



New microsatellite markers for the neotropical malaria vector *Anopheles nuneztovari sensu lato*

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ABSTRACT. *Anopheles nuneztovari sensu lato* consists of cryptic species and genetic lineages, one of which is an important human malaria vector in the northern part of South America. Population structure and evolutionary genetics studies may help in the definition and delimitation of the species and lineages within this species complex, which is relevant information for organizations involved in malaria control efforts. In this study, 10 new microsatellite markers were isolated from 2 repeat-enriched genomic libraries of *A. nuneztovari s.l.* and were characterized in 37-48 mosquitoes of this species. All loci were highly polymorphic and encompassed 5-25 alleles per locus. The observed (H_o) and expected (H_E) heterozygosities ranged from 0.354 to 0.866 and from 0.613 to 0.932, respectively. Six of the 10 new loci showed significant deviations from the Hardy-Weinberg equilibrium, and no linkage disequilibrium was detected. The loci described in this study were more polymorphic than the 18 previously characterized loci and appear to be promising markers for use in investigating the fine-scale population genetic structure

and the boundaries of the cryptic species and lineages within the *A. nuneztovari* complex.

Key words: Malaria vector; Microsatellite markers; Genetic diversity; Population genetics; Speciation