

Mitochondrial genome assembly and comparative mitogenomics of five snake mackerels (Perciformes, Gempylidae).

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Abstract

The Gempylidae (snake mackerels) family, belonging to the order Perciformes, consists of about 24 species described in 16 genera primarily distributed in tropical, subtropical, and temperate areas worldwide. Despite substantial research on this family utilizing morphological and molecular approaches, taxonomy categorization in this group has remained puzzling for decades prompting the need for further investigation into the underlying evolutionary history among the gempylids using molecular tools. In this study, we characterized and compared eight complete mitochondrial genomes for five Gempylidae species [Neopinnula minetomai, Neopinnula orientalis, Rexea antefurcata, Rexea prometheoides, and Thyrsites atun] using Ion-Torrent sequencing. Using Bayesian Inference and Maximum-Likelihood tree search methods, we investigated the evolutionary relationships of seventeen Gempylidae species using mitogenome data. In addition, we estimate divergence times for extant gempylids. We identified two major clades that formed approximately 48.05 (35.89 – 52.04 mya) million years ago; Gempylidae 1 [Lepidocybium flavobrunneum, Ruvettus pretiosus, Neopinnula minetomai, Neopinnula orientalis, and Epinnula magistralis], and Gempylidae 2 [Thyrsites atun, Promethichthys prometheus, Nealotus tripes, Diplospinus multistriatus, Paradiplospinus antarcticus, Rexea antefurcata, Rexea nakamurai, Rexea prometheoides, Rexea solandri, Thyrsitoides marleyi, Gempylus serpens, and Nesiarchus nasutus]. The present study demonstrates the superior performance of complete mitogenome data compared to individual genes in phylogenetic reconstruction. In addition to Cytochrome c oxidase subunit 1, NADH dehydrogenase subunit 2, and Cytochrome b, which are frequently employed in phylogenetic investigations, NADH dehydrogenase subunit 5 provided adequate resolving power. Analyses of selection pressure revealed purifying selection is predominant in Gempylidae mitogenomes. By including T. atun individuals from different regions we demonstrate the potential for the application of mitogenomes in species phylogeography.

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