Kevin F. 103  
 Jones, Kara J. 1363  
 Jones, Matt J. 1230  
 Jones, Matthew L. 440  
 Jones, Sophie 510, **1186**  
 Jones, Susan A. 564  
 Jones, Stephen L. 535  
 Jones-Engel, Lisa 671  
 Jongsakul, Krisada 1063  
 Jori, Giulio 1211  
 Jörnhagen, Louise 901  
 Joseph, Don 1291  
 Joshi, Deepak 505  
 Joshi, Sudhaunshu 1438  
 Joshi, Sangeeta B. 1034  
 Joy, Teresa 215  
 Joyce, Kevin 1409  
 Jules, Mihigo 1018  
 Juliano, Jonathan J. 357, 363, 364, 368, 889  
 Juliao, Patricia 391, 485, 1124, 1125  
 Juma, Elizabeth 787, 839  
 Juma, Jane 1040  
 Jun, Gao 1101
- Jung, Suk-Chan 580  
 Junghanss, Thomas **784**  
 Jupatanakul, Natapong 1232, 1372  
 Justo, Carlos 253  
 Juwara, Musa S. 1419
- K**
- Kabanywany, Abdunoor M. K. **861, 1473**  
 Kabayiza, Alain 10  
 Kabayiza, Allan 906, 906  
 Kabesch, Michael 1109  
 Kabikira, Fredrick 325  
 Kabir, Mamun 1027  
 Kabore, Achille M. **1038, 1448**  
 Kaboré, Jacques **811**  
 Kabula, Bilali **197, 226, 1204**  
 Kabyemela, Edward 541  
 Kachani, Malika 1068  
 Kachur, S. Patrick 11, 332, 398, 833, 836, 1469, 1473, 1476, 334, 460, 843, 1356, 9  
 Kaddumukasa, Mark **709**  
 Kadivane, Samuel 1409  
 Kadjo, Blaise 53  
 Kaewhiran, Surachai 1093  
 Kaewma, Benjawan 1101  
 Kafkova, Jirina 891  
 Kafuko, Jessica 695, 800, 918  
 Kaguthi, Grace **952**  
 Kahigwa, Elizeus A. 1473  
 Kahindi, Samuel 752, 1385  
 Kahitsi, Wilson 546  
 Kahle, Kristen 635, **926**  
 Kahn, Jim G. 687  
 Kahn, Maria 849  
 Kain, Kevin C. 1449  
 Kaindo, Emanuel W. **688**  
 Kaita, Ibrahim M. 1051  
 Kakeeto, Stella 892  
 Kakoly, Nadira S. **1407**  
 Kakoma, Jean-Baptiste 651  
 Kakuma, Ritsuko 801  
 Kakuru, Abel 540  
 Kalam, Adil 1380  
 Kalayanarooj, Siripen 1082, 102  
 Kaldas, Rania M. 69  
 Kaldor, John 576, 616  
 Kaldor, John M. 1404  
 Kalemba, Lems 566  
 Kalilani-Phiri, Linda 1438  
 Kalinga, Akili 483  
 Källander, Karin **804**  
 Kalolella, Admirabilis 11, 290, 332, 460, 896, 1469, **334**  
 Kalsy, A 1041  
 Kama, Mike 1411  
 Kamatenesi-Mugisha, Maud K. 860
- Kamau, Edwin 4, 1308  
 Kamau, Luna 1389  
 Kamdem, Ramsay S. T. 408  
 Kamga, Henri-Lucien F. 380  
 Kamgue, Eric 1475  
 Kamhawi, Shaden 472  
 Kaminta, Sylvester 590  
 Kamissoko, Yaya 84  
 Kamm, Kelly B. 1262, **1479**  
 Kampango, Ayubo 404  
 Kampmann, Beate 1285  
 Kampondeni, Samuel 1427  
 Kamuliwo, Mulakwa 73, 165, 727, 1180, 1340  
 Kamy, Moses 316, 372, 379, 466, 540, 549, 892, 314, 319, 462, 553, 719  
 Kanagawa, Shuzo 788  
 Kanchana, Aiemporn 339  
 Kandeel, Amr 1237  
 Kande, Ballah 464  
 Kandula, Deepika 166  
 Kaneko, Osamu 974  
 Kang, Gagandeep 516, 1031  
 Kang, Hae Ji 53  
 Kang, Seungwon **580**  
 Kang, Seokyoung **1372**  
 Kangwana, Beth B. P. **838, 878**  
 Kanki, Phylis 657  
 Kanoute, Moussa B. 280, 664, 898  
 Kansal, Sangeeta 534  
 Kanyala, Estelle 1062  
 Kao, Chuan-Liang 1099  
 Kapella, B.K. 1473  
 Kapin'a Kanyanga, Muzala 1045  
 Kapisi, James A. **316, 372**  
 Kapito-Tembo, Atupele 857, 857  
 Kappe, Stefan 178, 187  
 Kapulu, Melissa C. **1456, 1458**  
 Kar, Shantanu K. **521**  
 Karana, Orise 1475  
 Karanja, Diana M. S. 1434, 1442, 1443, 1444, 1033, 1428, 1432  
 Karanja, Peris 544  
 Kareem, Kevin 455  
 Karema, Corine **10, 779, 906, 906, 1350, 1351**  
 Karhemere, Stomy 455  
 Karikari, Patrick 802  
 Karim, Zachary 501, 705, 706, 1191, 1192, **1193**  
 Kariuki, Simon 854, 1437, 1468  
 Kariuki, Samuel K. M. 247  
 Kasiti, Jacqueline 613  
 Kaslow, Sarah R. 982  
 Kasper, Amelia M. **19**  
 Kasper, Matthew R. 589, 929, **1044, 1413, 85**  
 Kassahun, Aysheshm 814  
 Kasteng, Frida 804  
 Kasthuri, Raj S. 661, 661, 1164, 138
- Katabarwa, Moses 647, 1118, 312  
 Katabira, Elly 709  
 Katana, Abraham 1403  
 Kathcart, April 4  
 Kato, Cecilia Y. 594  
 Kato, Yasuyuki **788**  
 Kattula, Deepthi **1031**  
 Katwan, Elizabeth **1254**  
 Katz, Mark 1242  
 Kaufusi, Pakieli 117  
 Kaur, Gaganjot 1486  
 Kaur, Harparkash **328**  
 Kavare, Emmy 1444  
 Kavish, Reginald 968  
 Kawai, Satoru 974  
 Kawamura, Akira 1461  
 Kavar, Ziad S. 761  
 Kawazu, Shin-ichiro 974  
 Kayatani, Alexander K. 4  
 Kayentao, Kassoum 280, 336, 389, 787, 1436  
 Kayiwa, Denis 325  
 Kayondo, Jonathan 216, 400  
 Kayungwa, Benjamin 727  
 Kazacos, Kevin R. 129  
 Kazimirova, Maria 577  
 Kazura, James 50, 480, 700, 1483, 423  
 Ke, Hangjun **1188**  
 Kearney, Michael 121, 812, 818  
 Kearns, Therese 489, **604**  
 Keasey, Sarah L. 1397  
 Keating, Joseph 468, 903, 1435  
 Keck, James 1336  
 Kedenge, Sarah 838, **878**  
 Keenan, Jeremy D. 29  
 Kefyalew, Takele 386, 387  
 Keil, Martin 491  
 Keiser, Jennifer 531, **1122, 1447**  
 Keita, Adama D. 641, 782  
 Keita, Mohamed 336  
 Keita, Modibo 782  
 Keita, Mahamadou M. 782  
 Keita, Sory I. 478, 641, 740  
 Kelleher, Alan 1128  
 Keller, Angela J. **1444**  
 Keller, Tracey L. 1297  
 Kelley, James F. **117**  
 Kello, Amir B. 1271  
 Kelly, Jane X. 431  
 Kelly, Rosmarie 222  
 Kelly-Hope, Louise 32, 642, 484, 644  
 Kemgne, Eugenie A. M. **144**  
 Kemp, David J. 64, 68, 602  
 Kemp, Steve 613  
 Kempaiah, Prakasha 501, 705, **706, 707, 797, 957, 1191, 1192, 1193**  
 Kenangalem, Enny 155, 1424  
 Kendjo, Eric 862, 863, 863, 864, 1344

The number(s) following author name refers to the abstract number.

- Kennedy, Luma 725, 1386  
 Kersgard, Colleen M. **1295**  
 Keshinro, Babajide 958  
 Kessler, Evan 982  
 Kester, Kent 177  
 Ketoh, Guillaume 967  
 Keven, John 480  
 Khadime, Sylla 1166  
 Khairnar, Krishna 862  
 Khalil, Eltahir A. G. 1144  
 Khamadi, Samoel 1244  
 Khamag, Haneen 817  
 Khamis, Asma R. 880  
 Khamis, Iddi S. 35  
 Khan, Ashraful 1048  
 Khan, Anum 1161  
 Khan, Ashraf I. 42  
 Khan, Ashraful I. 46  
 Khan, Farhat 176, 716  
 Khan, Iqbal A. 46  
 Khan, Ikhlal A. 679  
 Khan, M. Salah Uddin 1056, **413**, 1039  
 Khan, Mohammad I. **1061**  
 Khan, Shabana I. 679  
 Khan, Shahid M. 978  
 Khan, Wasif Ali 210, 367  
 Khanam, Farhana 42, 43, 44, 518  
 Khanam, F. 1041  
 Khanam, Farhana 1410  
 Khantikul, Nardlada 406  
 Kharabora, Oksana 357, 889  
 Khasewa, Joab **658**  
 Khassawneh, Basheer 232  
 Khetani, Vikram 152, 1114, 1147  
 Khin, Hnin Su Su 1021  
 Khlaimanee, Nittaya 578  
 Khoa, Pham Thi 729  
 Khumalo, Zwebuka 1173  
 Kiang, Richard 944  
 Kibona, Mary 800  
 Kien, Duong Thi Hue 1398  
 Kigozi, Ruth 314, 892, 1439  
 Kihara, Jimmy 1429, 1430  
 Kikuchi, Mihoko 526, 637  
 Kikuvi, Gideon M. 273  
 Kikwai, Gilbert 943  
 Kilembe, Bernard 308  
 Kilima, Stella 1353  
 Killeen, Gerry F. 738, 910, 904  
 Killingbeck, Sarah 629  
 Killoran, Kristin E. **648**, 1004  
 Kilmarx, Peter H. 1040, 1252  
 Kilpatrick, A. Marm **1230**, 1217  
 Kim, Dong 127  
 Kim, Dohyeong **395**  
 Kim, Hyung 689, 689  
 Kim, Heung-Chul 736  
 Kim, Julia 1333  
 Kim, Nguyen Dang 356  
 Kim, Seong Yoon **1235**  
 Kim, Yohan 6, 995  
 Kimani, Tabitha M. **52**, 273  
 Kimmel, Rhonda 497, 700  
 Kinabo, Grace D. 1402  
 Kinara, Stephen 316, 372  
 Kindrachuk, Kristen 1494  
 Kinfu, Yohannes 1360  
 King, Chwan-Chuen **1099**  
 King, Christine A. 668  
 King, Charles H. **50**, 423, **1445**  
 King, Christopher L. 721, **993**, 992  
 King, David S. 103  
 King, Jonathan D. 646  
 King, Russell 733, 734  
 Kingston, Hugh 1165  
 Kipp, Aaron 955, 1127  
 Kirby, Matthew 8  
 Kiremire, Bernard T. 860  
 Kirinoki, Masashi 526  
 Kirkpatrick, Beth D. 1011  
 Kirkwood, Betty 804  
 Kironde, Fred 83, 709, 876  
 Kirwan, Daniela E. 1401  
 Kishore, Kamal 1404  
 Kisinza, William 197, 226, 1204  
 Kissinger, Jessica C. 672  
 Kitashoji, Emi **785**  
 Kitau, Jovin **195**, 197  
 Kitron, Uriel 18, 222, 563, 749, **816**, **822**, 1222, 1445  
 Kitron, Uriel D. 745  
 Kitsutani, Paul 241  
 Kitwika, Winston A. 473  
 Kityo, Robert 566  
 Kivaju, Zuhura 8  
 Kiware, Samson S. **399**, **1358**  
 Kiwou, Moses 891  
 Kizito, Fred 892  
 Kizza, Moses 875, 875  
 Kjetland, Eyrun F. 1278, 1279, 1280, 1433  
 Klarkowski, Derryck 845, 846  
 Klarmann, Ute 519, **522**  
 Klei, Thomas R. 649, 1117  
 Kleim, Jörg-Peter 435  
 Klein, Terry A. 736  
 Kleinschmidt, Immo 8, 729, 968, **1467**, 693  
 Klempa, Boris 577  
 Kleppa, Elisabeth 1278, **1279**, 1280, 1433  
 Kleschenko, Yuliya 190, 714, 715  
 Klimov, Alexander 1249  
 Kline, Daniel 748  
 Klion, Amy D. 740, 782  
 Klis, Sandor 780  
 Klunghong, Chonticha 104  
 Knee, Jacqueline S. **1263**  
 Knight, Nancy 953  
 Knight, Rob 600  
 Knopp, Stefanie **35**, 1446  
 Knox, Tessa B. **921**, 1206  
 Ko, Albert I. 19, 451, 1420  
 Ko, H. Y. 1099  
 Koba, Wade R. 1450  
 Kobayashi, Taiichiro 788  
 Kobylinski, Kevin C. **507**  
 Kochel, Tadeusz J. 18, 418, 622, 627, 1135, 1222, 593, 603, 618  
 Kodama, Yukinobu 168  
 Koech, Margaret C. 176  
 Koella, Jacob C. 1355  
 Koffi, David 344  
 Kofoed, Poul-Erik 835, 1338  
 Kohler, Casey **1191**  
 Kojiro, Maiko 785  
 Kok, Gerdalize 162, 1175  
 Koka, Hellen S. **412**  
 Kolapo, Usman 1131  
 Kolappan, C 242  
 Kolevic, Lenka 1400  
 Kolibab, Kristopher 175  
 Kollie, Karsor 306  
 Komba, Aldegunda 800  
 Kombila, Maryvonne 869, 1344  
 Komisar, Jack 4, 5  
 Konah, Stephen 705, 706, 957  
 Konah, Stephan 707, 1191, 1193  
 Konate, Amadou T. 1331  
 Konate, Drissa 712, 973  
 Konate, Lassana 722  
 Konate, Sidiki 336  
 Koné, Abdoulaye K. 1335  
 Kone, Mamady 1337  
 Kone, Penali L. 344  
 Kong, Deok-Hoon 665  
 Kongpatanakul, Supornchai 435  
 Kool, Jacob 1411  
 Koopman, James S. 1281  
 Kopel, Eran 829  
 Koporc, Kim 120  
 Koppel, Amanda L. 203  
 Kopydlowski, Karen 945, 1270  
 Koram, Kojo 1327  
 Koram, Kwadwo A. 1162, 1196, 1332, 276  
 Korkusol, Achareeya 578  
 Kormanovski, Alexander 254  
 Kornelis, Dieuwke 976  
 Koroivueta, Josefa 1404  
 Koroma, Joseph B. **300**  
 Korovou, Samuel 1411  
 Korpe, Poonum S. **1027**  
 Kosek, Margaret 885, 887  
 Kosgei, Jacklyn 1468  
 Koski, Kristine G. 1121  
 Koster, Michael P. 279  
 Kotloff, Karen 514, 1059, 1060, 513, 515, 961  
 Kouanda, Seni 292, 402, 956  
 Koudou, Benjamin G. **302**  
 Koura, Ghislain K. 371, 374  
 Kouriba, Bourema 7, 1335  
 Kourouma, Nana 1059, 1060  
 Kourout, Moussa 783  
 Kovac, Pavol 42, 45  
 Kovacic, Vanja **71**, 76  
 Kozar, Michael R. 676  
 Kralova, Jana 791  
 Kramer, Kenton J. 1168  
 Kramer, Laura D. 228, 561, **564**, 1217, 1230, 425  
 Kramer, Randall 395, 1353  
 Krastins, Bryan 45  
 Krattiger, Anatole 1291  
 Krause, Peter 60, 1025, **61**  
 Krause, Rachel J. **1121**  
 Krcmery, Vladimir **791**, **793**, **891**, **893**, **895**  
 Kreishman-Deitrick, Mara 945, 1270  
 Kremser, Peter G. 703  
 Kreppel, Katharina S. **58**, **739**, 741  
 Krieger, Marco 850  
 Krishna, Sanjeev 1454  
 Kroeger, Axel 747  
 Krolewiecki, Alejandro 1151  
 Kronmann, Karl 790  
 Krudsood, Srivicha 343  
 Kruize, Yvonne C. 1109  
 Ku, Chia-Chi 1099  
 Kuan, Guillermina 113, 633, 805, 1246  
 Kubio, Chris 414  
 Kublin, James G. 187, 871  
 Kubofcik, Joseph **478**  
 Kuchuloria, Tinatin 1266  
 Kuganatham, P 16  
 Kuhn, Walter F. 1239  
 Kukula, Vida A. **317**  
 Kukutla, Phanidhar **25**, 202, 1365  
 Kulkarni, Prasad 1285, 1408  
 Kulkarni, Rajan P. 296  
 Kulkova, Nada 791, 793, 893, 895  
 Kulohoma, Benard **79**  
 Kular, Dinish 72, **1149**  
 Kumar, Kamlesh 270  
 Kumar, Nirbhay 169, 500  
 Kumar, Rajiv 535  
 Kumar, Sunny 491  
 Kumar, Sanjai 496, 701  
 Kumar, Sanjeev 990  
 Kumar, Sumit 1198  
 Kumar, T.R. Santha **189**  
 Kumar, Urwashi 990  
 Kumar, Varun 241  
 Kumar Singh, Ahishek 534  
 Kumaraswami, V 242  
 Kundu, Subodh K. 773  
 Kunene, Simon 166, 469  
 Kunstadter, Peter **808**  
 Kurane, Ichiro 1392  
 Kuri-Morales, Pablo 634  
 Kuris, Armand 757  
 Kurniawan, Agnes **123**  
 Kurosaki, Tomoaki 168  
 Kurz, Nadine 489

The number(s) following author name refers to the abstract number.

