

Schistosomes (or bloodflukes) are digenetic trematodes in the family Schistosomatidae that normally parasitize birds and mammals, and utilize aquatic snails as intermediate hosts. Bloodflukes in the genus *Schistosoma* are responsible for causing human schistosomiasis, a parasitic disease of major public health importance, afflicting over 200 million people worldwide, mainly in sub-Saharan Africa. Although three main schistosome species namely, *Schistosoma mansoni*, *S. haematobium*, and *S. japonicum* cause human schistosomiasis, in Africa, *S. mansoni* is the most widespread, and probably the most important schistosome species afflicting human populations. It has been observed that there is a substantial amount of phenotypic variation in *Schistosoma* species. Genetic heterogeneity of schistosomes may contribute to the frequently observed phenotypic variations in parasite biological characteristics such as infectivity, virulence or drug response. This work was undertaken in order to help in the development of accurate means of fluke identification at any life-stage. In order to achieve this, a thorough knowledge of their population genetic structures is needed to facilitate control/eradication efforts. Being both phenotypically and selectively neutral, microsatellites for developing a genetic analysis assay and studying the genetic structures of a range of schistosome species was investigated.

Five microsatellite loci were used to study the level of genetic diversity of 7 populations in *S. mansoni* obtained from 7 different endemic localities in Kenya. Genomic DNA from individuals in the different parasite populations was amplified using the polymerase chain reaction (PCR) and the amplification products sequenced using the ABI 377 sequencer. A total of 416 individual worms were genotyped across the five loci.

All the five loci were highly polymorphic, with the mean number of alleles per parasite population ranging from 11 to 43. The expected heterozygosity (HE) ranged from 0.4978 to 0.7944 while the observed heterozygosity (H_o) values ranged from 0.5896 to 0.7874 in all the populations. None of the *S. mansoni* populations studied were in Hardy-Weinberg equilibrium. The pairwise F_{ST} values for the seven populations studied were moderately high 0.084 - 0.210 ($P < 0.01$) indicating genetic differentiation between the populations. The genetic distances, DA and standard genetic distances D_s between the seven populations were high (0.275 - 0.546 for the (DA) distances and 0.334 - 1.075 for the (D_s) distances). Phylogenetic trees constructed using the genetic distance values showed a clustering pattern that did not relate to geographic origin of the populations investigated. This study concludes that populations of *S. mansoni* in Kenya are remarkably diverse genetically, but geographical location may not be a major factor in the observed diversity.