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**Population Structure Of The Malaria-transmitting Mosquitoes *A. Arabiensis* And *A. Gambiae* In Nigeria Using Sequences Of The Mtdna *Coi* Gene**

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The malaria vectors *Anopheles arabiensis* and *A. gambiae* s.s. are found sympatrically throughout Nigeria, with *A. arabiensis* more common in the northern dry savannah and *A. gambiae* prevalent in the southern rainforest. *A. gambiae* exists as two distinct molecular forms throughout Nigeria, M and S. To assess population structure of these mosquito species and molecular forms, we used sequence data from the cytochrome oxidase I (COI) mitochondrial gene. We found evidence of an historical population expansion in *A. gambiae* S form and in three northern populations of *A. arabiensis*, estimated to have occurred over 200,000 years ago, using neutrality tests and mismatch distribution. As was expected in expanded populations with high dispersal ability, neither species followed the model of isolation by distance. We detected two common haplotypes between M and S forms and three common haplotypes between *A. arabiensis* and *A. gambiae*, including one shared between all three taxonomic units. These shared haplotypes are suggestive of ancestral polymorphisms or gene flow through introgression. In a neighbor-joining tree based on genetic distances, M and S forms from the same localities segregated into different clusters, supporting assortative mating between them. However, *A. gambiae* S form clustered with *A. arabiensis*, suggesting a closer relationship between *A. arabiensis* and S form than between M and S forms. Understanding how processes such as population expansions and gene flow shape the population structure of mosquito vectors will aid in predicting the response of these species to factors such as climate change and human population expansion.