- Kuschner, Robert A. 418  
 Kushner, Adam L. 286  
 Kuzmin, Ivan 566  
 Kwak, Byung Hyung 676  
 Kwambai, Titus 271  
 Kwambana, Brenda 1419  
 Kwarteng, Alexander 522  
 Kwarteng, Anthony **1176**  
 Kweza, Patience 1252  
 Kwiatkowski, Dominic 503, 999  
 Kwityn, Clifford 1034  
 Kwofie, Kofi D. **256**  
 Kwon, Chang-hee 580  
 Kyabayinze, Daniel 463, 1307, 1309, **1020**  
 Kyari, Fatima 1274  
 Kyebambe, Peterson S. **656**  
 Kyelem, Carole G. 377  
 Kyelem, D. 483  
 Kyle, Dennis E. 431, 866, 867, 989  
 Kyobotungi, Catherine 1360
- L**
- LaBaer, Josh 41  
 Labbé, Pierrick 1205  
 LaBeaud, A. Desiree 50, **423**, 721  
 Laclette, Juan P. 98, 1076, 99  
 Lacoste, Maryjane 880  
 LaCrue, Alexis N. 431  
 Lafferty, Kevin 757  
 LaForce, Marc 1408  
 Lafosse, Elsie 47  
 Lafuente-Monasterio, Maria Jose 1325  
 Lage, Regina C. G. 529  
 Laguna-Torres, Victor A. **1135**, 942, 1400  
 Lai, Chih-Yun 1394  
 Lakwo, Tom L. **520**  
 Lal, Sham 340, 341  
 Lalji, Shabbir 546, **918**  
 Lalloo, David 362, 1441  
 Lam, Felix 1345  
 Lam, Polo C. H.. 24  
 Lambert, Lynn 1423  
 Lamberton, Poppy H. L. 479  
 Lamine, Diakité Moussa 1337  
 Lammie, Patrick 482, 645  
 Lampah, Daniel A. 155, 1424  
 Lan, Nguyen T. P. 637  
 Lanata, Claudio F. 516, 941, 1248, 1258  
 Laney, Sandra J. 1489  
 Lang, Jean 110, 630  
 Lanou, Herman 292  
 Lantagne, Daniele S. 1252  
 Lanteri, Charlotte A. **837**, 1063  
 Lantz, Chris 438  
 Laquer, Kari 176
- Larbi, Irene A. 1109  
 Larissa Aurore Tobola, Bouyoukou Hounkpatin **703**  
 LaRocque, Regina C. 42, 43, 45, 1410, 41, 1041  
 Larrauri, Luis 446  
 Larsen, David 1180  
 Larsen, David A. **12**, **468**, **694**, 1435  
 Larson, Erik 629  
 Larson, Nick 1213  
 Larson, Peter S. **915**, **917**  
 Larsson, Catherine 1011  
 Lasanajak, Yi 761  
 Laserson, Kayla 513, 514, 515, 952, 961, **453**, 1403  
 Latourette, Matthew 1427  
 Lau, Colleen 118  
 Lau, Louis 1395  
 Lau, Rachel 862  
 Lauby-Secretan, Beatrice 141  
 Laucella, Susana A. 1153  
 Laufer, Miriam K. 871, 1438, **857**, **857**  
 Laurens, Matthew B. 5, 7, 1335  
 Laver, Susan M. L.. 1252  
 Law, Charity W. 1167  
 Lawal, Ismail 958  
 Lawrie, Alison 3  
 Lazo, John S. 537  
 Le, Binh **1209**  
 Le, Christy 1002  
 Le, Huu Tho 246  
 Le, Minh Nhat 246  
 Le Bras, Jacques 862, 863, 863, 864, 868  
 Le Nagard, Hervé 868  
 Ledermann, Jeremy P. 1377, 566  
 Lee, Angela 1357  
 Lee, Andrew H. 439  
 Lee, Bi-Yao 1119  
 Lee, Bruce Y. 127, 296  
 Lee, Ming-Chieh 877  
 Lee, Marcus C. S. 439  
 Lee, Patricia J. 683  
 Lee, Sue 548, 1269  
 Lee, Susan Shin-Jung 1119  
 Leed, Susan E. 683  
 Leeds, Janet M. 103  
 Leepitakrat, Surachai 578  
 Legac, Jenny 677  
 Legros, Mathieu **872**  
 Lehane, Michael 71, 76  
 Leiby, David A. 905, 905  
 Leitner, Gabriel 797  
 Leitner, Wolfgang W. 611, 611  
 Lekpor, Cecilia E. 333  
 Lele, Albertine K. **337**  
 Lemey, Philippe 17, 119  
 Lemma, Seblewengel 903  
 Lemnge, Martha M. 861  
 Lemos, Larissa S. 250  
 Lengeler, Christian 1328
- Lenhart, Audrey 281, 724, 786  
 Lennon, Niall J. 429  
 Lennox, Gayle 1254  
 Leon, Juan S. 1255  
 Leontsini, Elli 774, 775, 963, 965  
 Leow, Kak S. 560  
 Lepore, Timothy 60  
 Lepore S.R., Timothy J. 59  
 Lerdprom, Rujira 877  
 Leroy, Didier 681, 986  
 Lesage, Pierre-Loup 1345  
 Lescano, Andrés G. 227, 259, 445, 640, 929, 1196, 1223  
 Lescuyer, Arlette 1451  
 Leshem, Eyal **829**  
 Leslie, Toby 454, **461**  
 Lesser, Adriane 1353  
 Lessler, Justin 1082  
 Letizia, Andrew **951**  
 Leung, Daniel T. **42**, 43, 45, **518**, 1041, 1410  
 Leung, Zachary 1470  
 Leutner, Silke 980  
 Levens, Joshua 592  
 Levin, Joshua Z. 429  
 Levine, Jessica 54  
 Levine, Myron M. 236, 513, 515, 961, 1288, 514, 1059, 1060  
 Levine, Rebecca 563  
 Levy, Danielle 1275  
 Levy, Karen 1042  
 Levy, Michael Z. 275, 825  
 Lewallen, Susan 1268, 1271  
 Lewis, Kayla 1240  
 Lewis, Michael D. 981  
 Lezama, Percy 1055  
 Lhermitte-Vallarino, Nathaly 40  
 Li, Hongmin 1071  
 Li, Jianyong 24  
 Li, Jian 665  
 Li, Lixin 103  
 Li, Li 1104  
 Li, Qigui 840, 841  
 Li, Shanping 389  
 Li, Tao 189, 449  
 Li, Tiger 1099  
 Li, Xiangming **1461**  
 Li, Yu 455  
 Li, Yuexin 834, 834  
 Liang, Ai Wei 110  
 Liang, Li 719  
 Liang, Song 960  
 Liang, Yousheng 532  
 Liao, Hua-Xin 632  
 Libraty, Daniel H. 15  
 Lichtner, Franz 1459  
 Lieberman, Marya 1240  
 Lieshout, L. V. 1434  
 Lietman, Tom M. 29  
 Lievens, Marc 188  
 Liles, W. C. 1449  
 Lillebø, Kristine **1278**, 1279, 1280
- Lilue, Jingtao 1499  
 Lim, Burton K. 53  
 Lim, Chang-kweng 1392  
 Lim, Jacqueline K. **1016**, 1017  
 Lim, Kee-Chong 1035  
 Lim, Pharath **985**  
 Lim, Yvonne A. L. 248  
 Lima, Aldo A. M. **517**, 1049  
 Lima, Helena C. A. V. 19  
 Lima, Marcelo d. Lima. 265, 266  
 Noélia L. Lima. 517  
 Limbach, Keith 495  
 Limkittikul, Kriengsak 1016, 1017, 1101  
 Lin, Feng-Chang 363  
 Lin, Jingwen **978**  
 Lin, Jessica T. 357, **689**, **689**, **889**  
 Lin, Ren-Yong 449  
 Lin, Zhaoting 983  
 Linares-Perez, Nivaldo 944, 1249  
 Lindblade, Kim 485, 626, 938, 1124, 1125, 1243, 391  
 Lindh, Jenny 191, 214, 217  
 Lindo, John F. 1130  
 Lindquist, Susan 1297  
 Lindroth, Erica **67**  
 Lindsay, Robbin 1090, 1287  
 Lindsay, Steve 191, 214, 217, 1220, 1388, 464, **1419**  
 Lindsay, Thomas 1419  
 Lindsley, Craig W. 730  
 Lingam, Raghu 804  
 Linser, Paul 1362  
 Linthicum, Kenneth K. 211  
 Liomba, Mike 857, 857  
 Liong, Kek-Yee 983  
 Lipkin, W. Ian 1103  
 Lissandrin, Raffaella 448, 1067  
 Little, Kristen M. **485**, **1124**, **1125**, **1478**  
 Littrell, Megan **1021**, **1299**, 1300  
 Liu, Canhui 1113, 1487  
 Liu, Jenny 342, **684**, 1174  
 Liu, Jie 512, 1380  
 Liu, Kun 1464  
 Liu, Lucy 60  
 Liu, Mingli 313, **663**  
 Liu, Mingshun 625  
 Liu, Shipping 23  
 Liu, Xia 175  
 Liu, Yunhua 23  
 Liu, Yue 1027  
 Livengood, Jill A. **619**, 1013, 1014  
 Liyanaage, Jayantha 410  
 Llanos, Fernando 446  
 Llanos, Fiorella 1341  
 Llanos-Cuentas, Alejandro 885, **887**, **1270**, 1341  
 Llergo, Jose L. 1320  
 Llewellyn, Martin S. 981  
 Llinás, Manuel 439  
 Lloyd, Bradley 790

The number(s) following author name refers to the abstract number.

- Lloyd, Natasha 61  
 Lo, Aminata Cole 346, **349**  
 Loayza, Manuel J. **108**  
 Lobigs, Mario 1228  
 Lobo, Cheryl 667  
 Lobo, Neil 752, 1219, 1231  
 Locke, Emily 183  
 Logarajah, Shankar 1209  
 Logue, Kyle 208, **559**  
 Logvinenko, Tanya 41  
 Loker, Eric S. **527**  
 Lokoel, Gilchrist 271  
 Lon, Chantap 720, 1303  
 Long, Carole A. 171, 183, 185, 186, 712, 973, 1457, 441  
 Long, Kanya 724, 1386, 622  
 Long, Lewis S. 586, 736, 750, 1199  
 Long, Romnie 1015  
 Long, Thavy 530, **1035**, **1451**  
 Lopera-Mesa, Tatiana M. 712, 973  
 Lopez, Ana M. 186  
 Lopez, Beatriz 485  
 Lopez, Brenda 805  
 Lopez, Beatriz 1124, 1125  
 Lopez, Gerard 485, 486, 1124, 1125, 1259  
 Lopez, Jose 1401  
 López, María Reneé 938, **626**, 1243  
 Lopez, Maria T. 1073  
 López, Pedro G. 599  
 Lopez, Roger 1246  
 Lopez, Victor 737  
 López, Yilmarsy 599  
 López Monteon, Aracely 533  
 Lopez-Urbina, Maria T. 249  
 Lopez-Urbina, Teresa 94  
 Lorenz, Lena M. **511**, 742  
 Lorenzo, Micaela A. 108  
 Lorono, Ruben 565  
 Lorono-Pino, Maria 565  
 Lotsima, Jean Pierre 639  
 Lotspeich Cole, Leda 496  
 Lou, Zhongzi 1071  
 Loua, Kovana 503  
 Louis, Christos **70**  
 Loukas, Alex 131  
 Lourenço, Tiago C. 93  
 Lourens, Chris **858**  
 Lovegrove, Maribeth 645  
 Lovejoy, Candace 103  
 Lovin, Diane D. 207  
 Lowell, Joanna 800  
 Lozada, Michelle 1258  
 Lu, Chan Woon 1454  
 Lu, Feng 665  
 Lu, Peng 505, **744**
- Luby, Stephen P. 965, 1039, 1241, 1262, 1407, 1414, 1417, 1418, 1479, 413, 773, 774, 777, 940, 775, 1056, 963, 46, 410  
 Lucantoni, Leonardo 1211  
 Lucas, Carmen M. 259, 1196  
 Lucas, John 912  
 Lucas, Keira 23  
 Lucchi, Naomi W. **854**, 843, 850  
 Luchavez, Jenny 457  
 Luciano, Jacinta 404  
 Lucke, Andrew J. 147  
 Luckhart, Shirley 218, 916, 1370, 1462  
 Ludwig, John T. 289  
 Lugo-Roman, Luis A. 259  
 Luhanga, Misheck 1472  
 Lui, James 1128  
 Luka, Madalitso 1472  
 Luke, Catherine 1011  
 Lukenge, Matthew **400**  
 Lukens, Amanda 347, 1325, **675**, 1201  
 Lukindu, Martin **1387**  
 Lukwesa, Chileshe 1045  
 Lule, John 1409  
 Lule, Swaib A. 875, 875  
 Luna, Concepción 1151  
 Luna, Giannina 237, 244, 929  
 Lund, Andrea **222**  
 Lundblom, Klara 902  
 Lungu, Chris 12, 468, 694, 1180  
 Lunze, Karsten 1477  
 Luo, Ping 1086  
 Luong, ThuLan 840  
 Lupidi, Giulio 1211  
 Lusinde, Rosemary 918  
 Lusingu, John P. A. **2**, 179, 696  
 Lust, Lydia 519  
 Lustigman, Sara 649, 1117  
 Luswata, Charles 184, 280, 1337  
 Lutomiah, Joel **211**, 412, 605, 613  
 Lutwama, Julius 566  
 Luty, Adrian J.F. 696, 697, 710, 711  
 Luy, Betty 619  
 Luyai, Anthony 761  
 Luzzatto, Lucio 435  
 Lwande, Olivia W. L. **605**, 613  
 Lwetoijera, Dickson W. **194**, 732  
 Ly, Alioune B. 550, 1466  
 Ly, Po 354  
 Lyaruu, Eugene A. 473  
 Lyaruu, Peter 836  
 Lyimo, Thomas 836  
 Lyke, Kirsten E. 5, 7, 1335  
 Lynch, Caroline 328  
 Lynch, Michael 10  
 Lynch, Michael F. 382  
 Lyon, Jeffrey 176  
 Lyons, Arthur **1089**, 1096
- Lyu, Andrew C. T. 115

## M

- Ma, Jennie 1027  
 Ma, Ming 24, 1213  
 Mabey, David 950  
 Mabunda, Samuel 1356  
 Mabuza, Aaron **162**, **1175**  
 Macallan, Derek C. 1137  
 Macareo, Louis 796  
 MacArthur, Chad 30, 1268  
 MacArthur, John R. 1473  
 Macasocol, Durinda 1082  
 MacDonald, Nicholas 1455  
 Mace, Kimberly E. **382**  
 Macete, Eusébio 1356  
 Machado, Paulo Roberto L. 813  
 Machado, Ricardo L. D. **702**  
 Machalkova, Renata 893, 895  
 Machicado, Jorge D. **125**  
 Machoe, Elias 404  
 MacInnis, Bronwyn 503, 999  
 Macintyre, Fiona 437  
 Mackay, Andrew J. 230  
 Mackenzie, Charles D. **523**, 647  
 Macleod, Annette 811  
 MacLeod, Bruce 450  
 Madanista, Mwayi 1438  
 Madrid, Cesar 603  
 Madrill, Nicole 523  
 Maffei, Joseph G. 564  
 Magak, Ng'wena G. 698  
 Magalhães, Izanelda 1305  
 Magalhaes, Ricardo J. S. 1448  
 Magán-Marchal, Noemí 681, 986  
 Maganga, Mussa 836, 843  
 Magatte, Ndiaye 1166  
 Magesa, Stephen 197, 226, **1204**  
 Maggy Ntuku, Henry 1328  
 Magill, Alan J. 164, 1272  
 Magloire, Roc 1242  
 Magnussen, Pascal 340, 341, 781, 831  
 Magtanong, Ruth V. 1445  
 Magwisha, Henry B. 473  
 Mahajan, Babita 701  
 Mahama, Emmanuel 338, 653, 654  
 Mahama, Princess R. **794**  
 Mahamar, Almahamoudou 664, 898  
 Mahanty, Siddhartha 93, 96, **97**, 1075  
 Maharaj, Payal D. 562  
 Maharaj, Rajendra 381, **690**, 1173  
 Mahdy, Mohammed A. K. **248**  
 Maher, Steven P. 438  
 Mahmud, Abdullah A. 87, 597  
 Mahmud, Rohela 248
- Mahmud, Zahid H. 777  
 Maia, Marta 742  
 Maier, Elizabeth A. 1382  
 Maiga, Assadou 223  
 Maiga, Deogratius 163  
 Maïga, Hamidou 746  
 Maiga, Oumar 782  
 Maina, Martin W. **1187**  
 Maire, Nicolas 450  
 Maiteki-Sebuguzi, Catherine **549**, 573  
 Majam, Victoria 496, 701  
 Majambere, Silas 194, 642, 732  
 Majanja, Janet 936  
 Majji, Sai 190, 715, 996  
 Makadi, Marie-Françoise 1285  
 Makazi, Patrick M. 644  
 Makepeace, Benjamin L. **1484**, 1486  
 Makio, Albina 412  
 Makori, Euniah 543  
 Makoundou, Patrick 1205  
 Malaga, Edith 1157  
 Malama, Costantine 1045  
 Malaviya, Paritosh 534, 826  
 Malboeuf, Christine M. 429  
 Malecela, Mwelecele N. **308**, 483, 642  
 Malek, M. A. 518  
 Malekani, Jean 566  
 Malekela, Erasmo **800**  
 Maleki, Monika 237  
 Malele, Imna I. **473**  
 Malheiros, Antonio F. 250  
 Malhotra, Indu **721**, 993  
 Malik, Naiela 328  
 Malima, Robert 197, 968, 1204  
 Malishee, Alpha 1358  
 Maliti, Deodatus 739, **741**  
 Malm, Keziah L. 1022, **1327**, **1354**, 401, 832  
 Malone, Joseph 1439  
 Malone, John B. 121, 812, 818  
 Malunga, Phidelis 899  
 Mamessier, Audrey 110  
 Mammen, Mammen P. 15  
 Mamo, S. 780  
 Mamova, Alexandra 791, 793  
 Mamun, Md. A 775  
 Manah, Abdul Marsudi **360**  
 Manangazira, Portia 1040, 1252  
 Mancilla-Ramírez, Javier 1152  
 Mancini, Emiliano 205, 998, 999  
 Mancuso, James **958**  
 Mand, Sabine 522  
 Manda, Hortance 737  
 Mandike, Renata 546, 800, 861  
 Mandro, Michel **768**  
 Manetsch, Roman 431  
 Manga, Akhenaton 1313, 1330  
 Mangham, Lindsay 337  
 Mangwiro, Clement 71, 76  
 Mann, Andrea 290, 896, 1360

The number(s) following author name refers to the abstract number.

- Manne, Jen **275**  
 Manneh, Jainaba 1380  
 Mannor, Kara 1425  
 Manrique, Paulo **1200**  
 Manske, Magnus 503  
 Manson, Willem L. 780  
 Mansour, Sameh S. **1106**  
 Mantel, Nathalie 630  
 Manu, Alexander 653, 654  
 Manyando, Christine **787**  
 Manzi, Fatuma 388, **1284**  
 Mao, Sivanna 985  
 Maokola, Werner 388  
 Marada, Jozef 895  
 Marcet, Paula 563, 749  
 Marchant, Tanya 1284  
 Marchetti, Elisa 1408  
 Marcinkiewicz, Cezary 1463  
 Marcombe, Sebastian **726**  
 Marcos, de Almeida E. 850  
 Marcos, Luis A 125  
 Marcsisin, Sean **840**  
 Maregeya, Emmanuel 1471  
 Marenjo, Dulcisaria 404  
 Margolis, Harold 1097  
 Marianelli, Leonardo 754  
 Marin, Silvia 887  
 Mariné, Geisi F. Mariné. 265  
 Marinotti, Osvaldo 204  
 Markotter, Wanda 566  
 Maro, Athanasia 1380  
 Maro, Venance P. 1402  
 Marquart, Louise 436, 853  
 Marra, Peter P. 1230  
 Marrone, James R. 270  
 Marris, Carl 1042  
 Marsh, Kennan 523  
 Marsh, Kevin 874, 881, 902, 1132  
 Marshall, John M. **972, 1003**  
 Marshall, Robert J. 1426  
 Martellet, Lionel **1285**  
 Mårtensson, Andreas 9, 779, 901, 988, 1306, 1316, 1322, 1351  
 Martey, Pamela 283  
 Martin, Akogbeto C. **198**  
 Martin, Coralie **40**  
 Martin, Diana **949**  
 Martin, Greg 951  
 Martin, Julie S. 1126  
 Martínez, Antonio 681  
 Martínez, Dianny 598  
 Martínez, Dalila Y. **251, 1341**  
 Martínez, Lily 575, 581, 823  
 Martinez, Luis J. 922, 1096  
 Martinez, Mara 1069  
 Martinez, Norma H. **1226, 1227**  
 Martins, Lívia C. 1103  
 Martins, Moara S. **812, 818**  
 Martins-Filho, Olindo 539  
 Martinson, Francis 368  
 Marube, Elizabeth 1343, 1440
- Marukutira, Tafireyi **652**  
 Marx, Melissa A. 1045  
 Maryada Venkata Rami, Reddy 1005  
 Marzal, Miguel 93, **1075**  
 Masanja, Irene M. **843**  
 Masanja, Mary 388  
 Masembe, Charles 216, 400, 1387  
 Maser, Pascal 475  
 Maserati, Roberta 448  
 Masiga, Daniel 211, 613  
 Maskery, Brian 1016, 1017  
 Maslen, Gareth 999  
 Mason, Carl J. 1047, 1380  
 Massaga, Julius 915  
 Massambu, Charles 844  
 Massougbdji, Achille 371, 374, 696, 697, 710, 711, 1364  
 Massung, Robert F. 594  
 Mast, Eric 410  
 Masue, Denis 197  
 Masumbe, Palmer N. 318  
 Masuoka, Penny M. 736  
 Maticchiero, Amy C. **1217**  
 Matete, Daniel O. 1432, 1434  
 Matey, Elizabeth J. 1428, 1443, 1444  
 Mathanga, Don P. 552, 830, 888, 857, 857, 1472  
 Mather, Michael W. 431, 499, 1188  
 Mathew, Anuja 102, **427**  
 Mathias, Derrick K. 167  
 Mathieu, Els 31, 34  
 Mathieu-Daude, Françoise 299  
 Mathison, Blaine A. **130, 1018**  
 Matias, Abrahan 1467  
 Matias Arnez, Abrahan 729  
 Maticchiero, Amy M. 561  
 Mátiz, Maria Ines 281  
 Matoke, Damaris **1389**  
 Matowo, Johnson 197, 968, **723**  
 Matowo, Nancy S. **396**  
 Matthews, Krista 189  
 Matthews, Stephen 877  
 Mattia, Kimberly-Anne M. **635, 926**  
 Matts, Paul J. 638  
 Matusse, Júlio 404  
 Matute, Maria Luisa 819  
 Matyi, Stephanie 202  
 Mauch, Verena 1250  
 Maude, Richard J. **548, 886, 1165, 1269**  
 Maude, Rapeephan R. 886, 1165  
 Mäusezahl, Daniel **941, 1248, 1258**  
 Maves, Ryan C. 259, 1053, 1123, 593, 1044  
 Mawejje, Henry D. **193, 1210**  
 Mawili, Denise P. 852
- Mawili-Mboumba, Denise P. 869, **1344**  
 Mawindo, Patricia 1438  
 Mawole, Johansan 891  
 Maxwell, Nikki 1409  
 May, Linda 1109  
 Mayan, Ismail 461  
 Mayanja, Harriet 719  
 Mayaud, Philippe 950  
 Mayer, Bryan T. **1281**  
 Mayieka, Lilian M. **1244**  
 Mayor, Alfredo **990**  
 Mayur, Desai M. 962  
 Mayxay, Mayfong 983, 988, 1316  
 Mazimba, Arthur 574, 1339, 1477  
 Mazitschek, Ralph 1297  
 Mbabazi, Phoebe K. **335**  
 Mbabu, Murithi R. 49  
 Mbacham, Wilfred F. 144, 318, 337, 86, 1475  
 Mbae, Cecilia K. M. **247**  
 Mbando, Donnan 308  
 Mbanefo, Evaristus C. **526**  
 Mbare, Oscar O. **1388**  
 Mbata, Geoffrey H. 473  
 Mbaye, Amicoleh 375  
 Mbenda Behalal, George 298  
 Mberu, Blessing 1360  
 Mbeye, Nyanyiwe M. **1133**  
 Mbodj, Sidiya **659**  
 Mboera, Leonard **1353**  
 Mbokazi, Frans 162, 1175  
 Mbonye, Anthony K. 340, 341  
 Mboup, Souleymane 347, 504, 1201  
 Mbulli, Innocent A. 1475  
 Mbusa, Ben 1409  
 Mbwili, Clara 165  
 McAuliffe, Isabel 129  
 Mcavin, James 1063  
 McBride, Colleen 285  
 McCabe, Colton 1193  
 McCall, Philip 194, 724, **747, 1207, 1212**  
 McCann, Robert S. **1221**  
 McCardle, Patrick W. **578**  
 McCarroll, Jennifer 121, 812, 818  
 McCarter, James 311  
 McCarthy, Florence 301  
 McCarthy, James 57, 329, 604, 612, 853, **436, 489**  
 McCarthy, William 945, 1270  
 McCarty, Kathleen M. 962  
 McChesney, James D. 679  
 McClellan, Lucy 1254  
 McCollum, Andrea 455  
 McCoy, John P. 472  
 McCracken, John 239, 485, 944, 626, **938, 1243**  
 McCracken, Michael K. **426**  
 McCulley, Nicholas 840
- McCullough, Hazel E. **1282**  
 McCunn, Maureen 286  
 McDermott, Cathy 678  
 McDonald, Mirna J. 150  
 Mcdonald, Warren 23  
 McDonnell, Joseph 604  
 McElroy, Peter 197, **695, 800, 843, 880, 890, 918**  
 McEntee, Benjamin J. 620  
 McFadde, Geoffrey I. 147  
 McGeorge, Rachael 1194  
 McGrath, Mairi A. 1006  
 McGrath, Shannon 6  
 McGready, Rose 1324  
 McKerrow, James 530, 1035  
 McKibben, Maxim J. 721  
 McManus, Donald P. 1071  
 McMillan, David 68  
 McMillan, Joseph 222, 563, **749**  
 McMorrow, Meredith **836, 843**  
 Mcneal, Monica M. 1382  
 McNulty, Nathan 1485  
 McNulty, Samantha N. **1485**  
 McReynolds, Larry A. 1113  
 Mead, Daniel G. 222, 563  
 Méda, Bertrand 956  
 Meda, Nicolas 1062  
 Medang Owono, Matthieu 1344  
 Medeiros, Daniele B. A. 119, 1103  
 Medina-Izquierdo, Juan F. 1097  
 Meek, Sylvia 398, 804, 1019  
 Meharie, Andargachew Mulu M. 419  
 Mehta, Anand 666  
 Mehta, Khanjan 289  
 Mehta, Shruti H. 16  
 Meibalan, Elamaran **666**  
 Mejia, Aurelio 1016, 1017  
 Mejia, Amelita L. 270  
 Mejia, Rojelio **488**  
 Mekasha, Addis 386  
 Mekonnen, Moges K. M. **345**  
 Melanson, Vanessa R. 618, 1148  
 Melchor, Angel 624  
 Melendez, Astrid X. T. O. 451  
 Meléndez, Marlon 1376  
 Melendez, Victor 676, 840, 841  
 Melo, Paulo S. 1098  
 Meltzer, Eyal 829  
 Melvin, Palesa 30  
 Membe, Gladys 1438  
 Memish, Ziad A. 390  
 Menacho, Silvio 825  
 Menard, Didier 457, 502  
 Mendoza, Ana Patricia 931  
 Mendoza, Guillermo 99  
 Mendoza, Patricia 640  
 Mendoza-Martinez, Cesar 1152  
 Menéndez, Clara 990, 1167  
 Menezes, Claudio 472  
 Menezes, Tais 477  
 Meng, Shi 176



