184

ASSOCIATION OF AUTOCIDAL GRAVID OVITRAPS WITH REDUCED RATES OF CHIKUNGUNYA VIRUS INFECTION IN PUERTO RICO

Tyler M. Sharp[1], Olga Lorenzi[1], Veronica Acevedo[1], Chelsea Major[1], Brad J. Biggerstaff[2], Janice Perez-Padilla[1], Jorge Munoz-Jordan[1], Stephen Waterman[1], Roberto Barrera[1]

[1]Centers for Disease Control and Prevention, San Juan, PR, United States, [2]Centers for Disease Control and Prevention, Fort Collins, CO, United States

There are currently no effective and sustainable interventions to prevent infections with viruses transmitted by *Aedes* mosquitoes. Since 2012, four communities in Puerto Rico have been participating in a field trial of a recently developed autocidal gravid ovitrap (AGO). After 3 AGO traps were placed in >85% of homes in two intervention communities, adult *Ae. aegypti* mosquito populations were reduced by ~80% compared to two non-intervention communities. The introduction of chikungunya virus (CHIKV) to Puerto Rico in May 2014 provided an opportunity to determine if AGO traps were associated with CHIKV infection rates in humans and mosquitos in these communities. To estimate the seroprevalance of CHIKV infection in intervention and non-intervention communities, 377 houses were randomly selected. Participating household members provided a blood specimen and completed a questionnaire on demographics, recent illnesses, and mosquito avoidance practices. Serum specimens were tested by IgG ELISA to detect historic CHIKV infection. During November 2015 and February 2016, a total of 233 (62%) households from the four communities agreed to participate. Mean age of participants (53 years) was greater than that of all eligible residents (49 years). Mean age of participants from intervention communities was not significantly different from those from non-intervention communities. Among 152 and 175 participants from non-intervention and intervention communities, historic CHIKV infection was detected in 69 (45%) and 40 (23%) participants, respectively. The observed two-fold difference in the prevalence of CHIKV infection in intervention compared to non-intervention communities may be associated with the lower measured mosquito densities in communities where AGO traps are present. Additional analyses are being performed to adjust anti-CHIKV antibody prevalence with respect to sampling design, community differences, and participation rates. These findings may implicate AGO traps as an effective and sustainable community intervention to prevent infections transmitted by *Ae. aegypti* mosquitos.

185

BACTERIAL COMPOSITION OF LARVAL BREEDING SITES OF AFRICAN *AEDES AEGYPTI* AND ITS EFFECT ON VECTORIAL CAPACITY

Laura B. Dickson[1], Davy Jiolle[1], Guillaume Minard[2], Isabelle Moltini-Conclois[1], Diego Ayala[3], Christophe Paupy[4], Claire Valiente Moro[2], Louis Lambrechts[1]

[1]Insect-Virus Interactions Group, Department of Genomes and Genetics, Institut Pasteur, URA CNRS 3012, Paris, France, [2]Ecologie Microbienne, UMR CNRS 5557, USC INRA 1364, VetAgro Sup, FR41 BioEnvironment and Health, Université Claude Bernard Lyon 1, Villeurbanne, France, [3]CIRMF, BP 769, Franceville, Gabon, [4]UMR MIVEGEC IRD 224 CNRS 5290 UM1 UM2, Montpellier, France

Like other animals, insects establish symbiotic associations with microbial communities that shape their individual phenotype and fitness. In particular, the native gut bacteria of insect vectors can modulate their immunity and susceptibility to human pathogens. Compared to vertebrates, insects have more labile gut bacterial associations that are under strong influence of the environment. Thus, habitat-related differences in bacterial communities could mediate an environmental influence on vector-borne pathogen transmission. We investigated whether differences in the bacterial communities of larval breeding sites may drive variation in vectorial capacity of the mosquito *Aedes aegypti*, a major vector of dengue, Zika, and chikungunya viruses. In Sub-Saharan Africa, *Ae. aegypti* larvae develop both in domestic habitats such as human-associated containers and in sylvatic habitats such as rock pools or tree holes. Comparison of natural sylvatic and domestic breeding sites in Gabon by metataxogenomics revealed contrasted bacterial communities in the water and, to a lesser extent, in the midgut of adult *Ae. aegypti* emerging from these breeding sites. To test whether exposure to different bacteria during larval development may differentially affect adult vectorial capacity, we created gnotobiotic larvae using a selection of four bacterial isolates from the natural breeding sites in Gabon. Mono-association with *Enterobacter*, *Salmonella*, *Arthrobacter*, or *Rhizobium* bacterial isolates during larval development resulted in significant differences in pupation rate. In addition, larvae exposed to the *Arthrobacter* isolate had larger bacterial loads in adult midguts pre and post blood meal, showed decreased antibacterial activity in adult hemolymph, and were less susceptible to dengue virus infection. No differences in adult lifespan were detected between the different gnotobiotic treatments. Together, our results provide the proof of principle that habitat-related differences in larval exposure to bacteria can drive variation in adult mosquito immunity and vectorial capacity.

186

THE IMPORTANCE OF HUMAN POPULATION CHARACTERISTICS IN MODELING MOSQUITO VECTORS: A COMPARATIVE ANALYSIS OF MODEL COMPONENTS

Julie Obenauer Motley, Andrew Joyner, Megan Quinn

East Tennessee State University, Johnson City, TN, United States

The current Zika virus epidemic in the Western hemisphere is representative of the confluence of global climate change and infectious disease expansion, and vector modeling represents a pertinent and timely method to analyze the environment associated with Zika-carrying mosquitoes. Among many mosquito species distribution models, there are varying opinions on which variables are most predictive and, consequently, should be included in modeling efforts. While climate variables (e.g., mean temperature, mean precipitation) are routinely included, some argue that human population dynamics, in the form of population density and socioeconomic status, should also be included. This project aimed to test the importance of including human population characteristics by modelling the Zika virus vector *Aedes aegypti* in the Southeastern United States with climate variables, population density, and poverty characteristics. A. aegypti occurrences, global climate data, and population characteristics were obtained from publicly available sources and sampled at a resolution of 2.5 arc-minutes. Data pre and post-processing was completed in ArcMap 10.3 and models were created in Maxent v.3.3.3k. Four models were developed for this project: a climate-only model, a climate and population density model, a climate and poverty model, and a combined model with climate, population density, and poverty. Models were evaluated by comparing test and training area under the curve metrics, omission and commission errors, and variable jackknifing results. The climate-only model performed poorly compared to models with human population characteristics. The combined model was the best fit, though the model with climate and population density had a lower commission rate (21.0% and 20.6%, respectively). Jackknife results for the full model showed that population density was the most significant contributor to the model. This research indicates that more consideration should be given to human population characteristics when modelling mosquito habitats.