

Title: Geographic differentiation at multiple loci in *Anopheles gambiae* populations from São Tomé and Príncipe (West Africa)

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Abstract- *Anopheles gambiae* is a major vector of *Plasmodium falciparum*, the causative agent for the most lethal form of human malaria. One possible malaria control effort is through the use of genetically manipulated insect vectors. However, the knowledge of the origin, structure and dynamics of the involved *An. gambiae* populations is an essential prerequisite for the success of such an effort. Because of their geographic isolation, islands are simplified settings for natural experimental studies of vector control strategies. Two potential sites for these studies are the islands of São Tomé and Príncipe located off the west coast of Africa. In this study we carried a phylogeographic analysis aimed at understanding the evolutionary origins of *A. gambiae* populations from both islands using mitochondrial and nuclear loci. Mosquito samples were collected from São Tomé (~100 individuals from 2 populations), Príncipe (~50 individuals from one population) and various countries from continental Africa (~400 individuals from 9 countries). We sequenced portions of the ITS region of the rDNA, Intron I of the *kdr* gene, and the ND5 mitochondrial gene. Analysis of the mtDNA gene revealed extensive genetic divergence between São Tomé and Príncipe island populations. Results also suggest a recent origin of mtDNA haplotypes possibly from Nigeria, Cameroon, and the Central Republic of Africa. On the contrary, analysis of the nuclear genes indicates a possible origin of the island populations from Angola. Possible explanations of these results are discussed, particularly in relation to historical human migration routes.