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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of *Pomadasys kaakan* (Perciformes: Haemulidae)

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ABSTRACT

Pomadasys kaakan (Cuvier 1830) is a fish found in coastal waters that is widely distributed in the Western Indo-Pacific Ocean and plays an important role in commercial fisheries. The complete mitochondrial genome of *P. kaakan* was determined for the first time in this study. The genome was 16,808 bp in length and consisted of 13 protein coding genes, 22 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes, and one noncoding control region. The overall base composition was estimated to be A: 27.1%; T: 24.7%; C: 31.7%; and G: 16.5%, with an AT bias of 51.8%. Molecular phylogenetic analysis suggested that *P. kaakan* was clustered with species of genera *Plectorhinchus*, *Diagramma*, and *Parapristipoma*, which also belonged to the Haemulidae family. Furthermore, the Haemulidae family was closely related to the group containing Oplegnathidae, Kyphosidae, Teraponidae, and Lutjanidae. These results may provide molecular information for the species evolution and phylogenetic status of *P. kaakan* in the suborder Percoidei.

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Pomadasys kaakan (Cuvier 1830) belongs to the Haemulidae family of order Perciformes and is a kind of coastal water fish that is widely distributed in the Western Indo-Pacific Ocean. It inhabits turbid inshore waters with sandy to muddy bottoms to a depth of 75 m, and feeds on crustaceans and fish (Kuiter and Tonozuka 2001). It is also a commercially important fish for fisheries worldwide. Recently, no *Pomadasys* species mitogenome sequence has been available online. In this study, the complete mitochondrial sequence of *P. kaakan* was determined and analyzed for the first time, and the phylogenetic status of P. kaak*an* was also investigated.

The *P. kaakan* species was collected from Yangjiang city, Guangdong Province, China (21°52′81″N, 111°47′56″E) in October 2019 by commercial trawling. The total genomic DNA was extracted from tissues using the DNA isolation kit (TIANGEN, China). The specimen was deposited at the laboratory of the College of Animal Science and Technology in the Zhongkai University of Agriculture and Engineering, Guangzhou, China (http://www.zhku.edu.cn/, Rishen Liang is the contact peerson, email: cheetahliang@126.com) under the voucher number ZK-201907DP01, and the muscle tissue was placed in storage in 95% ethanol, DNA samples were stored in the refrigerator at −20 °C in the laboratory. Sequencing of The mitogenome was performed on the Illumina Novaseq 6000 platform and assembled using the de novo assembler SPAdes 3.11.0 (Dmitry et al. 2016). The complete mitochondrial genome was annotated using MITOS (http://mitos.bioinf.uni-leipzig.de/index.py). The circular genome map was drawn using Organellar Genome DRAW v1.2 (Lohse et al. 2007).

The complete mitogenome sequence of *P. kaakan* was determined to be 16,478 bp in length (GenBank accession number: MW421307), and the overall base composition of the genome was 27.1% A, 16.5% G, 24.7% T, and 31.7% C. At 51.8%, the AT content (51.8%) was higher than the GC content (48.2%). The structural organization of the genome consisted of 38 genes, containing 13 protein coding genes, 22 transfer RNA genes, two ribosomal RNA genes, and one control region. Most genes were encoded on the heavy strand, except for the ND6 and 8 tRNA genes (tRNA^{Gln}, RNA^{Ala}, RNA^{Asn}, tRNA^{Cys}, tRNA^{Tyr}, tRNA^{Ser}, tRNA^{Glu}, tRNA^{Pro}), which were identical to those of other vertebrates (Zhang et al. 2019; Lv et al. 2018; Sun and Xu 2018). All protein-coding genes used ATG as a start codon except for COI, which started with GTG. The patterns of stop codons were diverse in different genes: five genes ended with TAA (ND1, ND2, ATPase8, ND4L, and ND5), one ended with TAG (ND6), one ended with AGG (COI), and the remaining genes had

