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**Population Structure and Taxonomic Status of putative *Anopheles albitarsis* G (Diptera: Culicidae) using Mitochondrial DNA COI Gene Sequences.**

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Previous data based on the complete (1537bp) mitochondrial DNA (mtDNA) cytochrome oxidase I (COI) gene sequences, suggested that the phylogenetic pattern of the neotropical mosquito *Anopheles albitarsis* s.l. and within-species genetic distances, support the existence of previously unidentified species. To analyze the genetic relatedness and taxonomic status of samples of putative cryptic species, within the *albitarsis* complex, three Brazilian Amazonian localities (Eastern Amazon River, Western Amazon River and Itaituba) were assessed using 78 partial (668bp) sequences of the COI mtDNA gene. A haplotype network identified *A. marajoara*, *A. albitarsis* B, putative *A. albitarsis* G and detected an unidentified clade, among the 34 haplotypes. Multiple species were detected in all three localities and *A. albitarsis* B was found only in Itaituba. *Anopheles marajoara* has been implicated as an important regional vector of malaria in Amazonian Brazil, and understanding the population structure and behavior of *A. marajoara* and putative sister species contribute to vector control and identifying and predicting malaria transmission patterns.