
Keynote Forum October 30, 2017

Zoology & Microbiology 2017



International Conference on

Zoology, Microbiology & Medical Parasitology

October 30-November 01, 2017 | Chicago, USA



Jay R Stauffer

Penn State University, USA

Controlling vectors and hosts of Schistosomes in Lake Malawi

Schistosomiasis is a parasitic disease of major public health importance in many countries in Africa, Asia, and South America. The disease is caused by trematodes of the genus *Schistosoma* that require specific freshwater snail species to complete their life cycles. Prior to 1985, the open waters of Lake Malaŵi were free from schistosome transmission. Over the past decades, however, the prevalence of urinary schistosomiasis has increased dramatically in the southern part of the lake. We found the prevalence of human schistosomiasis in school-aged children to be negatively correlated with the density of molluscivorous fishes. Specifically, the increase in infection rate in southern Lake Malawi between 1978 and 1991 is coincident with the reduction in numbers of snail-eating fishes. During 2003, we determined the relative abundance of molluscivorous fishes and snail density at 18 sites throughout the lake, and schistosome infection in school-aged children living in selected lake shore communities of Lake Malaŵi. At the 18 sites sampled in 2003, we found that snail abundance decreased with an increase in abundance of snail-eating fishes. Furthermore, the 2003 samples showed that the abundance of snail-eating fishes increased and there was a reduction in schistosomiasis in school-aged children in Chembe Village. We believe that we will not observe a return to the 1978 infection rates until these fishes continue to increase and inhabit shallower waters. The transmission of the disease may be further complicated.

We postulated that a strain of *S. haematobium* from other parts of Africa, which was introduced into the Cape Maclear region of Lake Malaŵi by tourists, was compatible with *Bulinus nyassanus*—which is a close relative of *B. truncatus*, and interbred with the indigenous strain of *S. haematobium*, which ultimately produced via introgression a strain that can use both *B. globosus* and *B. nyassanus* as intermediate hosts. This actively evolving situation involving intermediate snail–host switching and decline of *Trematocranus placodon*, a natural cichlid snail predator, will impact on transmission of urogenital schistosomiasis within the local communities and on tourists who visit Lake Malaŵi.

Speaker Biography

Jay R Stauffer is a Distinguished Professor of Ichthyology at Penn State University. His international work has involved the transfer of research results and technology to both the local governments and the people of Malawi. The Smithsonian (1988:144-155) highlighted his early work on Lake Malaŵi and the British Broadcasting Corporation (BBC) used him as a primary consultant on fishes and used his underwater videos in several of their productions, including *Blue Planet*. In 2006, he co-authored an educational brochure entitled *Bilharzia in Lake Malaŵi – What are the Facts*, that was published in both English and Chechewa, the most widely used language in Malaŵi (<http://sfr.psu.edu/research/labs/stauffer/lake-malawi/general/bilharzia/view>). His international studies also gave him the opportunity to describe several species of fishes from Malaŵi and Nicaragua, and to study the adverse impact of the introduction of African tilapia on native species.

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Ruben Bueno Mari

Laboratories Lokímica, Spain

Vector control strategies in the framework of the fight against emerging arboviruses: The example of *Aedes albopictus* management in Spanish Mediterranean cities


Mosquitoes are considered as the most dangerous ectoparasites of the world. The ubiquity of these insects, intense haematophagic behavior of females, high bioecological plasticity of many species and the role as vectors of a great variety of pathogens, has made this animal group a serious public health hazard for centuries. Nowadays the Asian tiger mosquito, *Aedes albopictus*, is probably one of the best exponents of this concern. This invasive species recently detected in the last decades in new continents such as America, Africa, Oceania and Europe, is a potential vector of several arboviruses like dengue (DENV), zika (ZIKV) or chikungunya (CHIKV) in urban and periurban environments. These viruses are currently emerging worldwide, especially in tropical and temperate regions where vectors are capable of proliferating and reach high population densities. In Spain, the species was first collected in 2004 and currently is well distributed across the Mediterranean fringe. It is well established in some of the most important cities of the country like Barcelona, Valencia and Murcia, among others. Simultaneously in Spain DENV, ZIKV and CHIKV are diseases frequently imported by tourists and immigrants infected in endemic countries. This context of increasing incidence and spread of potential local vectors, high infection rates of these arboviruses in tropical countries and globalization, that facilitates quick and continuous human movements all over the

