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Phylogeny of the Funestus Group and phylogeography of the Sundaicus Complex, main malaria vectors in Africa and Asia

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Abstract

Recent advances in systematics and molecular identifications have allowed a clarification of phylogenetic relationships and a simplification of species identification among and within sibling species or *Anopheles* groups. The presentation of the latest data on the Funestus Group and the Sundaicus Complex is highlighting the importance of precisely identifying the species, assessing relationships among members of complex, and testing phylogenetic hypotheses involving closely related *Anopheles* species to conduct adequate and efficient vector control strategies.

The Funestus Group comprises 27 closely related species distributed in Africa and Asia including major malaria vectors on both continents. Based on ribosomal (ITS2, D3) and mitochondrial (COI, COII) sequences, a new systematic scheme is presented which reflects the evolutionary relationships within species of this group. Hypothetic biogeographic scenario of the Afrotropical and Oriental species is also examined in relation to the new phylogeny and estimates of divergence time. The Sundaicus Complex is distributed along the Asian coast where it is known as one of the main malaria vector. Recent molecular works using a ribosomal (ITS2) and two mitochondrial (COI, Cyt-b) sequences have allowed the recognition of three species for which phylogeographic evolutionary scenario is presented along with the malaria risk linked to specific human activities.