The number(s) following author name refers to the abstract number.

- Meng, Zhaojing 37, 1008, 1010  
 Menk, Jeremiah 1480  
 Menon, Jayaram 946  
 Menon, Mahesh **268**  
 Mens, Petra F. 326  
 Mensah, David Y. **832**  
 Mensah, George T. **767**  
 Mensah, Jubin 519  
 Menten, Joris 534  
 Mentré, France 868  
 Meral Esen, Meral 703  
 Mercer, Luke 1147  
 Mercereau-Puijalon, Odile 502  
 Mero, Chacha 197  
 Meschino, Steve 1015  
 Mesele, Tamiru 387  
 Mesfin, Nebiyu 235  
 Meshnick, Steven R. 365, 368, 391, 689, 689, 889, 600, 609, 615  
 Mesirov, Jill 1421  
 Messenger, Louisa A. **729, 981**  
 Messer, William B. **116**  
 Messina, Jane P. 21, 391  
 Messina, Joseph P. 1221  
 Mestra, Laureano **309, 1138**  
 Metcalf, Jessica 863, 863, 1023, 933  
 Metenou, Simon **37, 97**  
 Metta, Emmy 332  
 Mey, Sitech 282  
 Meymandi, Sheba K. 817  
 Meza, Ericka 1200  
 Meza, Rina A. 589, 85, 1044  
 Mgohamwende, Fidelis 844, 846  
 Mharakurwa, Sungano **1464**  
 Mich, Vann 241  
 Michael, E. 308  
 Michel, Kristin 26, **751, 1363**  
 Michelin, Ruel **611**  
 Michels, Meta **106, 430**  
 Michuki, George 605, 613  
 Mickum, Megan L. 761  
 Middaugh, Russell C. 1034  
 Midega, Janet T. 881  
 Miguel, Sanjoaquin 362  
 Mihoko, Kikuchi 168  
 Mika, Angela 68, 602  
 Mikhail, Amy 461  
 Mikhailov, Alexei 120  
 Mikolasova, Gertruda 791  
 Mikoleit, Matthew 1039, 1409  
 Mikolon, Andrea 1039, 1056  
 Mikulasova, Petra 893  
 Miles, Melody 314, 884, 892, **1439**  
 Miles, Michael A. 474, 981  
 Milhous, Wilbur K. 1091, 431  
 Miller, Asia 1478  
 Miller, Ann K. 150, 435  
 Miller, Barry 51, 566  
 Miller, Brad 1161  
 Miller, John M. 12, 468, 694, 1180, 165, 1340  
 Miller, Lori 176  
 Miller, Louis H. 185  
 Miller, Melanie 1128  
 Miller, Nancy E. 38  
 Miller, Nathan 729  
 Miller, Robert 894  
 Miller, Tom 582  
 Miller, W. Allen 1105  
 Milligan, Paul 349, 547, 693, 1313, 1330, 1342, 1436  
 Millogo, Athanase 447  
 Mills, Stephen 807  
 Mills-Robertson, Felix C. **590**  
 Milman, Jessica 178  
 Milner, Dan 347, 504, 1421  
 Milner, Erin 676  
 Milord, Marie Denise 645  
 Minakawa, Noboru 917, 378  
 Minaya, Percy 1249  
 Minior, Thomas 291, 572  
 Minja, Jubilate 197  
 Mintz, Eric 47, 513, 514, 515, 1045, 1409, 1411, 961, 1040, 1252  
 Miranda, Aracelis **1160**  
 Miranda, José C. 821  
 Miranda, MariLynn 1353  
 Miranda, Maria C. 1012  
 Mireji, Paul 211  
 Mirembe, Florence 876  
 Miri, Emmanuel 1346  
 Misiani, Eunice 162, 1173, 1175  
 Misikova, Eva 895  
 Missé, Dorothee 213  
 Mita-Mendoza, Neida K. **973**  
 Mitchell, Sara N. 554  
 Mitprasat, Mashamon 1303  
 Mitraka, Elvira 70  
 Mitre, Edward 648, 1004, 1007  
 Mitreva, Makedonka 1485  
 Miura, Kazutoyo 171, **183, 185, 1456, 1457**  
 Mizero, Liévin 1471  
 Mkoba, Clarence **332**  
 Mkocho, Harran 592  
 Mkude, Sigsbert 846  
 Mobegi, Victor A. **503**  
 Mochly-Rosen, Daria 1142  
 Modak, Joyanta K. 87, 597, 1407  
 Modi, Radhika 1192  
 Modiano, David 510  
 Modrek, Sepideh 342  
 Moebius, Jacqueline 280  
 Moehrl, Joerg 436, 437  
 Moeker, Janina 145  
 Mogsale, Vittal **1017**  
 Moguel, Barbara B. **98, 99**  
 Mohamadou, Siribie **13**  
 Mohamed, Abdinoor H. **1481**  
 Mohamed, Hanan 647  
 Mohamed, Mahdi R. 1204  
 Mohammed, Hamish 1372  
 Mohammed, Khalifa 1436  
 Mohammed, Khalfan A. 35, 1446  
 Mohammed, Nader 461  
 Mohandas, Naria 1171  
 Mohareb, Emad W. 245, 934, 1106, 1237  
 Mohasin, M. 42, 45  
 Mohler, James P. 1386  
 Mohlin, Frida 602  
 Mohon, Abu Naser 210  
 Mohr, Sharif 451  
 Möhrle, Jörg 435  
 Moi, Meng Ling **1392**  
 Moir, Juan Carlos 938  
 Moiroux, Nicolas 213, **971, 1364**  
 Mok, Sachel **983**  
 Moke, Fenny 961  
 Mølbak, Kåre 516  
 Molden, Todd 1214  
 Molestina, Robert E. **261**  
 Molina-Cruz, Alvaro **997**  
 Molla, Yordanos B. M. **274**  
 Molten, Fabrizio 197  
 Molteni, Fabrizio **546, 695, 890, 918**  
 Molyneaux, Neil D. 1098  
 Molyneux, Gemma **1112**  
 Molyneux, Malcolm E. 365, 708  
 Mombouli, Jean 455  
 Mondal, Dinesh 1026  
 Monkanna, Taweesak 578  
 Monroy, Eric 82  
 Montagu, Dominic 342  
 Montalvo, Raul 1401  
 Montano, Silvia 446, 1094, 1413, 1373  
 Montell, Craig 1371  
 Montenegro, Sonia 1400  
 Montgomery, Joel M. 237, 244, 456, 486, 931, 942, 953, 1259, 271, 588  
 Montgomery, Scott 902  
 Montgomery, Susan P. 1428, 1432, 1434, 1443, 1444  
 Monti, Feliciano 1467  
 Montomoli, Emanuele 1408  
 Moody, M. Anthony 632  
 Moon, James E. 4  
 Moonasar, Devanand 162, **1173, 1175**  
 Moonga, Hawela 12, 468, 694, 1340  
 Moore, Anne 1009, 1116  
 Moore, Christopher C. 267  
 Moore, Jason 742  
 Moore, Julie M. 991  
 Moore, Marnijina **306**  
 Moore, Sarah 742  
 Moore, Sarah J. 910  
 Moore, Sean R. 517, **1382, 1049**  
 Moore, Vanessa 36  
 Moormann, Ann 497, 700  
 Moorthy, Vasee S. 5  
 Mora, Eric 1100  
 Moraleda, Cinta 1167  
 Morales, Maria Luisa 244, 942  
 Morales, Sandra S. **928**  
 Morales Ruiz, Sandra S. **420**  
 Morales-Fernandez, Maria L. **237**  
 Mordmüller, Benjamin 703, 709  
 Moreira, Andres 607  
 Moreira, Wilfried 538  
 Morel, Marion 980, 1451  
 Moreno, Laura 1073  
 Moreno, Norma A. 98  
 Mores, Christopher N. 426, 428  
 Moretz, Samuel E. 183, 1457  
 Morgan, Douglas R. 1376  
 Morgan, Juliette 1018, 1356, 404  
 Morgan, Sian 1208  
 Mori, Akio 206, **207**  
 Mori, Nicanor **1373**  
 Morimoto, Konosuke 246  
 Morin, Merribeth 183  
 Moritz, Mark 960  
 Moriuchi, Hiroyuki 246  
 Morlais, Isabelle 167  
 Morris, Alexandra 1345  
 Morris, C. Paul **1004**  
 Morris, Sheldon 175, 496  
 Morris, Ulrika **901, 1306**  
 Morris-Jones, Steve 1251  
 Morrissey, Joanne M. 431, 499, 1188  
 Morrison, Amy C. 18, 112, 418, 622, 728, 1222, 1386, 724, 737  
 Morrison, Robert 541  
 Morrissey, Anne B. 1402  
 Mortensen, Deborah S. **152, 1114, 1147**  
 Mortimer, Peter S. 638  
 Morton, Lindsay 989  
 Moscoso, Fabiola 938, 1243  
 Moseley, Pope 706  
 Moses, Cynthia 455  
 Moses, Lina M. 48  
 Mosha, Franklin W. 8, 968, 197, 226  
 Mosha, Jacklin F. **545**  
 Mosher, Aryn W. 1268, 1271  
 Mossel, Eric C. 1377  
 Mosser, David 477  
 Mota, Diogenes C. 1420  
 Mota, Rosa M. S. 517  
 Motta, Amarilis 626  
 Mouchet, François 213  
 Moudy, Robin M. **199, 1386**  
 Moulia, Catherine 40  
 Moulton, Lawrence H. 240  
 Mounsey, Kate **57, 612**  
 Mourão, Marina M. **762**  
 Moureau, Gregory 587

The number(s) following author name refers to the abstract number.

- Moussa, Kone 344  
 Moussa, Sadi 84  
 Moussiliou, Azizath 1364  
 Moutairou, Kabirou 697, 710, 711  
 Moyano, Luz M. **446**, 1072, **1078**  
 Moyes, Catherine L. 21  
 Mpabuka, Etienne **655**  
 Mpairwe, Harriet 875, 875  
 Mpamba, Chipo 574  
 Mpeka, Betty 1020  
 Mpimbaza, Arthur 314, **892**, 1439  
 Mremi, Irene 308, 483  
 Mrisho, Mwifadhi 388  
 Msangi, Shandala 197  
 Msellem, Mwinyi I. 880, 890, 901, 695  
 Mshinda, Hassan 388  
 Mtapuri-Zinyowera, Sekesai 1040  
 Mtshali, Andile 1278  
 Mu, Jianbing 185, 982  
 Mubi, Marycellina 1306  
 Mubiru, Denis 1409  
 Mubiru, James N. 1146, 1143  
 Muchiri, Eric 50, 423, 721, 1445  
 Muchiri, Geoffrey 1443  
 Mudenda, Ntombi **121**  
 Muehlenbachs, Atis 463, 1307, **1309**  
 Muehlenbein, Michael P. 670  
 Mueller, Ellen 1490  
 Mugalura, Frances 546  
 Muggaga, Olive 462, 553  
 Mugri, Regina 136  
 Mugumbate, Grace **397**  
 Muhangi, Lawrence 875, 875  
 Muhindo, Mary 540  
 Muhoho, Ng'ethe 1445  
 Muiruri, Samuel 50, 423  
 Mukabana, Richard W. 450  
 Mukabana, Wolfgang R. 909  
 Mukabayire, O. 655  
 Mukabayire, Odette 789  
 Mukadam, Rabia 857, 1438  
 Mukantwali, E. 655  
 Mukarugwiro, Beata 1350  
 Mukerabirori, Aline 1471  
 Mukhopadhyay, Amitava 467, 920  
 Mukoko, Dunstan A. 644  
 Mukunzi, Silvanos 936  
 Mukwaya, Louis 216, 400, 1387  
 Mulabya, Fred 1409  
 Mulder, C.E.G. 729  
 Mulenga, Modest 899  
 Mulenga, Musapa 1390  
 Mulet, Teresa 681, 986  
 Mulholland, Eddie 604  
 Muli, John M. 891  
 Mulindahabi, Monique 10  
 Muller, Gunter C. 972  
 Müller, María Luisa 938  
 Mulondo, Jerry 463, 1307  
 Mulrooney, Carol 675  
 Mulwa, Francis 605, 606  
 Mumba, Peter 73  
 Mumbengegwi, Davis R. 315, 674, **809**  
 Munde, Elly **1183**, 1184  
 Mungai, Peter 721, 992, 993, 1445  
 Mungofa, Stanley 1040, 1252  
 Munoz, Beatriz 592  
 Munoz, Benito 675  
 Muñoz, Fredy 485, 1124, 1125  
 Munoz, Jorge 1397  
 Munoz-Jordan, Jorge 1097  
 Munyua, Peninah M. **49**  
 Murangi, Amos 1409  
 Murata, Eri 498  
 Muratova, Olga 184, 223, 1455  
 Murithi, Rees 613  
 Murphy, Jittawadee 178, 1463, 4, 1199  
 Murphy, Robert L. 657  
 Murphy, Sean C. 187  
 Murphy, Trudy 410  
 Murray, Hugh 57  
 Murugasampillay, Sivakumaran 695  
 Murungi, Linda 902  
 Musabyimana, J.p. 655  
 Musenga, Erick 1045  
 Mushayi, Wellington 1252  
 Musila, Lillian 412  
 Muskavitch, Marc A. 753, 1216, 1210  
 Musonera, F. 655  
 Mussa, Abdul 1356  
 Mutapi, Francisca **1036**  
 Muth, Sinuon 889  
 Mutisya, James 412, 605  
 Mutka, Tina S. 431  
 Mutuku, Francis M. 1445  
 Muvunyi, Zuberi 894  
 Muzari, Odwell 731  
 Mvalo, Tisungane 368  
 Mwabulanga, Adam 894  
 Mwaengo, D. 655  
 Mwandama, Dyson A. **350**, 552, 830, 888  
 Mwangelwa, Boyd 574  
 Mwangungulu, Stephen P. **692**  
 Mwangwa, Florence 316, 372  
 Mwanyika, Henry 450  
 Mwanza, Mercie 165  
 Mwanza Ingwe, Mercy 1340  
 Mwatele, Cassian 644  
 Mwesigwa, Savannah A. **1154**  
 Mweya, Clement 197  
 Mwingira, Upendo J. 308, **483**, 303, **642**  
 Mwinula, Juma 894  
 Mwinzi, Pauline N. M. 1428, 1432, 1434, 1442, **1443**, 1444  
 Mwita, Alex 546  
 Mychalecky, Josyf 1026  
 Myers, Bennett Myers 495  
 Mzungu, Elton 993  


---

**N**  
 N'Fale, Sagnon 912  
 N'Guessan, Tiacoh L. 344  
 N'Goran, Eliézer K. 1447  
 Na-Bangchang, Kesara 158  
 Nabirye, Christine 803  
 Nadler, Steven A. 1462  
 Naeyer, Luke 1248  
 Nafuka, Sylvia N. **674**  
 Nagarkatti, Rana **539**  
 Nahum, Laila A. 762  
 Nair, Shalini **1169**, 1324  
 Najnin, Nusrat 1418  
 Nakalembe, Miriam 1307, 1309  
 Nakanjako, Damalie 1020  
 Nakaya, Helder I. 529  
 Nakayiki, Teddie 566  
 Nakazibwe, Christine 987  
 Nakeleme, Miriam **463**  
 Nakhasi, Hira L. 472, 783, 979, 1452  
 Namamba, Jabir 861  
 Nambozi, Michael **899**  
 Namulanda, Victor 891  
 Namusoke, Fatuma **876**  
 Nanayakkara, NP D. 433, 682  
 Nani Mudin, Rose 634  
 Naniima, Peter 759  
 Nankabirwa, Joaniter I. **379**  
 Nankya, Florence 549, 573  
 Naquira, Cesar G. 1068  
 Narahari, S R. 638  
 Naranjo, Nelson J. **218**  
 Narayanan, Jothikumar 854  
 Nare, Bakela 1147  
 Nartey, Alexander A. A. **571**  
 Narum, David L. 185, 1455  
 Naser, Abu M. 773  
 Nash, Theodore E. 93, 97, **445**, 1075  
 Nasidi, Abdussalam 1375  
 Nasirova, Emilyya 922  
 Nasr, Nabil N. 248  
 Nasr, Sussann 314, 462, 553, 879, 892, 1439  
 Nasreen, Sharifa 1479  
 Nasrin, Dilruba 513, 514, 515, 961  
 Nassirou, Baido 29  
 Natamba, Barnabas 372  
 Natarajan, Gayathri **1452**  
 Nataro, James P. 513, 515, 961, 514  
 Naulikha, Jackie 660  
 Naumov, Anatoli 438  
 Naumova, Elena 1031  
 Naushin, Tania 774  
 Navarrete-Perea, Jose **99**  
 Nawrocki, Lauren D. 258  
 Nayiga, Susan **803**  
 Nchimbi, Happy 11, 334, **460**  
 Ndao, Momar 109, 756  
 Ndayiragije, Diane 1471  
 Ndege, Chacha 1204  
 Ndegwa, Linus 1244  
 Ndi, Andre 136  
 Ndiath, Mansour 1330  
 Ndiath, Mahamadou M. **294**  
 Ndiath, Mamadou O. **970**  
 Ndiath, Ousmane M. 225  
 Ndiaye, Daouda **77**, **255**, 346, 347, 504, 712, 1201  
 Ndiaye, Jean-Louis 550, 779, 255, 346, **1313**, 1330, 1342, 1351, **547**, 77, 294, 781, 349  
 Ndiaye, Magatte **346**  
 Ndiaye, Mouhamadou 347, 77, 255  
 Ndiaye, Magatte 349, 547, 781, 864  
 Ndiaye, Maguette 1313  
 Ndiaye, Mouhamed 1330, **1342**  
 Ndiaye, Yaye Die 255, 347  
 Ndiaye, Youssooupha 547, 1313, **1330**  
 Ndiabazza, Juliet **875**, **875**  
 Ndiop, Medoune 919  
 Ndir, Omar 77, 255, 347  
 Ndive, Sarah N. 337  
 Ndjo'oh, Joseph 298  
 Ndombi, Eric M. 1033  
 Ndong, Ignatius C. 337  
 Ndour, Cheikh T. 781  
 Nduati, Eunice W. **1132**  
 Nduba, Videlis N. 952  
 Ndula, Miranda 969  
 Ndumbe, Peter M. 380  
 Ndungu, Francis M. **874**  
 Ndyomugenyi, Richard 340, 341  
 Neafsey, Daniel E. 1201, 1210, 1422, 188  
 Neatherlin, John 456, 486  
 Nébié, Issa 467, 1331  
 Neesanant, Pimnapar 1380  
 Negash, Kassahun 908  
 Negrete, Erasmo 82  
 Negri, Vanesa 1151  
 Negroustoueva, Svetlana 393  
 Nelson, Kara L. 959  
 Nelson, Randall 60  
 Nene, Vish 613, 1030  
 Nerima, Barbara 475  
 Nerurkar, Vivek R. 117  
 Newbold, Chris 441  
 Newby, Gretchen 684

The number(s) following author name refers to the abstract number.

