The complete mitochondrial genome of the grass emperor, Lethrinus laticaudis (Perciformes: Lethrinidae)

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ABSTRACT

The grass emperor Lethrinus laticaudis is a coral reef fish that has high value to fisheries and is vulnerable to overharvesting. The complete mitochondrial genome was assembled from approximately 5.5 million reads produced by Illumina MiSeq. The 16,758 bp consisted of 13 protein-coding genes, 22 transfer RNA genes and two ribosomal RNA genes (12S and 16S). The genes and RNAs were typically ordered and oriented on the complete mitogenome. Sequence was validated using the MitoAnnotator pipeline on the Mitofish webserver (Iwasaki et al. 2013). Our findings are consistent with what was described in Table 1. Moreover, the base composition was A, 32%, T, 18.7%, G, 21.3%, C, 28% with an A+T base content (50.7%) similar to other Teleosts. De novo annotations of the mitogenome were computed using the MitoAnnotator pipeline on the Mitofish webserver (Iwasaki et al. 2013). The complete mitogenome of L. laticaudis was aligned against the mitogenomes of closely related species chosen based on the classification of bony fishes (Betancur et al. 2013) and considering their availability in GenBank. The phylogenetic tree (Figure 1) showed that our mitogenome grouped together with the other Lethrinidae species. The Sparidae as well as the Nemipteridae species grouped together and formed a sister clade to the Lethrinidae (Figure 1). Our findings are consistent with what was previously reported.
Table 1. Detailed structure of Lethrinus laticaudis mitogenome (KU530221).

| Locus      | Position | Codon         | Intergenic bases (bp) |
|------------|----------|---------------|-----------------------|
| tRNA-Phe   | 1-68     | H             | 68                    |
| 12S rRNA   | 69-1023  | H             | 955                   |
| tRNA-Val   | 1023-1101| H             | 79                    |
| 16S rRNA   | 1100-2905| H             | 1806                  |
| tRNA-Leu   | 2906-2980| H             | 75                    |
| ND1        | 2981-3952| H             | 972                   |
| tRNA-Ile   | 3957-4025| H             | 69                    |
| tRNA-Gln   | 4026-4096| H             | 71                    |
| tRNA-Met   | 4095-4166| H             | 72                    |
| ND2        | 4166-5212| H             | 1047                  |
| tRNA-Trp   | 5214-5284| H             | 71                    |
| tRNA-Ala   | 5284-5352| L             | 69                    |
| tRNA-Asn   | 5355-5427| L             | 73                    |
| OL         | 5427-5465| H             | 39                    |
| tRNA-Cys   | 5465-5531| L             | 67                    |
| tRNA-Tyr   | 5533-5602| L             | 70                    |
| COX1       | 5611-7155| H             | 1545                  |
| tRNA-Ser   | 7158-7227| L             | 70                    |
| tRNA-Asp   | 7231-7302| H             | 72                    |
| COX2       | 7310-8008| H             | 699                   |
| tRNA-Lys   | 8001-8077| H             | 77                    |
| ATP8       | 8078-8245| H             | 168                   |
| ATP6       | 8258-8941| H             | 684                   |
| COX3       | 8941-9726| H             | 786                   |
| tRNA-Gly   | 9727-9797| H             | 71                    |
| ND3        | 9798-10148| L             | 351                   |
| tRNA-Arg   | 10149-10213| H             | 65                    |
| ND4L       | 10216-10512| L             | 297                   |
| ND4        | 10506-11891| H             | 1386                  |
| tRNA-His   | 11887-11955| H             | 69                    |
| tRNA-Ala   | 11957-12013| H             | 57                    |
| tRNA-Leu   | 12030-12102| H             | 73                    |
| ND5        | 12121-13941| L             | 1821                  |
| ND6        | 13938-14459| L             | 522                   |
| tRNA-Glu   | 14460-14528| L             | 69                    |
| CYTB       | 14533-15729| H             | 1197                  |
| tRNA-Thr   | 15674-15746| H             | 73                    |
| tRNA-Pro   | 15745-15814| L             | 70                    |
| D-Loop     | 15815-16758| H             | 944                   |

Figure 1. Phylogenetic tree of 11 closely related species including Lethrinus laticaudis based on the analysis of mitogenome sequences. The mitogenomes were aligned in Geneious using ClustalW alignment method with default settings. Poorly aligned positions and indels were removed with Gblock v 0.91b (Castresana 2000; Dereeper et al. 2008) using default settings and the D-Loop region was also excluded (total length: 15,323 bp). A heuristic maximum likelihood (ML) search was conducted using RaxML HPC v8 (Stamatakis 2006) on XSEDE, implemented in the CyberInfrastructure for Phylogenetic Research (CIPRES) portal v3.3 (http://www.phylo.org/portal2, Miller et al. 2010). Lutjanus johnii was set as the outgroup species for our analysis. A rapid bootstrap analysis and a search for best-scoring ML tree were performed. Robustness of the nodes was assessed with 1000 bootstrap replicates.
described in Betancur et al. (2013) and validate the accuracy of our mitogenome and species sample. The present genomic information will help lay the foundations for more detailed understanding of the biological and genetic diversity of the species, and contribute to its conservation and sustainable management.

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