The complete mitochondrial genome of an eelpout *Lycodes ygreknotatus* (Teleostei: Zoarcidae)

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**ABSTRACT**

Here, we report the complete mitochondrial genome of the eelpout *Lycodes ygreknotatus*. The mitogenome is 16,486 bp in length and has the typical vertebrate mitochondrial gene arrangement, which contains 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and one D-loop region. The overall nucleotide base composition of *L. ygreknotatus* is 26.29%, 25.32%, 30.43%, and 17.96% for A, T, C, and G, respectively. Phylogenetic analysis of 14 fish species showed that *L. ygreknotatus* and *Lycodes toyamensis* were clustered into one branch.

**Lycodes** is one of the most diverse and widespread genera of eelpouts, containing over 60 species distributed in the North Pacific, Arctic, and Atlantic oceans (Anderson and Fedorov 2004). These fishes are typical inhabitants of the continental shelf and benthic zone, and play a key role in the bottom ichthyocenoses (Toyoshima 1985). To date, limited genetic information is available for *Lycodes* species, which constrains the population genetics studies. In this study, we reported the complete mitochondrial genome of *Lycodes ygreknotatus*, which mainly distributed in the Sea of Okhotsk, for the first time.

Samples of *L. ygreknotatus* was purchased from Qingdao Haiheng Company (Qingdao, China), and deposited at Marine Biology Herbarium, Weike Biotech Company (Qingdao, China). Total genomic DNA was extracted using marine tissue extraction kit (CWBiO, Beijing, China). The complete mitogenome of *L. ygreknotatus* was amplified using PCR with six pairs of primer designed based on the mitochondrial genome of *Lycodes toyamensis* (Miya et al. 2003).

The complete mitochondrial genome of *L. ygreknotatus* is 16,486 bp in length and is composed of 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes (12S rRNA and 16S rRNA), and one D-loop region. The mitochondrial gene arrangement of *L. ygreknotatus* is similar to that observed in the most vertebrates. Majority of the genes were encoded on the H-strand, while one protein-coding gene (ND6) and eight tRNA genes (*tRNA^Gin^*, *tRNA^Ala^*, *tRNA^Asn^*, *tRNA^Cys^*, *tRNA^Tyr^*, *tRNA^Ser^*, *tRNA^Glu^*, and *tRNA^Arg^*) were encoded on the L-strand. The base composition of the entire mitogenome is 26.29% for A, 25.32% for T, 30.43% for C, and 17.96% for G, which showed a slight AT (51.61%) bias. All start codons for the protein-encoding genes of *L. ygreknotatus* mitogenome are ATG except for COI, which is initiated with GTG. The open reading frames (ORFs) of five genes (ND1, COI, ATPase 8, ND4L, ND5, ND6, and Cytb) were ended with TAA or TAG, while the ORFs of the reminder genes were terminated with incomplete stop codons, either TA (ND2 and COIII) or T (COII, ATPase6, ND3, and ND4). The incomplete stop codons were also found in many other fishes, such as *Glyptothorax zainaensis*, *Rhynchobatus australiens*, *Macropodus erythropherus* (Li et al. 2016; Si et al. 2016; Yu et al. 2016). Among the mitochondrial protein-coding genes, ND5 (1839 bp) is the longest, and ATPase 8 (168 bp) is the shortest. The two ribosomal RNA genes, 12S rRNA (945 bp) gene and 16S rRNA (1688 bp) gene, are located between *tRNA^Phe^* and *tRNA^Leu(^UUR^)*, separated by *tRNA^Val^*. The D-loop region is 851 bp in length, which is located between *tRNA^Phe^* and *tRNA^Pro^*.

In order to investigate the phylogenetic position of *L. ygreknotatus*, maximum likelihood analysis was carried out with complete mitochondrial genome sequences from 13 fish species. As shown in Figure 1, *L. ygreknotatus* was clustered with its congeners species *L. toyamensis*, and the two *Lycodes* species had the closest relationship with *Pholis crassispina*. This information would be useful for population genetics studies of *L. ygreknotatus*, and for extending our knowledge about the evolutional relationship of Zoarcidae.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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