- Newman, Robert 10  
 Newmann, Mercy 81  
 Newton, Paul N. 328, 983, 988, 1316, 1412  
 Newton, Sam 338  
 Ng, Jun Li 110  
 Ng'ang'a, Zipporah 925, 1244  
 Nga, Cao T. P. 637  
 Ngabo, Fidele 10  
 Nganga-Wanjiku, Lucy 953  
 Ngasala, Billy E. 1306, 1322, 861  
 Nge, Nabi 363  
 Ngigi, Julius 1300  
 Ngigi, Margaret 52  
 Ngilangwa, David P. 890  
 Ngondi, Jeremiah 1346  
 Ngongang, Eric O. 318  
 Ngongo, Ngashi 1333  
 Nguah, Samuel B. 1314  
 Nguetta, Simon-Pierre A. 351  
 Nguku, Patrick M. 1051, 1375  
 Nguon, Chea 354  
 Nguyen, Chilinh 1002  
 Nguyen, Jennifer 1209  
 Nguyen, Lien Thi Kim 580  
 Nguyen, Megan 905, 905  
 Nguyen, Quang N. 807  
 Nguyen, Sara A. 491  
 Nguyen, Tien K. T. 807  
 Nguyen, Vu 181  
 Ngwa, Alfred 375  
 Nhabomba, Augusto 1167  
 Ni, Jinfei 1371  
 Ni, Xingwei 1071  
 Niang, Abdoulaye 746  
 Niangaly, Amadou 7, 1335  
 Niangaly, Moussa 336  
 Nichol, Stuart 51, 1381  
 Nicholson, Sarah C. 1033  
 Nicholson, William N. 609  
 Nicolas, Violaine 53  
 Nicoletti, Alessandra 1077  
 Nicosia, Alfredo 1456  
 Nielsen, Carrie 884, 1439, 879  
 Nielsen, Tyler J. 258  
 Nieto, Javier 945  
 Nieto, Melissa 945  
 Nieto Sosa, Liliana 754  
 Nieto-Sanchez, Claudia P. 824  
 Niezgodna, Michael 271, 566  
 Nigo, Maurice M. 639  
 Nikiema, Rosalie 869  
 Niles, Jacquin C. 442  
 Nilles, Eric 1411  
 Nilsen, Aaron 431, 834, 834  
 Nimbura, Marc 894  
 Nimmannitya, Suchitra 1082  
 Nimmo, Derric 1208  
 Nimri, Laila F. 232  
 Ninsiima, Boaz 462, 553  
 Nisalak, Ananda 15, 1093  
 Nisalak, Ananda 104, 1082, 102  
 Nishimura, Sei 369  
 Nizame, Md. Fosiul A. 963, 1417  
 Njagi, Kiambo 544  
 Njagi, Leonard M. 417  
 Njau, Joseph D. 1473, 1476  
 Njau, Ritha 800, 861  
 Njenga, M. Kariuki 271, 943, 49, 273  
 Njenga, Sammy 486, 644, 1259  
 Nji, Akindeh M. 1475  
 Njie, Fanta 1436  
 Njiri, James 936  
 Njogu, Julius 1360  
 Njua, Clarisse 136  
 Njuabe, Theresia M. 337  
 Njuguna, Henry 953  
 Njuguna, Patricia 1  
 Njunda, Anna L. 380  
 Nkanga, Mayen 1277, 1289  
 Nkhoma, Standwell 1169, 1324  
 Nkimberg, Manka 1339, 1477  
 Nkonwa, Inocent 791, 893  
 Nkrumah, Francis 1332  
 Nkwocha, Omeni 1359  
 Noedl, Harald 367, 988, 1316  
 Noh, Jinhyeong 580  
 Noh, John C. 96  
 Noisakran, Sansanee 628  
 Nokes, James N. 247  
 Nokes, Nokes 1244  
 Noland, Gregory 1346  
 Noor, Abdissalan 838, 1360, 881  
 Noordin, Rahmah 310  
 Norgan, Andrew P. 851  
 Norris, Douglas E. 210, 585  
 Nosten, François 983, 988, 1169, 1316, 1324, 435  
 Nouatin, Odilon Paterne 710, 697, 711  
 Noukpo, Herbert 213  
 Nour El-Din, El-Shaimaa M. 69  
 Novotny, Joe 166, 469  
 Nsanzabana, Christian 355  
 Nseng, Gloria 1467  
 Nshala, Andreas 303, 308, 483  
 Nsobya, Samuel L. 987  
 Nsoh, Maxwell 338  
 Ntale, Muhammad 876  
 Nuckols, John T. 1228  
 Nunes, Keley 932  
 Nunes, Kelley N. B. 119  
 Nunes, Marcio Roberto T. 932, 119, 1103  
 Nuñez, Andrea 429  
 Nuñez, Jorge 259, 640  
 Nuramo, Adamu Addissie 287  
 Nurudeen, Ikumapayi U. 1419  
 Nuruzzaman, Md. 963  
 Nussenzweig, Victor 133  
 Nutman, Thomas B. 36, 37, 39, 242, 304, 478, 488, 492, 740, 782, 1008, 1010, 1110  
 Nwadike, Jones 1277, 1289  
 Nwakanma, Davis 369, 375, 503, 205  
 Nwankwo, Lawrence 1359  
 Nwobi, Benjamin 34  
 Nyachieo, Dhillon 456, 953  
 Nyaga, Victoria 902  
 Nyaku, Mawuli 31, 34  
 Nyakundi, Ruth 993  
 Nyambura, Janet 936  
 Nyandigisi, Andrew 838, 878  
 Nyawira, Rose 936  
 Nyemazi, Jean Pierre 10  
 Nygren, Benjamin 47, 961, 1416  
 Nyingilili, Hamisi S. 473  
 Nyirenda, Oswald 857, 857  
 Nzamba, Joseph 1344  
 Nzangwa, Timothy 1311
- ## O
- 
- O'Brien, Connor 1321  
 O'Connell, Kathryn 1021, 1299, 1300, 1360  
 O'Meara, Wendy P. 1343  
 O'Neil, Mike 434, 683  
 O'Neill, Paul M. 1115  
 O'Reilly, Ciara E. 513, 961, 514, 515  
 O'Rourke, Peter 436  
 O'Brien, Jack 503  
 O'Donoghue, Peter 1453  
 O'Neil, Gregory 467  
 Oakgrove, Khouchy S. 1189  
 Oakley, Miranda S. 496, 701  
 Obanda, Vincent 605, 613  
 Obare, Peter 847  
 Obed, Samuel 256  
 Obeng, Benedicta B. 1109  
 Oberhelman, Richard A. 1400  
 Obi, Larry 1261  
 Obidike, Ifeoma C. 146, 233  
 Obiri, Dorotheah 288  
 Obonyo, Charles 839  
 Obuobi, Frank 590  
 Ocaña, Victor 415  
 Ochiai, R. Leon 1061  
 Ochieng, Benjamin 513, 514, 515  
 Ochieng, Caroline A. O. 100, 412  
 Ochieng', Melvin 567  
 Ochoa, Theresa J. 806, 1258, 1482  
 Ochola, Elizabeth A. 1432, 1434, 1428  
 Ochola, Lyticia 698  
 Ocholla, Harold 1190  
 Ocholla, Steven 936  
 Ochomo, Eric O. 200  
 Ockenhouse, Christian F. 4, 5, 174, 716, 1308, 176, 177, 1459  
 Odegaard, Justin 975  
 Odek, Willis 572  
 Odero, Chris 1468  
 Odero, Kennedy 486, 1259  
 Odhiambo, Frank 453, 1403  
 Odhiambo, Gladys O. 1442  
 Odiere, Maurice R. 1442  
 Odongo, Wycliffe 543, 1343  
 Odonkor, Gabriel 571  
 Oduro, Albert 543, 1440  
 Oduro, Abraham R. 1162, 1196, 1332  
 Oduru, Gloria 875, 875  
 Odusami, Oluwakemi 621  
 Oelschlaeger, Stephan 414  
 Oesterholt, Mayke 696  
 Offianan, André T. 864  
 Offouga, Laetitia C. M. 852  
 Ofoefule, Sabinus 233  
 Ofori, Micheal F. 170  
 Ofori-Anyinam, Akua B. 80  
 Ofula, Victor O. 421  
 Ogada, Edna 902  
 Ogange, Lorraine 1260  
 Ogbole, Omonike O. 408  
 Ogola, Eric 271  
 Ogolla, Sidney 411  
 Ogonda, Lilian 1183  
 Oguike, Mary C. 1202  
 Ogutu, Bernhards 176, 467, 839, 847, 920  
 Oh, Taek kyu 855  
 Ohashi, Kazunori 201  
 Ohrt, Colin 433, 434, 682, 837, 840, 841, 844, 845, 846, 164  
 Ohta, Nobuo 792  
 Ojeda, Sergio 1246  
 Ojikutu, Bisola 291, 572, 1131  
 Ojo, Tolulope 1224  
 Okafor, Henrietta U. 787  
 Okal, Michael N. G. 217  
 Okany, Charles 1141  
 Okebe, Joseph 369, 375  
 Okechukwu, Emeka 1131  
 Okedi, Loyce M. 820, 1210  
 Okello, Grace 501  
 Oketch, Samuel 271  
 Okeyo, Winnie A. 1183, 1184  
 Okhamafe, Augustine O. 326  
 Okiring, Jaffer 372, 987  
 Okoh, Chukwuyem 160  
 Okorofo, Iheanyichi 1346  
 Okoth, Edward 1444  
 Okoth, George 953  
 Okudo, Charles 859  
 Okuma, Peter O. 947  
 Okumu, Fredros O. 396, 910  
 Okumu, Wilson 1183, 1184  
 Olack, Beatrice 953  
 Oladejo, John 1375  
 Oladepo, Oladimeji 342  
 Olang, George 1468  
 Olang, Evelyn A. 909  
 Olano, Victor Alberto 281

The number(s) following author name refers to the abstract number.

- Olaya, Sandra 446  
 Olayemi, Sunday 1141  
 Oliveira, Ana Cecilia A. Xavier. 718  
 Oliveira, Guilherme 529, 762  
 Oliveira, Jefferson S. O. 1049  
 Oliver, Ericka 867  
 Oliver, JoAnne 564  
 Olkowski, Sandra 622  
 Olliaro, Piero L. 779, 900, 1351, 324  
 Olotu, Ally 177, 179  
 Olson, Ken E. 204, 937, 1377  
 Olsson, Daniel 902  
 Omalu, Innocent C. J.. 1140  
 Omar, Abdiasis 390  
 Omballa, Victor 567, 943  
 Ombok, Maurice 961, 1221, 1468  
 Omemo, Peter 271  
 Omer, Rihab A. 1064  
 Omer, Samia A. 1144  
 Omolo, Jared 273  
 Omondi, Angela 859  
 Omondi, David 211  
 Omere, Richard 513, 514, 515, 961  
 Onapa, Ambrose W. 520  
 Ondari, Daniel 456  
 Ondigo, Bartholomew 698  
 ONeal, Seth E. 1072, 1078  
 Ong, Weibin 560  
 Ong'echa, John 501, 705, 706, 707, 797, 957, 1191, 1192, 1193, 839  
 Ongoiba, Aissata 280, 389  
 Ongus, Juliette 421, 943  
 Onsrud, Mathias 1279  
 Onwuchekwa, Uma 1059, 1060  
 Onwujekwe, Obinna 827  
 Onwujekwe, Ogochukwu 827  
 Onyango, Clayton 1244  
 Onyango, Kevin O. 839  
 Onyango, Wycliffe 1440  
 Onyeabor, Onyekachi S. 384, 385  
 Onyia, Mgbodichi 1359  
 Ooi, Eng Eong 115, 424  
 Opara, Gift 1359  
 Opere, Christiana 590  
 Operario, Darwin J. 1380  
 Opisa, Selpha 1442  
 Opiyo, Elizabeth 820  
 Opoka, Robert O. 542, 1336, 717, 1276  
 Opot, Benjamin 936  
 Oppong, Samuel 401, 1022  
 Orandle, Marlene 1423  
 Orang-Ojong, Barnabas B. 337  
 Ord, Rosalynn L. 667  
 Ordoñez, Luis 108  
 Oremo, Jared 1416  
 Oren, Deena 1461  
 Orenstein, Evan W. 236, 1288  
 Orenstein, Lauren A. V. 236, 1288  
 Oresanya, Olusola 1346  
 Oriá, Reinaldo B. 517  
 Oriango, Robin 752, 1385, 1440  
 Oriero, Eniyoun 375  
 Orimba, Vincent 453  
 Orinda, George 1183, 1184, 705  
 Orinde, Austine B. 273  
 Orish, Verner N. 384, 385  
 Orji, Bright C. 1277, 1289  
 Orozco, Marcela 816, 822  
 Orr, John M. 585  
 Orr, Steven B. 115  
 Orr-Gonzalez, Sachy 1423  
 Ortega, Corrie 997  
 Ortega, Ynes R. 1265  
 Ortiz, Ernesto 237, 244, 942  
 Ortiz, Jose 938  
 Osada, Yoshio 526  
 Osarfo, Joseph 831  
 Oscar, Oscar 1273  
 Osei, Isaac 1273  
 Osei, Joseph H. N. 256  
 Osei-Akoto, Alex Y. 802  
 Osei-Atweneboana, Mike Y. 479  
 Osei-Kwasi, Mubarak 414  
 Oser, Rebecca C. 572  
 Osier, Faith 902, 994  
 Osilo, Emmanuel 540  
 Osorio, Jorge E. 619, 1013, 1014, 1378, 629, 1016, 1017, 1083  
 Osta, Mike A. 27  
 Osterbauer, Beth 316, 372  
 Osuna, Finnley 936  
 Otchere, Joseph 491  
 Oteng, Eugene K. 441  
 Othieno, Lucas 549  
 Otiende, Mark 881  
 Otieno, Eric 501  
 Otieno, Godfrey Allan 176, 839  
 Otieno, Kephas 1437  
 Otieno, Lucas 176, 839  
 Otieno, Michael 705  
 Otieno, Peter 1468  
 Otieno, Ronald 1416  
 Otieno, Walter 176  
 Otolorin, Emmanuel 1277, 1289  
 Otozi, Rita 1359  
 Otsuka, Yasushi 229  
 Otsyula, Nekoye N. 176, 179  
 Ott, Amy C. 1163  
 Ottesen, Eric 1038, 1448, 483  
 Ottomassathien, Darren 1275  
 Ouattara, Amed 7  
 Ouattara, Aminata 463, 1307  
 Ouédraogo, Amidou 467  
 Ouédraogo, Alphonse 467, 920, 1331  
 Ouedraogo, André Lin 1177, 1331  
 Ouédraogo, Adja M. 956  
 Ouedraogo, Esperance 1331  
 Ouedraogo, Gautier H. W. 292  
 Ouédraogo, Jean-Bosco 447, 463, 1211, 1307, 1458  
 Ouédraogo, Macaire S. 377  
 Ouédraogo, Robert K. 1211  
 Ouédraogo, Smaïla 371, 374  
 Ouedraogo/Nikiema, Leatitia 292  
 Ouellette, Marc 538  
 Oullo, David 224  
 Ouma, Collins 200, 1183, 1184  
 Ouma, Caroline 1409  
 Ouma, Peter 1403, 1437  
 Oumar, Gaye 1166  
 Oumbouke, Welbeck A. 196  
 Oundo, Joseph 515, 925, 421, 513, 514, 943, 1244  
 Ovalle Bracho, Clemencia E. 1159  
 Overgaard, Hans J. 281, 786, 1256, 1263, 1334  
 Oviedo, Yisela 1253  
 Owaga, Chrispin 543, 752, 1343, 1385, 1440  
 Owens, Lauren 1339, 1477  
 Owino, Martin O. 1444  
 Owino, Simon O. 991  
 Owston, Michael 1143  
 Owuor, Mercy 1260  
 Owusu-Agyei, Seth 179, 338, 653, 654, 847, 1327  
 Oyegbami, Banji 134  
 Oyibo, Wellington 1307  
 Oyieke, Florence 191  
 Oyugi, Jessica 1472  
 Ozaki, Masayo 1346, 1359
- P**
- P, Shinta 1219  
 Pablo Martinez de Salazar, Pablo 703  
 Pacheco, M. Andreina 669, 670, 671, 1197  
 Pacheco-Yepepe, Judith 252, 254  
 Padilla, Beatriz 1258  
 Padilla, Norma 391  
 Padmanabha, Harish 20  
 Padte, Neal 1461  
 Paes, Cheryl 926  
 Page, Wendy 604  
 Paintain, Lucy Smith. 1333  
 Paintsil, Elijah 276  
 Pajuelo, Monica 1081  
 Pakpour, Nazzy 1462  
 Pakuta, Elizabeth 455  
 Palacios, Gustavo 1103  
 Palermo, Pedro M. 227  
 Palma, Sandra P. 89  
 Palmer, Carolyn G. 1261  
 Palmer, Stephanie L. 1268, 1271  
 Pamen-Ngako, Joelle 337  
 Pan, William 1079  
 Panchalingam, Sandra 513, 514, 515, 925, 961  
 Pande, James 957  
 Pandit, Jayesh 838, 878  
 Panella, Nick 566  
 Paniagua, Gloria Luz 82  
 Panyanivong, Phonepasing 1412  
 Paolino, Kristopher 4  
 Papadi, Bhavesh 130  
 Paphavee, Lertsethtakarn 1380  
 Paploski, Igor A. D. 19  
 Paraiso, Noel 1439  
 Parameswaran, Poornima 429  
 Paranjape, Gandhali 1408  
 Paredes, Adriana 93, 1075  
 Paredes, Antonio 938, 1243  
 Paredes, Maribel 887  
 Paris, Daniel H. 1412  
 Park, Daniel J. 984, 1201, 504  
 Park, Gregory S. 331  
 Park, Mi Yeoun 1235, 1236  
 Parker, Daniel 877  
 Parker, Josephine 1212  
 Parker, Zahra 621  
 Parobek, Christian M. 364  
 Parr, Jason 369  
 Parra, Marcela 175  
 Parshuku, Joyce P. 691  
 Parsons, Michele 514, 1040, 513, 515  
 Partidos, Charalambos D. 619, 629, 1013, 1014, 1083, 1378  
 Parveen, Shahana 963, 1056, 1241  
 Pasay, Cielo 57, 612  
 Pascual, Aurélie 153  
 Paskova, Lucia 895  
 Passos, Luzia Márcia R. 1095  
 Passos, Sara T. 477  
 Patel, Akruiti 1114  
 Patel, Apurva K. 150  
 Patel, Dipali 1463  
 Patel, Jaymin C. 357, 391, 485, 1124, 1125  
 Patel, Minal 410  
 Patel, Roopal 906, 906  
 Patel, Sunali 783  
 Patel, Saurabh D. 984  
 Paternina, Luis E. 575, 581, 823  
 Paternina-Gómez, Margaret 575, 581, 823  
 Pates Jamet, Helen 921, 1206  
 Patil, Teja 462, 553  
 Patiño, Lilian 1055, 1044  
 Patipong, Suchart 407  
 Patterson, Amy E. 1346, 1359  
 Patterson, Noelle B. 495, 1461  
 Patton, Elizabeth 393  
 Paul, Ajay 1252  
 Paul, Repon C. 410  
 Paul, Sanjib K. 886

The number(s) following author name refers to the abstract number.

