

## The complete mitochondrial genome of *Chelidonichthys spinosus* (Scorpaeniformes: Triglididae) from Jiangsu Province, China

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### ABSTRACT

In this study, we present the complete mitogenome and a phylogenetic analysis of *Chelidonichthys spinosus* characterized using Illumina next-generation and Pacific Biosciences (PacBio, Menlo Park, CA) sequencing technologies. The complete mitochondrial genome is a circular molecule 16,511 bp in length and contains the same set of 37 mitochondrial genes (13 protein-coding genes, two ribosomal RNA (rRNA), 22 transfer RNA (tRNA)), and a control region as other bony fishes. The base composition of the entire mitogenome showed a slight AT bias. Phylogenetic analysis of the mitogenome of *C. spinosus* fully resolved it in a clade with other species classified to the Triglididae. The mitogenome data produced in this study provide the genomic resources available for future evolutionary studies.

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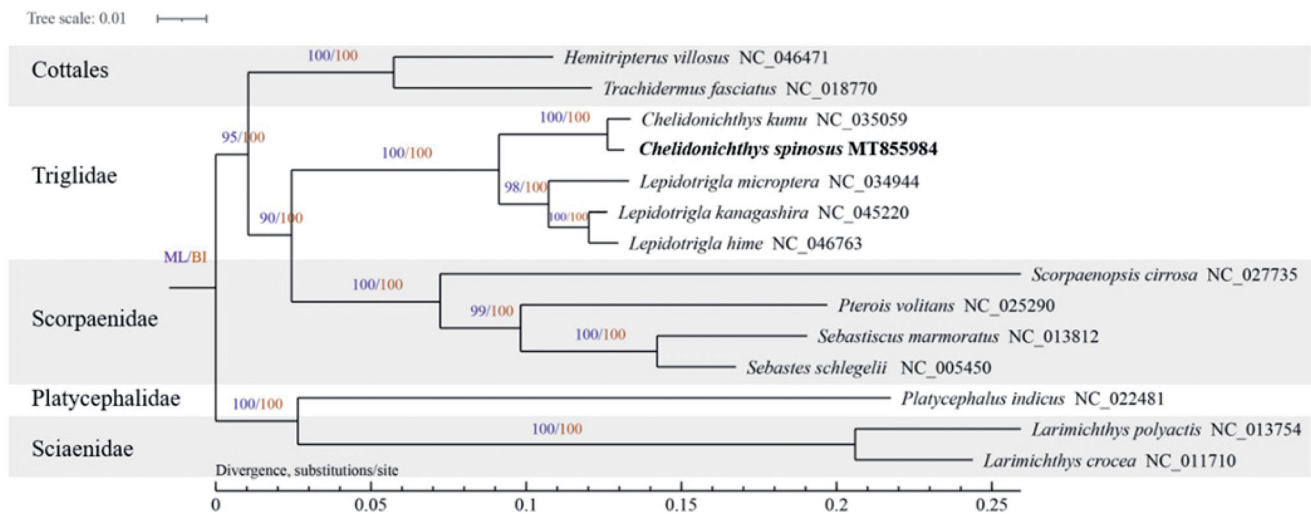
*Chelidonichthys spinosus*;  
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*Chelidonichthys spinosus* (McClelland, 1844) is classified in the order Scorpaeniformes, and is an important economic fish species in China. It is mainly distributed in the Yellow Sea, East China Sea, and South China Sea, and is also reported from the coastal waters of Korea and Japan (Ni and Wu 2006). *Chelidonichthys spinosus* is a low yield migratory fish that inhabits inshore warm bottom waters with sandy-mud substrates. Although molecular barcode analyses have been performed on *C. spinosus* (Kim et al. 2012), its complete mitogenome has yet to be deciphered. In the present study, the complete mitochondrial genome of a specimen of *C. spinosus* Jiangsu Province, China, was determined to contribute to the systematics and phylogenetic history of this species.

A specimen of *C. spinosus* (no. LQ20050701) was collected from the Coastal survey of Jiangsu Province (121°45'E, 32°15'N) on May 2020 and deposited in the museum of Jiangsu Marine Fisheries Research Institute (Yanping Wang, [Olindo@126.com](mailto:Olindo@126.com)). In this study, the purified mitochondria from muscle tissue were homogenated by differential centrifugation, and subsequently, DNA was isolated following Sambrook and Russell (2001). The complete mitogenome sequence of *C. spinosus* was characterized using Illumina next-generation and Pacific Biosciences (PacBio, Menlo Park, CA) sequencing technologies and an analysis of the phylogenetic relationships among Scorpaeniformes with two species in the order Perciformes designated as outgroups was performed. The mitochondrial genome was assembled using GetOrganelle v1.6.4 and the SPAdes-3.13.1 package, annotated using the online MITOS tool.

The complete mitogenome of *C. spinosus* is 16,511 bp in length (GenBank accession number: MT855984) and shares a high level of gene synteny with most vertebrates (Wolstenholme 1992; Boore 1999). The mitogenome consists of 13 typical vertebrate protein-coding genes, 22 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes (12S rRNA and 16S rRNA), and two major non-coding regions (control region and L-strand replication origin). Most of the mitochondrial genes of *C. spinosus* are encoded on the H-strand, except for ND6 and eight tRNA genes (Gln, Ala, Asn, Cys, Tyr, Ser-UCN, Glu, and Pro) which are encoded on the L-strand. The overall nucleotide composition of the heavy strand is 25.20% T, 31.18% C, 26.61% A, and 17.01% G, with anti-G bias and a slight excess of AT as typical in most fishes (Miya et al. 2001, 2003). The 13 protein-coding genes account for 69.43% of the complete mitogenome. The *C. spinosus* mitogenome also contains a small subunit rRNA (12S rRNA) and a large subunit rRNA (16S rRNA), which are 946 and 1692 bp in length, respectively.

To investigate the phylogenetic relationships of *C. spinosus* and other species classified in the Scorpaeniformes, the MtREV+I+G+F model was determined to be the best nucleotide substitution model, phylogenetic trees (Figure 1) were inferred using maximum-likelihood (ML) and Bayesian inference (BI) analyses by PhyML 3.0 and MrBayes-v3.2.7a respectively based on the complete mitochondrial sequences. The consensus topology of phylogeny trees for 12 Scorpaeniformes species shows that the Triglididae and Scorpaenidae are sister families. Each superfamily in



**Figure 1.** Phylogenetic tree using the complete mitochondrial sequences of *Chelidonichthys spinosus* and representative Scorpaeniformes. The sequences are downloaded from GenBank and the phylogenetic tree is constructed by maximum-likelihood (ML) and Bayesian inference (BI) methods. The bootstrap values and posterior probabilities are presented at the nodes. The mitogenome sequence obtained in this study is highlighted in bold font.

Scorpaeniformes is monophyletic, and the genus *Chelidonichthys* and *Lepidotrigla* are fully resolved in a clade in the Triglidae.

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## Disclosure statement

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

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## Data availability statement

Mitogenome data supporting this study are openly available in GenBank at nucleotide database, <https://www.ncbi.nlm.nih.gov/nucleotide/MT855984>,

Associated BioProject, <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA693658>, BioSample accession number at <https://www.ncbi.nlm.nih.gov/biosample/SAMN17393319>, and Sequence Read Archive at <https://www.ncbi.nlm.nih.gov/sra/SRR13494716>.

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