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Mitochondrial DNA Part A

DNA Mapping, Sequencing, and Analysis

ISSN: 2470-1394 (Print) 2470-1408 (Online) Journal homepage: http://www.tandfonline.com/loi/imdn21

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To cite this article: Pierre Feutry, Peter M. Kyne, Zaiqing Peng, Lianghao Pan & Xiao Chen (2016) Complete mitochondrial genome of the Freshwater Whipray Himantura dalyensis, Mitochondrial DNA Part A, 27:3, 1589-1590, DOI: 10.3109/19401736.2014.958682

To link to this article: http://dx.doi.org/10.3109/19401736.2014.958682

Mitochondrial DNA

http://informahealthcare.com/mdn
ISSN: 2470-1394 (print), 2470-1408 (electronic)

Mitochondrial DNA Part A, 2016; 27(3): 1589–1590
 DOI: 10.3109/19401736.2014.958682

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the Freshwater Whipray *Himantura dalyensis*

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Abstract

The complete mitochondrial genome of the Freshwater Whipray *Himantura dalyensis* is presented in this study. It is 17,693 bp in length and contains 37 genes in typical gene order and transcriptional orientation observed in vertebrates. There were a total of 86 bp short intergenic spacers and 22 bp overlaps in the genome. The overall base composition was 31.4% A, 25.5% C, 13.2% G and 29.9% T. Two start codons (GTG and ATG) and two stop codons (TAG and TAA/T) were found in 13 protein-coding genes. The length of 22 tRNA genes ranged from 68 (tRNA-*Cys* and tRNA-*Ser2*) to 75 bp (tRNA-*Leu1*). The origin of L-strand replication (OL) was found between the tRNA-*Asn* and tRNA-*Cys* genes. The base composition of the control region (1940 bp) was similar to the whole mitogenome.

Keywords

Dasyatidae, *Himantura dalyensis*, mitochondrion

History

Received 7 August 2014
Accepted 23 August 2014
Published online 17 September 2014

The Freshwater Whipray *Himantura dalyensis* (Rajiformes: Dasyatidae) is a poorly-known euryhaline batoid which is listed as Data Deficient on the IUCN Red List of Threatened Species (Kyne, 2011). It was only recently described as distinct from *H. polylepis* (a senior synonym of *H. chaophraya*), which occurs in South-East Asia (Last & Manjaji-Matsumoto, 2008). *Himantura dalyensis* is distributed across tropical northern Australia in estuarine and river environments, although its full extent of occurrence remains unconfirmed and it may also be present in southern New Guinea (Kyne, 2011; Last & Manjaji-Matsumoto, 2008). Here we provide the whole mitogenome of *H. dalyensis.*

A tissue sample (fin clip) was collected from a specimen of *H. dalyensis* captured and released in Nourlangie Creek, a tributary of the South Alligator River, Kakadu National Park, Northern Territory, Australia, under KadaduResearch Permit RK805. The experimental protocol and data analysis methods follow Chen et al. (2014). The complete mitogenome of *H. dalyensis* was a circular molecule 17,693 bp in length (GenBank accession No. KM244769). It contains 37 genes encoding 13 proteins, 2 ribosomal RNAs, 22 transfer RNAs and 1 control region. Gene order and transcriptional orientation are typical for a vertebrate species (Figure 1). The mitochondrial genes have a total of 86 bp short intergenic spacers in 19 different locations ranging from 1 to 13 bp, and overlapping by a total of 22 bp in 4 different locations from 1 to 10 bp.The overall base composition of the *H. dalyensis* mitogenome is 31.4% A, 25.5% C, 13.2% G and 29.9% T. The AT content (61.3%) is slightly higher than the GC content, as observed in other vertebrates.