- Pavlis, Oto 1057  
 Pavlov, A. 483  
 Pavluck, Alex 482  
 Paw-Sang, Luis 264  
 Pawar, Atmaram 233  
 Paye, Jusufu 301  
 Paykel, Joanna 1013, 1014  
 Payne, Amanda 47  
 Paz, Hector 945  
 Paz, Jorge 955  
 Paz-Soldan, Valerie 18, 728, 1386  
 Pazoles, Pamela 427, 1087  
 Pearl, Jocelynn R. 439  
 Pearson, Mark S. 131  
 Pechacova, Daria 891  
 Peck, Roger 304  
 Pecor, James E. 750  
 Peixe, Ricardo G. 38  
 Peixoto-Rangel, Alba L. 38  
 Pelle, Roger 1030  
 Pem, Deki 158  
 Peña, Rodolfo 1376  
 Penali, Louis K. 351, 864  
 Peñataro, Pablo 885, 887  
 Penfold, Suzanne 1284  
 Pengsaa, Krisana 1101  
 Penlap, Véronique 86  
 Pernetier, Cedric 971  
 Penny, Melissa 182  
 Pensulo, Paul 857, 857  
 Pepper, Lauren 1297  
 Pereira Bruno, Fernando 140, 1450  
 Perez, Dominique 1384  
 Perez, Juan 1135  
 Perez, Maria de los Angeles 113  
 Perez Brandan, Cecilia 494  
 Pérez-Doria, Alveiro 575, 581, 823  
 Periago, Maria V. 1129  
 Perkins, Alex 1220  
 Perkins, Douglas 501, 705, 706, 707, 797, 957, 1191, 1192, 1193, 839  
 Perkins, Mark D. 457  
 Pernas, Lena 1496  
 Perng, Guey C. 628  
 Perniciaro, Jamie 609  
 Person, Bobbie 35, 1260, 1416, 1446  
 Perumal, Kaliraj 1005, 1488  
 Peruski, Leonard 239  
 Peshu, Judith 881  
 Peters, Bjoern 6, 995  
 Peters, David H. 295  
 Peterson, David S. 991  
 Peterson, Stefan 569  
 Petri, Jr., William A. 1026, 1238, 1245, 512, 1027  
 Petruccelli, Christopher 1311, 848  
 Pfaff, Jennifer 635  
 Pffarr, Kenneth 519, 522  
 Pfeil, Johannes 321  
 Phasomkusolsil, Siriporn 192  
 Phelps, Benjamin R. 1131  
 Philip, Sairu 638  
 Phillips, Allison A. 1174  
 Phillips, Aaron T. 937, 1377  
 Phillips-Howard, Penelope 453, 1403  
 Phipps, Tenisha C. 208, 559  
 Phiri, Kamija S. 1133, 1441  
 Phok, Sochea 1021  
 Phong, Nguyen C. 327, 356  
 Picado, Albert 534, 826  
 Piccinini, Renata 797  
 Piccoli, Luca 448, 1067  
 Pichyangkul, Sathit 720  
 Pickering, Amy J. 1418  
 Pickering, Darren 68, 131  
 Pickett, Gavin 706  
 Picos, Victor 624  
 Pierce, Kristen 1011  
 Pierce, Raymond J. 762  
 Pierce, Susan K. 874  
 Piermarini, Peter M. 730, 1368  
 Pierre, Dorny 93  
 Pietri, Jose E. 916  
 Pike, Andrew 1371  
 Pike, Robert 602  
 Pikula, Jiri 1057  
 Pilat, Sandra 1167  
 Pilingana, Portipher 574  
 Pillai, Dylan R. 862  
 Pillay, Pavitra 1278, 1433  
 Pilotte, Nils 650, 1489  
 Pimentel, Guillermo 1266  
 Pina, Raquel A. 718  
 Pinder, Margaret 375, 464, 1419  
 Pindolia, Deepa K. 1352  
 Pineda, Ines 1258  
 Pineda, Miguel A. 1006  
 Pineda, Stephen 1143, 1146  
 Pineda, Vanessa 253  
 Pinto, Joao 205, 998, 999  
 Pinto da Silva, Eliana 932  
 Pinyorattanachote, Arunya 358  
 Piola, Patrice 322  
 Piriou, Erwan 411  
 Pitcher, Sylvie 555  
 Pitt, Catherine 693, 1342  
 Plante, Kenneth 927, 1383  
 Plewes, Katherine 548  
 Plieskatt, Jordan L. 167, 1034  
 Pliikaytis, Brian 1408  
 Plotkin, Marya 880  
 Plowe, Christopher V. 7, 351, 871, 1335  
 Pocquet, Nicolas 1205  
 Podust, Larissa 530  
 Poe, Amanda C. 391  
 Pogliano, Joe 1128  
 Pogliano, Kit 1128  
 Pohanka, Miroslav 1057  
 Poinson, Anne 74, 299  
 Poirot, Eugenie 398  
 Polhemus, Mark 174, 176  
 Polich, Erin 1357  
 Pollack, Henry 1126  
 Pollett, Simon 1044  
 Poldsomboon, Suppaluck 1224  
 Pombi, Marco 998, 999  
 Pondja, Maria 404  
 Ponnusamy, Loganathan 600, 609, 1386  
 Poole, Catherine B. 1113  
 Poole-Smith, B. Katherine 109  
 Poolthin, Suteera 907  
 Popper, Stephen J. 625  
 Porco, Travis C. 29  
 Porter, John D.H. 653, 654  
 Porter, Michael D. 716  
 Portugal, Silvia 280, 389  
 Post, Rory J. 479  
 Postels, Douglas 1425  
 Potchen, Michael J. 1427  
 Pothin, Emilie 882, 882  
 Pou, Sovitj 834, 834  
 Poulidakos, Panagiotis 1137  
 Poulsen, Sally-Ann 145  
 Pumo, Tchouassi D. 606  
 Povelones, Michael 27  
 Pova, Marinete M. 669  
 Pow-Sang, Luis 648  
 Powell, Tim 619, 1083  
 Powers, Ann 566, 930, 937, 1377  
 Poyer, Stephen 1299, 1300  
 Prabhu, Prince R. 1005, 1488  
 Prachumsri, Jetsumon 877  
 Pradines, Bruno 153, 864  
 Praet, Nicolas 95, 447  
 Prapansilp, Panote 1426  
 Prasad, Abhishek N. 1108  
 Prasanphanich, Nina S. 761  
 Preiser, Peter R. 983  
 Premji, Zul 861, 1306  
 Prescott, Joseph 54  
 Pretell, E J. 445  
 Prevots, D. Rebecca 541, 1337  
 Preziosi, Marie- Pierre 1273, 1285, 1408  
 Price, Dana 558  
 Price, Richard N. 155  
 Price, Ric N. 551  
 Price, Richard N. 1424  
 Priest, Patricia 771  
 Prigge, Sean 189  
 Prins, Frans 978  
 Pritchard, David I. 124  
 Prithiviraj, Bharath 600  
 Pritt, Bobbi S. 851  
 Privat-Maldonado, Angela 1156  
 Privett, Natalie 810  
 Prom, Satharath 720, 1303  
 Prompitayarut, Wiboonwun 1093  
 Promstaporn, Sommai 578  
 Protopopoff, Natacha 8, 968  
 Pruckler, James 47  
 Pruszyński, Catherine 1208  
 Psutka, Rebecca 771  
 Puddicombe, Babajide J. 134  
 Puddicombe, Tolulope A. 134  
 Pullan, Rachel 307, 386, 544  
 Punguyire, Damien 790  
 Puray-Chavez, Maritza 1055  
 Purkayastha, Anjan 783  
 Purnell, Sue 802  
 Puschnik, Andreas 632, 1395  
 Putnak, Robert 1096  
 Putong, Nimfa M. 785  
 Pyae Phyo, Aung 1324  
 Pyarali, Fahim F. 286  
 Pybus, Brandon 837, 841, 840
- 
- Q**
- Qadri, Firdausi 41, 42, 43, 44, 45, 46, 518, 1041, 1048, 1410  
 Qin, Zhenpeng 331  
 Quagraine, Josephine E. 491  
 Quang, Huynh H. 327, 356  
 Quasie, Olga 590  
 Quaynor, Helena 256  
 Queiroz, Adriano 813  
 Queiroz, Alice N. 932  
 Queiroz, Rafaella F. Q. 1399  
 Queiroz, Tássia L. 19  
 Querino, Vladimir A. 1420  
 Quick, Robert 1260, 1416  
 Quimice, Lazaro 1167  
 Quintanar-Quintanar, María E. 254  
 Quintó, Llorenç 990  
 Quispe, Ana 1270  
 Quites, Humberto F. 38  
 Qureshi, Ammar 435  
 Qureshi, Shahida 1380  
 Quyen, Than Ha 1398  
 Qvit, Nir 1142
- 
- R**
- Raballah, Evans 705, 706, 707, 957, 1191, 1192, 1193  
 Rabelahasa, Eleonore 1471  
 Rabiou, Mansur M. 1274  
 Rabone, Muriel E. 763  
 Rachid-Viana, Giselle M. 669  
 Raddell, Kellie 1240  
 Raharimanga, Vaomalala 608, 1406  
 Raharinjatovo, Jacky 1300  
 Raheerampinaina, Gisele 262  
 Rahman, Anisur 46  
 Rahman, Mohammad Arif 42, 43  
 Rahman, Mahmudur 410, 773

The number(s) following author name refers to the abstract number.

- Rahman, Mizanur 410  
 Rahman, M. Ridwanur 548, 886  
 Rahman, Mahfuzur 774  
 Rahman, M. Waliur 1056  
 Rahman, Waliur 886  
 Rai, Madhukar 72  
 Raikhel, Alexander 23, 209  
 Rajab, Mohamed 800  
 Rajasingham, Anangu 961  
 Rajerison, Minoarisoa 58  
 Rakers, Lindsay 1118  
 Rakotomalala, Emma 444  
 Rakotondrazaka, Mahenina 444  
 Rakunuea, Teretia 771  
 Ralston, Katherine 1497  
 Ram, Pavani K. 777, 940, 963, 1241, 1257, 1262, 1418, 1479, 1755, 1417  
 Ramadan, Mohamed A. 1066  
 Ramamoorthi, Roopa 1291  
 Raman, Dharmpal P. 525  
 Raman, Jaishree 381, 690  
 Ramanathan, Roshan 1290  
 Ramandanirainy, Prisca 444  
 Ramarakoto, Charles-Emile 608, 1406  
 Rambaut, Andrew 17  
 Ramesh, Akshaya 1483  
 Ramirez, Juan-David 981  
 Ramirez, Jose L. 1372  
 Ramos, Ana 1270  
 Ramos, Mariana 1247  
 Ramos, Ryan 939  
 Ramos-Ligonio, Angel 533  
 Rampton, Melanie 612  
 Ramsan, Mahdi 197, 695, 918  
 Ramsey, Janine M. 275  
 Ranallo, Ryan T. 1460  
 Ranarivelo, Lalasoanirina 146  
 Rand, Alison 386  
 Randall, Amber 1408  
 Randall, Louise 708, 708  
 Randolph, Thomas 52  
 Randremanana, Rindra 262  
 Randriamanantena, Fanomezantsoa 1406  
 Rangsing, Ram 786  
 Rani, M.R. Sandhya 1098  
 Rankin, Steven E. 164  
 Ransom, Janet 945, 1270  
 Ranson, Hilary 966  
 Rao, Ramakrishna U. 1111  
 Rao, V. Bhargavi 856  
 Raphemot, Rene 730  
 Rascoe, Lisa N. 129  
 Rascon, Alberto 530, 1035  
 Rasgon, Jason L. 585  
 Rashu, Rasheduzzaman 43  
 Rashwan, Nour 490  
 Rasmussen, Zeba A. 516  
 Rasoul, Bareza A. 438  
 Raswiswi, Eric 381, 1173  
 Rausch, Kelly 1455  
 Ravel, Guillaume 630  
 Ravi, Bhaskara 55  
 Ravines, Romy R. 451  
 Ravis, William 945, 1270  
 Ray, Prabhati 434  
 Rayner, Julian C. R. 440  
 Razafiarimanga, Zara 444  
 Razafimahefa, Julien 444  
 Razakandrainibe, Romy 444  
 Razaki, Osse 198  
 Razek, Tarek 286  
 Razuri, Hugo 237, 244, 588, 931, 942  
 Read, Andrew F. 751  
 Reaves, Erik J. 244, 929, 942, 1247  
 Reavill, Drury 1143  
 Rebar, Edward J. 439  
 Reber, Jodi 615  
 Recuenco, Sergio 271  
 Reed, Steve 4, 174  
 Regna, Kimberly 753  
 Regules, Jason A. 4  
 Reich, Michael R. 275  
 Reichard, Gregory 676  
 Reiffer, Andre 771  
 Reighard, Derek A. 776  
 Reimer, Lisa 208, 480, 559  
 Reiner, Robert C. 18, 1229  
 Reiner, Jr., Robert C. 1222  
 Reis, Eliana A. 528  
 Reis, Mitermayer G. 19, 451, 528, 1098, 1420  
 Reis, Renato B. 451  
 Reisen, William K. 562  
 Reiser, Hannah 1240  
 Reiter, Karine 185  
 Reithinger, Richard 386, 387  
 Relman, David A. 625  
 Remais, Justin V. 617  
 Remoue, Franck 74, 213, 299, 1465  
 Remy, Christine 920  
 Ren, Ruilin 290, 896, 1360  
 Renom, Montserrat 1167  
 Ressonner, Rose 951  
 Reyes, Jorge 128  
 Reyes, Lissette 485, 626, 1124, 1125  
 Reynolds, Mary G. 455  
 Reynolds, Simone L. 68, 602  
 Reynoso, Manuel 589  
 Rezende, Wanderson Rezende C. 1034  
 Rhatigan, Joseph 1283  
 Rheingans, Richard 1120, 1264, 1415, 1288  
 Rhod Larsen, Anders 81  
 Riarte, Adelina 1151  
 Ribacke, Ulf 984  
 Ribeiro, Guilherme S. 19, 451, 1420  
 Ribeiro, Isabela 1305  
 Ricciardi, Alessandra 756  
 Rice, Benjamin 671, 1197  
 Rich, Stephen 1026  
 Richard, Stephanie A. 516  
 Richard, Vincent 608, 1406  
 Richards, Allen L. 591, 614, 603  
 Richards, Frank 312, 646, 647, 1118, 1346, 1359  
 Richardson, Barbra A. 660  
 Richardson, Jason H. 507, 586, 618, 736, 750, 1199, 65, 178  
 Richardson, Jason J. 578  
 Richie, Nancy 176  
 Richie, Thomas L. 5, 6, 190, 264, 495, 714, 715, 995, 996, 1162, 1196, 178, 1461  
 Richman, Adam 189, 982  
 Riddle, Mark S. 568  
 Riediger, Irina N. 1420  
 Riehle, Michael 215  
 Riewpaiboon, Arthorn 1017  
 Rigg, C 63, 815  
 Rigg, Chystrie 253  
 Rigonis, Cynthia 560  
 Riley, Eleanor 177  
 Riley, Lee W. 813  
 Rios, Maria 623, 1107  
 Rios, Paul 85  
 Rios, Sandra 257  
 Rios, Zonia M. 112  
 Rippon, Emily J. 193  
 Riscoe, Erin 834  
 Riscoe, Michael K. 431, 834  
 Ritchie, Scott 731  
 Rivard, Robert 1266  
 Rivas, Ariel 797  
 Rivas, Enrique 1012  
 Rivera, Andrea 93  
 Rivera Medina, Maribel 1012  
 Rivera-Aguilar, Victor 252  
 Riveron, Jacob M. 969  
 Roark, Gary L. 361  
 Roberts, Jacqueline 9  
 Roberts, Megan 524, 1115  
 Roberts, Rachel 3  
 Robinson, Annie 262  
 Robinson, James E. 1085  
 Robinson, Katherine A. 953  
 Robinson, Lisa A. 1449  
 Roca Feltrer, Arantxa 1441  
 Roca-Feltrer, Arantxa 354, 362  
 Rocha, Claudio 1053, 1123  
 Rochford, Rosemary 411, 668  
 Rodrigues, Amabelia 835, 998  
 Rodrigues, Amabélia 999, 1338  
 Rodrigues, Sueli G. 119, 932  
 Rodriguez, Ana 973  
 Rodriguez, Ane 1320  
 Rodriguez, David 1249  
 Rodriguez, Julian 219  
 Rodriguez, Mary L. 1069  
 Rodriguez, Nilyan 599  
 Rodriguez, Silvia 91, 95, 96, 443, 446, 1068, 1072, 1077, 1078  
 Rodriguez Barraquer, Isabel 16  
 Rodriguez-Delgado, Rosa 1152  
 Rodriguez-Perez, Mario 75  
 Rodulfo, Hectorina 598, 599  
 Roe, R. Michael 600, 725  
 Roestenberg, Meta 5, 713  
 Roetync, Sophie 874  
 Rogawski, Elizabeth T. 365  
 Roger, Tine C. K. 1166  
 Rogers, David W. 554  
 Rogers, William 357, 364, 889  
 Rogerson, Stephen J. 365, 708  
 Rogier, Christophe 608, 1406  
 Rojas, R. 63, 815  
 Rojo, Raziell 1097  
 Rojo, Liliana 530  
 Rollend, Lindsay 61  
 Rollins, Sean 41, 1410  
 Rollins, S.M. 1041  
 Rollinson, David 35, 763, 1446  
 Roman, Elaine 880  
 Romani, Franco R. 1094  
 Romani, Lucia 576, 616, 1404  
 Rombo, Lars 835, 1338  
 Romero, Ada 931  
 Romero, Candice 237, 244, 942  
 Romero, Elsa G. 1384  
 Romero, Luis R. 581  
 Romero-Vivas, Claudia 1372  
 Romig, Thomas 1064  
 Ronan, Jambou 344  
 Ronca, Raffaele 510  
 Rono, Hillary 596  
 Rono, Josea 902, 994  
 Ronsmans, Carine 950  
 Rook, Kimberly 940  
 Rooslamati, Indri 155  
 Rooth, Ingegerd 994  
 Roper, Cally 864, 1195  
 Rosas, Gabriela 99  
 Roschnik, Natalie 1466  
 Rose, Joan B. 959  
 Rosenbaum, Marieke 640, 1413  
 Rosenthal, Philip J. 355, 677, 719, 987, 1203  
 Rosenzvit, Mara 1069  
 Roseric, Azondekon 198  
 Ross, Leila S. 1325  
 Ross-Degnan, Dennis 295  
 Rossi, Cindy 421  
 Rossi, Shannan L. 927, 1383  
 Rotella, David 1114  
 Rothman, Alan L. 15, 1087, 102  
 Rouamba, Noel 1307  
 Rouhani, Saba 1466  
 Rouhier, Matthew F. 1368  
 Rourke, Michelle 118  
 Routh, Janell 1045, 1409  
 Routray, Paramita 766  
 Roux, Guillaume 262  
 Rowcliffe, Kerryn 356, 1453

The number(s) following author name refers to the abstract number.