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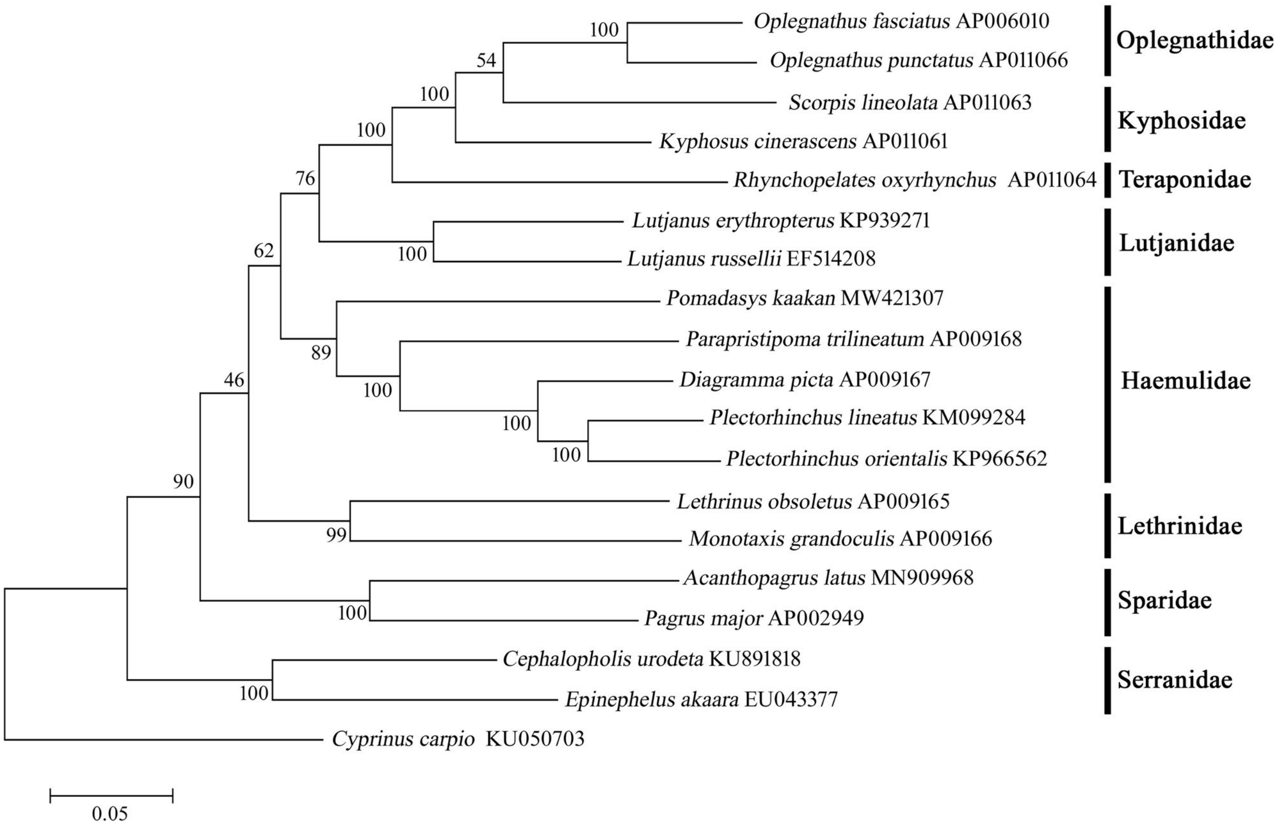

Figure 1. Molecular phylogenetic tree of *Pomadasys kaakan* and 17 other related species of suborder percoidei based on 12 protein-coding gene sequences constructed using the maximum likelihood method.

incomplete stop codons, TA (ATPase6, COIII) or T: COII, ND3, ND4, and Cyt b.

The molecular phylogenetic tree was constructed based on 12 protein coding genes from *P. kaakan* and 17 other related species of suborder percoidei with species *Cyprinus carpio* as outgroup, using a maximum-likelihood method with 1000 replicates in MEGA version 7.0 (Kumar et al. 2016). The results showed that *P. kaakan* was tightly clustered with species in the group *(Plectorhinchus lineatus* + *Plectorhinchus orientalis* + *Diagramma picta* + *Parapristipoma trilineatum*), which also belonged to the Haemulidae family. For the phylogenetic relationships of Haemulidae within other families of suborder Percoidei, the tree revealed that the Haemulidae group was a sister to the cluster including the Oplegnathidae, Kyphosidae, Teraponidae, and Lutjanidae families. This mitochondrial genome provides important genomic information for species evolution and phylogenetic analysis of genus *Pomadasys* and the Haemulidae family (Figure 1).

Disclosure statement

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

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov] (https://www.ncbi.nlm.nih.gov/) under the accession no. MW421307. The associated BioProject, SRA, and BioSample numbers are PRJNA765495, SRR16027455, and SAMN21561908 respectively.

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