Complete mitochondrial genome characteristics and phylogenetic position of *Lycodes brevipes* Bean, 1890

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**ABSTRACT**

*Lycodes brevipes* is one of the representative species of zoarcid fishes with little genetic information. The complete mitochondrial genome sequence of *L. brevipes* was sequenced by long PCR and primer walking methods. The mitogenome is a circular molecule of 16,537 bp in length including the structure of 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNA genes and two non-coding regions (origin of light strand replication and control region). The present study also revealed the phylogenetic relationship of this species at the molecular level using NJ algorithm. The mitogenome of *L. brevipes* provides essential genetic data for further phylogenetic and evolutionary analyses.

The Chukchi Sea is located at high latitudes and one of the most sensitive waters to climate change. In polar marine ecosystem, the environmental characteristics seriously shape the temporal and spatial distributions of fishes. The eelpouts of genus *Lycodes* is comprised of about 62 species as the largest group of zoarcid fishes distributed in the Arctic Ocean and adjacent waters, and is well known for currently the most species-rich genus, providing a great potential for Arctic marine speciation and genetic analysis (Anderson 1994; Møller and Gravlund 2003). However, species identification of *Lycodes* is often difficult due to similar morphological characteristics. *Lycodes brevipes* Bean, 1890 is one of the representative species of this genus with little phylogenetic analysis (Møller and Gravlund 2003). To understand its genetic background and clarify the phylogenetic position, sufficient genetic information of *L. brevipes* is needed and helpful for effective management and conservation of this species.

The voucher specimen was collected from Chukchi Sea continental shelf (168.2°W, 69.3°N) during the 6th Chinese National Arctic Research Expedition (CHINARE 6) in 2014, and deposited at the Third Institute of Oceanography, SOA. In this study, the complete mitochondrial genome (mitogenome) of *L. brevipes* was sequenced and phylogenetic topology of *Lycodes* species was reconstructed.

Long PCR and primer walking methods are employed to amplify the mitogenome sequence of *L. brevipes* with 37 pairs of primers (Miya and Nishida 1999). It was a typical circular form with 16,537 bp in length (GenBank number MK133251) and comprised of 37 coding and two non-coding regions. The 37 coding regions include 13 protein-coding genes, 22 transfer RNA genes (tRNAs), two ribosomal RNA genes (12S and 16S rRNAs), and two mainly non-coding regions (origin of light strand replication/Ol and control region/CR). Most of these genes are encoded on the H-strand, except for ND6 and eight tRNA genes (tRNA\(^{Gin}\), tRNA\(^{Ala}\), tRNA\(^{Aso}\), tRNA\(^{Cys}\), tRNA\(^{Thr}\), tRNA\(^{Ser}\), tRNA\(^{Glu}\), and tRNA\(^{Pro}\)) that are oriented to the L-strand. The arrangement of all genes is in accordance with most other vertebrates (Cheng et al. 2012; Wang et al. 2018). The overall base composition is as follows: 25.6% for A, 25.0% for T, 18.6% for G, and 30.8% for C, with a slight A + T-rich feature (50.6%).

Adjacent genes overlap by 31 bp in nine different locations from 1 to 10 bp, smaller than those in most mammals (40–46 bp; Broughton et al. 2001), and have gaps of 43 bp in nine different locations from 1 to 24 bp. The putative Ol is 40 bp long, located in the WANCY region (tRNA\(^{Gin}\)-tRNA\(^{Ala}\), tRNA\(^{Aso}\)-tRNA\(^{Cys}\), tRNA\(^{Thr}\)-tRNA\(^{Pro}\)). The CR of *L. brevipes* located between the tRNA\(^{Asp}\) and the tRNA\(^{Phe}\) genes is determined to be 865 bp in length. Except for COI starting with GTG, the remaining 12 protein-coding genes start with ATG. Seven protein-coding genes are inferred to terminate with TAA (ND1, ND2, COI, ATP8, ATP6, COII, and ND4L), three with TAG (ND3, ND5, and ND6), and three with incomplete stop codons T– (COII, ND4, and Cyt b).

Phylogenetic relationship was reconstructed by MEGA 6.06 (Tamura et al. 2013) based on the mitogenome sequences of *L. brevipes* and seven other Arctic fish species. The NJ tree (Figure 1) also showed that all species can be easily distinguished from each other with the high bootstrap values. The species *L. brevipes* was closer to the generic species than other species. The genus *Lycodes* species first formed a monophyly, and then they clustered with other Arctic fish species. The complete mitochondrial genome of *L. brevipes* reported in this study would facilitate further phylogenetic analysis and population genetics of this species.

**KEY WORDS**

Lycodes brevipes; phylogenetic position; mitochondrial genome; Zoarcidae

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