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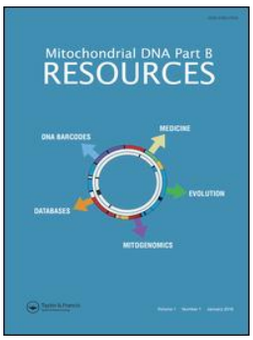

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MITOGENOME ANNOUNCEMENT

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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 order and orientation on as well as the A + T base content (50.7%) was similar to what is found in other Teleosts. A phylogenetic tree with the most closely related species available in GenBank was built to validate *L. laticaudis* mitogenome.

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Genome; *Lethrinus laticaudis*; mitochondrion

Lethrinus laticaudis Alleyne & Macleay, 1877 is an exploited species of Lethrinidae that occurs in tropical waters of western Pacific and southeastern Indian oceans throughout southern Indonesia, Australia, Papua New Guinea, Solomon Islands and New Caledonia (Carpenter & Niem 2001). They mainly inhabit brackish and marine water with adults common over shallow (<50 m) coral reef habitats and their juveniles occupying seagrass meadows and mangrove forests (Carpenter & Niem 2001; Travers et al. 2010). The species is considered an excellent eating fish and is targeted by commercial fishers and recreational anglers across northern Australia (Coleman 2003). Although the grass emperor is considered robust to fishing pressure (Grubert et al. 2010) due to its high reproductive capacity (i.e. serial batch spawners, high spawning frequency, high batch fecundity) (Ayvazian et al. 2004), it is heavily exploited in some areas. Genetic information on the species' stock structure is required to support future decisions on fisheries management and ensure the sustainability of exploited populations. In this study, we determine the complete mitogenomic sequence for *L. laticaudis* using a next generation sequencing approach.

Genomic DNA was extracted from a tissue sample (WAM16-001) using Qiagen DNAesy 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 (O_L) 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%, 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

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Table 1. Detailed structure of *Lethrinus laticaudis* mitogenome (KU530221).

	Position				Codon			
Locus	Start	Stop	Strand	Length (bp)	Start	Stop	Anti-codon	Intergenic bases (bp)
tRNA-*Phe*	1	68	H	68			GAA	0
12S rRNA	69	1023	H	955				−1
tRNA-*Val*	1023	1101	H	79			CAC	−2
16S rRNA	1100	2905	H	1806				0
tRNA-*Leu*	2906	2980	H	75			GAG	0
ND1	2981	3952	H	972	ATG	TAA		4
tRNA-*Ile*	3957	4025	H	69			TAG	0
tRNA-*Gln*	4026	4096	L	71			GTC	−2
tRNA-*Met*	4095	4166	H	72			TAC	−1
ND2	4166	5212	H	1047	ATG	TAA		1
tRNA-*Trp*	5214	5284	H	71			ACC	−1
tRNA-*Ala*	5284	5352	L	69			CGT	2
tRNA-*Asn*	5355	5427	L	73			TTG	−1
OL	5427	5465		39				−1
tRNA-*Cys*	5465	5531	L	67			ACG	1
tRNA-*Tyr*	5533	5602	L	70			ATG	8
COX1	5611	7155	H	1545	ATT	TAA		2
tRNA-*Ser*	7158	7227	L	70			TCA	3
tRNA-*Asp*	7231	7302	H	72			CTG	7
COX2	7310	8008	H	699	ATG	AGA		−8
tRNA-*Lys*	8001	8077	H	77			TTT	0
ATP8	8078	8245	H	168	ATG	TAA		12
ATP6	8258	8941	H	684	ATG	TAA		−1
COX3	8941	9726	H	786	ATG	TAA		0
tRNA-*Gly*	9727	9797	H	71			CCA	0
ND3	9798	10148	H	351	ATG	TAG		0
tRNA-*Arg*	10149	10213	H	65			TCG	2
ND4L	10216	10512	H	297	ATG	TAA		−7
ND4	10506	11891	H	1386	ATG	AGG		−5
tRNA-*His*	11887	11955	H	69			GTG	1
tRNA-*Ala*	11957	12013	H	57			CGC	16
tRNA-*Leu*	12030	12102	H	73			GAA	18
ND5	12121	13941	H	1821	ATA	TAA		−4
ND6	13938	14459	L	522	ATG	TAG		0
tRNA-*Glu*	14460	14528	L	69			CTT	4
CYTB	14533	15729	H	1197	ATG	TAA		−56
tRNA-*Thr*	15674	15746	H	73			TGT	−2
tRNA-*Pro*	15745	15814	L	70			GGG	0
D-Loop	15815	16758	H	944				0

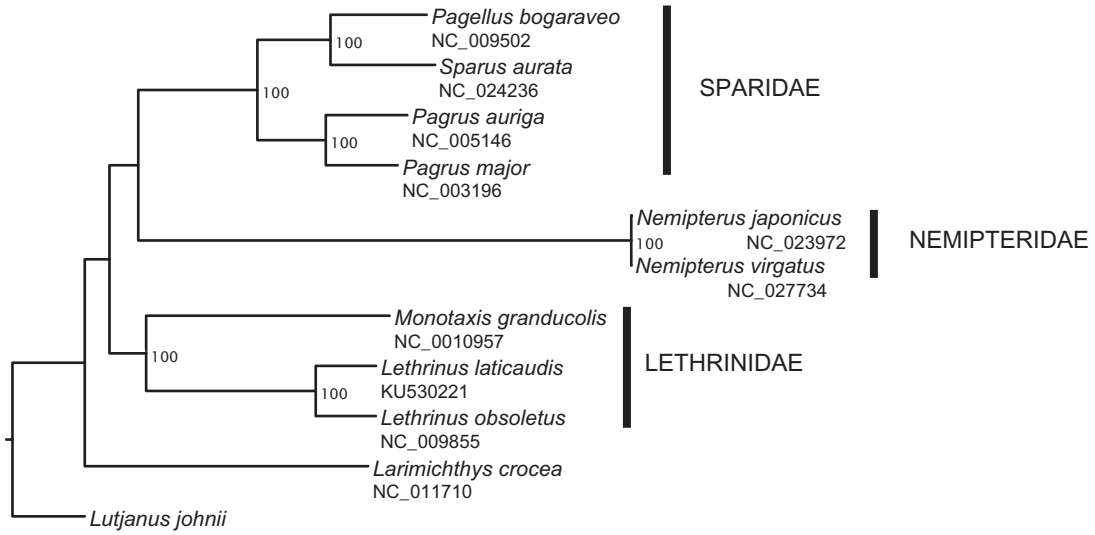

Figure 1. Phylogenetic tree of 11 closely related species including *Lethrinus laticaudis* based on the analysis of mitogenome sequences. The mitogenomes were aligned in Geneious using ClustalW alignment method with default settings. Poorly aligned positions and indels were removed with Gblock v 0.91b (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.

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Disclosure statement

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

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