world, has motivated the Spanish Ministry of Health to declare DENV, ZIKV and CHIKV as priority notifiable diseases in our country. Our presentation is focused on how this conjunction of epidemiological and entomological issues is approached based on integrative vector control strategies. The entomological interventions surrounding imported cases of DENV, ZIKV and CHIKV in order to evaluate (surveillance-monitoring) and minimize (control) the risk of disease amplification at local scale will be a mandatory topic for all public administrations involved in Municipal Public Health during the next years.

Speaker Biography

Ruben Bueno Mari finished his PhD in 2010 from the University of Valencia (Spain) and obtained the Special Doctorate Award in the field of Natural Sciences two years later. He is an active Member of several scientific associations at national and international level, highlighting his role as Member of the Board of the European Mosquito Control Association (EMCA). He also collaborates with several scientific journals as member of the Editorial Board, is an Expert Advisor of the Iberoamerican Society of Scientific Information (SIIC) and has published more than 60 scientific publications in journals related with the fields of medical and veterinary entomology, applied zoology and public health. He currently cooperates with several universities and other academic institutions in superior teaching issues related with his field of expertise (medical entomology, vector control and vector-borne diseases) and is the Head of the Department of Research and Development (R+D) of a leading company in environmental health called Laboratorios Lokímica.

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 Notes:



Kuppuswamy N Kasturi

US Food and Drug Administration, USA

Real-Time PCR for detection of *Salmonella* spp. in environmental samples


The methods currently used in FDA field laboratories and other public health laboratories for detecting *Salmonella* in food /environmental samples require 2 days and have limited sensitivity. We describe the development and validation of a real-time PCR method that detected *Salmonella* and presence of group D in 24 h. Primers and probes specific to the *invA* gene of *Salmonella*, group D, and Enteritidis serovar were designed and evaluated for the inclusivity and exclusivity using a panel of 329 *Salmonella* isolates consisting 126 serovars from 32- O groups and 22 non-*Salmonella* environmental organisms. The *invA*-, group D-and Enteritidis - specific sets identified the isolates accurately. The PCR method was 100% inclusive for *Salmonella* spp and had a detection limit of 2 copies of *Salmonella* DNA per reaction. A Single-laboratory validation performed on 1,741 environmental samples demonstrated that the PCR method detected 55% more positives than the VIDAS method that is currently used. The method is more specific

and did not report any false-negatives. The receiver operating characteristic (ROC) analysis documented excellent agreement between the results from the culture and PCR methods (area under the curve, 0.90; 95% confidence interval of 0.76 to 1.0) confirming the validity of the PCR method. The validated PCR method will help to strengthen public health efforts through rapid screening of *Salmonella* spp. in environmental samples.

Speaker Biography

Kuppuswamy N Kasturi after completing DSc from the University of Paris South, France, pursued postdoctoral studies at the Beatson Institute for Cancer Research, Glasgow, Scotland, United Kingdom and then worked as a Member of Microbiology Faculty at Mount Sinai Medical Center, New York, USA prior to joining USFDA as a Microbiologist in 2002. He has published more than 50 papers in reputed international journals and has been serving as an Editorial Board Member of *International Journal of Food Science, Nutrition and Dietetics*.

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 Notes:

Keynote Forum October 31, 2017

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Michael Kosoy

Fort Collins, USA

Movement ecology of rats of the genus *Rattus* and global distribution of rat-associated *Bartonella* species

Statement of the Problem: Animal movement resulting from intentional or unintentional human activity can introduce pathogens into new geographic areas. The objective of this study focuses on introduction of zoonotic agents via invasive rat species (*Rattus norvegicus* and *R. rattus*) to the US seaports from other continents. The bacterial zoonotic pathogens associated with commensal rats include several species of *Bartonella*.

