




# Complete mitochondrial genome of the hydrozoan jellyfish *Blackfordia virginica* Mayer, 1910 (Cnidaria; Hydrozoa; Leptothecata) with phylogenetic analysis

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## ABSTRACT

In this study, we analyzed the complete mitochondrial genome of the hydrozoan jellyfish *Blackfordia virginica*. The genome was a linear form (15,109 bp long, 73.6% AT), including 13 protein-coding genes (*cox2*, *atp8*, *atp6*, *cox3*, *nad2*, *nad5*, *nad6*, *nad3*, *nad4L*, *nad1*, *nad4*, *cytB*, and *cox1*), 2 tRNAs (tRNA-Met and tRNA-Trp), and 2 rRNAs (12S and 16S RNA). The genome structure of the *B. virginica* was completely identical to mitochondrial genomes of other hydrozoans that belonged to Leptothecata and Anthoathecata. Molecular phylogenetic analysis within hydrozoan species showed that *B. virginica* was the closest to the hydrozoan *Laomedea flexuosa*.

## ARTICLE HISTORY

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## KEYWORDS

Hydrozoa; *Blackfordia virginica*; mitochondrial genome; molecular phylogeny tree

## Introduction

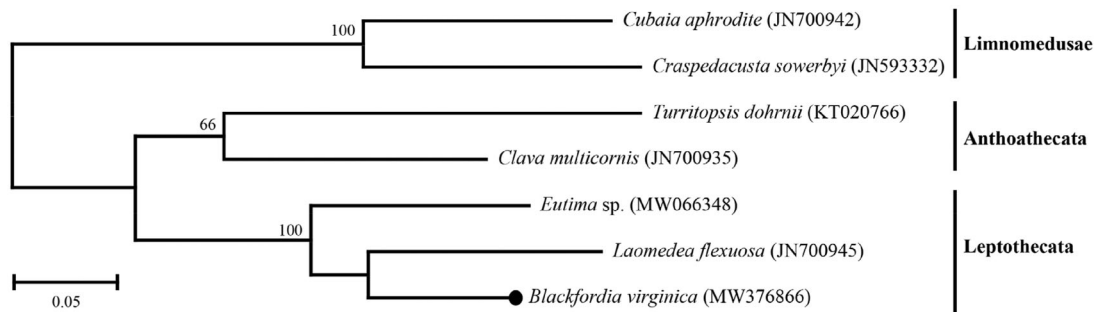
Leptothecata (thecate hydroids) is an order of hydrozoans in the phylum Cnidaria. They show great morphological variations among species according to their mode of development, growth stages, and defensive structures (Maronna et al. 2016). The hydrozoans have a complex life cycle, including a polyp stage, a medusa stage, or both, and their polyps are always living in colonies which grow rapidly on rocks and shells. Based on the morphology, their taxonomy has been described for a long time (Cornelius 1995a, 1995b), and until now approximately 2300 species of Leptothecata have been documented in public database (WoRMS 2020). Recent molecular phylogenetic approaches have improved the deep relationships among species of the Leptothecata, suggesting the addition of new clades in this order (Maronna et al. 2016). Considering the huge numbers of species, there are insufficient molecular data for a more accurate classification of the true relationship.

The hydrozoan jellyfish *Blackfordia virginica* Mayer, 1910 (Cnidaria; Hydrozoa) is a member of the Leptothecata (WoRMS 2020). It was first described from the Black Sea and has been considered a native species there. However, to date, it is considered an invasive species due to the worldwide expansion via trading by ships (Mills and Sommer 1995). In this study, we first described and analyzed the complete mitochondrial genome structure of *B. virginica*. In addition, molecular phylogenetic analysis was performed using five hydrozoans, including three Leptothecata.

The specimen of *B. virginica* was collected from Songsangyo (37°12'22.4"N, 127°01'24.2"E) in South Korea, on 7 July 2020. Genomic DNA was extracted from the whole

body by using the cetyl trimethylammonium bromide (CTAB) method (Richards et al. 2003) and the remaining part of the specimen was stored in the Department of Biotechnology, Sangmyung University, Korea (Accession No. EN424). The whole mitochondrial genome was sequenced on MGISEQ-200 platforms, and paired-end reads of mitogenome sequences were assembled and annotated using Getorganelle version 1.7.1a (Jin et al. 2020), MITOS (Bernt et al. 2013), and Geneious version 9.1.3 (Geneious, Auckland, New Zealand), respectively. A molecular phylogeny tree was constructed based on concatenated amino acid sequences of 13 protein-coding genes (PCGs) in MEGA X (Kumar et al., 2018). The molecular phylogenetic analysis method has been described in our previous study (Karagozlu et al. 2019).

The total length of the complete mitochondrial genome of *B. virginica* was evaluated as 15,109 bp in length (GenBank No. MW376866; 31.6% A, 42% T, 12.3% C, and 14.1% G). The genome contained 13 PCGs (*cox2*, *atp8*, *atp6*, *cox3*, *nad2*, *nad5*, *nad6*, *nad3*, *nad4L*, *nad1*, *nad4*, *cytB*, and *cox1*), 2 rRNAs (12S and 16S rRNA), and 2 tRNAs (tRNA-Met and tRNA-Trp). The order of 17 mitochondrial genes of *B. virginica* was completely identical to other Leptothecata, such as *Eutima* sp. (MW066348) and *Laomedea flexuosa* (JN700945), and also *Clava multicornis* (JN700935) and *Turritopsis dohrnii* (KT020766) belonging to the Anthoathecata (Kayal et al. 2012). Specifically, only 16S rRNA encoded in minority strand and short *cox1* fragment (about 100 bp) was found at the end of 16S rRNA like other Leptothecata species (Kayal et al. 2012). Mitochondrial genes of *B. virginica* have one start codon (ATG) and two stop codon (TAA/TAG). The TAA stop



**Figure 1.** Molecular phylogenetic tree of Hydrozoidina. The tree was constructed with the concatenated amino acid sequences of 13 mitochondrial protein coding genes using the maximum-likelihood algorithm (JTT matrix-based model) with 1000 bootstrap replicates. A black dot represents *Blackfordia virginica* determined in this study.

codon was found in all the mitochondrial PCGs, except TAG in *nad5*.

The phylogenetic relationships of the class Hydrozoa were investigated (Figure 1). The molecular phylogenetic tree showed that *B. virginica* was clustered with other Leptothecata species, and *L. flexuosa* is the closest species to *B. virginica*. The genome sequence data in this study provide additional data for phylogenetic classification among hydrozoan species.

## Disclosure statement

No potential conflict of interest was reported by the author(s).

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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 MW376866 (<https://www.ncbi.nlm.nih.gov/nucore/MW376866>).

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