

The complete mitochondrial genome of *Diagramma pictum* (Perciformes: Haemulidae)

Ming Chen^{a,b,c}, Guowei Liao^a, Zibo Li^a, Houhua Chen^a, Kai Zhang^{a,b,c} and Rishen Liang^{a,b,c}

^aCollege of Animal Science and Technology, Zhongkai University of Agriculture and Engineering, Guangzhou, China; ^bGuangdong Provincial Water Environment and Aquatic Products Security Engineering Technology Research Center, Guangzhou, China; ^cGuangzhou Key Laboratory of Aquatic Animal Diseases and Waterfowl Breeding, Guangzhou, China

ABSTRACT

The painted sweetlips *Diagramma pictum* (Thunberg 1792) is an important fish for commercial fisheries which is widely distributed in the Indo-West Pacific Ocean. It can change its external coloration and pattern during their lives. The complete mitochondrial genome of *D. pictum* was determined in this study. The genome was 16,531 bp in length and consisted of 13 protein coding genes, 22 transfer RNA (tRNA), 2 ribosomal RNA (rRNA), and one noncoding control region. The overall base composition was estimated to be A: 27.5%; T: 24.7%; C: 30.9% and G: 16.9% with AT bias of 52.2%. The molecular phylogenetic result revealed that *D. pictum* did not form an independent branch but was tightly clustered inside the *Plectorhinchus* groups, closely related to the species *Plectorhinchus chaetodonoides*, indicating the close relationships between genera *Diagramma* and *Plectorhinchus*. These results may provide important genomic information for species evolution and mitogenome based phylogenetic analyses of *D. pictum* in the family Haemulidae.

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The painted sweetlips *Diagramma pictum* (Thunberg 1792) is an important fish for commercial fisheries. It belongs to the family Haemulidae of order Perciformes. It is widely found throughout the coastal inshore waters around the Indo-Western Pacific Ocean. Morphologically, *D. pictum* displayed diverse appearance and can change its external coloration and pattern during its life. Juvenile *D. pictum* has longitudinal dark bands along its body, as it grows to adult, the bands increased and break into numerous small round spots, making the juvenile quite distinct from its adult form (McKay 1984, 2001). In this study, we determined the complete mitochondrial sequence of *D. pictum* and analyzed the genome structure and organization as well as its phylogenetic status within the family Haemulidae.

The painted sweetlips *D. pictum* was collected from Nanao city, Guangdong Province, China (22°53'38"N, 114°48'88"E) in July 2019 by setting nets. The sample was deposited in the laboratory of College of Animal Science and Technology, Zhongkai University of Agriculture and Engineering, Guangzhou, China (23°37'93"N, 113°45'15"E, voucher number: ZK-201907DP01, collector Information: Rishen Liang, cheetahliang@126.com). Total genomic DNA was extracted from tissues using the Animal Genomic DNA isolation kit (TIANGEN, China). Sequencing of the mitogenome was performed on Illumina Novaseq 6000 platform and assembled

using the de novo assembler SPAdes 3.11.0 (Dmitry et al. 2016). The annotations were performed with MITOS web server (<http://mitos.bioinf.uni-leipzig.de/index.py>) and the circular genome map was drawn using OGDRAW v1.2 (Lohse et al. 2007).

The complete mitogenome of *D. pictum* was circular and of 16,531 bp in length (GenBank accession number: MW411454), typically containing 13 protein coding genes, 22 transfer RNA (tRNA), 2 ribosomal RNA (rRNA), and 1 non-coding region. The overall base compositions of the genome were 27.5% for A, 16.9% for G, 24.7% for T, 30.9% for C, respectively. The AT content (52.2%) was higher than the GC content (47.8%). The genome structure, organization and base compositions were identical to those of other vertebrates (Zhang et al. 2019; Kim et al. 2020; Tabassum et al. 2020). 13 protein-coding genes found in *D. pictum* mitogenome use ATG as a start codon except for *COI*, which started with GTG. The use of stop codons varied among different genes, five genes ended with TAA: *ND1*, *ND2*, *ATPase8*, *ND4L* and *ND5*, one ended with TAG: *ND6*, one ended with AGG: *COI*, the remaining genes had incomplete stop codons, TA (*ATPase6*, *COIII*) or T: *COII*, *ND3*, *ND4* and *Cyt b*.

