

Mitochondrial genome characterization and phylogenetic analysis of bird schistosome *Trichobilharzia szidati*

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ABSTRACT

In the present study, the complete mitochondrial genome of *T. szidati* was assembled by next generation sequencing (NGS). We found that the complete mitochondrial genome of *T. szidati* is 14,303 bp in length and consists of 3023 (21.1%) adenine, 1153 (8.1%) cytosine, 3432 (24.0%) guanosine and 6695 (46.8%) thymine. The genome contains 12 conserved core protein-coding genes (*atp6*, *cox1*, *cox2*, *cox3*, *nad1*, *nad2*, *nad3*, *nad4*, *nad4L*, *nad5*, *nad6*, *CYTB*), 21 tRNA genes, 2 rRNA genes and 1 D-loop region. Phylogenetic analysis showed that *T. szidati* has a close relationship with *T. regent*. Knowledge of mitochondrial genome of *T. szidati* could provide useful information for the further studies of evolutionary biology, epidemiology and species identification.

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Trichobilharzia is a kind of thread-like schistosome and it is distributed in birds worldwide (Yakhchali et al. 2016). It was reported that there were over 30 species in this kind of schistosomes (Loker 2009). *T. szidati* is one of the species that belongs to Schistosomatidae, Trematoda (Brant and Loker 2009). *T. szidati* can only parasitize in specific birds hosts whereas its larvae could penetrate, transform and migrate in all kinds of hosts (Le et al. 2002). In freshwater, the larva of *T. szidati* has the ability to penetrate human skin. Besides, it may cause human cercarial dermatitis (Martin Kašný 2011). Adult worms of *Trichobilharzia* cause extensive damage as they migrate and lay larvae in their preferred site (either the nasal mucosa or visceral capillaries) of infection (Zbikowska 2005). In the present study, the mitochondrial genome of *T. szidati* from China was sequenced. Its genetic characteristics and phylogenetic status was assessed in order to provide useful information for further study on trematode evolution.

Trichobilharzia szidati cercariae were collected from host snail *Lymnaea stagnalis* in Henan, China. (34°40'E; 112°21'N) and was stored in Henan Agricultural University (No. Tsz002). Total genomic DNA was isolated from this specimen according to Webster et al (Webster et al. 2007), and was stored in the sequencing company (BGI Tech, Shenzhen, China). We constructed sequencing libraries using a NEB Next Ultra II DNA Library Prep Kit (NEB, Beijing, China) following the manufacturer's instructions. Whole genomic sequencing was performed using an Illumina HiSeq 2500 Platform (Illumina,

San Diego, CA, USA). The mitogenome was assembled and annotated as reported (Li, Liao, et al. 2018; Li, Wang, et al. 2018; Li et al. 2019; Li et al. 2019a).

The complete mitochondrial genome of *T. szidati* is 14,303 bp in length and consists of 3023 (21.1%) adenine, 1153 (8.1%) cytosine, 3432 (24.0%) guanosine and 6695 (46.8%) thymine. The genome contains 12 conserved core protein-coding genes (*atp6*, *cox1*, *cox2*, *cox3*, *nad1*, *nad2*, *nad3*, *nad4*, *nad4L*, *nad5*, *nad6*, *CYTB*), 21 tRNA genes, 2 rRNA genes and 1 D-loop region. The *T. szidati* mitochondrial genome sequence was submitted to GenBank under the accession number of MG570047.

We used maximum likelihood (ML) and Bayesian inference (BI) to create phylogenies based on the combined gene alignment (Li, Yang, et al. 2018; Li et al. 2019b; Li, Ren, et al. 2019). The ML analysis was performed with RAxML (Stamatakis 2014), while bootstrap values were calculated using 1,000 replicates to assess node support (Li, He, et al. 2020). Bayesian analyses were performed with MrBayes v3.2.6 (Ronquist et al. 2012). Phylogenetic analysis showed that *T. szidati* has a close relationship with *T. regent* (Semyenova et al. 2017) (Figure 1).

Disclosure statement

The authors have declared that no competing interests exist.

