

1 Supplementary material

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Table 1. Gene sequences located and analysed for *S. bovis*

<i>S. bovis</i> sequences	Degree of identity according to databases		
	BLAST at NCBI	SchistoDB	Sanger
rRNA5-8S genome (155 bp) FJ588862	Genus <i>Schistosoma</i>	100% <i>S. mansoni</i> 99% <i>S. haematobium</i> 100% coverage	96% <i>S. curassoni</i> 100% coverage
18S rRNA genome (1,864 bp) AY157238	Genus <i>Schistosoma</i>	99% <i>S. mansoni</i> 93% <i>S. haematobium</i> 100% coverage	99% <i>S. curassoni</i> 100% coverage
rRNA-28S genome (3,829 bp) AY157266	Genus <i>Schistosoma</i>	98% <i>S. mansoni</i> 86% <i>S. haematobium</i> 100% coverage	99% <i>S. curassoni</i> 100% coverage
ITS 1 genome, between 18S and 5.8S (457 bp) FJ588862	Genus <i>Schistosoma</i>	95% <i>S. mansoni</i> 87% <i>S. haematobium</i> 100% coverage	98% <i>S. curassoni</i> 100% coverage
ITS 2 genome, between 5.8S and 28S (313 bp) AF146030	Genus <i>Schistosoma</i>	93% <i>S. mansoni</i> and <i>S. haematobium</i> 100% coverage	97% <i>S. curassoni</i> 100% coverage
Tetraspanin 23 genome (1,620 bp) JX844194	Genus <i>Schistosoma</i>	94% <i>S. haematobium</i> 85% <i>S. mansoni</i> 100% coverage	89% <i>S. curassoni</i> 91% <i>S. mattheei</i> 85% <i>S. intercalatum</i> 100% coverage
Tetraspanin 23 genome (1,617 bp) JX844196	Genus <i>Schistosoma</i>	93% <i>S. haematobium</i> 86% <i>S. mansoni</i> 100% coverage	89-99% <i>S. curassoni</i> 92-95% <i>S. mattheei</i> 83-95% <i>S. intercalatum</i> 100% coverage
Tetraspanin 23 genome (291 bp - 1,620 bp) JX844194	No homology with other schistosomes	89% <i>S. haematobium</i> 87% <i>S. mansoni</i> 87% <i>S. japonicum</i> Overlapping in small parts of the sequence	60-61% <i>S. intercalatum</i> 60-65% <i>S. margrebowiei</i> 61-65% <i>S. curassoni</i> 60% <i>S. guineensis</i> 65% <i>S. mattheei</i> 57-60% <i>S. rodhaini</i> 100% coverage
14-3-3 protein genome (832 bp) DQ176433	Genus <i>Schistosoma</i>	99% <i>S. haematobium</i> 92% <i>S. mansoni</i> 100% coverage	98% <i>S. curassoni</i> 100% coverage
Glutathione S- transferase genome (781 bp) M87800	Genus <i>Schistosoma</i>	99% <i>S. haematobium</i> 90% <i>S. mansoni</i> 100% coverage	98% <i>S. curassoni</i> 100% coverage

Repeat sequence 1 genome (203 bp) DQ831697	<i>S. curassoni</i> , <i>S. mattheei</i> and <i>S. haematobium</i>	85%–95% <i>S. haematobium</i> 76%–83% <i>S. mansoni</i> No 100% coverage	82-100% <i>S. curassoni</i> 80% <i>S. mattheei</i> 100% coverage
Repeat sequence 2 genome (227 bp) DQ831700	<i>Schistosoma haematobium</i> group	94% <i>S. haematobium</i> 100% coverage	85-95% <i>S. curassoni</i> 87-94% <i>S. mattheei</i> 92-93% <i>S. margrebowiei</i> 100% coverage
Repeat sequence 3 genome (161 bp) DQ831699	Genus <i>Schistosoma</i>	94% <i>S. haematobium</i> 89% <i>S. mansoni</i> 100% coverage	89% <i>S. curassoni</i> 92% <i>S. margrebowiei</i> 100% coverage
Repeat sequence 4 genome (216 bp) Mitochondrial	<i>Schistosoma haematobium</i> group	95% <i>S. haematobium</i> Almost 100% coverage	94-96% <i>S. curassoni</i> 95-100% <i>S. mattheei</i> 85-97% <i>S. margrebowiei</i> 100% coverage
COX-1 DQ831698 (503 bp) AY318827	Genus <i>Schistosoma</i>	90% <i>S. haematobium</i> 80% <i>S. mansoni</i> 100% coverage	65-77% <i>S. curassoni</i> 83% <i>S. guineensis</i> 55-75% <i>S. mattheei</i> 100% coverage
Mitochondrial COX-1 (1,224 bp) AJ519521	Genus <i>Schistosoma</i>	89% <i>S. haematobium</i> 80% <i>S. mansoni</i> 100% coverage	72-94% <i>S. curassoni</i> 84% <i>S. guineensis</i> 73% <i>S. mattheei</i> 100% coverage
Mitochondrial 12S rRNA (801 bp) FJ897168	Genus <i>Schistosoma</i>	84-95% <i>S. haematobium</i> 84% <i>S. mansoni</i> 100% coverage	98% <i>S. curassoni</i> 91-94% <i>S. guineensis</i> 100% coverage
Mitochondrial 16S rRNA (390 bp) EU513556	Genus <i>Schistosoma</i>	93% <i>S. haematobium</i> 84% <i>S. mansoni</i> 100% coverage	96% <i>S. curassoni</i> 100% coverage

