

TABLE
Mitochondrial genome information and definitive hosts of *Parastrongyloides trichosuri*, representative Strongyloididae species and outgroup used in this study

Species/strain	Accession No.	Length (nt)	Annotation	Definitive host ^a	Publication
<i>Strongyloides fuelleborni fuelleborni</i> (L)	PV564809	24,335	36 genes	Non-human primates, human	n.a.
<i>Strongyloides fuelleborni fuelleborni</i> (S)	OL672152	14,037	36 genes	Non-human primates, human	n.a.
<i>Strongyloides papillosus</i>	NC_028622	13,909	<i>nad4</i> missing	Ruminants	n.a.
<i>Strongyloides vituli</i>	NC_066507	14,624	36 genes	Cattle	n.a.
<i>Strongyloides venezuelensis</i>	NC_028229	15,956	<i>trnV</i> missing	Rodents	n.a.
<i>Parastrongyloides trichosuri</i>	BK075097	13,809	36 genes	Marsupials	This study
<i>Strongyloides ratti</i>	NC_028623	16,609	<i>trnV</i> missing	Rat	n.a.
<i>Strongyloides stercoralis</i>	NC_028624	13,751	<i>trnD</i> missing	Human, dogs	n.a.
<i>Strongyloides cebus</i>	NC_066659	16,948	<i>trnN</i> duplicate	Non-human primates	n.a.
<i>Schistosoma mansoni</i>	NC_002545	14,415	-	Human, other mammalian hosts	(1)
<i>Schistosoma japonicum</i>	KU196417	14,088	-	Human, other mammalian hosts	(2)

a: definitive host information was obtained from.⁽³⁾ n.a.: not available.

Percent	Clade	Reads	Taxon	Reads	Rank	Code	Taxonomy	ID	Scientific Name
50.09	64777263	64777263	U	0	0	0	unclassified		
49.91	64556180	42327	R	1	1	1	root		
49.82	64428942	464965	R1				cellular organisms		
48.40	62595382	884041	R2	2	2	2	Bacteria		
43.71	56533339	220035	P				Pseudomonadati		
38.76	50132350	775938	R3				Pseudomonadota		
0.00	7	0	C				delta/epsilon subdivisions		
0.00	7	0	O				Deltaproteobacteria		
0.00	7	0	F				Bradymonadales		
0.00	6	0	G				Bradymonadaceae		
0.00	6	0	S				Bradymonas		
0.00	1	0	G				Bradymonas sediminis		
0.00	1	1	S				Persicimonas		
0.00	1	1	R3				Persicimonas caeni		
0.00	1	1	S				environmental samples		
0.00	1	1	R3				uncultured bacterium		
0.00	1	1	R3				unclassified Bacteria		
0.00	1	1	S				unidentified bacterial endosymbiont		
1.06	1366052	61624	R2	2759			Eukaryota		
0.99	1282505	18285	R3	33154			Opisthokonta		
0.94	1214047	0	K	33208			Metazoa		
0.94	1214047	0	K1	6072			Eumetazoa		
0.94	1214047	0	K2	33213			Bilateria		
0.94	1214047	0	K3	33511			Deuterostomia		
0.94	1214047	0	P	7711			Chordata		
0.94	1214047	0	P1	89593			Cranialia		
0.94	1214047	0	P2	7742			Vertebrata		
0.94	1214047	0	P3	7776			Gnathostomata		
0.94	1214047	0	P4	117570			Teleostomi		
0.94	1214047	0	P5	117571			Euteleostomi		
0.94	1214047	0	P6	8287			Sarcopterygii		
0.94	1214047	0	P7	1338369			Dipnotetrapodomorpha		
0.94	1214047	0	P8	32523			Tetrapoda		
0.94	1214047	0	P9	32524			Amniota		
0.94	1214047	0	C	40674			Mammalia		
0.94	1214047	0	C1	32525			Theria		
0.94	1214047	0	C2	9347			Eutheria		
0.94	1214047	0	C3	1437010			Boreoeutheria		
0.94	1214047	0	C4	314146			Euarchontoglires		
0.94	1214047	0	O	9443			Primates		
0.94	1214047	0	O1	376913			Haplorrhini		
0.94	1214047	0	O2	314293			Simiiformes		
0.94	1214047	0	O3	9526			Catarrhini		
0.94	1214047	0	O4	314295			Hominidae		
0.94	1214047	0	F	9604			Homininae		
0.94	1214047	0	F1	207598			Homo		
0.94	1214047	0	G	9605			Homo sapiens		
0.94	1214047	1214047	S	9606					

Fig. 1: taxonomic profiling of filtered reads by Kraken 2 reveals bacterial contamination dominated by *Pseudomonadota*.

