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Reduced levels of genetic variation in *Aedes albopictus* (Diptera: Culicidae) from Manaus, Amazonas State, Brazil, based on analysis of the mitochondrial DNA *ND5* gene

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ABSTRACT. *Aedes albopictus*, a mosquito originally from Southeast Asia, is considered to be one of the main vectors of dengue fever, yellow fever and other arboviruses. We examined the genetic variability and population structure of 68 individuals of *Ae. albopictus* collected from five neighborhoods of the city of Manaus, based on the mitochondrial gene coding for NADH dehydrogenase subunit 5 (*ND5*). Two haplotypes were found, separated by a single mutational event (T ↔ C), with extremely low levels of genetic variability ($h = 0.187 \pm 0.059$; $\pi = 0.00044 \pm 0.00014$). Based on AMOVA, we concluded that most of the variation (99.08%) occurred within populations, though the levels of variation were not significant. Neutrality tests (Tajima's *D* and Fu's *Fs*) were non-significant, indicating that these populations are in genetic equilibrium. The most frequent haplotype (H1) is restricted to Brazilian populations of *Ae. albopictus*, while the rarer haplotype (H2) is shared with populations from the United States and Asia. We suggest that the reduced variability and low genetic structure identified in our study is a consequence of the recent introduction of this species in Manaus, possibly through a founder effect, followed by expansion throughout the city neighborhoods. Genetic similarity would therefore be due to insufficient time to have accumulated genetic differences between the populations of *Ae. albopictus* and not to extensive gene flow among them.

Key words: Dengue; Population genetics; Mitochondrial gene; Vector control

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