

## Complete mitochondrial genome of *Lepidotrigla alata* (Osteichthyes: Triglidae) with phylogenetic consideration

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### ABSTRACT

The complete mitochondrial genome of *Lepidotrigla alata* was sequenced in this study. The genome sequence is 16,512 bp in length, comprising 13 protein-coding genes, 22 *tRNA* genes, two *rRNA* genes, and one control region. Overall base composition is 26.46% A, 25.05% T, 17.22% G, and 31.27% C. Phylogenetic analysis indicated that *L. alata* was close to *L. guentheri* and *L. microptera*, and each genus in the family Triglidae was monophyletic. This study can provide valuable information for future evolutionary studies on *L. alata* and Triglidae.

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As a member of Triglidae, *Lepidotrigla alata* (Houttuyn, 1782) broadly distributes in Western Pacific (Richards 1992; Jin 2006). It is a kind of warm water fish and generally inhabits in sandy mud bottom of the tropical and temperate seas. *L. alata* mainly feeds on benthic animals and is a bycatch object of trawl nets. The meat is of good quality and can be sold fresh (Ni and Wu 2006). Mitochondrial DNA was reported to play important roles in the studies of population genetics, phylogeny, and evolution (Boore and Brown 1998; Curole and Kocher 1999; Minegishi et al. 2005). However, no information as to the complete mitochondrial genome of *L. alata* can be found by far. In this study, the complete mitochondrial genome of *L. alata* was sequenced and analyzed to evaluate its phylogeny and evolution.

A specimen of *L. alata* was collected from the spawning ground in the coastal waters of Jiangsu Province (32°20'N, 122°40'E) in 2019 and deposited in the East China Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences (Xiaojing Song, [xiaojingsong23@163.com](mailto:xiaojingsong23@163.com)) under the voucher number ZYCLC19042301. During the extraction of total genomic DNA, a part of muscle tissue was used, and the TIANGEN animal genomic DNA extraction kit (China) was selected according to the manufacturer's instruction. Then, the complete mitochondrial sequence was characterized by using Illumina MiSeq platform, and assembled by the SPAdes (Bankevich et al. 2012). The annotation of genes was employed by using the online software MitoAnnotator (<http://mitofish.aori.u-tokyo.ac.jp/annotation/input.html>) (Iwasaki et al. 2013).

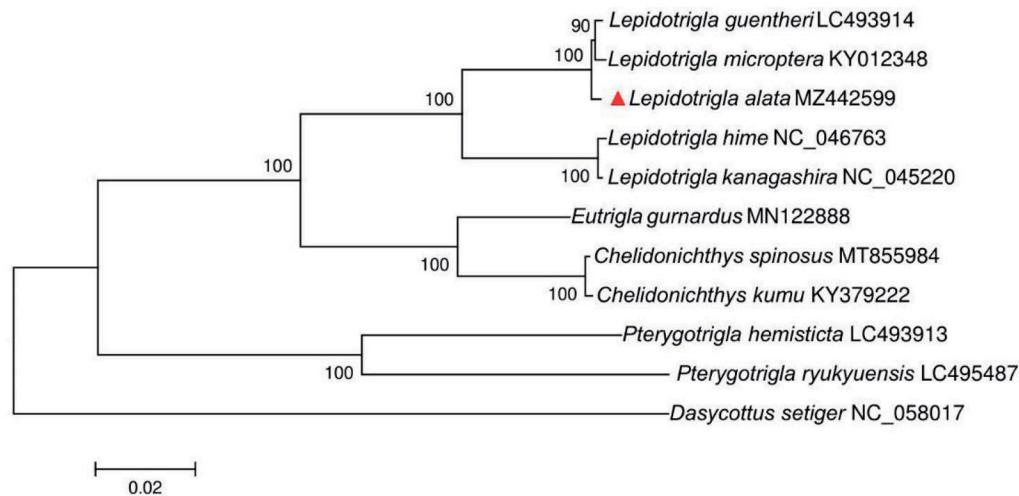
Results showed that the complete mitogenome of *L. alata* (16,512 bp, GenBank accession number: MZ442599) has an overall base composition of 26.46% for A, 25.05% for T, 17.22% for G, and 31.27% for C. The content of A + T is 51.51%, which showed an anti-G bias that was typical in most fishes (Miya et al. 2001, 2003). The mitogenome has two *rRNA* genes, 22 *tRNA* genes, 13 protein-coding genes, and one control region. Apart from the *ND6* gene and eight *tRNA* genes (*tRNA-Gln*, *Ala*, *Asn*, *Cys*, *Glu*, *Pro*, *Ser*, and *Tyr*) encoded on the L-strand, most genes are on the H-strand. There were two types of start codons (ATG and GTG) and four types of stop codons (AGG, TAA, TA, and T) in 13 protein-coding genes. In addition, D-loop (with a length of 838 bp) has a higher A + T content (59.31%) when compared with A + T content of the whole mitogenome sequence.

In order to investigate the phylogenetic relationships of *L. alata*, mitochondrial genome sequences of nine fish species in the family of Triglidae were analyzed together with *Dasycottus setiger* as outgroup species. Multiple alignment of gene sequences was performed by using ClustalW version 1.83 (Thompson et al. 1997) with default parameters. The maximum-likelihood (ML) phylogenetic trees were constructed by MEGA7 (Kumar et al. 2016), and tree topology was evaluated by 1000 bootstrap replicates. The *L. alata* represented the closest relationship with *L. guentheri* and *L. microptera*, and clustered as one group, then pooled together with *L. hime* and *L. kanagashira*. Each genus in Triglidae was monophyletic, and *Lepidotrigla* was the sister genus of the ancestor of *Eutrigla* and *Chelidonichthys* (Figure 1).

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**Figure 1.** Phylogenetic tree of *L. alata* and representative Triglidae based on the complete mitochondrial sequences (with *D. setiger* as outgroup). The topology of phylogenetic tree was inferred from maximum-likelihood method. Bootstrap supports for each analysis are indicated at the nodes.

## Disclosure statement

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

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## Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI (<https://www.ncbi.nlm.nih.gov/>) under the accession number MZ442599. The associated BioProject, SRA, and BioSample numbers are PRJNA743139, SRR15018814, and SAMN19998322, respectively.

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