

Mosquito diversity and arbovirus detection in Paraguay: First evidence of dengue and chikungunya virus infection in field populations

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Abstract

Arboviruses are mosquito-borne viruses of major public health importance, particularly in tropical and subtropical regions. In Paraguay, dengue (DENV) and chikungunya (CHIKV) viruses are among the most epidemiologically relevant; however, studies integrating mosquito and arbovirus surveillance remain scarce. This study aimed to characterize mosquito assemblage composition across different ecological settings and investigate arbovirus circulation in field-collected mosquitoes. A total of 4,595 mosquitoes (609 pools) were collected between 2013 and 2024 from urban, rural, and Atlantic Forest environments in Paraguay. Twenty-six mosquito species were identified, with *Culex quinquefasciatus* (55.3%) as the most abundant, followed by *Aedes (Ochlerotatus) scapularis* (13.3%). *Aedes aegypti* (7.3%) was mainly associated with urban areas. Diversity analyses showed higher alpha diversity and greater gamma diversity in the Atlantic Forest and lower values in rural areas, whereas high beta diversity indicated substantial species turnover among locations. Molecular screening by real-time RT-PCR detected no evidence of West Nile, Saint Louis encephalitis, Venezuelan equine encephalitis, Mayaro, yellow fever, Zika, or Oropouche viruses. In contrast, *A. aegypti* pools tested positive for DENV (n = 3; 2021 and 2023) and CHIKV (n = 3; 2023). Phylogenetic reconstruction confirmed the circulation of DENV-4 Genotype II (lineage B.1.1), DENV-2 Genotype II (F.1.1.2), and CHIKV East/Central/South African (ECSA) lineages in Paraguay, all closely related to human outbreak-associated sequences. These findings provide the first molecular evidence of arbovirus infection in field-collected mosquitoes in Paraguay and emphasize the importance of integrated entomological and viral surveillance.