We compared our *D. pictum* mitogenome sequence with *Diagramma picta* obtained from GenBank (AP009167), *D. picta* is a synonymy of *D. pictum* and *D. pictum* is a valid

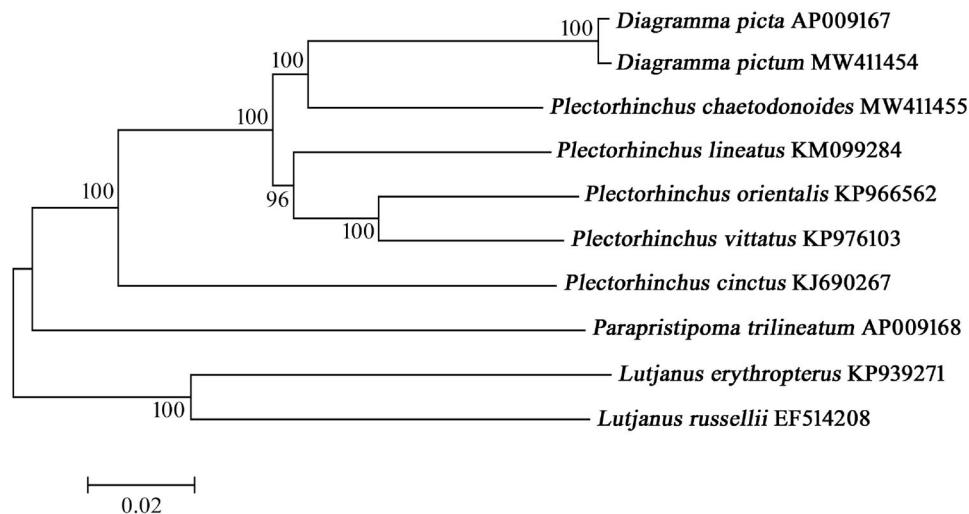


Figure 1. Molecular phylogenetic tree of *Diagramma pictum* with other Haemulidae species based on nucleotide sequences of 12 protein coding gene sequences constructed by maximum likelihood method. The accession number and species sites for these species are as follows: *Diagramma picta*(AP009167); *Diagramma pictum*(MW411454); *Plectorhinchus chaetodonoides*(MW411455); *Plectorhinchus lineatus*(KM099284); *Plectorhinchus orientalis*(KP966562); *Plectorhinchus vittatus*(KP976103); *Plectorhinchus cinctus*(KJ690267); *Parapristipoma trilineatum*(AP009168); *Lutjanus erythropterus*(KP939271); *Lutjanus russellii*(EF514208).

name (McKay 1984; McKay 2001; Froese and Pauly 2020). The result showed that there were 70 bp variable sites between the two samples and the sequence divergence value was 0.004%, indicating that some sequence variation and molecular differentiation exist at the intraspecific level. To investigate the molecular phylogenetic status of *D. pictum* in the family Haemulidae, mitogenome sequences of 7 Haemulidae and 2 Lutjanidae species available online in GenBank were downloaded and analyzed. Lutjanidae species were closely related to Haemulidae species and were used as outgroups (McKay 1984; Miller and Cribb 2007). The molecular phylogenetic tree was constructed based on the nucleotide sequences of 12 proteins coding genes (except for *ND6*) by RAxML 8.0 using maximum-likelihood method with GTR+G+I model (Figure 1). The result revealed that *D. pictum* in our study was tightly clustered with *D. picta*. Species in *Diagramma* did not form an independent branch but were located inside the *Plectorhinchus* groups, closely related to *Plectorhinchus chaetodonoides*, and they were sister to cluster *Plectorhinchus orientalis* + *Plectorhinchus vittatus* + *Plectorhinchus lineatus*, revealing the close relationships within *Diagramma* and *Plectorhinchus*. This result was consistent with the previous phylogenetic studies of the Haemulidae fish (Sanciangco et al. 2011; Tavera et al. 2018). This mitochondrial genome provides important genomic information for species evolution and phylogenetic analyses of *D. pictum* in the family Haemulidae.

Disclosure statement

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

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Data availability statement

The data that support the findings of this study are openly available in "NCBI" at <https://www.ncbi.nlm.nih.gov/>, reference number MW411454.

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