

The complete mitochondrial genome of a parasitic flatworm *Senga ophiocéphalina* (Cestoda: Bothriocephalidae)

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ABSTRACT

Mitochondrial DNA of nematodes undergoes frequent rearrangements, so it is a very good model for studying the mitochondrial genome evolution. The complete mitochondrial genome of a parasitic nematode *Senga ophiocéphalina* was sequenced and annotated. The 13,816 bp-long genome contained 12 protein-coding genes (*atp8* gene was missing), two ribosomal RNAs, 22 transfer RNAs, and a 391 bp non-coding region. Phylogenetic analysis showed that *S. ophiocéphalina* forms a monophyletic cluster with the remaining two Bothriocephalidae species.

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Mitochondrial DNA of nematodes undergoes frequent rearrangements, which makes it a good model for studying the mechanisms of mitochondrial genome evolution (Hu & Gasser 2006). Phylogenetic relationships within Bothriocephalida, a relatively recently established order (previously Pseudophyllida) of tapeworms that mostly parasitise on teleost fish (Kuchta et al. 2008), are still disputable (Brabec et al. 2015). To fully resolve these, it will be necessary to employ a marker capable of providing good phylogenetic resolution. The complete mitogenome provides better phylogenetic resolution and precision relative to traditional markers (Sebastián et al. 2011), but mitogenome sequences are currently available only for two *Schyzocotyle* (syn. *Bothriocephalus*) species in Bothriocephalidae family (syn. Ptychobothriidae). Hence, to help future researches resolve the phylogenetic relationships within this order, we have sequenced the whole genome of an Asian parasitic fish tapeworm belonging to a different genus within the Bothriocephalidae, *Senga ophiocéphalina*.

Senga ophiocéphalina specimen was collected from the Zhegui reservoir (103°19' E, 23°56' N), near Mile city in Yunnan province. The specimen is stored in the Aquatic Organisms Museum of Guangdong Ocean University under the accession number SO02052015YN. DNA was extracted using the Aidlab kit. Twenty-two primer pairs were used to amplify the entire mitochondrial genome sequence (GenBank accession number: KX434430). The genome is rather small (13,816 bp), all genes are transcribed in the same direction, and it lacks the *Atp8* gene, all of which are common features for nematode genomes (usually 13.6–14.3 kb). Hence, it

contains only 12 protein-coding genes, along with the usual 22 tRNAs and 2 rRNAs. Eleven protein-coding genes use AUG start codon and UAG or UAA stop codons. *Cox3* gene uses GUG as start and an abbreviated UAA (UU-) as stop codon. All these are common in invertebrate mtDNA (Hu & Gasser 2006). Similar to a parasitic nematode *Strongyloides stercoralis* (Hu et al. 2003), the studied genome also has extremely high T content (55.9%) and extremely low C content (8.3%), resulting in a very strong A + T bias (70.1%).

Phylogenetic position of *S. ophiocéphalina* was estimated using maximum-likelihood, implemented in RaxmlGUI (with 1000 bootstrap replications) (Silvestro & Michalak 2012), and the Bayesian inference (BI), implemented in MrBayes version 3.26 (default settings, four MCMC chains, 6.34×10^6 generations) (Ronquist & Huelsenbeck 2003), approaches. Mitogenome sequences of all 23 available cestode species, and a trematode *Dicrocoelium dendriticum* as outgroup, were retrieved from the GenBank. Analyses were performed on concatenated 12 mitochondrial protein-coding genes and 2 rRNA genes (12,444 bp). GTR + G + I was chosen as the best nucleotide substitution model for both analyses. Apart from a somewhat ambiguous position of *Versteria mustelae*, both dendrogram topologies were identical (Figure 1; only BI dendrogram is shown). *Senga ophiocéphalina* formed a monophyletic cluster with the remaining two Bothriocephalidae species (with high statistical support), which then formed a sister clade with Diphylobothriidae family. Apart from the ambivalent position of Dipylidae, the overall dendrogram topology is highly congruent with the results of Cheng et al. (2016).

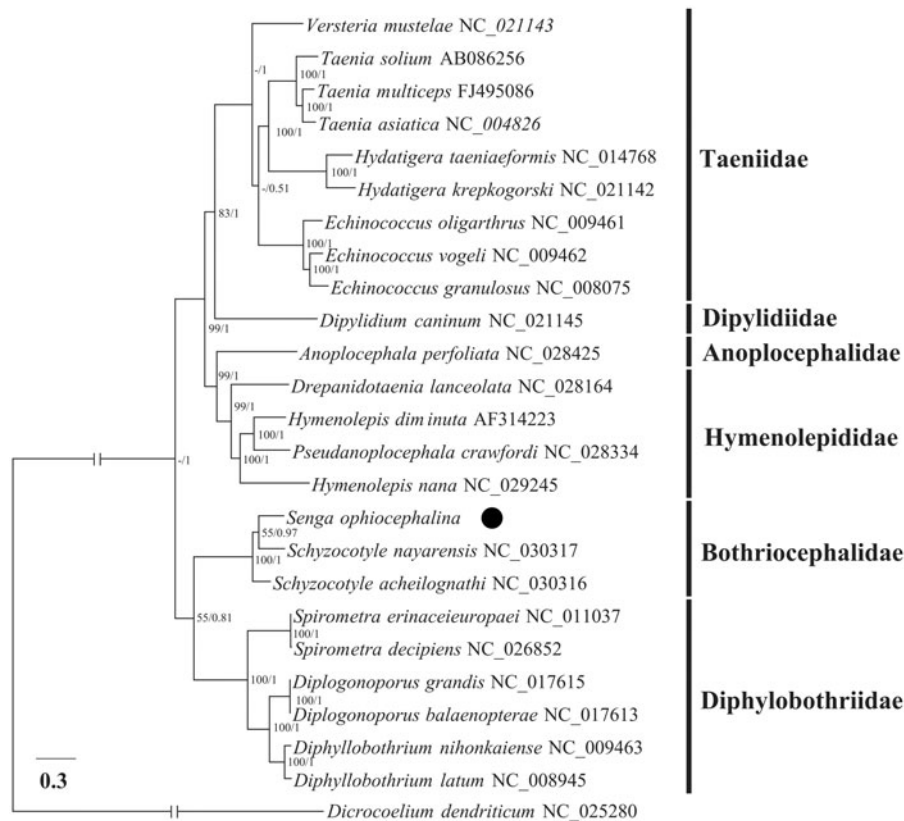


Figure 1. Phylogenetic dendrogram showing the evolutionary relationships among *S. ophioccephalina* (highlighted by a black dot), all 23 cestode species are available in GenBank and a trematode *D. dendriticum* as an outgroup. Maximum-likelihood and the Bayesian analyses were performed using partial genomes. Scale bar corresponds to the estimated number of substitutions per site. Both bootstrap support (first number) and the Bayesian posterior probability values (second number) are displayed next to the nodes. Values lower than 70 are displayed as -. GenBank accession numbers indicated in the figure.

Disclosure statement

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