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Abstract

Identifying the vectors of *Anolis* malaria transmission in Puerto Rico.

Vector-borne diseases are a global health priority, particularly in the tropics and sub-tropics. Even though, malaria infection in rodents helped us made significant progress understanding the molecular aspects of infection, we know less about how ecological relationships influence transmission. Anole lizards in Puerto Rico are an ideal animal model to understand the ecological aspects of *Plasmodium* transmissions because the host is highly abundant, diagnostics are simple and transmission frequent. Anole lizards in Puerto Rico are infected by three *Plasmodium* species (two infecting erythrocytes *P. azurophilum* and *P. floridense*; and one that infects leukocytes, *P. leucocytica*). Even though we know the basic ecological aspects driving transmission in this host-parasite system, the vector(s) are currently unknown. The purpose of our study is to identify a narrow list of candidate vectors for the three *Plasmodium* species infecting Anole lizards in Puerto Rico. The field trapping has been carried out using six CDC traps placed at El Verde Field Station and across the University of Puerto Rico- Rio Piedras. After the collections, the insects are placed on ethanol 95% and stored for classification. A dissecting microscope is used for selecting and identifying each mosquito by family and genus. Once is identified, a DNA extraction and a nested PCR is done to determine if the mosquito is infected or not. Based on literature, we have selected a candidate list of six genres (5 of them belong to the *Culicidae* family and one to the *Psychodidae*). In general, the traps have been collecting more of other families of *Diptera* than mosquitoes. Therefore, we plan to use a source of CO₂ to attract more mosquitoes to the traps. The identification of this list will contribute to studying the vector's life cycle, incorporating the results in models to explain the potential source of spatial heterogeneity in transmission.