

## MOLECULAR STUDIES OF *CULEX* MOSQUITOES IN SÃO PAULO STATE, BRAZIL

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*Culex* is one of the most extensive genera of Culicidae and taxonomically one of the least well known. Many mosquitoes of this genus are pathogen vectors and belong to complexes. *Cx. quinquefasciatus* is considered an urban plague and transmits filariases and arbovirus diseases. Its immature stages develop in aquatic bodies compromised by domestic and industrial effluents. Studies of genetic variation in mosquitoes are crucial in the definition of intraspecific variations and species distinction. We studied intra- and interspecific variations of *Culex* mosquitoes in two areas in São Paulo State: Parque Ecológico do Tietê (PET) and Pariquera Açu (PA). Mitochondrial markers COI and ND4 (used in population studies, phylogeny and species distinction) were used. PCR sizes were similar to those found in other mosquitoes. ND4 analysis showed no significant differences among *Cx. quinquefasciatus* samples. Differences of up to 11% were observed between *Cx. quinquefasciatus* and *Cx. nigripalpus* and of up to 2% among *Cx. nigripalpus*. COI sequence divergence among *Cx. quinquefasciatus* was 1.2%. These differences could be used to distinguish the two populations, which have suffered different pressures from insecticides and environmental pollution. The PET population is constantly subject to the effects of pollution and is showing insecticide resistance, whereas the human presence has had less impact on the environment in PA. Supported by FAPESP