

## Population genetic structure of *Anopheles arabiensis* on the island of La Réunion (Indian Ocean), a candidate for SIT-based control.

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La Réunion is a small island (c.a. 2,500 km<sup>2</sup>) located in the Indian Ocean, off the East coast of Madagascar. Malaria was eradicated from the island following comprehensive malaria control programs implemented in the early 1950s, including vector control and quinine prophylaxis. However, residual vector populations still thrive on the island requiring uninterrupted epidemiological and entomological surveillance in order to prevent re-emergence of the disease. Each year, Public Health Services indeed detect some imported cases from surrounding countries where malaria is endemic and considerable effort is devoted to control the local vector population.

*Anopheles arabiensis* is the only member of the *An. gambiae* complex and the only potential malaria vector present on La Réunion, though its brief life cycle and its exophilic and zoophilic behavior were found to be key elements in maintaining the eradication status of the disease on the island. Mosquitoes usually occur at relatively low densities and are restricted to the coastal plain, where they develop in discrete, geographically isolated pockets of suitable habitat. For all these reasons, and because of geographical and genetic isolation from the core of the species' range in continental Africa, this limited mosquito population is a candidate for eradication by the Sterile Insect Technique. Although this technique was used in several large-scale mosquito control projects in the 1970's, for a variety of reasons none of these projects were successfully brought to completion. Recent advances in molecular entomology, genetic engineering and remote sensing however, have renewed interest in the Sterile Insect Technique for controlling mosquito populations, because these advances may remove some major technical problems that have constrained its use in the past.

Here, we aimed at providing a clear and exhaustive description of the malaria vector's population genetic structure on the island, as a prerequisite to assess feasibility and relevance of the implementation of a SIT-based control strategy directed against *An. arabiensis*. We explored extant genetic variability and its distribution within and between *An. arabiensis* mosquito populations sampled in three discrete locations on La Réunion, representing the three major foci where *An. arabiensis* larval development sites are known to occur.

Genetic diversity was assessed from allelic and genotypic frequencies observed at ten microsatellite loci spread throughout *An. arabiensis* chromosomes. We found strong evidence for genetic differentiation between the sub-populations suggesting little dispersal between them. All commonly used indices detected reduced genetic variability in our samples suggesting small population size. Calculation of quantitative estimates of the effective population size ( $N_e$ ) using moment-based estimators strengthened these findings, providing  $N_e$  estimates in the hundreds with upper 95% confidence limits below 1,500. Altogether, our results suggest that the *An. arabiensis* population from La Réunion is suitable for SIT-based control operation: small effective population size of the resident population would indeed limit the number of sterile insects to be released, and restricted geographic distribution and low dispersal between geographic isolates would allow precise identification of the most appropriate release points.