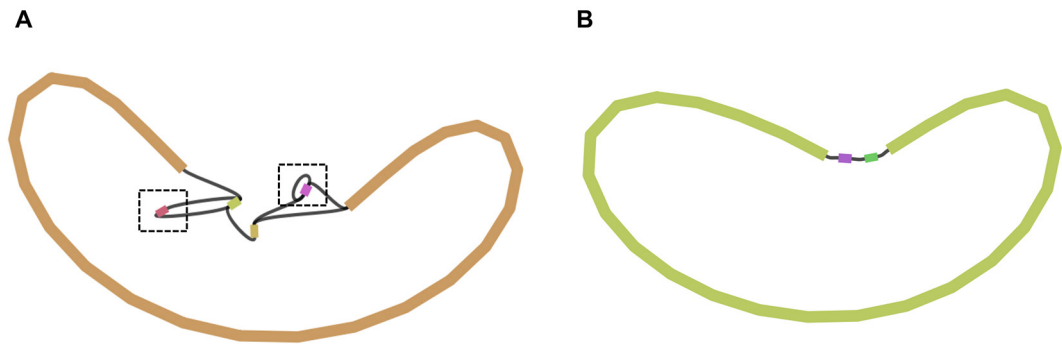


Fig. 2: circular representation of the mitochondrial genome assembly of *Parastrongyloides trichosuri* in this study, visualized using Bandage v0.8.1. (A) The initial assembly failed to form a circular genome due to the presence of two repeated fragments (indicated by the dotted box). (B) A circular mitochondrial genome was successfully reconstructed by manually removing the two repeated fragments.

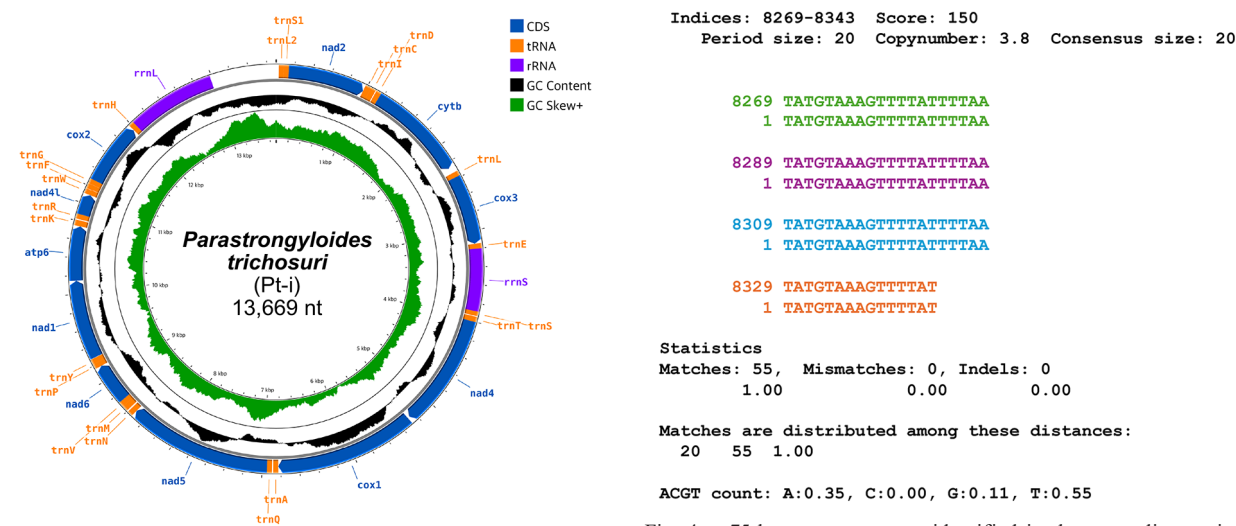


Fig. 3: circular map of the incomplete mitogenome of *Parastrongyloides trichosuri* (Pt-i; GenBank: NC_028620).

Fig. 4: a 75-bp repeat segment identified in the noncoding region. Green, purple, and blue indicate three 20-bp repeat units, and orange shows an additional 15-bp short repeat sequence.

REFERENCES

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