processes to kill malaria parasites in the midgut. These studies enhance our understanding of the effects of human blood factors on malaria parasite transmission and will ultimately support the development of novel strategies for control.

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GENETIC STRUCTURE OF *AEDES AEGYPTI* (DIPTERA: CULICIDAE) USING MICROSATELLITE AND MITOCHONDRIAL MARKERS IN CAMEROON (CENTRAL AFRICA)

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Aedes aegypti is considered as the worldwide vector of dengue, yellow fever and chikungunya. In West-Central Africa, the species is summarized as sylvan, breeding far from human dwellings and biting preferentially animals rather than humans. Therefore this mosquito is not considered as an efficient vector. However, its biology in this area is actually much more complex since this mosquito occurs in a wide spectrum of environments ranging from sylvan to urban. Also its diversity and its implication in transmission of arboviruses are probably largely underestimated. In order to better assess the diversity of *Ae. aegypti* in Central Africa, we undertook a study on the genetic diversity and structure of 19 populations originated from Cameroon. 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. In addition to morphological characters (McClelland's criteria), we used seven microsatellite and two mitochondrial markers (COI and ND4). All microsatellites were found polymorphic. Across all loci, allelic richness and heterozygozity ranged respectively from 2.6 to 4.0 (3.4 +/- 0.4) and from 0.33 to 0.52 (0.45 +/- 0.05), suggesting high level of genetic diversity across populations. Analysis from microsatellite data also revealed a strong genetic structure of populations (Fst =0.080, P<10-6); using the bayesian approach results suggested two genetic clusters. The analysis of COI and ND4 genes resulted in the detection of 30 (S= 50; ϖ = 0.090) and 10 (S= 18; ϖ = 0.002) haplotypes, respectively, confirming thus the high level of diversity in Cameroonian populations in comparison with data previously described outside Africa. The phylogeographical analysis of mtDNA polymorphism suggested the possible existence of two lineages across cameroonian populations of *Ae. aegypti* and recent demographic changes. The origin of these lineages and their implications on the epidemiology of arboviruses in Cameroon are discussed.

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MICROGEOGRAPHIC GENETIC DIVERSITY OF THE MALARIA VECTOR *ANOPHELES DARLINGI* FROM CORDOBA AND ANTIOQUIA, COLOMBIA

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Anopheles darlingi competence for transmitting *Plasmodium falciparum*, *P. vivax* and *P. malariae* has been documented. It is an important malaria vector in various endemic regions such as Antioquia and Cordoba, two states in western Colombia. Because knowledge of vector population genetics is important for malaria control programs, this study was conducted to test genetic variation of *An. darlingi* at the microgeographic scale (~100 km), from five localities in Cordoba and Antioquia. Eight microsatellite loci and *COI* gene sequences were analyzed. Estimated F_{ST} indicated moderate to low genetic differentiation (MS F_{ST}= 0.01343; *COI* F_{ST} =0.02457) between states and estimates of *COI* nucleotide divergence were similar among populations from both states. mtDNA data agreed with microsatellite results showing the existence of demographic equilibrium with no signal of bottleneck and a common demographic history between *An. darlingi* populations from Cordoba and Antioquia. A neighbor-net network showed that *An. darlingi* populations from Colombia are genetically closer to Central American populations and more differentiated from populations of Brazil, Peru and French Guiana. This study suggests the existence of high gene flow between *An. darlingi* populations of Cordoba and Antioquia and therefore, integrated vector control strategies could be developed for this region.

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MOSQUITO VISION: MOLECULAR EVOLUTION AND FUNCTIONAL CHARACTERIZATION OF THE OPSINS IN *ANOPHELES GAMBIAE* AND *AEDES AEGYPTI*

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A novel strategy to reduce incidence of vector-borne diseases involves manipulating mosquito vision to disrupt mating, host detection or oviposition such that their populations and vector capacity decline. Developing an understanding of mosquito vision at the molecular level is fundamental to explore the feasibility of this approach. Opsins are G-protein coupled receptors (GPCRs) that interact with photons to initiate a phototransduction signaling cascade, involved with a visual response. Typically, insects have three classes of opsins to visualize ultraviolet, short, or long light wavelengths. Gene expression of arthropod opsins is detected in the eye and that of the related gene pteropsin, which is believed to regulate circadian rhythm, is detected in the brain. Previously, we identified 11 and 10 opsin genes in *Anopheles gambiae* and *Aedes aegypti*, respectively, as part of the complete genome sequencing projects. Here, newly-available expressed sequence tag (EST) data and homology-based analyses were used to improve opsin annotations. An extensive reverse transcriptase PCR (RT-PCR) study revealed sex and stage specific expression of opsins in *A. aegypti*. Expression of all opsins except *op7* and *op11* was confirmed in *A. gambiae* adult using a real time quantitative RT-PCR approach. *In situ* hybridization of *op3* and *op8* in *A. aegypti* was consistent with that reported for orthologs in the *Drosophila melanogaster* eye. Phylogentic analyses were conducted using ~300 opsin gene sequences from invertebrates and vertebrates and used to predict the function of each mosquito opsin. Our phylogenetic analyses indicate that a complex pattern of duplication events underlie the radiation of the opsin gene family in insects, been this novel paralogous gene lineages with respect to vertebrates. The long wavelength opsin gene family has expanded in mosquitoes; perhaps this is tied to their visual needs during periods of low light intensity when they are most active. Future research is aimed at characterizing the spectral sensitivity of mosquitoes opsins to confirm their functions.