0.2Genome size
● 14,091–16,901 bpBootstrap
● Fully resolved
● RAXML/Mrbayes

GC Content

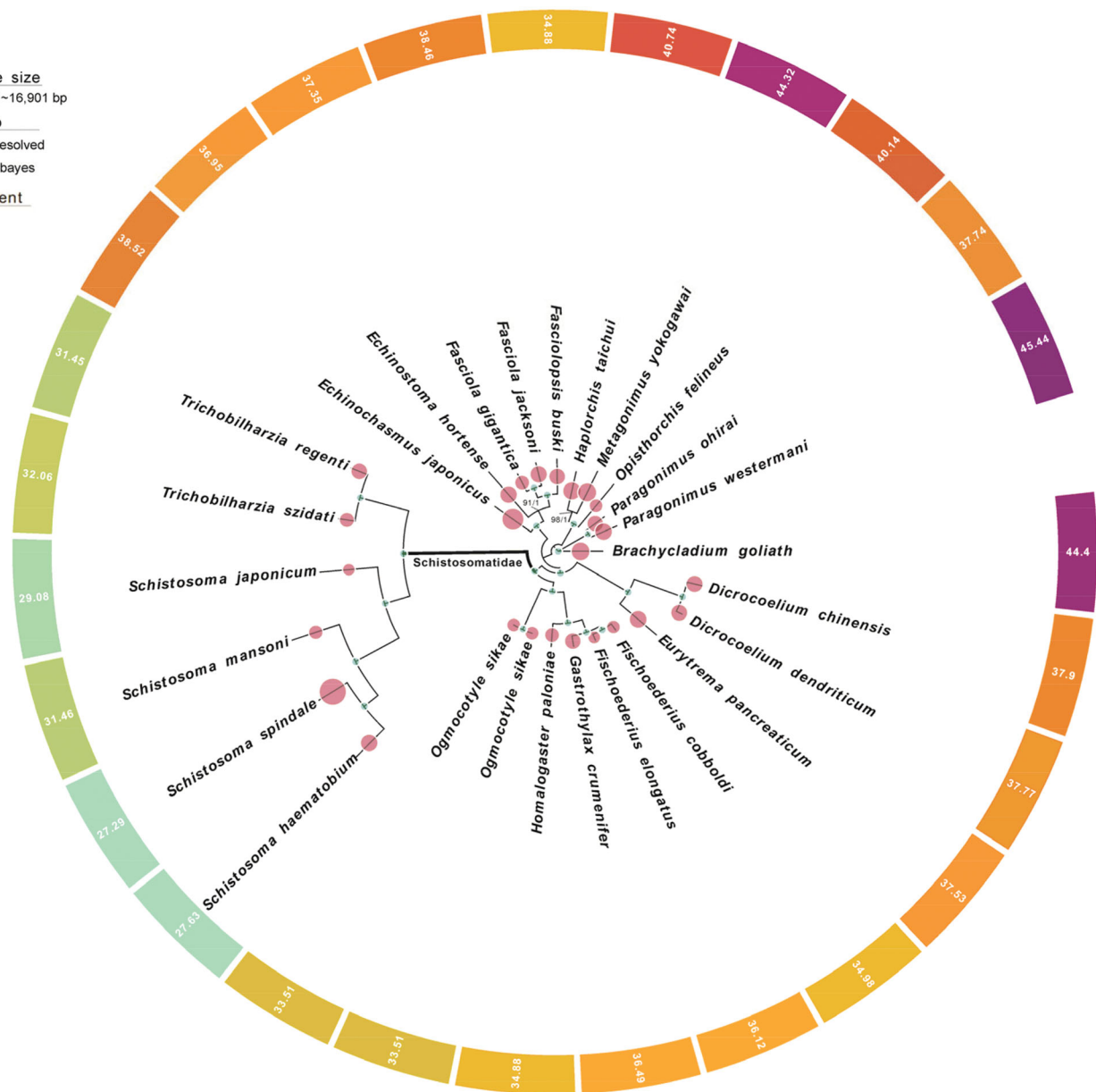
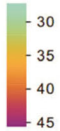


Figure 1. Phylogenetic relationships of 26 digeneans based on Bayesian inference and maximum likelihood analysis of 12 protein-coding genes. Support values are bootstrap values (before slash) and bayesian posterior probabilities (after slash). *Brachycladium goliath* (KR703278); *Dicrocoelium chinensis* (KF318786); *Dicrocoelium dendriticum* (KF318787); *Echinostoma japonicas* (KP844722); *Echinostoma hortense* (KR062182); *Eurytrema pancreaticum* (KP241855); *Fasciola gigantica* (KF543342); *Fasciola jacksoni* (KX787886); *Fasciolopsis buski* (KX169163); *Fiscoederius cobboldi* (KX169164); *Fiscoederius elongates* (KM397348); *Gastrothylax crumenifer* (KM400624); *Haplorchis taichui* (KF214770); *Homalogaster paloniae* (KT266674); *Metagonimus yokogawai* (KC330755); *Ogmocotyle sikae* 1 (KR006934); *Ogmocotyle sikae* 2 (NC_027112); *Opisthorchis felineus* (EU921260.2); *Paragonimus ohirai* (KX765277); *Paragonimus westermani* (KX943544); *Schistosoma haematobium* (DQ157222.2); *Schistosoma japonicum* (JQ781206); *Schistosoma mansoni* (NC_002545); *Schistosoma spindale* (DQ157223); *Trichobilharzia regent* (DQ859919).

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