

Phylogeography and genetic diversity of *Aedes aegypti*, the dengue and yellow-fever mosquito in Cape Verde

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Phylogeography and genetic diversity of *Aedes aegypti*, the dengue and yellow-fever mosquito in Cape Verde.

Aedes aegypti is the most important mosquito vector of dengue and yellow fever, two of the most significant mosquito-borne viral diseases in the world. Due to the lack of antiviral therapy or vaccination, reducing dengue transmission depends only on mosquito control. In the archipelago of Cape Verde (West Africa) in November 2009 a dengue epidemic was declared with more than 20,000 people affected, 174 hemorrhagic fever cases and six deaths. The presence of *Ae. aegypti* in the archipelago was reported since 1931. In this study we aim to clarify the origins and population history of *Ae. aegypti* in Cape Verde by analyzing the variability of the mitochondrial gene NADH dehydrogenase subunit 4 (ND4). We analyzed 42 mosquitoes from three islands (Santiago, Brava and Fogo) collected before and after the dengue outbreak (2007/2010). ND4 sequences of 360bp revealed seven haplotypes, three of which are Cape Verde specific (haplotype diversity =0.637 and nucleotide diversity =0.002). All haplotypes were closely related and formed a star-like structure typical of expanded populations. In a comparison with 194 published haplotypes (including 6 African *Aedes* sp. outgroups), sequences from Cape Verde occurred in a basal clade mainly associated with West African mosquito populations. Our results suggest a high genetic diversity and a West African origin for this insular mosquito population. We found no evidence of new recent founder events that could be associated with the unique dengue outbreak in 2009.