NADH

Mitochondrial NADH subunit 6 (592 bp) FJ897164	<i>S. curassoni</i> and <i>S. haematobium</i> (100% and 94% coverage and 80% identity) <i>S. guineensis</i> (92% identity and 70% coverage)	84% <i>S. haematobium</i> 69-86% <i>S. mansoni</i> 100% coverage 81%-93% <i>S. japonicum</i> (overlapping only occurred in very small regions)	85% <i>S. curassoni</i> 62-67% <i>S. margrebowiei</i> 70% <i>S. intercalatum</i> 65-75% <i>S. guineensis</i> 62-65% <i>S. mattheei</i> 100% coverage
Mitochondrial NADH consensus x3 (2,215 bp) Sub 4, 3, 1	<i>Schistosoma haematobium</i> group	81% <i>S. haematobium</i> 70% <i>S. mansoni</i> Almost 100% coverage 68% <i>S. japonicum</i> No 100% coverage	92% <i>S. curassoni</i> 56-68% <i>S. margrebowiei</i> 56-75% <i>S. guineensis</i> 56-68% <i>S. mattheei</i> 100% coverage

Mitochondrial NADH subunit 4 (700 bp) HM594942	<i>S. curassoni</i> (100%), <i>S. margrebowiei</i> (75%) and 95% coverage	82% <i>S. haematobium</i> 68-83% <i>S. mansoni</i> 100% coverage 76%-86% <i>S. japonicum</i> , (overlapping only occurred in very small regions)	88-92% <i>S. curassoni</i> 75% <i>S. margrebowiei</i> 78% <i>S. intercalatum</i> 75% <i>S. guineensis</i> 59-68% <i>S. mattheei</i> 100% coverage 95% <i>S. curassoni</i>
Mitochondrial NADH subunit 3 (369 bp) HM594942	<i>S. curassoni</i> (94% identity and 100% coverage)	76% <i>S. mansoni</i> 75% <i>S. japonicum</i> 136-362 bp overlapping 88%-95% <i>S. haematobium</i> and almost 100% coverage	70-85% <i>S. margrebowiei</i> 75% <i>S. intercalatum</i> 73% <i>S. guineensis</i> 79% <i>S. mattheei</i> 100% coverage
Mitochondrial NADH subunit 1 (678 bp) HM594942	<i>S. curassoni</i> (94% identity and 99% overlapping)	70% <i>S. mansoni</i> 66% <i>S. japonicum</i> 83% <i>S. haematobium</i> Almost 100% coverage in all	92% <i>S. curassoni</i> 58-68% <i>S. margrebowiei</i> 78% <i>S. intercalatum</i> 72% <i>S. guineensis</i> 78% <i>S. mattheei</i> 70% <i>S. rodhaini</i> 100% coverage

*Specific sequences selected for each case are highlighted in colour.

Table 2. Degree of ITS-1 and ITS-2 sequence identity regarding schistosome species in the different databases

<i>Schistosoma</i> spp. sequence	Degree of identity according to BLAST databases at NCBI	SchistoDB	Sanger
ITS-2 nuclear genome, between 5.8S and 28S (311 bp) GU257398	All species from the genus <i>Schistosoma</i>	92% <i>S. mansoni</i> 91% <i>S. haematobium</i> 81% <i>S. japonicum</i> 100% coverage	89-97% <i>S. bovis</i> 90-92% <i>S. intercalatum</i> 91% <i>S. curassoni</i> 89-93% <i>S. guineensis</i> 90-95% <i>S. margrebowiei</i> 78-96% <i>S. mattheei</i> 81-93% <i>S. rodhaini</i> 100% coverage
ITS-1 nuclear genome, between 18S and 5.8S (457 bp) GU257398	All species from the genus <i>Schistosoma</i>	95% <i>S. mansoni</i> 88% <i>S. haematobium</i> 86% <i>S. japonicum</i> 100% coverage	84-98% <i>S. bovis</i> 81-99% <i>S. intercalatum</i> 77-98% <i>S. curassoni</i> 81-96% <i>S. guineensis</i> 96-98% <i>S. margrebowiei</i> 78-97% <i>S. mattheei</i> 85-96% <i>S. rodhaini</i> 100% coverage

* Specific sequences selected for each case are highlighted in colour