



Supplementary Materials

Table S1: Urine samples with hybrid eggs. Number of eggs of pure *S. haematobium* and hybrids (*S. haematobium* x *S. bovis*) based on COX1 and ITS2 genes in each sample.

Locality Name	No. of Eggs/Urine Sample	Age	Sex	Sequence Identification		Genetic Profile
				mtDNA COX1	rDNA ITS2	
NIAKHAR	Urine1 1 egg 1 egg	10	M	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> <i>S. haematobium</i> x <i>bovis</i>	<i>S. haematobium</i> Hybrid (type1)
	Urine2 4 eggs 1 egg	14	M	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> <i>S. haematobium</i> x <i>bovis</i>	<i>S. haematobium</i> Hybrid (type1)
	Urine3 3 eggs 2 eggs	15	M	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> <i>S. haematobium</i> x <i>bovis</i>	<i>S. haematobium</i> Hybrid (type1)
	Urine4 9 eggs 1 egg	11	M	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> <i>S. haematobium</i> x <i>bovis</i>	<i>S. haematobium</i> Hybrid (type1)
	Urine5 2 eggs 1 egg	7	F	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> <i>S. haematobium</i> x <i>bovis</i>	<i>S. haematobium</i> Hybrid (type1)
	Urine6 1 egg 2 eggs	11	M	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> <i>S. haematobium</i> x <i>bovis</i>	<i>S. haematobium</i> Hybrid (type1)
	Urine7 7 eggs 3 eggs	11	M	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> <i>S. haematobium</i> x <i>bovis</i>	<i>S. haematobium</i> Hybrid (type1)
KHOMBOLE	Urine8 18 eggs 2 eggs	10	M	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> <i>S. haematobium</i> x <i>bovis</i>	<i>S. haematobium</i> Hybrid (type1)
	Urine9 12 eggs 1 egg	10	M	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> <i>S. haematobium</i> x <i>bovis</i>	<i>S. haematobium</i> Hybrid (type1)
	Urine10 21 eggs 3 eggs	10	M	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> <i>S. haematobium</i> x <i>bovis</i>	<i>S. haematobium</i> Hybrid (type1)
	Urine11 13 eggs 2 eggs	10	M	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> <i>S. haematobium</i> x <i>bovis</i>	<i>S. haematobium</i> Hybrid (type1)
	Urine12 14 eggs 2 eggs	10	M	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> <i>S. haematobium</i> x <i>bovis</i>	<i>S. haematobium</i> Hybrid (type1)
NDIAT HENE	Urine13 2 eggs 1 egg	10	M	<i>S. haematobium</i> <i>S. bovis</i>	<i>S. haematobium</i> <i>S. haematobium</i>	<i>S. haematobium</i> Hybrid (type2)

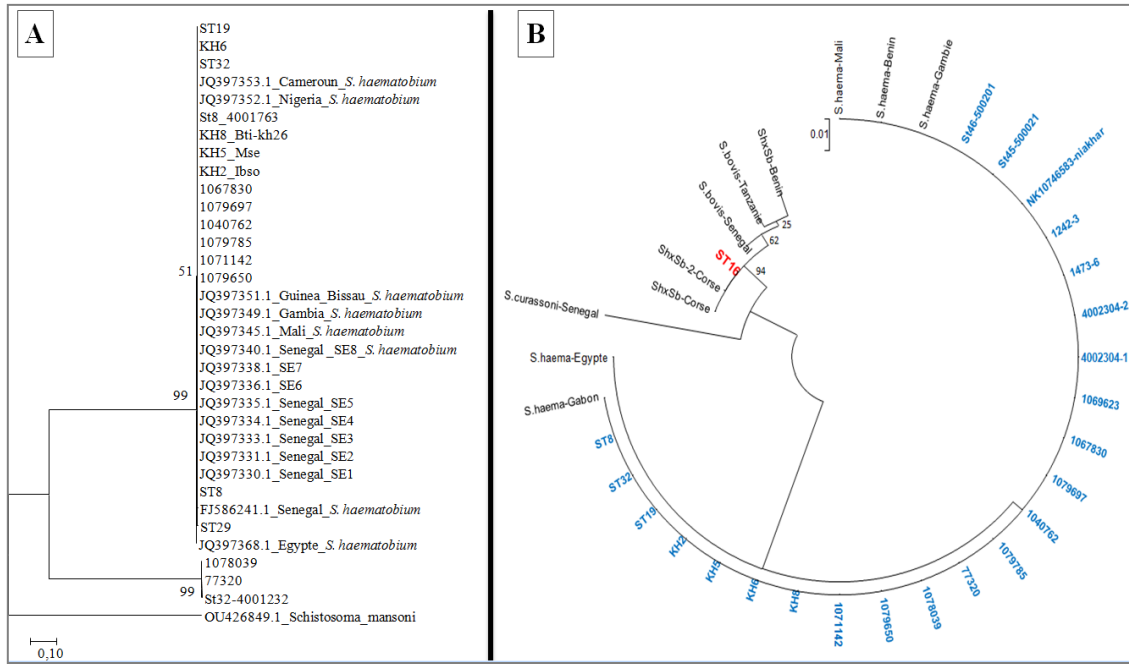


Figure S1: Phylogenetic tree with the gene COX1. This tree is derived from the maximum likelihood analysis of cox1 mitochondrial sequences from *Schistosoma haematobium*. The phylogeny of cox1 data was rooted with an *S. mansoni* haplotype (OU426849.1) (A) and *S. curassoni* (AJ519521.1) (B). All cox1 sequences were uploaded to the GenBank nucleotide data base. Clade support values for each node are maximum parsimony bootstrap percentages.