




The complete mitochondrial genome of the hydrozoan jellyfish *Spirocodon saltatrix* (Cnidaria; Hydrozoa; Anthoathecata) with phylogeny analysis

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ABSTRACT

In the present study, we sequenced and analyzed the complete mitochondrial genome of the hydrozoan jellyfish *Spirocodon saltatrix*. The mitochondrial genome was a linear form (15,752 bp long, 70.4% AT), consisting of 13 protein coding genes (*cox1*, *cox2*, *atp8*, *atp6*, *cox3*, *nad2*, *nad5*, *nad6*, *nad3*, *nad4L*, *nad1*, *nad4*, and *cytB*), two tRNAs (tRNA-Met and tRNA-Trp), and two rRNAs (12S and 16S). Mitochondrial gene arrangement of the *S. saltatrix* was completely identical to already-known mitochondrial genomes of hydrozoans. Molecular phylogenetic analysis using 13 protein-coding genes showed that *S. saltatrix* was closely related to the hydrozoan *Clava multicornis*.

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Hydrozoa; *Spirocodon saltatrix*; mitochondrial genome; phylogeny analysis

Hydrozoa is one of the five representative classes in the subphylum Medusozoa, and it consists of more than 90% species of medusozoans (Daly et al. 2007). In addition, hydrozoans show the most morphological diversity in the Medusozoa (Kayal et al. 2015). Recent molecular studies have improved our understanding of their phylogeny (Kayal et al. 2015), but many relationships among the sibling species in hydrozoans remain largely unknown.

The hydrozoan jellyfish *Spirocodon saltatrix* Tilesius 1818 (Cnidaria; Hydrozoa; Anthoathecata) is a single species within the genus (Schuchert 2020). Until now, there is no molecular data for this species, excluding 5S ribosomal RNA sequence (GenBank No. K02349). Here, we determined the complete mitochondrial genome of *S. saltatrix*, and investigated its genomic structures and molecular phylogenetic relationships to other hydrozoans using their genomes.

Environmental specimens of *S. saltatrix* were collected from Masan Bay (35°09'06.3"N, 128°35'54.3"E) in South Korea, on 27 March 2013. Total genomic DNA (gDNA) was extracted from umbrella tissue using the cetyltrimethylammonium bromide (CTAB) DNA extraction method (Ausubel et al. 1989) and the remaining part was stored in the Department of Biotechnology, Sangmyung University, Korea (Accession No. AZ 9-3). Next generation sequencing (NGS) was subjected to the gDNA (Miseq, Illumina, USA), and paired end reads of mitochondrial genome sequences were assembled and annotated using MITObim (Hahn et al. 2013), MITOS (Bernt et al. 2013), and Geneious 9.1.3 (Geneious, Auckland, New Zealand), respectively. A molecular phylogeny tree was reconstructed using concatenated amino acid sequences of 13 protein-coding genes (PCGs) in MEGA X (Kumar et al. 2018). The


method of the phylogenetic tree has been described in our previous study (Karagozlu et al. 2019).

The complete mitochondrial genome of *S. saltatrix* sequence was 15,752 bp in length (GenBank No. MT150265; 30.4% A, 40% T, 14% G, and 15.6% C). The genome contained 13 PCGs (*cox1*, *cox2*, *atp8*, *atp6*, *cox3*, *nad2*, *nad5*, *nad6*, *nad3*, *nad4L*, *nad1*, *nad4*, and *cytB*), two tRNAs (tRNA-Met and tRNA-Trp), and two rRNAs (12S, 16S rRNA). In addition, it had a long non-coding region (656 bp; 17.4% A, 17.8% T, 28.4% C, and 36.4% G) between *cox1* and 16S rRNA. The 17 mitochondrial genes arrangement of *S. saltatrix* was completely identical to those of Anthoathecata hydrozoans, including *Clava multicornis* (JN700935), *Hydra sinensis* (JX089978), *Hydra oligactis* (EU237491), and *Turritopsis dohrnii* (KT020766). The arrangement, however, was different to other Trachylinae hydrozoans, in which 16S rRNA encoded only in minority strand. Mitochondrial PCGs of *S. saltatrix* used a single start codon (ATG) and three stop codons (TAA, TAG, and TGA). The most frequent codon in the genome was TTT (409 times, 7.8%).

Molecular phylogeny tree (Figure 1) using proteins of 13 mitochondrial PCGs of eight hydrozoan species showed that all Anthoathecata species were clustered together, and the *S. saltatrix* was the closest to *Clava multicornis*, followed by *T. dohrnii*. The present study provides additional mitochondrial genome data of the hydrozoans for understanding the molecular genetic basis of hydrozoans.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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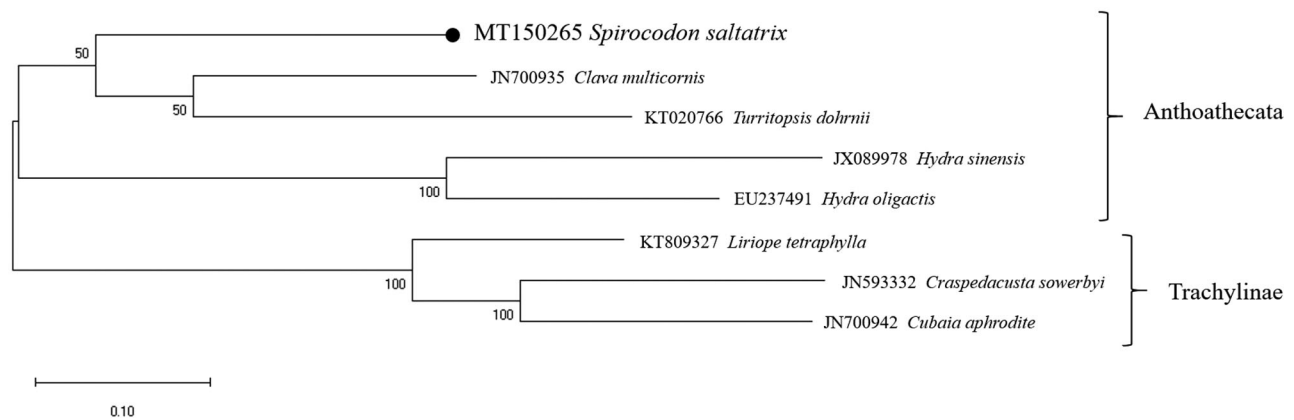


Figure 1. Molecular phylogeny of hydrozoans. The tree was reconstructed using concatenated amino acid sequences of 13 mitochondrial protein-coding genes and the maximum-likelihood (ML) algorithm with the JTT matrix-based model in MEGA X software. Bootstrap proportions (BP) of the 1000 times replications were incorporated into the ML tree. The branch lengths are proportional to the scale given. *Spirocodon saltatrix* determined here represents with a black dot.

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Data availability statement

The data that support the findings of this study are openly available in GenBank with the accession number MT150265 (<https://www.ncbi.nlm.nih.gov/nucleotide/MT150265>).

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