MITOCHONDRIAL GENOME SEQUENCING AND PHYLOGENETIC STUDIES OF FEATHER BACK CHITAL, *Chitala chitala*

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Executive Summary

The featherback chital or clown knifefish (*Chitala chitala*) is categorized as an endangered species in Bangladesh whereas, in global context, the fish is considered as near threatened species. The study aimed to characterize the mitochondrial genome sequencing of *Chitala chital*a and to explore phylogenetic history. Featherback chital fish specimens were collected from the Netrokona district of Bangladesh for investigating mitogenome sequencing during February 2021 to June 2022. The genomic DNA was extracted from the fish tissue using the DNeasy® Blood and Tissue Kit according to the manufacturer's manual. After confirming the species by DNA barcoding technology, the mitochondrial DNA was extracted with mitochondrial DNA isolation kit. The next generation sequencing (NGS) was performed using the Illumina MiSeq platform. The process of NGS was performed from South Korea. The MiSeq raw reads were assembled using the Geneious® Prime 2020.0.3 software to construct a complete mitogenome of *C. chitala*. The circular gene map of *C. chitala* was drawn by OGDRAW software and the phylogenetic tree was constructed by MEGA7 program. The complete mitochondrial genome was 16248 bp in size. The mitogenome formed a circular double-stranded DNA molecule containing a total of 37 mitochondrial genes (13 protein-coding genes, 2 ribosomal RNA genes and 22 transfer RNA genes) with two non-coding regions, an origin of light strand replication (OL) and a displacement loop (D-loop), similar structure with other fishes of Teleostei. The phylogenetic tree demonstrated its close relationship with osteoglossiform fishes. The complete mitogenome of *Chitala chitala* (GenBank accession number: ON764424) showed 92.87 % identity to another species, *Chitala ornata* (AP008923.1), followed by 91.42 % identity with *Chitala lopis* (AP008922.1). Sequence of the complete mitochondrial genome of *C. chitala* would be an essential resource for studying population genetic structure and conservation management of the endangered fish species.

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