

Anopheles arabiensis, an important vector of malaria in sub-Saharan Africa shows great versatility in utilizing a broad range of larval habitats. Most studies on the population genetic structure of this species have focused on adult mosquitoes collected mainly indoors and have found populations within relatively short distances to be panmictic. Various authors suggested that the incipient speciation between the chromosomal forms of *Anopheles gambiae* s.s. in West Africa involved adaptation to different habitats of larvae. To investigate if similar process occurs in *An. arabiensis*, we analyzed samples from four different larval habitats alongside a sample of adult mosquitoes collected indoors at eight microsatellite loci. We tested the hypothesis that *An. arabiensis* is subdivided into populations that are adapted to exploit different larval habitats. Overall, the level of genetic differentiation among the larval subpopulations was low with the mean pairwise F_{st} estimate based on information from all the loci being 0.0232 ($P=0.1691$) although differentiation was only significant for comparisons between certain larval samples and the adult samples. In addition, there was strong evidence against subdivision among larvae when multilocus simultaneous assignment tests were used. These results do not provide sufficient support for the hypothesis that *An. arabiensis* is subdivided into subpopulations that specialize to exploit different larval habitats.