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

Taillebois, Laura; Crook, David; Saunders, Thor; Williams, Samuel M.; Ovenden, Jennifer R.

Published in: Mitochondrial DNA Part B: Resources

DOI: 10.1080/23802359.2016.1166076

E-pub ahead of print: 18/04/2016


General rights
Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

• Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
• You may not further distribute the material or use it for any profit-making activity or commercial gain
• You may freely distribute the URL identifying the publication in the public portal

Take down policy
If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.
The complete mitochondrial genome of the grass emperor, Lethrinus laticaudis (Perciformes: Lethrinidae)

Laura Taillebois, David A. Crook, Thor Saunders, Samuel M. Williams & Jennifer R. Ovenden

To cite this article: Laura Taillebois, David A. Crook, Thor Saunders, Samuel M. Williams & Jennifer R. Ovenden (2016) The complete mitochondrial genome of the grass emperor, Lethrinus laticaudis (Perciformes: Lethrinidae), Mitochondrial DNA Part B, 1:1, 277-279, DOI: 10.1080/23802359.2016.1166076

To link to this article: https://doi.org/10.1080/23802359.2016.1166076

© 2016 The Author(s). Published by Taylor & Francis.

Published online: 18 Apr 2016.

Submit your article to this journal

Article views: 125

View related articles

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

Laura Taillebois\(^a,b\), David A. Crook\(^b\), Thor Saunders\(^c\), Samuel M. Williams\(^d\) and Jennifer R. Ovenden\(^d\)

\(^a\)North Australia Marine Research Alliance, Charles Darwin University, Darwin, NT, Australia; \(^b\)Research Institute for the Environment and Livelihoods, Charles Darwin University, Darwin, NT, Australia; \(^c\)Department of Primary Industry and Fisheries, Northern Territory Government, Berrimah, NT, Australia; \(^d\)Molecular Fisheries Laboratory, School of Biomedical Sciences, The University of Queensland, St. Lucia, QLD, Australia

**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 order and orientation on the complete mitogenome were computed using the MitoAnnotator pipeline on the Mitofish webserver (Iwasaki et al. 2013). Our findings are consistent with what was described in *L. laticaudis* using a next generation sequencing approach.

Genomic DNA was extracted from a tissue sample (WAM16-001) using Qiagen DNAasy Blood and Tissue Kits (Qiagen, Germantown, USA) following the manufacturer’s instructions. The purified genomic DNA was processed (Illumina, San Diego, CA) on a MiSeq Illumina platform at the AGRF (Australian Genomics Research Facilities). The MiSeq run yielded 5,601,280 sequences with a read length of 300 bp. The mitogenome was assembled from paired end sequences. The reads were first mapped against the complete mitochondrial genome of *Larimichthys crocea* (Scianidae, GenBank Accession Number NC_011710) in Geneious version 9.0.2 (http://www.geneious.com, Kearse et al. 2012). The 8163 mapped reads were then assembled *de novo* to produce a 16,758 bp length mitogenome assembly (GenBank Accession Number: KU530221). Indels were validated or corrected based on depth and sequence quality. The overall mean coverage was 145 (min = 2; max = 410; SD = 47.9). *De novo* annotations of the mitogenomic sequence were computed using the MitoAnnotator pipeline on the Mitofish webserver (Iwasaki et al. 2013).

The complete mitogenome of *L. laticaudis* consisted of 13 protein-coding genes, 22 transfer RNA (tRNA), 2 ribosomal RNA (rRNA) as well as two non-coding regions namely the origin of light strand replication (OL) and the control region (D-Loop). The genes and RNAs were typically ordered and oriented between the two strands of the mitogenome as described in *Table 1*. Moreover, the base composition was A, 32.2%, T, 18.7%, G, 21.3%, C, 28% with an A + T base content (50.7%) similar to other Teleosts. To validate our mitogenome and assist with future taxonomic and phylogenetic studies, *L. laticaudis* mitogenome 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
Table 1. Detailed structure of Lethrinus laticaudis mitogenome (KU530221).

<table>
<thead>
<tr>
<th>Position</th>
<th>Locus</th>
<th>Start</th>
<th>Stop</th>
<th>Strand</th>
<th>Length (bp)</th>
<th>Start</th>
<th>Stop</th>
<th>Anti-codon</th>
<th>Intergenic bases (bp)</th>
</tr>
</thead>
</table>
|          | tRNA-Phe | 1 68 | H | 68 | GAA | 0
|          | 12S rRNA | 69 1023 | H | 955 | CAC | 0
|          | tRNA-Val | 1023 1101 | H | 79 | 0
|          | 16S rRNA | 1100 2905 | H | 1806 | GAG | 0
|          | tRNA-Leu | 2906 2980 | H | 75 | 4
|          | ND1     | 2981 3957 | H | 972 | ATT | 1
|          | tRNA-Ile | 3957 4025 | H | 69 | TAG | 2
|          | tRNA-Gln | 4026 4096 | L | 71 | GTC | 2
|          | tRNA-Met | 4095 4166 | H | 72 | 0
|          | ND2     | 4166 5212 | H | 1047 | ATG | 1
|          | tRNA-Trp | 5214 5284 | H | 71 | ACC | 1
|          | tRNA-Ala | 5284 5352 | L | 69 | CGT | 2
|          | tRNA-Asn | 5355 5427 | L | 73 | TTA | 2
|          | OL      | 5427 5465 | L | 39 | 0
|          | tRNA-Cys | 5465 5531 | L | 67 | ACG | 1
|          | tRNA-Tyr | 5533 5602 | H | 70 | 0
|          | COX1    | 5611 7155 | H | 1545 | 0
|          | tRNA-Ser | 7158 7227 | L | 70 | TCA | 3
|          | tRNA-Asp | 7231 7302 | H | 72 | CTG | 7
|          | COX2    | 7310 8008 | H | 699 | AGA | 8
|          | tRNA-Lys | 8001 8077 | H | 77 | 0
|          | ATP8    | 8078 8245 | H | 168 | 12
|          | ATP6    | 8258 8941 | H | 684 | 0
|          | COX3    | 8941 9726 | L | 786 | TTA | 0
|          | ND3     | 9798 10148 | H | 351 | 0
|          | tRNA-Arg | 10149 10213 | H | 65 | TCG | 2
|          | ND4L    | 10216 10512 | H | 297 | 0
|          | ND4     | 10506 11891 | H | 1386 | AGG | 5
|          | tRNA-His | 11887 11955 | H | 69 | GTG | 10
|          | tRNA-Ala | 11957 12013 | H | 57 | CGC | 16
|          | tRNA-Leu | 12030 12102 | H | 73 | AGA | 18
|          | ND5     | 12121 13941 | H | 1821 | 4
|          | ND6     | 13938 15729 | L | 522 | TGT | 56
|          | tRNA-Glu | 14460 14528 | L | 69 | 4
|          | CYTB    | 14533 15729 | L | 1197 | TAG | 0
|          | tRNA-Thr | 15674 15746 | H | 73 | 0
|          | tRNA-Pro | 15745 15814 | L | 70 | 0
|          | D-Loop  | 15815 16758 | H | 944 | 0

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.

Acknowledgements

The authors thank Mike Travers, Steve Newman and other staff from the Western Australian Department of Agriculture and Fisheries for sample collection and valuable comments.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

Funding information

This research was supported by the Fisheries Research and Development Corporation (Project 2013/017); and the researcher LT was supported by the North Australia Marine Research Alliance (NAMRA – AIMS/ANU/CDU/NT Government) post-doctoral Fellowship.

References


