

## Population Genetics of *Anopheles* mosquitoes in South Asia

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Population genetics has an important role to play in studies of *Anopheles* mosquitoes. Much recent research has focussed on the extent of gene flow i.e. movement of genes between populations, since this relates directly to malaria control e.g. the proposal to genetically modify mosquitoes to make them refractory to the malaria parasite, and the movement of insecticide resistance genes between populations (or species). Recent research has demonstrated that reliable inferences of gene flow require not only the determination of genetic population structure, but also the inference of population history e.g. population expansions, fragmentation events, etc. This talk will give an overview of my recent and ongoing research on the genetic population structure and population history of *Anopheles* species (including *An. dirus*, *An. maculatus*, *An. annularis*) in South Asia. A large-scale study of *An. dirus* using mitochondrial sequence data and microsatellites revealed evidence of population expansions in *An. dirus* species A (in Thailand, Laos and Cambodia) and *An. dirus* species D (in Thailand, Myanmar, Bangladesh and Assam). Expansions following population bottlenecks are probably due to increased availability of suitable habitat after periods of cooler, drier climate associated with 100,000-yearly glaciations. Taken together with results using mitochondrial sequence data from other species groups e.g. *An. maculatus* and *An. annularis*, a general pattern is revealed: high diversity from the Thai-Myanmar border northwestwards to Myanmar and Assam; low diversity and recent population expansion eastwards to Laos and Cambodia; and very reduced genetic diversity in southern Thailand. The presence of significant (but limited) population structure in *An. dirus* D indicates there are barriers to gene flow. The hypothesis of longer, more stable population histories in Assam relative to Southeast Asia due to the moderating influence of the Himalayas on periodic climate change was tested using mitochondrial sequence data from *An. dirus* and *An. philippinensis*. The genetic distinctiveness of populations from Assam, their higher genetic diversity and structured genealogies support this hypothesis. This has potential implications for malaria as genetically distinct populations may differ in key factors that relate to malaria transmission: anthropogenicity; vector competence; habitat preference; etc. The relevance of these findings to our understanding of the origin and maintenance of biodiversity in South Asia and its conservation will also be discussed.