

## ABSTRACT

### **Genealogy, distribution and history of haplotypes of *Aedes (Stegomyia) aegypti* ND4 from Brazil .**

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Knowledge about intrapopulation variation of biological vectors is critical for understanding the dynamics of the transmission of an infectious agent. The major objective of the present study is to characterize the variability of a fragment of the gene that codes for the subunit 4 of the mitochondrial Nicotinamide Adenine Dinucleotide Dehydrogenase – *ND4* among *Aedes aegypti* populations from Brazil comparing with that of several other countries.

Single nucleotide polymorphism was detected employing DNA sequencing techniques. Nucleotide sequences were analyzed using molecular variance (AMOVA), nested clade analysis (NCA) and mismatch distribution methods. Additionally, evolutionary relationships among haplotypes were estimated employing parsimony and maximum likelihood criterions.

The results show that the fragment is polymorphic, and that the populations of *Ae. aegypti* from Brazil are grouped into two genetically distinct, monophyletic clades.

Historical inferences support the hypothesis that one clade includes sequences from individuals that may be introduced in the Americas in the 17<sup>th</sup> and 18<sup>th</sup> centuries during the slave trade from Africa to America. The second clade consists of sequences of individuals that may be introduced in Brazil more recently, probably from Asian populations.

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