albimanus is not at demographic equilibrium likely due to population growth and historical geographic fragmentation at a regional scale. Pairwise coalescence analysis of population divergence (MDIV) indicates that migration increases as geographic distance decreases; however, a median-joining network depicted three divergent haplotype groups: (A) Nicaragua, Costa Rica and western Panamá; (B) central-eastern Panamá plus the Caribbean coast of Colombia, and (C) the Colombian Pacific coast plus Ecuador. Groups (A) and (C) are at demographic equilibrium whereas (B) has undergone population expansion. The time since expansion from the mismatch analysis is around 49,000 years ago (95% CI 17,237 - 87,276). Our findings do not support physical barriers to gene flow, but instead, Pleistocene geographic separation in eastern Panama and northern Colombia is the likely cause of population structure in *An. albimanus*.

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GENETIC STRUCTURE OF *AEDES ALBOPICTUS* IN CAMEROON (CENTRAL AFRICA)

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The Asian tiger mosquito, *Aedes albopictus* (Skuse, 1894), is an invasive species that expanded in all continents, including Africa. The species was first detected in Nigeria in 1991, and invaded Central Africa in 2000s, where it was recently implicated in emergences of arborviruses such as chikungunya and dengue. According to their geographical origin, the populations of *Ae. albopictus* are known to vary for biological characters (e.g. anthropophily) which are able to modulated the vectorial capacity of the species. To date, the origin of Central African populations is not determined, since the invasion of this region may have occurred from Nigeria, from a secondary introduction, or both. In order to assess the diversity of *Ae. albopictus* in Central Africa, we undertook a study on the genetic diversity and structure of populations originated from 12 Cameroonian locations. Samples were collected in 2007 according to North-South and West-East geographical transects representing all main bioclimatic regions. In each location, specimens were collected as larvae/pupae and reared to adult stage. We used six microsatellite and two mitochondrial markers (COI and ND5).

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EPIDEMIOLOGICAL IMPORTANCE AND POPULATION GENETICS OF THE HUMAN MALARIA MOSQUITO *ANOPHELES NILI SL* IN AFRICA

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Mosquitoes from the *Anopheles nili* group are major vectors of human malaria in forests and humid savannas of tropical Africa. Despite their epidemiological importance, basic data on their bionomics and genetics are crucially lacking, although such data are a requisite to properly devise and implement efficient and sustainable vector control strategies. Here, we present original data that contribute to fill this gap in our knowledge. *An. nili* specimens were collected in Senegal, Burkina Faso, Ivory Coast, Nigeria, Cameroon and the Democratic Republic of Congo by human landing catches and pyrethrum spray collections. Field-collected specimens were identified by PCR and their feeding preferences and infectious status were determined by ELISA. Eleven recently developed microsatellite loci were used to compare the level of genetic diversity and differentiation between 16 populations. *An. nili s.s.* was highly anthropophilic and partially endophagic and was the only member of the group collected out of Cameroon. Specimens of *An. ovengensis* and *An. carnevalei* collected in South Cameroon were highly exophagic and exophilic. All three species were found infected by *P. falciparum* with mean infection rates ranging 4.3-13.6% in *An. nili s.s.* (N=3646), 0.9% in *An. carnevalei* (N=516) and 1.0% in *An. ovengensis* (N=978). Genetic diversity indices were high in *An. nili s.s.*, and lower in *An. carnevalei* and *An. ovengensis*. High and significant levels of genetic differentiation were estimated across species (Fst>0.19, P<0.001). Within *An. nili s.s.*, the population structure is consistent with isolation by distance, although demographic and/or selective events probably resulted in a higher level of genetic isolation in marginal populations. This study confirmed that *An. nili s.s.* is the major malaria vector of the group and emphasized the exophagic behavior of *An. ovenegensis* and *An. carnevalei*. Genetic structure analyses fully supported former morphological and genetic studies, providing further support for the recent taxonomic classification within this group.

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SPECIES DELIMITATION IN SOUTH EAST ASIAN VECTORS OF MALARIA

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Many vectors of malaria belong to species complexes, which may differ in vector capacity and ecology. So efficient vector control relies on our ability to correctly identify both genetic and geographical species barriers. We have for this purpose developed a method for assessing reproductive boundaries in species complexes, using mitochondrial (cytochrome c oxidase 1) and nuclear genetic data (internal transcribed spacer 2), and we apply the method on three closely related species complexes; Anopheles subpictus (n=300), Anopheles sundaicus (n=375) and Anopheles vagus (n=200), all of which are closely related to each other. The previous morphological and genetic evidence for species delineation in the species complexes was also re-assessed. In all three cases it is found that the number of described species is different from our inferred number of species. Anopheles subpictus is found to contain at least 7 species, two of which are morphologically distinct, and have previously been described as separate species. There are also two cases of shared mitochondrial haplotypes between sympatric species, so identification based on mitochondrial genetic data can in these cases be misleading. ITS2 is found to be the most reliable species marker, but it may overestimate the number of species. Both Anopheles vagus and Anopheles sundaicus species complexes are found to only comprise of one species each, but in both species there are geographically isolated populations, which may have different ecological niches.

Ndo C., Antonio-Nkondjio C., Cohuet Anna, Kengne Pierre, Ayala D., Ngassam P., Morlais Isabelle, Fontenille Didier, Simard Frédéric. (2009)

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