

Origin and diversification of the human parasite *Schistosoma mansoni*

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Abstract:

Schistosoma mansoni is the most widespread of the human-infecting schistosomes, present in 54 countries, predominantly in Africa, but also in Madagascar, the Arabian Peninsula, and the Neotropics. Adult-stage parasites that infect humans are also occasionally recovered from baboons, rodents, and other mammals. Larval stages of the parasite are dependent upon certain species of freshwater snails in the genus *Biomphalaria*, which largely determine the parasite's geographical range. How *S. mansoni* genetic diversity is distributed geographically and among isolates using different hosts has never been examined with DNA sequence data. Here we describe the global phylogeography of *S. mansoni* using more than 2500 bp of mitochondrial DNA (mtDNA) from 143 parasites collected in 53 geographically widespread localities. Considerable within-species mtDNA diversity was found, with 85 unique haplotypes grouping into five distinct lineages. Geographical separation, and not host use, appears to be the most important factor in the diversification of the parasite. East African specimens showed a remarkable amount of variation, comprising three clades and basal members of a fourth, strongly suggesting an East African origin for the parasite 0.30–0.43 million years ago, a time frame that follows the arrival of its snail host. Less but still substantial variation was found in the rest of Africa. A recent colonization of the New World is supported by finding only seven closely related New World haplotypes which have West African affinities. All Brazilian isolates have nearly identical mtDNA haplotypes, suggesting a founder effect from the establishment and spread of the parasite in this large country.