Complete mitochondrial genome profile of Randall's threadfin bream, *Nemipterus randalli* and its phylogenetic analysis

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We characterized the complete mitogenome of *Nemipterus randalli* and performed comparative mitogenomic analysis with previously determined mitochondrial genomes belonging to the family Nemipteridae. Using Sanger sequencing, we identified a 16,642 bp mitogenome containing 37 genes (13 protein-coding, 2 rRNA, 22 tRNA) and a non-coding region. Its gene organization, nucleotide composition, tRNA secondary structure and codon usage are similar to other Nemipteridae mitogenomes. The phylogenetic analysis indicated that Nemipteridae is a monophyletic group. The present study forms the basis for further studies on the population genetics, evolution and phylogeny of *N. randalli* and its family.

Keywords: Mitogenome, *Nemipterus randalli*, nemipteridae, phylogeny, protein coding genes.

crucial role in deciphering the phylogenetic relationship between closely related species[6]. Phylogenetic analysis based on the full mitogenome offers higher resolution than partial mitochondrial gene sequences[7]. Mitochondrial DNA (mt-DNA) is typically circular with a size of about 16–17 kb and encodes 13 protein coding genes (PCGs) as well as 22 tRNAs, 2 rRNAs and a control region[8]. Mitochondrial DNA plays a crucial role in evolutionary and population genetics[9] due to its haploid nature, high mutation rate, and lack of genetic recombination[10]. Understanding the profile of the mitogenome is very important as it provides clues to the species taxonomy, phylogeny, adaptation mechanisms and evolutionary consequences in different habitats[11]. Among 62 species belonging to the Nemipteridae family, only six complete mitogenomes are still available. Out of these six available mitogenomes, two are from the genus *Scolopsis* and the remaining from the genus