

Microsatellite typing reveals strong genetic structure of *Schistosoma mansoni* from localities in Kenya.

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Genetic diversity and population structure of seven populations of *Schistosoma mansoni* sampled in Kenya were assessed using five microsatellite markers. The mean number of alleles per locus, expected heterozygosity in Hardy-Weinberg equilibrium and pairwise F_{ST} values ranged from 5.2 to 10.7, 0.5-0.8 and 3.6-27.3%, respectively. These data reveal that *S. mansoni* populations in Kenyan have relatively high levels of genetic diversity and is significantly differentiated. Our data combined with information on biogeography support the hypothesis that the strong genetic structure in Kenyan schistosomes is as a result of limited gene flow and large population sizes. Resistance to anthelmintics has not been reported among the Kenyan schistosomes, we hypothesize that this is probably due to the very little gene flow among populations, thereby limiting opportunities for the spread of rare alleles that might confer resistance to the drugs.