

those in people with no history of dengue. Our results suggest that the level of antibodies can be used as a proxy for mosquito bite exposure and a measure of dengue fever risk.

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EVALUATION OF PREDICTIVE MAPS FOR *Aedes aegypti* LARVAL HABITATS IN TWO URBAN AREAS OF COSTA RICA

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The abundance of *Aedes aegypti* can be associated with urban structure and tree cover, which conceals and protects containers. The purpose of this study was to create and evaluate predictive maps for *Ae. aegypti* larval habitats in Puntarenas and Carpio, two very different urban environments in Costa Rica. Linear regression models for number of mosquito larval habitats had been developed for Puntarenas, and they showed a significant association with tree cover when corrected by the number of locations evaluated ($R^2 = 0.650$, $p < 0.001$). Land cover maps were created from Quickbird satellite imagery of both sites. Data was extracted from 50 by 50 m cells, and parameters from the model were used to create predictive maps by determining the expected number of *Ae. aegypti* positive larval habitats in all cells that cover the urban areas. To evaluate maps, cells were randomly selected, and entomological evaluations were performed. Four categories were created for the number of larval habitats per cell: low (0-1), medium (2-3), high (4-5), and very high (6 or more). For both sites, the expected number of wet containers in sample cells fell within the 95% confidence interval of predicted values. In Puntarenas, 382 wet containers were identified, container index was 22.5% and Breteau index 43.7. Expected and observed categories of *Ae. aegypti* larval habitats per cell in Greater Puntarenas were significantly correlated ($p = 0.037$). Only 32.5% of cells harbored the exact number of expected habitats, 74% contained the expected number +/- 2 habitats, and only 16% underestimated total larval habitats. In Carpio, 693 wet containers were identified, container index was 11.4% and Breteau Index 24.7. Expected and observed categories of *Ae. aegypti* positive habitats per cell were not significantly correlated in Carpio. Only 50% of cells contained the expected number +/- 2 habitats, and 29% underestimated the total observed. The most frequent *Ae. aegypti* larval habitats in Puntarenas included outdoor containers and miscellaneous objects, while larval habitats in Carpio were commonly human-filled, such as drums and buckets. These maps and models may be considered adequate for areas like Puntarenas, whereas they do not seem to apply for Carpio. Tree cover may provide useful information in sites where *Ae. aegypti* larval habitats include mostly outdoor rain-filled containers, as opposed to sites where containers are greatly affected by the need for water storage.

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CLIMATIC VARIABILITY AND LANDSCAPE HETEROGENEITY IMPACT URBAN MOSQUITO DIVERSITY AND VECTOR ABUNDANCE AND INFECTION

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Urban habitat heterogeneity can modify patterns of interactions across species and lead to spatially fine grained differences in β -diversity patterns and their associated ecosystem services. Here, we study the impacts of landscape heterogeneity and climatic variability on: (i) the richness and diversity patterns of mosquitoes (Diptera: Culicidae) and (ii) the abundance and West Nile virus infection rate of the house mosquito, *Culex pipiens*, in Chicago, USA. We conducted a four year long study (2005-2008) in 8 sites

that captured a gradient of urban heterogeneities. We found a total of 19 mosquito species, a representative sample of mosquito species richness in the area, according to both model estimation ($\text{Chao2} \pm \text{S.E.} = 20.50 \pm 2.29$) and faunal records for Chicago. We found that heterogeneity in the landscape was the best predictor of both mosquito species richness and diversity, with the most heterogeneous landscapes harboring the largest number of species. In general there were no changes in species richness over the years that could be associated with weather patterns and climatic variability (WPCV). In contrast, changes in diversity evenness showed signatures of WPCV. Our results also showed that WPCV had major impacts on house mosquito abundance and West Nile virus mosquito infection rate (MIR) patterns. Although MIR was independent of mosquito diversity, it was associated with overall mosquito abundance, which had a convex association with species richness (i.e., abundance increases to a point after which it decreases as function of species richness). Finally, our results highlight the importance of considering dominant vector species as part of a community of vectors, whose biodiversity patterns can directly or indirectly impact the risk of infectious disease transmission.

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NON-LINEAR IMPACTS OF CLIMATIC VARIABILITY ON *Aedes aegypti* POPULATION REGULATION

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Aedes aegypti is one of the most common urban tropical mosquito species and an important vector of dengue, chikungunya, and yellow fever viruses. It is also an organism with a complex life history where larval stages are aquatic and adults are terrestrial. This ontogenetic niche shift could shape the density dependent regulation of this and other mosquito species because events that occur during the larval stages impact adult densities. Here, we present results from simple density-dependence mathematical models fitted using maximum likelihood methods to weekly time series data from Puerto Rico and Thailand. Density dependent regulation was strong in both populations. Analysis of climatic forcing indicated that populations were more sensitive to climatic variables with low kurtosis (i.e., climatic factors highly variable around the median) rainfall in Puerto Rico and temperature in Thailand. Changes in environmental variability appear to drive sharp changes in the abundance of mosquitoes. The identification of exogenous factors forcing the sharp changes in disease vector populations using their statistical properties, such as kurtosis, could be useful to assess the impacts of changing climate patterns on the transmission of vector-borne diseases.

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THE ROLE OF SWINE IN THE ECOLOGY OF JAPANESE ENCEPHALITIS VIRUS TRANSMISSION OF SOUTHERN VIETNAM

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Japanese encephalitis virus (JEV) is a mosquito-borne flavivirus disease of major public health importance and is endemic to both north and south Vietnam. Swine populations play a role in JEV transmission as both a reservoir and amplifying host. In general, infected adult pigs support transient but high titer viremia and remain asymptomatic. In contrast, naïve piglets exhibit fever and experience weight loss, and gilts or sows who become infected from 40-80 days of gestation often abort or give birth to stillborn mummified fetuses. In some JEV-endemic countries, swine vaccination is performed within commercial livestock sector to prevent losses in reproductive performance of breeding herds. Here we review previous unpublished studies of JEV seroprevalence