- Rowe, Alexander K. **295**, 382  
 Rowe, Samantha Y. 295  
 Rowland, Mark 8, 461, 729, 968  
 Rowland, Tobin 621  
 Rowlinson, Emily 1266  
 Roy, Rajasree 97  
 Roy, Sourav 209  
 Roy, Sharon 485, 1124, 1125, 1259  
 Roy, Smriti 775  
 Royals, Michael 1014  
 Ruangsirarak, Ponlawat 339  
 Rubahika, Denis 879, 892, 314  
 Rubio, Camilo 20  
 Rucker, Joseph 926  
 Ruddock, Jacinth S. 487, 536  
 Rudra, Carole 1241  
 Rueangweerayut, Ronnatrai **435**  
 Rueckert, Paul 310  
 Rueda, Leopoldo M. 586, 736, **750**, 1199  
 Ruiz, Joaquin 806, 1482  
 Ruiz, Marilyn O. **745**  
 Rukundo, Alphonse 10, 906, 906  
 Rumunu, John 1357  
 Runge-Ranzinger, Silvia 747  
 Rupperecht, Charles 271, 566  
 Rusine, J. 655  
 Russell, Bruce 983  
 Russell, Richard 1374  
 Russell, Tanya L. 1231, 1358  
 Rutagwera, Marie-Reine I. **1181**  
 Ruth, Annette M. **772**  
 Ruth, Laird 486  
 Rutta, Acleus M. S. **14**  
 Rutta, Edmund 1286  
 Rwantangle, Absalom 1409  
 Rwenyonyi, Charles Mugisha 83  
 Ryan, Elizanbeth M. 429  
 Ryan, Edward T. 41, 42, **43**, 45, 518, 1048, 1410, 1041  
 Ryan, Terence 638  
 Rzepecka, Justyna 1006
- S**
- S, Aery 83  
 Sa, Juliana M. 712, **982**  
 Saade, Camille A. **769**  
 Saadou, Issifou 703  
 Saavedra, Herbert 91  
 Saavedra, H. 445  
 Saavedra Romero, Marlon P. **220**  
 Saavedra-Rodriguez, Karla 725  
 Sabeti, Pardis C. 984, 1201  
 Sabitu, Kabir 1051  
 Saboori, Shadi 1264, 1415  
 Sacarlal, Jahit 179  
 Sack, David A. 210  
 Sack, R. Bradley 516  
 Sacko, Moussa 1466
- Sacks, David 535  
 Sadowski, Brett W. 683  
 Sadumah, Ibrahim 1260, 1416  
 Saenz, Fabian 431, 867  
 Sáenz, Fabián E. **873**  
 Safeukui, Innocent **1171**  
 Saganda, Wilbrod 1402  
 Sagar, Sangeetha 1015  
 Sagara, Issaka 184, 223, 1337  
 Saguti, Fredy 163  
 Saha, Amit 42, 43, **44**, 46  
 Saha, Nirod Chandra 46  
 Saha, Samir K. 87, 240, 597, 1407  
 Saha, Tusar T. **209**  
 Sahadeo, Nikita S. D. **1084**  
 Sahli, Michelle W. **1257**, 1262  
 Sahr, Foday 300  
 Sahu, Bikash 496, **701**  
 Sahu, Priyadarshi S. **90**  
 Sahu, Rajnish 433, 679, **680**, **680**, 682  
 Said, Khadija 880  
 Saidy, Kalifa 375  
 Saijo, Masayuki 1392  
 Sáinz, Teresita 82  
 Saito, Mayuko 446, 1400  
 Saito, Tais B. **88**, 1058  
 Saiyasombat, Rungrat 565, **1105**  
 Sajid, Mohammed 978  
 Sakhria, Sonia 587  
 Salawu, Oluwakanyinsola 146  
 Salazar, Elsa 598  
 Salazar Moreno, Wayra Y. **795**  
 Salazar-Lindo, Eduardo 1400  
 Saldaña, Azael 63, 253, 1160, 815  
 Salim, Nahya 179  
 Saliou, Ramani 1311  
 Salje, Henrik **1082**  
 Sallah, Neneh 1419  
 Sallau, Adamu 1346, 1359  
 Salmon, Gabriela 237  
 Salmon-Mulanovich, Gabriela 588  
 Salum, Abdullah R. 918  
 Sam, Baramy 985  
 Samad, Rasheda 886  
 Samalvides, Frine 1341  
 Samb, Badara **722**  
 Sampaio, Ingrid C. S. 1049  
 Sampong, Lily B. 401, **1022**  
 Samudio, Franklyn 1160  
 Samuels, Aaron 482, **825**  
 Sanchez, Daniel R. 817  
 Sanchez, Juan F. 227, 929, 1223  
 Sanchez, Nery 1246  
 Sande, John 1472  
 Sandeu, Maurice Marcel **1364**  
 Sandiford, Simone 1366, **1371**  
 Sandlund, Johanna **135**  
 Sandoval, Carlos 488  
 Sandoval, Diana 91
- Sang, Rosemary 211, 412, 421, 605, 606, **613**  
 Sangaré, Alassane 236  
 Sangaré, Hama 30  
 Sangaré, Laura R. 660  
 Sangare, Moussa B. 641, 782  
 Sangthong, Rassamee 284  
 Sanogo, Zana L. 478, 641, 740  
 Sanon, Antoine 299  
 Sanon, Souleymane 1331  
 Sanou, Adama 377  
 Sanou, Antoine 912  
 Sanou, Armande K. 13  
 Sansa, Megan 1331  
 Santa Maria, Maria Luiza S. 1095  
 Santamaria, Ana Maria 253  
 Santana, Bibiana G. 756  
 Santana, Francisco S. 451  
 Santelli, Ana Carolina 1305  
 Santivañez, Saul 1065, **1068**, **1069**  
 Santolamazza, Federica 205  
 Santos, Andreia C. 451  
 Santos, Daiana 1420  
 Santos, Joara S. 818  
 Santos-Argumedo, Leopoldo 973  
 Sanz, Laura M. 986, 1320  
 Sar, Borann 241  
 Sarkar, Dhiman 146  
 Sarkar, Rajiv 1031  
 Sarker, Rouha Anamika 775  
 Sarmiento, Diana 281  
 Sarpong, Bernard K. 590  
 Sarr, Demba 991  
 Sarracino, David 45  
 Sasaki, Hitochi 168  
 Sasmono, R. Tedjo **101**  
 Satake, Akiko 378  
 Satimai, Wichai 339, **358**, 406, 407  
 Satoguina, Judith 503  
 Satoh, Yoshitaka 1114  
 Satoskar, Abhay R. 1452  
 Sattabongkot, Jetsumon 167, 357, 559, 665  
 Sauerbrey, Mauricio 1118  
 Sauerwein, Robert W. 5, 180, 713, 1177, 1186  
 Saul, Allan 1050  
 Saunders, David 720, 1063, 1303  
 Savadogo, Léon G. 377  
 Savioli, Lorenzo 35  
 Savji, Nazir 1103  
 Savranskaya, Tatyana 174, 1463  
 Savuth, Chin 241  
 Sawadogo, Simon P. 746, 1211  
 Sawers, Larry 260, 798, **954**, **1136**  
 Sawyer, Lynette 667  
 Sayeed, Md. Abu 44  
 Sayeed, Shameq 297  
 Sazzad, Hossain M. S. 1056
- Scaraffia, Patricia Y. **22**, **1367**  
 Schaefer, Jennifer 1254  
 Schaffner, Stephen F. 1201  
 Schal, Coby 1386  
 Schallig, Henk D. F. H. 326  
 Schats, Remko 180  
 Schatzkin, Eric 342  
 Schaumburg, Frieder 703  
 Schechtman, Deborah 1142  
 Scheel, Molly D. **1002**  
 Scheirer, Jessica L. 618, **1148**  
 Schellenberg, David 388, 833, 856, 1330, 1333, 1469  
 Schellenberg, Joanna 1284  
 Schelling, Esther 52, 273  
 Schiaffo, Charles E. 531  
 Schieffelin, John S. 48, 1085, 1275  
 Schijman, Alejandro 822  
 Schildgen, Oliver 237  
 Schildgen, Verena 237  
 Schilkey, Faye D. 1108  
 Schilling, Katharine A. **513**, 1260, 1416  
 Schlatter, Joel 548  
 Schlein, Karen 342  
 Schlein, Yosef 972  
 Schmaedick, Mark A. 203  
 Schmid, Michael A. **425**, **631**  
 Schmidlin, Sandro 1328  
 Schmidt, Robert 1143  
 Schmidt, Wolf-Peter 766  
 Schneider, Kyle 757  
 Schneider, Kristan 871  
 Schoepp, Randal 421  
 Schofield, Louis 1167  
 Scholzen, Anja 180, 713  
 Schountz, Tony **54**  
 Schreiber, Mark 101  
 Schriefer, Albert **813**  
 Schroeder, Jay 1214  
 Schuenzel, Erin 1226, 1227  
 Schuster, Anthony 357  
 Schuster, Angela 792, 1406  
 Schwabe, Christopher 1467  
 Schwarte, Silvia 457  
 Schwartz, Alanna **1203**  
 Schwartz, Eli 829  
 Schwarz, Alexandra 579  
 Schwarz, Daniel 797  
 Schwenk, Robert 178, 716, **995**  
 Sciotti, Richard J. **537**, **676**  
 Scitutto, Edda 99  
 Scobie, Heather M. **1411**  
 Scott, Anthony 902  
 Scott, Chuck 945  
 Scott, Charles 1270  
 Scott, Marilyn E. 1121  
 Scott, Phillip 477  
 Scott, Thomas W. 18, 21, 622, 728, 1222, 1386, 1220  
 Se, Youry 720, 988, 1303, 1316  
 Sea, Darapiseh 720, 1303

The number(s) following author name refers to the abstract number.

- Seah, Ching Ching 110  
 Sebati, Konji 1291  
 Secor, W. Evan 1033, 1028, 1428, 1432, 1434, 1443, 1444  
 Sedegah, Martha 6, 178, 495, 995, 1461  
 Segura-Cervantes, Enrique 1152  
 Sehgal, Ravinder N. 1189  
 Seidman, Jessica C. 592  
 Seidu, Razak 281, 786, 1256  
 Sekonde, Edward 844, 845, 846  
 Sekulsoki, Silvana 436  
 Sekyi, Modupe A. 1273  
 Seligman, Stephen J. 1267  
 Selvarajah, Suganya 926  
 Sembene, Malick 550, 1466  
 Sembene, Mbacké P. 225  
 Semenya, Amma A. 1033  
 Semnani, Roshanak T. 492  
 Semrau, Katherine 574, 1339, 1477  
 Senaratne, Niroshini 984  
 Séné, Papa Diogoye 504  
 Senkoro, Keshini 1353  
 Serhir, Bouchra 924  
 Serjan, Alicia 1153  
 Serme, Luc 13  
 Serre, David 208, 502, 559, 1483  
 Sesar, Jillian 1128  
 Sesay, Santigie 300, 301  
 Sesay, Sanie S. 362, 1441  
 Sessions, Wendy 1242  
 Seth, Misago 163  
 Sette, Alessandro 6, 995  
 Severson, David W. 62, 206, 207, 557, 1002, 1369  
 Sevilla, Carlos R. 1055  
 Sevillano Tripero, Natalia 1035  
 Seydel, Karl 857, 1427, 1438  
 Seye, Mouhamadane M. 757  
 Seyfang, Andreas 1161  
 Seymour, Robert L. 1379  
 Seyoum, Aklilu 738, 904  
 Shade, Robert 1143, 1146  
 Shade, Robert E.  
 Shaffer, Jeffrey G. 1275  
 Shafik, Caroline F. 245  
 Shafique, Muhammed 398, 406, 1019  
 Shah, Mirat 127  
 Shah, Shamsul Azhar 360  
 Shakarishvili, Roman 1266  
 Shakely, Delér 9, 901  
 Shamba, Donat 1284  
 Shan, Jiao-Yu 449  
 Shandukani, Mbavhalelo 162, 1173, 1175  
 Shankar, Ravi 534  
 Shanks, G. Dennis 243, 327, 356  
 Sharakhov, Igor V. 557  
 Sharakhova, Maria V. 557  
 Sharief, Abdalla H. 1144  
 Sharker, M. a. Y. 1039  
 Sharker, Yushuf 1407  
 Sharkey, Alyssa 1333  
 Sharlow, Elizabeth 537  
 Sharma, Atashi 556, 556  
 Sharma, Ankur 1170  
 Sharma, Yagya D. 1185  
 Sharmin, Iffat 1241  
 Shaw, Jeffrey J. 250, 821  
 Shaw, Robert 554  
 Shaw, Timothy 54  
 Shayo, Elizabeth 1353  
 Sheehy, Susanne 3  
 Sheele, Johnathan 1430, 55, 1429  
 Sheen, Patricia 1081  
 Shehu, Nathan Y. S. 657  
 Sheikh, Alaullah 41, 1041  
 Shek, Lynette 110  
 Shekalaghe, Seif 458  
 Shelite, Thomas R. 1058  
 Shepard, Donald S. 570, 583, 584, 634, 1088, 748  
 Sherwood, James A. 564  
 Shew, Kelly J. S. 479  
 Shewchuk, Tanya 1360  
 Shi, Meng 1162  
 Shield, Jenny 489, 604  
 Shiferaw, Welelta 814  
 Shim, So Hee 53  
 Shimogawara-Furushima, Rieko 792  
 Shin, E-Hyen 1235  
 Shin, E-Hyun 1236  
 Shin, Kirk 1161  
 Shin, Sang W. 209  
 Shirima, Kizito 388  
 Shiwalo, Ibrahim 1442  
 Shono, Yoshinori 201  
 Shott, Joseph P. 280  
 Shrestha, Sanjaya K. 1047  
 Shretta, Rima 1304, 1471  
 Shuaibu, Mohammed Nasir 168, 526  
 Shultz, Leonard D. 681, 986, 427  
 Sialumano, Mavis 1464  
 Siba, Peter 208, 480, 559, 1483  
 Sibindy, Samira 404  
 Sichitamba-Wamulume, Chibesa 165  
 Siddik, Md Ashraf uddin 46  
 Siddique, Abdullah 1027  
 Siddique, Shah Alam 46  
 Siddiqui, Asim A. 1185  
 Sidibé, Diak 236  
 Sidibe, Diakaridia 1059, 1060, 1288  
 Sidibé, Diakaridia  
 Sidibe, Yacouba 641  
 Sidibe, Youssoufa 664, 898  
 Siebert, James 1427  
 Siegl, Peter 431  
 Siekierka, John 1114  
 Sierra, Gloria M. 624  
 Sifuna, Peter M. 796  
 Sigaúque, Betuel 990  
 Sihuincha, Moises 1222  
 Sihuincha Maldonado, Moises 622  
 Sikaala, Chadwick 727, 738  
 Silamut, Kamolrat 548  
 Silapong, Sasikorn 1380  
 Silengo, Shawn 1083  
 Siles, Crystyan 422, 1102  
 Silharova, Barbora 893  
 Silué, Kigbafori D. 1447  
 Silumbe, Kafula 12, 468, 694, 1180  
 Silva, Adriano Q. 451  
 Silva, Clayton 932  
 Silva, Cassia 1129  
 Silva, Fernando J. 821  
 Silva, Giovanna G. 1413  
 Silva, Gisele M. C. 476  
 Silva, Joana C. 1025, 1030  
 Silva, Luciano K. 528  
 Silva, Maria 244  
 Silva, Maria E. 929  
 Silva, Marta M. N. 812, 818  
 Silva, Monaise M. O. 19  
 Silver, Karlee L. 1449  
 Sim, B. Kim L. 189, 982  
 Sim, Joan 983  
 Sim, Shuzhen 1372  
 Sima, Laura C. 962  
 Simmons, Cameron 933, 1398  
 Simmons, Graham 926  
 Simon, Gabriel 1485  
 Simonsen, Paul 483  
 Simwaka, Bertha 1182  
 Sindato, Calvin 197  
 Sinden, Robert E. 1456, 1458  
 Singa, Benson 660  
 Singh, Bijender 990  
 Singh, Balbir 1454  
 Singh, Om Prakash 535  
 Singh, Rudra Pratap 534, 826  
 Singh, Sheetalpreet 1411  
 Singhasivanon, Pratap 354  
 Sintasath, David 354, 398, 1019  
 Siqueira, João Bosco 634  
 Sirichaisinthop, Jeeraphat 877  
 Sirima, Bienvenu S. 1177  
 Sirima, Sodiomon B. 13, 467, 920, 1331, 779, 1351  
 Siripokasupkul, Raveewan 1303  
 Sirivichayakul, Chukiat 1016, 1017, 1101  
 Sirot, Laura K. 555  
 Sissoko, Seydou 1059, 1060  
 Sistro, Mark 475, 820  
 Sivasubramaniam, Selvaraj 1274  
 Siwo, Geoffrey H. 151, 154  
 Siyum, Yohannes D. S. 234  
 Skaflen, Marcus 438  
 Skarbinski, Jacek 552, 830, 1472  
 Skinner-Adams, Tina 143, 147, 1194  
 Sklar, Larry 1384  
 Skwarczynski, Mariusz 131  
 Slater, Hannah C. 1355  
 Slayton, Rachel B. 1040, 1252  
 Sliz, Piotrek 1325  
 Sloan, Lynne M. 851  
 Sloods, Theo 436  
 Slotman, Michel 508, 509, 1000  
 Slovak, Mirko 577  
 Slutsker, Laurence 453, 1437  
 Small, Scott T. 208, 559, 1483  
 Smallegange, Renate C. 212  
 Smer, Aiman M. 817  
 Smit, Cornelis H. 976, 1032  
 Smith, Bryan 678  
 Smith, David 1220  
 Smith, David F. 761  
 Smith, David L. 881, 1229  
 Smith, Emily 495, 715  
 Smith, Helen 71  
 Smith, Jared 1009  
 Smith, Joshua D. 585  
 Smith, Jennifer L. 596, 1274  
 Smith, Katherine M. 111  
 Smith, Lisa 1286  
 Smith, Monique A. 470  
 Smith, Nicole 1221  
 Smith, Pauline C. 1006  
 Smith, Roger 151, 154  
 Smith, Stephen C. 913  
 Smith, Sarah E. 289  
 Smith, Thomas A. 182, 743, 1340, 914, 903  
 Smith Gueye, Cara 684, 687, 1174  
 Smithers, Hannah M. 1462  
 Smrekova, Eva 791  
 Smyth, Gordon K. 1167  
 Snively, Callae S. 275  
 Snow, Grace E. 115, 424  
 Snow, Robert 838  
 Snow, Robert W. 544, 878  
 Soares, Alberto M. S. 517, 1049  
 Soares, Fabia C. 821  
 Sobral, Mariana Carolina M. 1095  
 Sobsey, Mark D. 1263  
 Sobuz, Shihab U. 512, 1380  
 Socheat, Duong 983, 988, 1303, 1316, 357, 364, 720  
 Soebiyanto, Radina P. 944  
 Sogoba, Nafomon 1337  
 Soheli, Badrul M. 940  
 Soisson, Lorraine A. 6, 7, 176, 995, 1459  
 Sokhna, Cheikh 225, 970, 1342  
 Sokolova, Jaroslava 791, 793, 891, 893  
 Sokolow, Susanne H. 757  
 Solanki, Nehal R. 496  
 Solano, Philippe 74



The number(s) following author name refers to the abstract number.

