The complete mitochondrial genome of the doubled-lined mackerel
*Grammatorcynus bilineatus* Rüppell, 1836 (Perciformes: Scombridae) from Beqa lagoon in Fiji

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ABSTRACT

The complete mitochondrial genome of the doubled-lined mackerel, *Grammatorcynus bilineatus*, was determined by the combination of high-throughput sequencing (HTS) and Sanger sequencing. The constructed mitochondrial genome of *G. bilineatus* was 16,537 bp in length, which harbors a canonical 37 genes (13 proteins, two ribosomal RNAs, and 22 tRNAs) and two non-coding regions (origin of light-strand replication (O<sub>L</sub>) and the D-loop control region). Among 38 genes, nine were encoded on its light strand (L), while the other 28 were on its heavy strand (H). Besides COX1 (GTG) and ATP6 (CTG), the other eleven protein-coding genes (PCGs) begin with a typical start codon (ATG). The phylogenetic tree showed that *G. bilineatus* was not clustered with the other species in the Scombridae, forming a clade for *Grammatorcynus*. The genetic information of *G. bilineatus* will provide useful information for the scientific management and conservation of the species in the genus.

According to FishBase (www.fishbase.org), *Grammatorcynus bilineatus* is one of two species in the genus *Grammatorcynus*, which is widely distributed in the Indo-Pacific from the Red Sea to the Andaman Sea (Collette and Gillis 1992). The higher gill raker numbers (18–24) and larger eye size of *G. bilineatus* have been known as the main morphological characters, which are distinct from its sole relative species, *Grammatorcynus bicornatus* (Silas 1963). However, the habitat of both species shares in Fiji, and their genetic information are essential to understand the sustainable stock distribution, and reproduction in any medium, provided the original work is properly cited.
The phylogenetic analysis revealed that *G. bilineatus* did not cluster with others in the family Scombridae, forming a distinct genus clade (Figure 1). Among the compared species in the family, *G. bilineatus* showed 84.40% and 83.79% identity to *Katsuwonus pelamis* and *Auxis thazard*, respectively. The genetic information of *G. bilineatus* will provide useful information for the scientific management and conservation of the species in the genus.

**Disclosure statement**

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

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**Data availability statement**

The data that support the findings of this study are available in [GenBank database] [Grammatorcynus bilineatus] at [https://www.ncbi.nlm.nih.gov/nucleotide/] with a reference number [GenBank Number: MT680627].

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**Figure 1.** Phylogenetic relationship of *Grammatorcynus bilineatus* with fish in the family Scombridae: A phylogenetic tree with the complete mitochondrial genome in the family Scombridae with Minimum Evolution (ME) algorithm (1000 bootstrap replicates). *Taracites asper* was used as an outgroup member.