The complete mitochondrial genome of *Toxotes chatareus* (Toxotes; Toxotidae; Carangaria) assembled by the next-generation sequencing data and phylogenetic analysis of Carangaria

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ABSTRACT

We present the complete mitochondrial genome of *Toxotes chatareus* yielded by the next-generation sequencing data in this study. The complete mitochondrial genome of *T. chatareus* has 16,543 bp and contained 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes, and a single control region (D-loop). The overall base composition was A 28.75%, C 29.80%, G 15.77%, T 25.68% and its gene arrangement was similar with other Carangaria mitochondrial genomes. Additionally, the phylogenetic relationships of 13 Carangaria species based on the complete mitochondrial genome was analyzed using the neighbor-joining method. The result showed *T. chatareus* was clustered with *L. lactarius* suggesting the close phylogenetic affinity they owned. Together, the complete mitochondrial genome of *T. chatareus* would be beneficial for the study of phylogenetic relationship, taxonomic classification and phyleogeography of the Carangaria.

**KEYWORDS**

*Toxotes chatareus*; mitochondrial genome; next-generation sequencing; phylogeny

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The 13 protein-coding genes were 11,433 bp in length, accounting for 69.11% of the whole mitogenome, which encodes 3,811 amino acids in total. The lengths of 12S rRNA located between tRNA\textsuperscript{Phe} and tRNA\textsuperscript{Val} and 16S rRNA located between tRNA\textsuperscript{Val} and tRNA\textsuperscript{Leu} were 959 bp and 1,697 bp, respectively. The control region (D-Loop) typically located between tRNA\textsuperscript{Pro} and tRNA\textsuperscript{Phe}, was 828 bp in length.

To further investigate the phylogenetic location of \textit{T. chatareus} in Carangaria, the phylogenetic relationship was constructed in this study. Specifically, we first downloaded the mitochondrial genome of 13 species (including 12 Carangaria species and \textit{Danio rerio}) in NCBI database. Then, the sequence alignment of these 14 species (including \textit{T. chatareus}) was conducted by multiple sequence alignment program ClustalW (Thompson et al. 1994) in BioEdit software (Hall 1999). At last, the phylogenetic tree was constructed using the neighbor joining (NJ) method with 10,000 bootstrap replications using MEGA7 (Kumar et al. 2016). The result of the phylogeny shows that \textit{T. chatareus} is clustered with the \textit{L. lactarius} (Figure 1), which is belongs to Lactariidae, suggesting close phylogenetic relationship they owned. We expect that the information of the complete mitogenome of \textit{T. chatareus} would be beneficial for the study of phylogenetic relationship, taxonomic classification and phylogeography of the Carangaria in the future.

Figure 1. Neighbor-Joining tree of 13 Carangaria and one outgroup (\textit{Danio rerio}) species based on the complete mitochondrial genome. The number at each node represents the bootstrap probability. The dark spot indicates the studied species.

Disclosure statement

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

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Data availability statement

The mitochondrial genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov under the accession number MW689259. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA592745, SRR11793814, and SAMN13439313, respectively.

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