- Sole, Catherine L. 606  
 Solomon, Anthony 1274  
 Solomon, Sunil Suhas 16  
 Solomon, Wesley 313  
 Solon, Juan-Antonio 305  
 Sombié, Issaka 377  
 Somda, Martin B. 74, **299**  
 Some, Fabrice 463, 1307  
 Somi, Geoffrey 800  
 Somuah, Stephen 1314  
 Sonde, Hesbon O. 421  
 Sondo, Blaise 292  
 Sonenshine, Daniel E. 55  
 Song, Dan 591  
 Song, Jin-Won 53  
 Song, Xuezheng 761  
 Sonnie, Mustapha 300  
 Sonoiki, Ebere **677**  
 Sopha, Chantha 985  
 Sopoh, Ghislain 780  
 Soremekun, Rebecca 827  
 Soremekun, Seyi 804  
 Sosa, Nestor **945**  
 Sosa-Estani, Sergio 819  
 Soto-Castellares, Giselle 1400  
 Sougoufara, Seynabou **225**  
 Soulama, Issiaka 920, 1331  
 Sourou Bankolé, Honoré 780  
 Sousa, Erica 1420  
 Sousa, Jason 837, 840, **841**  
 Sousa, Rosana 813  
 Sousa Jr., Edvaldo C. 119, 1103  
 Souza, Samaly S. **765**  
 Sow, Doudou **269**  
 Sow, Samba 1059, 1060, 1285, 1288, 236, 782  
 Sowe, Momodou 375  
 Spaccapelo, Roberta 716, 978  
 Sparks, Kansas 989  
 Spear, Robert C. 1037  
 Speare, Richard 604  
 Specht, Sabine 522, 523, 524  
 Speck, Rebecca M. 286  
 Spence-Lewis, Infanta M. N. **911**  
 Spencer, Bryan R. 905, 905  
 Spencer, Lynn 1440  
 Spicer, Jennifer 825  
 Spicknall, Ian **1046**  
 Spiropoulou, Christina F. 1381  
 Spray, David C. 140  
 Sprigg, Karajo 751  
 Spring, Michele 5, 176, **720**, 1459  
 Sreenivasan, Nandini **514**  
 Sreng, Sokunthea 985  
 Srichairatanakul, Utaiwan 720  
 Srijan, Apichai 1047  
 Srikiatkachorn, Anon 15  
 Srikiatkachorn, A. 102  
 Srikrishnan, Aylur Kailasom 16  
 Sriprakash, Kadaba S. 68  
 Srisatjarak, Wanna 877  
 Srisuwanporn, Termsang 1101  
 Srivastava, Anuradha **867**  
 Sriwichai, Sabaithip 720, 1303  
 Ssempebwa, John 319  
 Sserwanga, Asadu **314**, 892  
 St. Laurent, Brandyce **1219**, 752  
 Staedke, Sarah G. 379, 466, 549, 892, 314, 573, 803  
 Stancil, Jeffrey D. 1222  
 Stanford, Donald S. 679  
 Stanton, Michelle C. **32**  
 Stanzani, Valerio 1408  
 Stark, Damien 263  
 Starr-Spires, Linda D. **620**  
 Stauber, Christine 1263, **1416**  
 Stauffer, William 754  
 Stauff, Charles B. 937  
 Stauss-Grabo, Manuela 608  
 Steel, Cathy 304  
 Steen, Keith 1210  
 Steer, Andrew 576, 616, 1404  
 Steeves, Tanner 60  
 Stefanakis, Rianna 1291  
 Stein, Catherine M. 50  
 Steinhardt, Laura 1439, **1472**  
 Steinmann, Peter 122  
 Steketee, Richard W. 1340, 1435  
 Stell, Fred M. 725  
 Stenström, Thor Axel 281, 786, 1256, 1263  
 Stephens, H.A. 102  
 Stephenson, Rob 1476  
 Stepniewska, Kasia 712, **988**, 1316, 1324  
 Stergachis, Andreas 324  
 Steritz, Matthew 25, 202  
 Steven, Andrew 524, 977  
 Stevens, Eric 304  
 Stevenson, Jennifer 543, 685, 1343, **752**, **1385**, **1440**  
 Stevenson, Raz 800, 880  
 Stewart, Jenell 1413  
 Stienlauf, Shmuel 829  
 Stienstra, Ymkje **780**  
 Stijnberg, Deborah **1315**, 1347, 1348, 1349  
 Stiles, Jonathan 313, 663  
 Stiles-Ocran, J.B. 729  
 Stillwaggon, Eileen **260**, **798**, 954, 1136  
 Stinchcomb, Dan T. 619, 629, 1013, 1014, 1083, 1378  
 Stoddard, Robyn A. 1402  
 Stoddard, Steven T. **18**, 622, 1222, 220  
 Stolk, Wilma A. 33, 643  
 Stoller, Nicole E. **29**  
 Stone, Will **510**, 543, 1177  
 Storti-Melo, Luciane M. 702  
 Stoute, Jose A. 289, 1172  
 Straccini, Christine 109  
 Strachan, Daniel 804  
 Straif, Kurt 141  
 Straimer, Judith 439  
 Stramer, Susan L. 623  
 Streit, Thomas 482, 645  
 Stresman, Gillian 543, 685, 1440, **1343**  
 Strickman, Daniel 583, 584, 748  
 Strode, Clare 1390  
 Strosnider, William H. 776  
 Stuart, Ken 178  
 Stuckey, Erin M. **743**  
 Stullerova, Petra 793  
 Sturrock, Hugh 545, 1174, 596, **469**  
 Subramani, R 242  
 Subramanian, Shyamsundar 935  
 Suchard, Marc A. 17, 119  
 Suchdev, Parminder 486  
 Sudi, Wema 226  
 Sudiby, Heru 1219  
 Sugiharto, Victor A. **107**  
 Sukowati, Supratman 1219  
 Suleiman, Abdullah 695, 918  
 Sullivan, David J. 210  
 Sullivan, Kevin 879  
 Sullivan, William 1297  
 Sultana, Tania 41, 1410, 1041  
 Sumanadasa, Dulangi 145, **147**  
 Sumardi, S. 1219  
 Sumardi, Uun 430  
 Sumari, Debora 843  
 Sumba, Odada P. 668  
 Sumba, Peter O. 411  
 Summers, Jennifer A. 243  
 Sun, Longhua 1002  
 Sundar, Shyam 72, 534, 535, 826, 1149  
 Suon, Seila 985  
 Supali, Taniawati 310  
 Surangsirat, Surachai 1101  
 Surin, Johari 248  
 Sutamihardja, Awalludin **844**, **845**, **846**  
 Sutamiharja, Mochamad A. 844  
 Sutcliffe, James F. **1234**  
 Sutherland, Colin 329, 349, 353, 693, 870, 1186, 363, 1202  
 Sutherland, Laura J. 50, 423, 721  
 Suvada, Jozef 893  
 Suwito, S. 1219  
 Suwonkerd, Wannapa 1224  
 Suzuki, Brian 530  
 Suzuki, Motoi 246, 785  
 Svennerholm, Ann-Mari 44  
 Swai Ndealilia, Senyael 1380  
 Swamidoss, Isabel 328  
 Swanson, Scarlett 1384  
 Swe, Pearl M. **64**  
 Swedberg, Gote 83  
 Swierczewski, Brett 568  
 Switchenko, Jeffrey 961  
 Switzer, William M. 931  
 Swoyer, Ryan **935**  
 Sy, AlHousseynou 550  
 Sy, Ousmane 1342  
 Syafruddin, Din 1219  
 Sykes, Melissa L. **1145**  
 Sylla, Khadime **1302**  
 Sylla, Mamadou B. **1059**, 1060  
 Sztejn, Marcelo B. 7
- 
- T**
- Taaffe, Jessica E. **1423**  
 Taaka, Lilian 573, 803  
 Taal, Makie 375  
 Tacchini-Cottier, Fabienne 471  
 Tachibana, Mayumi 498  
 Tadele, Getnet 285, 1405  
 Tagbor, Harry 794, 831, 883, **1436**  
 Tagoe, Naakai 790  
 Tahita, Marc Christian **1312**  
 Tai, Qin-Wen 449  
 Takahashi, Daniele 19  
 Takala-Harrison, Shannon 871, 1335, 351  
 Takaoka, Hiroyuki 229  
 Takasaki, Tomohiko 1392  
 Takashima, Eizo 1457  
 Takem, Ebako N. 369, **375**  
 Takeshita, Nozomi 788  
 Takhampunya, Rattoo 578  
 Takken, Willem 212, 450, 508, 1000  
 Talaat, Kawsar R. 492, **1455**  
 Talbot, Julie **1283**  
 Taleo, George 1024  
 Talisuna, Ambrose 1020  
 Talkington, Deborah 47  
 Talledo, Michael J. 928  
 Talledo, Michael M. 420  
 Talley, Angela K. 5  
 Tamarozzi, Francesca 1067  
 Tambatamba, Bushimbwa 1045  
 Tami, Adriana **624**  
 Tamiru, Abreham 277  
 Tamminga, Cindy 6, 995  
 Tan, Asako 151, 154  
 Tan, Hwee Cheng 115  
 Tan, John C. 206  
 Tan, Kathrine R. 165  
 Tan, Lee Aun 27  
 Tang, Yuxiao 1408  
 Tanga, Mary J. 1150  
 Tangpukdee, Noppadon **343**  
 Taniuchi, Mami **512**, 1380  
 Tanjong, Rebecca A. E. **330**  
 Tanner, Marcel 388  
 Tannitisupawong, Darunee **1093**  
 Tanowitz, Herbert 487, 536, 140  
 Tapia, Milagritos 236, 1059, 1060, 1288  
 Tapia-Conyer, Roberto 634  
 Tapper, Marlene 1130  
 Tappero, Jordan 540

The number(s) following author name refers to the abstract number.

- Tarini, Ann 31, 298  
 Tarleton, Rick L. 494, 1153  
 Tarnagda, Zekiba **1062**  
 Tarning, Joel 548  
 Tasara, Faustinus P. 1040  
 Tassiba, M. E. 382  
 Tassinari, Wagner S. 451  
 Tatarsky, Allison 162, 1173, 1175  
 Tatem, Andrew J. 17, 166, 1352  
 Tatishvili, Nana 1266  
 Taweh, Fahn 459  
 Tay, Chwen 440  
 Taye, Aseged 312  
 Taylor, Andy 1251  
 Taylor, Aimee R. **1195**  
 Taylor, Jesse 669  
 Taylor, Lizeth 607  
 Taylor, Mark 11, 290, 334, 460, 522, 896  
 Taylor, Myra 1278, 1279, 1280, 1433  
 Taylor, Mark J. 481, 524, 977, 1112, 1115  
 Taylor, Steve M. 391  
 Taylor, Terrie E. 504, 871, 1427, 1438, 857, 857, 1425  
 Tchibola, Marie-Lou 869  
 Tchinda, Gervais G. 380  
 Tchioffo, Majoline T. **157**  
 Tchourbanov, Alexander 202  
 Team, Mкру 1344  
 Tedom, Tedom **86**  
 Teelen, Karina 1186  
 Teguate, Ibrahima 236, 1288  
 Teirlinck, Anne C. 180, **713**  
 Teixeira, Andrea 539  
 Teixeira, Bertinellys 598  
 Teixeira, Maria G. 1098  
 Teja-isavadharm, Paktiya 1303  
 Tejada, Romina A. 1094, 1413  
 Tekete, Mahamadou 348  
 Tekwani, Babu L. **433**, 679, 680, 680, **682**  
 Telfer, Sandra 58  
 Telford, III, Sam R. 59, 60  
 Tellez, Yolanda 429  
 Tello, Luis 1068  
 Tello, Raul 125  
 ten Bosch, Quirine A. **33**  
 Teng, An 55  
 Tenorio, Alexander 887  
 Teo, Andrew 708, 708  
 Teodori, Eleonora 554  
 ter Kuile, Feiko 324, 362, 897, 1133, 1436  
 ter Meulen, Jan H. 1015  
 Terashima, Angelica 125  
 Terer, Carolyn C. 1445  
 Terlouw, Dianne J. **1441**, 362  
 Terry, Frances 650  
 Tesfaye, Gezahegn 386, 387  
 Tesh, Robert 565, 1104  
 Teshima, Hayato 201  
 Teuscher, Franka 866  
 Tewari, Rita 1171  
 Thai, Kim 975  
 Thailayil, Janis 554  
 Thakur, Garib D. **525**  
 Thangamani, Saravanan **577**  
 Thanh, Nguyen Xuan 356  
 Thanh, Nguyen X. 327  
 Thao, Nguyen T. 637  
 Thapa, Laxmi B. 1047  
 Thavrin, Bou Kheng 1019  
 The Cysticercosis Working Group for Peru, For 446  
 Theander, Thor 510  
 Thera, Mahamadou A. 7, 1335  
 Thesing, Phillip C. 1438  
 Thiam, Cheikh 919  
 Thiam, Sylla 325, 908, **919**  
 Thielecke, Marlene 608, 1406  
 Thiem, Vu Dinh 1017  
 Thien, Nguyen Xuan 356  
 Thiombiano, Fatoumata 1177  
 Thior, Moussa 919  
 Thior, Pape Moussa 1313  
 Thirumalapura, Nagaraja 88  
 Tho, Le Huu 1017  
 Thomas, Alaina C. 164, **736**  
 Thomas, Marvin 1423  
 Thomas, Stephen J. 102, 1087, 1096, 1397, 1082  
 Thomas, Wayne 56  
 Thompson, Eloise 329  
 Thomsen, Edward 480  
 Thomson, Rebecca 11, **290**, 334, 460, 896  
 Thorn, Per 324  
 Thornton, Andy 485, 1124, 1125  
 Thornton, Haley 725  
 Thorogood, Margaret 801  
 Thoryk, Elizabeth A. 1015  
 Thriemer, Kamala 367  
 Thuma, Phil 1464  
 Thuy, Tran T. 637  
 Thwing, Julie 334, 460  
 Tiacoh, Landry N. 351  
 Tiago, Armino D. 1018  
 Tibbets, Clark 783  
 Tibenderana, James 804  
 Tibery, Cecilia 1011  
 Ticona, Eduardo 1401  
 Ticona, Maria 1267  
 Tidwell, James 757  
 Tiendrebeogo, Eli 292  
 Tietje, Kathy 849  
 Tigoï, Caroline 421, 613  
 Tilahun, Tekola 312  
 Tilley, Drake 85, 1044  
 Tilley, Drake H. 259, 589, 929, 1053, 1123, 1373  
 Tillus, Jeffrey 286  
 Timiryasova, Tatyana 1086  
 Timona, Lubica A. 791  
 Timoshevskiy, Vladimir A. 557  
 Timothy, Veenstra 1010  
 Tine, Roger K. 255, 294, 346, 349, 547, **781**  
 Tinelli, Carmine 448  
 Tinoco, Yeni 237  
 Tinoco, Yeny 244  
 Tinoco, Yeny O. **942**  
 Tintani, Francis 1336  
 Tinto, Halidou 402, 870  
 Tiono, Alfred B. 13, **467**, **920**, 1177, 1331  
 Tipmontree, Rungrawee **406**  
 Tirados, Inaki 71, **76**  
 Tisch, Daniel 1483  
 Tissera, Hasitha 1393  
 Titanji, Vincent 86  
 Titu, Abu Mohammad Naser 1056  
 Tiwary, Puja **72**, 1149  
 Tjitra, Emiliana 155, 1424  
 Tobgay, Tashi **158**  
 Toda, Mitsuru 1360  
 Todd, Jim 838  
 Toh, Xue Yun 110  
 Tokunaga, Naohito 498  
 Tolo, Youssouf 1335  
 Tolouei Semnani, Roshanak **36**, 1010  
 Tomaino, Francesca 1489  
 Tomás, Gonzalo 1151  
 Tomas, Gonzalo 1153  
 Tomayao, Agnes 1082  
 Tomczyk, Sara M. **277**  
 Tong, Carlos 588  
 Tong, Steven Y. C. 948  
 Tongren, Jon Eric 906, 906  
 Tonkoug, Paul 31  
 Topalis, Pantelis 70  
 Tora, Ababayehu **1405**  
 Torabi, Mohammad 215  
 Torii, Motomi 498  
 Torr, Steven 71, 76, 191  
 Torrero, Marina 1004  
 Torres, Cristina E. 158  
 Torres, Melissa **650**  
 Torres, Maria 1265  
 Torres, Melissa 1489  
 Torres, Sonia M. 885, 887  
 Torres-Montero, Jesús 533  
 Torto, Baldwin 606, 613  
 Tosh, Donna 176  
 Toth, Istvan 131  
 Totino, Paulo R. Rivas. 718  
 Totrov, Maxim 24  
 Toubali, Emily **30**, 1268, 1271  
 Tougher, Sarah 290, 896, 1360  
 Touray, Sunkaru **755**  
 Toure, Offianan A. **344**, 351  
 Towers, Cathy E. 1212  
 Towers, David P. 1212  
 Townend, John 375  
 Townes, Lindsay R. **888**  
 Townsley, Elizabeth **102**  
 Townson, Simon 524  
 Tozan, Yesim 321  
 Traina, Mahmoud I. **817**  
 Tran, Thang 55  
 Tran, Thanh 143  
 Tran, Thang C. 807  
 Tran, Tuan M. **389**  
 Traore, Abdoulaye 13  
 Traoré, Aminata 236  
 Traoré, Abdel Aziz 377  
 Traore, Abdramane 389  
 Traore, Alphonse 912  
 Traore, Abdel K. 641  
 Traore, Boubacar 280, 389, 641, 719  
 Traore, Bintou 1060  
 Traoré, Djeneba 236  
 Traore, Diahara 1466  
 Traore, Karim 712, 1335  
 Traore, Sekou 184  
 Traoré, Sékou F. 223, 641, 740  
 Traore, Yves 292  
 Trape, Jean François 225, 550, 970  
 Travassos, Mark **1335**  
 Travassos da Rosa, Amelia 565  
 Traylor, Zach 50, 423  
 Treger, Rebecca 491  
 Tremblay, Cecile L. 924  
 Trendell, Chris 676  
 Trenholme, Katharine 436  
 Triana, Paula R. 624  
 Triana-Alonso, Francisco J. 627  
 Triana-Alonso, Juana L. 627  
 Trichilo, Jessica 1460  
 Trigg, Kerim 457  
 Trimarsanto, Hidayat 101  
 Tripathi, Abhai 1232  
 Tripet, Frédéric 746  
 Tritten, Lucienne 1122  
 Troye-Blomberg, Marita 696, 697, 710, 711  
 Troyo, Adriana **607**  
 Trueba, Gabriel 1042  
 Trung, Trieu Nguyen 356, 327  
 Truong, Dzung V. 807  
 Truscott, James 307  
 Truyens, Carine 819  
 Try, Vorleak 985  
 Tsai, Hung-Chin **1119**  
 Tsai, Kun-Hsien 1099  
 Tsai, Lillian **1041**, 1410  
 Tsang, Victor C. W.. 446, 1072, 1077, 1078, 1079  
 Tsertsvadze, Tengiz 1266  
 Tshetu, Antoinette K. 391, 1328  
 Tsoumbou-Bakana, Gladys 869  
 Tsuboi, Takafumi 168, 498, 665, 1456, 1457  
 Tsuji, Moriya 1461  
 Tu, Zhijian 1462  
 Tuan, Ha M. 637  
 Tucker, Matthew 989

The number(s) following author name refers to the abstract number.

Tuicakau, Meciusela 1404  
 Tuikue Ndam, Nicaise 1364  
 Tuinsma, Marjon 30  
 Tukahebwa, Edridah M. 759  
 Tullo, Gregory 183, 1457  
 Tumwebaze, Patrick K. **987**  
 Tumwine, Lynnette 1309  
 Tunchan, Kalaya 358  
 Tungu, Patrick 197, 226, 1204  
 Tuong, Vo V. 637  
 Tupiza, Fernanda 1253  
 Turell, Michael J. 621  
 Turner, Alison V. 1456  
 Turner, Elizabeth L. 544  
 Turner, Gareth D. H. **1426**  
 Turner, Stephen 924  
 Turpo, Gladys 1267  
 Turscott, Martha 760  
 Tuxun, Tuerhongjiang **449**  
 Tweyongyere, Robert **759**  
 Twomey, Patrick 4, **678**  
 Tyavanagimatt, Shanthakumar  
 103  
 Tyner, Stuart 1063  
 Tzertzinis, George 1487

## U

Ubalee, Ratawan 357  
 Uchuya, Jorge 1267  
 Uddin, Md. Jasim 46  
 Uddin, Taher 42, 45, 1048  
 Uderzo, Eva 895  
 Udhayakumar, Venkatachalam  
 391, 843, 854  
 Ugarte, Cesar 955  
 Ugoagwu, Placid 657  
 Uhart, Marcela 640  
 Uisso, Cecilia 642  
 Ujiie, Mugen 788  
 Uliana, Silvia R. B. 1142  
 Ullman, Diane 945, 1270  
 Ulrich, Robert G. **1397**  
 Umar, Mary 1346  
 Umaru, John 646  
 Umulisa, Irene 10, 1350  
 Un Nissa, Tayyab 1380  
 Unal, Sandra 1205  
 Undurraga, Eduardo A. 634,  
 1088  
 Unicomb, Leanne 774, 775, 777,  
 963, 965, 1414, 1417, 1418  
 Unlu, Isik 748  
 Unnasch, Thomas R. 304, 647,  
 923, **1113**, **1487**, 75, 1118  
 Upton, Leanna M. 27  
 Urayai, Tanaka 1252  
 Urban, Britta 1132  
 Urnov, Fyodor D. 439  
 Ursing, Johan **835**, **1338**  
 Usmani-Brown, Sahar 60, 1025

Utzinger, Jürg 35, 122, 1447  
 Uwimana, Aline 1350  
 Uwimana, Zena **789**  
 Uwimbabazi, J.c. 655  
 Uyeki, Timothy 237, 244, 942  
 Uyeno, Leslie 1168

## V

Vaca, Maritza 128, 1253  
 Vaca, Sergio 82  
 Vaghjiani, Roshni R. 1352  
 Vaid, Nidhi 886  
 Vaidya, Akhil B. 499, 1188, 431  
 Vaillant, Michel 900  
 Valadez, Joseph 848  
 Valderrama, A 63, 815  
 Valdez, Edgar 795  
 Valença, Helio F. 821  
 Valencia, A. 1044  
 Valencia, Braulio 1270  
 Valencia, Diego E. 1068  
 Valente, Vanderson 1129  
 Valentiner-Branth, Palle 516  
 Valenzuela, Carla V. **955**  
 Valenzuela, Gabriela 873  
 Valenzuela, Jesus 389, 472  
 Valian, Adams 34  
 Valim, Clarissa **188**, 347, 1201,  
 1425  
 Valle, Ruben **1247**  
 van Dam, Govert G. 1433  
 van de Hoef, Diana L. 973  
 van de Vegte-Bolmer, Marga  
 180  
 Van de Wyngaerde, Marshall T.  
**618**, 1148  
 Van den Steen, Philippe E. 978  
 van der Vegte-Bolmer, Marga  
 1186  
 van der Ven, André J. A.. M..  
 180, 430  
 van der Werf, Tjip S. 780  
 van Diepen, Angela 976, **1032**  
 van Egmond, Loes 1032  
 van Eijk, Annemieke 1403, 453  
 Van geertruyden, Jean Pierre  
 235, 1020  
 van Gemert, Geert-Jan 180  
 van Lieshout, Lisette 180, 1433  
 Van Tyne, Daria 347, 504, 1201,  
**1421**  
 Van Voorhis, Wesley C. 187  
 van Wyk, Albert 328  
 van't Hoog, Anja 453, 952  
 Vanachayangkul, Pattaraporn  
 837, **1303**  
 Vanden Eng, Jodi 9  
 VanDerlip, Aaron 293  
 Vanderstraete, Mathieu **980**,  
 1451