Methodology & Theoretical Orientation: To conduct the proposed study, rat blood, tissue and ectoparasite samples were collected in Thailand, Vietnam, Madagascar, and several cities in the USA and Canada. Bacteria were cultured on agar supplemented with rabbit blood. *Bartonella* spp. were identified by sequence analysis of amplified fragments of 3-5 house-keeping genes.

Findings: The investigations have demonstrated that rats harbor *Bartonella* spp., most of which are clustered into a defined phylogenetic lineage that can be sub-divided further into a number of sub-clusters. This group was defined as *B. elizabethae* species complex. In Thailand, *Bartonella* was cultured from rats of eight *Rattus* spp. and the strains belonged to >20 genetic variants. Some of these *Bartonella* spp. were also identified in the USA seaports. The genetic diversity of *Bartonella* spp. found

in rats in the US cities was significantly lower than in Asia where these species are highly prevalent and extremely diverse.

Conclusion & Significance: The data suggest that some *Bartonella* spp., being evolutionary and ecologically associated with rats of the genus *Rattus*, have been dispersed from Asia to seaports around the globe where these bacteria have become established among domestic rats. The finding of *Bartonella* spp. in a high proportion of rats from around the globe suggests the need to investigate whether these agents might be responsible for cases of human pathology, especially in countries where *Bartonella*-infected rats arrive from Asian seaports.

Speaker Biography

Michael Kosoy is a Research Biologist and the Chief of Bartonella & Rodent-Borne Diseases Laboratory at the Division of Vector-Borne Diseases, Centers for Disease Control and Prevention (CDC). He is the author or co-author of >150 publications in area of ecology, evolution, zoology, microbiology, and epidemiology of infectious diseases. He has worked for many years in the area of ecology and epidemiology of zoonotic and vector-borne diseases. His international activities included, but not limited to P.R. China, Thailand, Vietnam, Kazakhstan, Georgia (Caucasus), Japan, Israel, Russia, Kosovo, Kenya, D.R. Congo, Peru, and Guatemala. His main research interests include disease ecology, evolution of pathogens, wildlife diseases, One Health movement, bioethics, and transdisciplinarity.

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 Notes:



Wenbin Tuo

United States Department of Agriculture/ARS, USA

Ostertagiosis and *Ostertagia ostertagi* interactions with the bovine host

Statement of the Problem: Parasitic nematodes are able to cross-regulate host immunity, evade immune surveillance, favoring their own survival. This is in part accomplished by producing bioactive molecules possessing potent immunoregulatory roles. *Ostertagia ostertagi* is a nematode parasite specifically infecting the gastric glands of the abomasum (4th stomach) of cattle. This most important parasite is highly prevalent in temperate regions worldwide and causes sustained production losses to the cattle industry. Gastrointestinal parasite control heavily relies on the use of anthelmintics; however, drug resistance is rapidly emerging and requires development of alternatives to drug control.

Methodology & Theoretical Orientation: Parasitic immune modulators were investigated by homologue search in the parasitic transcriptome and molecularly cloned/expressed/purified, and functionally characterized.

Findings: Upon infection with *O. ostertagi*, significant immune responses were readily detectable in the abomasum and its draining lymph nodes as early as day 3 post infection. However, host resistance to infection was not generated until after repeated infections. A number of parasitic immune modulators such as macrophage migration inhibitory factor (MIF) and

annexins were identified some of those were developmentally regulated and possessed active functions cross-regulating bovine host immune responses. Results suggested that immunosuppression mediated by parasitic immune modulators may be a mechanism by which the parasite evades host protective immunity.

Conclusion & Significance: Investigation of the host-parasite interaction, particularly immunomodulation mediated by parasitic-derived immune modulators, will aid in further understanding host-parasite interactions, host response to infection and parasite evasion, and facilitate the development of immunological control measures.

Speaker Biography

Wenbin Tuo has expertise in protozoan and nematode parasite infectious diseases in livestock species. He has devoted his professional career to understanding host-parasite interactions and development of immunologic control measures for parasitic infections in large ruminants. Vaccine candidates identified by antigen-specific CD4 T cells and parasitic immune modulators that are able to cross-down-regulate host protective immunity have been tested in numerous vaccine trials and some of the vaccines have been demonstrated to have significant protective efficacies. His ongoing research involves continued investigation of interplays between the parasites and hosts and identification and testing of protective candidate vaccines in ruminants.

