

Abstract

Understanding the genetic structure and transmission dynamics of *Plasmodium falciparum* parasites in malaria-endemic regions is crucial before the implementation of interventions. Located in a high-transmission region of western Kenya where *P. falciparum* is the predominant species, the Lake Victoria islands are ideal for feasibility of malaria elimination studies. We analyzed genetic variation in eight microsatellite loci to examine parasite population structure and gene flow patterns across five sites. High levels of genetic diversity were measured throughout the region (mean heterozygosity index = 0.84). The overall fixation index value between the sites was 0.044, indicating that approximately 5% of the overall allelic variation is due to differences between the populations. Based on these results, we concluded that parasite population structure in the studied islands is shaped by human migration patterns that maintain extensive parasite gene flow between the sites. Consequently, any malaria elimination and interventions strategies in the study area will have to be carried out broadly on all four islands and adjoining mainland region.