VanEkeris, Leslie 1362  
 Vanlandingham, Dana L. 1228  
 Vannavong, Anan 1263  
 Vannavong, Nanthasane 786  
 Vannier, Edouard 61  
 Varani, Stefania 696, 697, 710,  
 711  
 Vareta, Jimmy 504  
 Vargas, Andres 795  
 Vargas, Daniel 1467  
 Vargas, Jorge 603  
 Vargas, Martha 806, 1482  
 Vargas, Sandra Lucia 281  
 Varivann, Pin 241  
 Vasco, Karla 1042  
 Vasconcelos, Helena B. 119, 932  
 Vasconcelos, Pedro 932, **119**,  
**1103**  
 Vásquez, Daniel A. 1138  
 Vasquez, Gissella 588, 1223  
 Vasquez, Gabriela **724**  
 Vassal, Anna 804  
 Vasta, Gerardo R. 264  
 Vasudevan, Canjeeveram K. 16  
 Vaughan, Jefferson A. **1214**  
 Vaughn, Meagan **609**, **615**  
 Vazquez, Jesus 1097  
 Vazquez-Prokopec, Gonzalo 18,  
 222, 749, 1222  
 Veenstra, Timothy 37, 1008  
 Vega, Patricia d. 716  
 Veiga, Maria Isabel **1323**  
 Velasco-Salas, Zoraida I. 624  
 Velazquez, Peter 1171  
 Velez, Ivan D. 1016, 1017, 1138  
 Velmurugan, Soundarapandian  
 189, 982  
 Venancio, Thiago M. 529  
 Venkatesan, Meera **352**, 1195  
 Venkatesan, Malabi M. 1460  
 Vennervald, Birgitte 875, 875  
 Venter, Marietjie 605  
 Ventura, Carlos B. 1426  
 Vera, Huber 588  
 Verani, Jennifer 1243  
 Verastegui, Hector 941, 1248,  
 1258  
 Verastegui, Manuela 89, 1157,  
 1079, 1080  
 Verbel-Vergara, Daniel 581  
 Verhulst, Niels O. **212**  
 Verjovski-Almeida, Sergio 529  
 Vermeire, Jon J. 491  
 Vermund, Sten H. 1127  
 Verweij, Jaco J. 1433, 1434  
 Veyee, Vera 1475  
 Viana, D V. 250  
 Vianez, João 932  
 Viberg, Linda 489  
 Vicente, Jose L. 999  
 Vickers, Ivan 1130  
 Vicuña, Yosselin 488  
 Viebig, Nicola 3  
 Viera, Sara 681, 986  
 Vigil, Adam 660  
 Vilcarrero, Stalin 18, 422, 622  
 Villafane, Margarita 1135  
 Villar, Luis 1012  
 Villarama, Benito J. R. 785  
 Villaran, Manuel V. **603**  
 Villasante, Eileen 190, 264, 714,  
 715, 996  
 Villegas, Leopoldo 465  
 Villinger, Jandouwe 613  
 Villinski, Jeffrey T. 69  
 Vimos, Carlos 603  
 Vincent, Isabel M. **538**  
 Vincent, Naomi 480  
 Vincente, José L. 998  
 Vinetz, Joseph 689, 689, 885,  
 887  
 Viotti, Rodolfo 1153  
 Visser, Leo G. 180  
 Vitek, Christopher J. **1225**, 1226,  
**1227**  
 Vivarini, Aislan C. 476  
 Viviani, Simonetta 1408  
 Vizcaino, Lucrecia 724  
 Volkman, Sarah 188, 347, 504,  
 984, 1201, 1422  
 Vololonaiaina, Ramaroson 444  
 von Hohenberg, Max 331  
 von Seidlein, Lorenz 156  
 Von Thun, Annette M. **164**, 894  
 Voronin, Denis **977**  
 Vossbrinck, Charles 229  
 Vounatsou, Penelope 121  
 Vreden, Stephen G. S. 1326  
 Vu, Nancy **1401**  
 Vujcic, Jelena **777**, 1052, 1262,  
 1479  
 Vulule, John 453, 497, 501, 513,  
 514, 515, 685, 700, 705, 707,  
 957, 961, 1468

## W

Wachter, Keri 293  
 Wadegu, Meshack **936**  
 Wagar, Eric 1148  
 Wagman, Joseph **733**, **734**  
 Wagner, Jeffrey C. **442**  
 Wagner, James M. 935  
 Wagstaff, Simon 1112, 1115  
 Wahid, Isra 101  
 Waiboci, Lilian 567, 1244  
 Waitumbi, John **142**  
 Waitumbi, John N. 176  
 Wake, Rachel M. **1137**  
 Walakira, Andrew 462, 553, 987  
 Walhgren, Mats 876  
 Walker, Alan 128  
 Walker, David H. 1058

The number(s) following author name refers to the abstract number.

- Walker, Edward 200, 1389, 1468, 745, 1221  
 Walker, Kathleen 215  
 Walker, Larry A. 433, **679**, 680, 680, 682, 837  
 Walker, Martin **481**  
 Walker, Patrick **897**  
 Walker, Yatta 459  
 Walsh, Douglas 1063, 860  
 Walsh, Jennifer 572  
 Walsh, Laura 1035  
 Walson, Judd L. 660  
 Walters, Maroya S. **1409**  
 Walton, Shelley 57, 612, **56**  
 Wamani, Henry 569  
 Wamukoya, Marilyn 1360  
 Wamuyu, Maina G. 319  
 Wand, Handan 576, 616, 1404  
 Wandera, Bonnie 379  
 Wandinger-Ness, Angela 1384  
 Wang, Bo 665, **1370**, 1462  
 Wang, Chloe Q. 776  
 Wang, Jun-hua 449  
 Wang, Lin-Fa 413  
 Wang, Ruobing 178, 187  
 Wang, Shuo 1037  
 Wang, Wei-Kung **1394**  
 Wang, Xuelei X. 721  
 Wang, Ying 202  
 Wang, Yue 665  
 Wang', David 567  
 Wangeci, Gatei W. 247  
 Wangroongsarb, Piyaporn **370**, 398  
 Wangui, Julia 936  
 Wanionek, Kimberli 1011  
 Wanja, Elizabeth 859, 860, **621**  
 Wanjala, Christine L. **865**  
 Wanji, Samuel 481  
 Wannemuehler, Kathleen 1411  
 Wanzira, Humphrey 892  
 Warburg, Alon 814  
 Ward, Abigail **1345**  
 Ward, Brian 109  
 Ward, Danielle 649, 1117  
 Ward, Daniel A. **1172**  
 Ward, Honorine 1031  
 Ward, Stephen A. 1115  
 Wardhani, Puspa 101  
 Ware, Lisa 176  
 Warigia, Marion 211  
 Warimwe, George 137  
 Warrenfeltz, Susanne W. 672  
 Wartel-Tram, Anh 110  
 Washington, Charles H. 645  
 Wastling, Jonathan M. 1484, 1486  
 Watanabe, Emi 285  
 Waters, Norman C. 860, **1024**, **1453**  
 Wateska, Angela R. 296  
 Watmon, Ben 520  
 Watsierah, Carren A. 1184  
 Waweru, Evelyn W. 878  
 Weaver, Anne M. **1241**  
 Weaver, Scott C. 927, 1379, 1383, 1378  
 Webb, Emily 466, 549, 875  
 Weber, David J. 1376  
 Webster, Jayne 1333  
 Weetman, David 193, 966, 967, 998, **999**, **1210**  
 Weger, James 1378  
 Wegmann, Keith 834, 834  
 Wei, Wang **532**  
 Weil, Ana A. 43  
 Weil, Gary J. 33, 639, 1111, 1485  
 Weill, Mylène 967, 1205  
 Weinkopff, Tiffany S. **471**  
 Weinstein, Philip 118  
 Weintraub, Rebecca **293**, 1283  
 Weiss, Louis M. 140  
 Wekesa, Dennis 859  
 Wekesah, Frederick 1360  
 Weldon, Emma **283**  
 Wele, Mamadou **348**  
 Wellems, Thomas E. 982  
 Wellman, Michael 1428  
 Wen, Hao 449  
 Wen, Tzai-Hung 1099  
 Wenger, Edward A. **1178**  
 Were, Florence 1437  
 Were, Tom 501, 705, 706, 707, 957, 1191, 1192, 1193  
 Were, Vincent 1437, 1468  
 Wesson, Dawn 819  
 Wesson, Dawn M. 199, 725, 728, **1386**  
 West, Philippa A. **8**, 968  
 West, Sheila K. 592  
 Wettstein, Zachary S. **296**  
 Wheeler, Sarah S. 562  
 White, Chris 1021  
 White, Gregory S. 923  
 White, Karen 431  
 White, Lisa J. 886  
 White, Michael **177**, 179, 972  
 White, Nicholas J. 466, 548, 886, 983, 985, 988, 1165, 1316, 1426  
 White, Teresa J. 913  
 Whitehead, Stephen S. 1011  
 Whitehurst, Nicole 848, **1311**  
 Whitfeld, Margot 576, 616, **1404**  
 Whitman, Malcom 1297  
 Whitman, Tim 951  
 Whittaker, Joseph 611  
 Whittaker, Maxine 354, 1474  
 Whittembury, Alvaro 1267  
 Whitty, Christopher J. M. 461  
 Wichaidit, Wit **284**  
 Widdowson, Marc-Alain 241, 244, 942, 944, 1249, 237  
 Wiede, Marielle R. **1052**  
 Wiegand, Roger 675, 1201, 1325  
 Wiegand, Ryan 825, 830, 486, 1259, 1428  
 Wiesen, Eric 410  
 Wijayalath, Wathsala 190, 264, 714, 715  
 Wijesinghe, Rushika S. **1474**  
 Wilairatana, Polrat 343  
 Wilder-Smith, Annelies 110  
 Wilding, Craig S. 193, 966, 1210  
 Wilkerson, Richard C. 586, 750, 1199  
 Wilkins, Kimberly 455  
 Wilkins, Patricia P. 96, 129  
 Willey, Barbara 290, 896, 1333, 1360, **388**  
 William, Ryan 10  
 William, Timothy 946  
 Williams, April 439  
 Williams, Andrew R. 171, 1456  
 Williams, Carl 615  
 Williams, Chris 1421  
 Williams, Daniel 162  
 Williams, David **764**  
 Williams, Daniel 1175  
 Williams, Gail 305  
 Williams, John 1436  
 Williams, Katherine L. 1394, 1396  
 Williams, Maya 244, 416, 1102  
 Williams, Patience B. 333  
 Williams, Steven 650, 1489  
 Williams, Thomas N. 881  
 Williamson, John M. 953, 1434  
 Williamson, John W. 456  
 Willilo, Ritha 197  
 Willms, Kaethe 99  
 Wilschut, Jan C. 624  
 Wilson, David 681, 986  
 Wilson, Marianna 129  
 Wilson, Michael 491  
 Wilson, Michael D. 479  
 Wilson, Mary E. 813  
 Wilson, Mark L. 470, 888, 917  
 Wilson, Nick 243  
 Wilson, Nana O. **313**, 663  
 Wilson, Shona 759  
 Wilson, Wayne A. 258  
 Winch, Peter J. 775, 963  
 Wincker, Patrick 1025  
 Wineinger, Kristin 103  
 Wini, Lyndes 1474  
 Winikor, Jared 997  
 Winskill, Peter 479  
 Winter, Rolf 431, 834, 834  
 Winters, Anna M. **165**  
 Winters, Benjamin 73, 165, 727  
 Wirth, Dyann 188, 347, 1297, 1421, 504, 675, 984, 1201, 1325, 1422  
 Wiseman, Virginia 337  
 Wittenberg, Eve 583, 584  
 Wod-Ongom, Richard 1409  
 Woda, Marcia 427, 102  
 Wohlford, Eric M. **668**  
 Wojcik, Genevieve L. **1026**  
 Woldie, Mirkuzie 235  
 Wolfner, Mariana F. 555  
 Wolkon, Adam 879, 1472  
 Wondie, Yemataw Wondie 419  
 Wondimu, Hirut 814  
 Wondji, Charles S. 722, **969**  
 Wong, Chi-Huey 1461  
 Wong, Dawn M. 24  
 Wong, Ing Tien 1454  
 Wong, Joshua M. **456**, 953  
 Wong, Paolo A. 1055, 1094  
 Wongsrichanalai, Chansuda 357, 889  
 Woo, Kristie 1128  
 Woodard, Cassandra L. 860  
 Woodhall, Dana **1428**  
 Woodrow, Charles J. **868**  
 Woods, Emily 964  
 Woodward, Jimmy E. 1108  
 Woolsey, Aaron M. 1298, **1301**  
 Working Group on Chagas Disease in Bolivia and Peru 825  
 Working Group RDTs in Context 454  
 Worrell, Caitlin M. 486, **1259**  
 Wortman, Glenn 951, 1272  
 Worwa, Gabriella **562**  
 Wright, Alexandra 8  
 Wright, Alex 968  
 Wright, Gavin J. 171  
 Wright, Laura K. **1255**  
 Wright, Matthew 528  
 Wright, Melody L. R. **1198**  
 Wu, Douglass 1461  
 Wu, Jianyong 617  
 Wu, Shuenn-Jue 618  
 Wu, Y. 1041  
 Wu, Yi-Chieh 1394  
 Wu, Yimin **184**, 223, 1337, 1455, 1456  
 Wu, Ying 42, 45  
 Wu, Yukun 7  
 Wu-Hsieh, Betty 1099  
 Wuhler, Manfred 976  
 Wurapa, Eyako 936  
 Wurapa, Eyako K. 421, **790**  
 WWARN In Vitro Proficiency Pilot Project Group, on behalf of 1319  
 WWARN QA/QC Group 858  
 WWARN Toolkit Development Team, on behalf of the 1317  
 Wyatt, Nigel 1419  
 Wysocki, Vicki H. 1367  
 X  
 Xavier, Mariana S. 1305

The number(s) following author name refers to the abstract number.

Xayavong, Maniphet 850, 854  
 Xi, Zhiyong **505**  
 Xiao, Lihua 249  
 Xiao, Ningchuan 960  
 Xu, Guang 1058  
 Xu, Jiannong 25, **202**, 1365  
 Xu, Peng 45  
 Xu, Xiyan 1249  
 Xu, Yao 505  
 Xu Kelly, Jane 834, 834

## Y

Yadav, Prashant 470, **810**, 915,  
 1286, 1304, 1470  
 Yahata, Kazuhide 974  
 Yakob, Laith **305**  
 Yale, Gloria 108  
 Yalwala, Sancto J. **224**  
 Yaméogo, Téné Marceline **377**  
 Yan, Guiyun 200, 202, 865, 877,  
 1391  
 Yan, Hongbin 1071  
 Yanagi, Tetsu 168  
 Yanagihara, Richard 53  
 Yang, Amy 175  
 Yang, Alice **1143**, 1146  
 Yang, Yu-Rong 1071  
 Yang, Zhengyu 512  
 Yannick, Dari F. 1456  
 Yanow, Stephanie K. 1314  
 Yap, Peiling **122**  
 Yaro, Jean B. 1331  
 Yassine, Hassan 27  
 Yates, Travis W. 679  
 Yauri, Veronica 1157  
 Yaya Bocoum, Fadima I. K. **402**  
 Yazdanbakhsh, Maria 703, 760,  
 1109  
 Ye, Chunyan 1384  
 Y3, Maurice **392**  
 Ye, Yazoume 290, 393, 896, **1360**  
 Yeboah-Antwi, Kojo 574, **1339**,  
 1477  
 Yeda, Redemptah 859  
 Yen, T Y. 1099  
 Yenesew, Abiy 860  
 Yeo, Kee Thai **992**  
 Yeo, Tsin W. 155, 946, 1424  
 Yerbanga, Rakiswendé S. **394**  
 Yerbanga, Serge R. 1211  
 Yeung, Shunmay 328, **454**, 466  
 Ygoña, Stella 1082  
 Yi, Poravuth 983  
 Yohan, Benediktus 101  
 Yohanas, S 646  
 Yokobe, Lindsay 304  
 Yokoyama, Naoaki 974  
 Yoksan, Sutee 636  
 Yongchaitrakul, Siriporn **407**  
 Yongchavit, Kosol 720

Yoo, Dae-Hyun **1236**  
 Yoo, Mi-sun 580  
 Yoon, In-Kyu 15, 1087, 1093  
 Yoon, Steven 884, 879, 892,  
 1439  
 Yoshida, Lay Myint **246**  
 Younan, Mary 245  
 Younan, Rasha 1106  
 Young, Ginger 1013, 1014  
 Young, Sarah 1110  
 Younis, Iman 1237  
 Yount, Boyd 116  
 Yousif, Maitham G. **1043**  
 Youssef, Fouad G. 245  
 Yu, Jihnhee 940, 1241  
 Yu, Sun N. 29  
 Yu, Wanqin 25, 202, 1365  
 Yu, Yanan 42, 45, 1410  
 Yu, Y. 1041  
 Yubon, Nushara 435  
 Yugbare Belemsaga, Danielle M.  
 J. **373**, **376**  
 Yui, Katsuyuki 168  
 Yukich, Joshua O. 468, 694,  
 1340, **903**, 1435

## Z

Zaidi, Anita 1238, 1245, 1380  
 Zajdowicz, Jan 949  
 Zaman, K. 1479  
 Zaman, Umber 1245  
 Zambrana, Luís Enrique 1376  
 Zambrano, Betzana 1012  
 Zaongo, Silvére 1307  
 Zapata, Alejandra 1463  
 Zapor, Michael 951  
 Zariquiey, Carlos M. **640**  
 Zarroug, Isam 647  
 Zedar, Rebecca 1086  
 Zegers De Beyl, Celine 1019  
 Zeitler, Bryan 439  
 Zeituni, Amir E. 712  
 Zeldis, Jerome 152, 1114, 1147  
 Zelner, Jonathan L. 933  
 Zeng, Erliang 206  
 Zeng, Qiandong 1110  
 Zeng, Wu **570**  
 Zerihun, Mulat 1268, 1271  
 Zerlotini, Adhemar 529, 762  
 Zerpa, Rito 259, **1055**  
 Zeuz Capitán, Capitán 945  
 Zevallos, Juan C. 1012  
 Zhan, Bin 649, 1034  
 Zhang, Jin-Hui 449  
 Zhang, Lei 439  
 Zhang, Liang 676  
 Zhang, Lixin 1042  
 Zhang, Min **133**  
 Zhang, Peng 434  
 Zhang, Ruijun 632  
 Zhang, Veronica M. 860, 1453  
 Zhang, Xin **1363**  
 Zhang, Yaobi 30, 300  
 Zhang, Yanmin 591  
 Zhang, Yaobi 1448  
 Zhang, Zhiwen 593, 610  
 Zhao, Hui 455  
 Zhao, Jin-Ming 449  
 Zhioua, Elyes **587**  
 Zhou, Guoli 505  
 Zhou, Guofa 1391  
 Zhou, Hong 185, 186  
 Zhou, Xiao-Nong 122  
 Zhou, Zhaoxia 29  
 Zhu, Daming 1455  
 Zhumu, Bai 1101  
 Zimic, Mirko 95, 1077  
 Zimic, Mirko for the Cysticercosis  
 Working Group in Peru **1081**  
 Zimmerman, Peter 208, 559,  
 502, 1483  
 Zimmers, Jay 849  
 Zingue, Dezemon 1062  
 Zio, Muliadi 1219  
 Ziro, Odrie 1252  
 Zitha, Alpheus 162, 1175  
 Zollner, Gabriela 65, 67  
 Zollo, Paul H. A. 144  
 Zompi, Simona **629**, **632**, **1395**  
 Zongo, Issaka 463, 1307  
 Zornetzer, Heather 452, 805  
 Zorrilla, Víctor 227, 588, **1223**  
 Zottig, Victor 676  
 Zou, Zhen 209  
 Zucker, Jeremy 1110  
 Zulu, Siphon 1433  
 Zulu, Zuli 469  
 Zuluaga Idárraga, Lina M. 1318  
 Zumbo, Betty 1205  
 Zuniga, Concepcion 819  
 Zunt, Joseph R. 1094, 1373,  
 1413, 931  
 Zwang, Julien 779, 1351