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Lilia Gonzalez-Ceron

Regional Center for Research in Public Health, Mexico

Deciphering the participation of *Anopheline* species in the transmission of *Plasmodium vivax* in Mexico

Statement of the Problem: Malaria is a public health problem in tropical and subtropical regions of the world. In most Mexican territory, *P. vivax* transmission has been historical and remains in some malarious foci along the pacific coast and in the southern region, while *P. falciparum* was eliminated about eight years ago. In order to contribute to malaria control and elimination in the region, in southern Mexico we carried out several studies to discover vector and parasite factors involve in the *P. vivax* transmission. The purpose of this study was to investigate *P. vivax* genetic variation, and vector susceptibility, to identify vector-parasite factors favoring *P. vivax* transmission.

Methodology & Theoretical Orientation: The most abundant Anopheline vector species of different sites from Mexico were inbred under insectary conditions. *P. vivax* infected blood obtained from patients living in southern Mexico was used to test the mosquito susceptibility. The number of mosquitoes infected with oocyst and the number of oocysts per mosquito were recorded per colony and per mosquito species. Parasite genotype was determined and its association to vector susceptibility was analyzed.


Findings: The data exposed different *P. vivax* genotypes in southern Mexico that produced different degree of oocyst infection in *An. albimanus* and/or *An. pseudopunctipennis*, and *An. punctipennis*. Moreover, there were different colonies of two Anopheline species from distant geographic sites that showed similar susceptibility to southern parasites.

Conclusion & Significance: The finding suggests that *P. vivax* in southern Mexico comprises strains with different compatibility to the local Anopheline species. These mosquito vectors are distributed across the country and likely capable to sustain malaria transmission. On the other hand, the genetic pool of malaria parasites seem reduced to few genotypes, those more adapted to local vector species.

Speaker Biography

Lilia Gonzalez-Ceron, PhD. Parasitologist. Principal researcher of the Regional Centre of Research in Public Health, National Institute of Public Health, Chiapas, Mexico. She has been working with *P. vivax* malaria since 1986s, and has been involved in epidemiological studies, vector-parasite interactions, diagnosis and treatment. Also, she is interested in the evolutionary genetics of *P. vivax* in Mexico and its transmission dynamics.

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 Notes:



Yehudah L Werner

The Hebrew University of Jerusalem, Israel

Zoological research serving conservation

Zoology is important for human existence. Planning the conservation of the biosphere and of its species richness requires good alpha-taxonomy of animals. Yet much zoological research fails to serve this goal. Especially, two lines of research. First trendy genomic phylogeny studies that ignore or abuse morphology yield controversies and questions for example: whether to unite the lizard genera *Geckonia* and *Tarentola*, what are the species of *Hemidactylus* lizards hitherto lumped in Israel under *H. turcicus*? And are the morpho-taxa of *Testudo graeca* tortoises in the Levant real, despite genomic appearances? Second, investigations and debates about nomenclature, pitching priority against convention, and futile splitting of genera within a clade, such as the lizard *Agama*, waste the

time of zoologists. Zoologists should practice solid morphology-based, genomics-supported, alpha-taxonomy.

Speaker Biography

Yehudah L Werner is matriculated in 1949 from the Re'alli School (Biological Trend), Haifa. He has army service in 1948-50. He is an amateur and researcher of fishes, amphibians and reptiles. He studied Zoology at the Hebrew University of Jerusalem, MSc in 1956, PhD (summa cum laude) in 1961. He is in the University's staff since 1953 (TA), full Professor 1978, Emeritus 2000. He is the Co-founder, Society for Protection of Nature in Israel, 1953. Member, the Language Academy's Committee on Zoological Terms, 1963-99. He is the Editor of *Israel Journal of Zoology*, 1973-89. He is the President of Zoological Society of Israel, 1991-93. He has some 470 assorted publications, including a guide to the reptiles and amphibians of Israel (1995, Hebrew) and reptile life in the land of israel with comments on adjacent regions (2016, Chimaira).

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