Characterization of the complete mitochondrial genome of *Cottiusculus nihonkaiensis* (Scorpaeniformes, Cottidae) and phylogenetic studies of Scorpaeniformes

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**ABSTRACT**

In this study, the complete mitochondrial genome of *Cottiusculus nihonkaiensis* was presented, and we also discussed its mitochondrial characteristics. The full length of the mitochondrial genome was 16,612 bp, containing 13 protein-coding genes (PCGs), two ribosomal RNAs (12S and 16S), 22 transfer RNA genes (tRNA), one non-coding control region (CR) and one origin of replication on the light-strand. Overall base composition of the complete mitochondrial DNA was 26.4% A, 17.4% G, 31.5% C, 24.7% T. The phylogenetic tree suggested that *C. nihonkaiensis* shared the most recent common ancestor with *Gymnocanthus herzensteini*, *Gymnocanthus intermedius* and *Gymnocanthus tricuspid*. Overall base composition of the complete mitochondrial DNA was 26.4% A, 17.4% G, 31.5% C, 24.7% T, respectively, with a slight AT bias (51.1%). *C. nihonkaiensis* mitochondrial genes were mostly encoded on the heavy strand, and only ND6 and eight tRNA (Gln, Ala, Asn, Cys, Tyr, Ser, Glu and Pro) genes on the light strand coding. The start codons of the 13 PCGs encoding genes were ATG except for COI which was GTG, which is quite common in vertebrate mtDNA (He et al. 2015). Most of the stop codons were TAA or TĂ˘–, the stop codon of ND2 was CTA and the gene with TTA as the stop codon was COII. Most of the tRNAs could form a common cloverleaf secondary structure, except tRNA\(^{\text{Ser}}\) (GCT) gene without DHU stem (Han et al. 2016). The lengths of the two rRNA genes were 947 bp (12S rRNA) and 1,692 bp (16S rRNA), respectively, which located between the tRNAPhe and tRNALeu (TAA) and separated by the tRNA\(^{\text{Val}}\) gene. The length of the control region was 858 bp, located between tRNA\(^{\text{Pro}}\) and tRNA\(^{\text{Leu}}\).
In order to obtain the position and kinship of the *C. nihonkaiensis* within Scorpaeniformes, we constructed phylogenetic trees of Scorpaeniformes based on maximum likelihood (ML) method (Figure 1). According to the Akaike Information Criteria (AIC), the most suitable nucleotide sequence model was selected through MrModeltest 2.3 (Bozdogan 1987), and finally the most suitable model was GTR + I + G. The ML phylogenetic tree based on 13 PCGs of 36 species using the software RAxML 8.0 (Alexandros 2014). The results showed that *C. nihonkaiensis* shared the most recent common ancestor with *Gymnocanthus herzensteini*, *Gymnocanthus intermedius* and *Gymnocanthus tricuspid*.

**Disclosure statement**

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

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**Data availability statement**

The data that support the findings of this study are openly available in "NCBI" at [https://www.ncbi.nlm.nih.gov/nuccore/MK224511](https://www.ncbi.nlm.nih.gov/nuccore/MK224511). GenBank accession number: MK224511.1.

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