

# Genetic variability and heterogeneity of Venezuelan equine encephalitis virus vector *Ochlerotatus taeniorhynchus* (Diptera: Culicidae) populations of the Colombian Atlantic coast, based on microsatellite loci

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**ABSTRACT.** In Colombia, the mosquito *Ochlerotatus taeniorhynchus* has been identified as an efficient vector of the epidemic-epizootic Venezuelan equine encephalitis virus. We evaluated the genetic variability and heterogeneity of this mosquito in Colombian populations using eight microsatellite DNA loci. Two hundred and ten mosquito specimens collected from seven populations of the Colombian Atlantic coast (San Bernardo del Viento, Coveñas, Cartagena, Barranquilla, Ciénaga, Dibulla, and Riohacha) were analyzed. We found five polymorphic microsatellite loci, with 19 alleles giving 62.5% polymorphism; the mean number of alleles per locus was 3.8. The mean expected heterogeneity ranged from 0.568 to 0.660. Most of the polymorphic microsatellite loci were in Hardy-Weinberg disequilibrium, due to both deficit and excess of heterozygotes.

The  $F_{st}$  statistic gave a total value of 0.0369, reflecting low genetic differentiation among the populations and, as a consequence, a low degree of structuring among them, while gene flow was high ( $Nm = 6.52$ ); these findings point to genetic homogeneity among these populations. There was no significant linkage disequilibrium between genotype pairs of the various populations. We concluded that this mosquito is distributed in local populations along the Colombian Atlantic coast; these findings will be useful for developing strategies for controlling this vector.

**Key words:** *Ochlerotatus taeniorhynchus*; Genetic heterogeneity; Venezuelan equine encephalitis virus; Polymorphic microsatellite loci; Genetic variability