The size of the protein-coding genes found in *H. dalyensis*is are highly similar to its orthologs in the Rajiformes (Chen et al., 2014). Except for the *COI* gene using GTG as the start codon, the remaining 12 protein-coding genes were initiated by the typical ATG codon. The *COI* and *ND6* genes were terminated by the TAG codon, while the remaining genes employ TAA or incomplete T as the stop codon. The 12S and 16S rRNA genes were 964 and 1689 bp in length, respectively and located between the tRNA-*Phe* and tRNA-*Leu1* genes separated by the tRNA-*Val* gene. The length of the 22 tRNA genes ranges from 68 (tRNA-*Cys* and tRNA-*Ser2*) to 75 bp (tRNA-*Leu1*). They intersperse along the mitogenome and form three conserved tRNA clusters (IQM, WANCY, and HSL). All tRNAs could fold into a typical clover-leaf secondary structure, except tRNA-*Ser2*, which had lost the dihydrouridine (DHU) arm and replaced it by a simple loop. A 34 bp insert was identified as the origin of L-strand replication (OL) between the tRNA-*Asn* and tRNA-*Cys* genes within the WANCY cluster. It forms a stable hairpin structure (8 bp stem and 13 bp loop) as the original signal. The control region was 1940 bp in length, located between the tRNA-*Pro* and tRNA-*Phe* genes. The base composition of the control region

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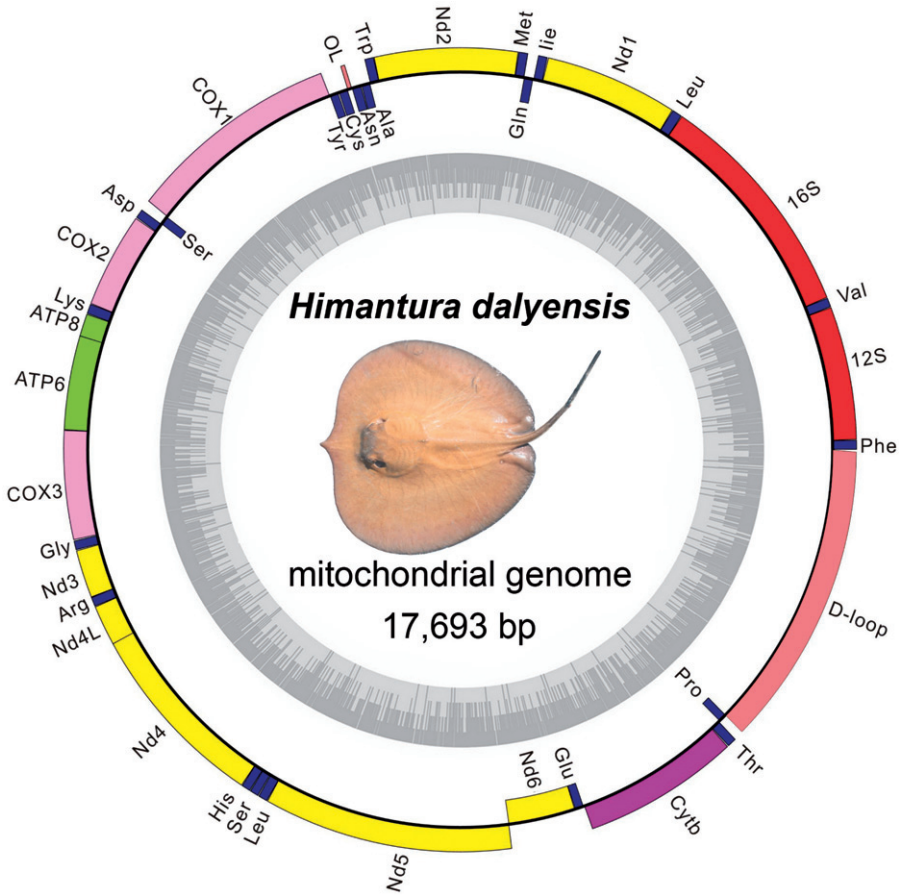

Figure. 1. Mitogenomic map of *Himantura dalyensis*. Photo credit: Peter M. Kyne (note most of tail missing).

(29.7% A, 25.3% C, 15.2% G and 29.8% T) is similar to the whole mitogenome.

Declaration of interest

This study was supported by the National Natural Sciences Foundation of China (41006080) andthe Marine Biodiversity Hub, a collaborative partnership supported through funding from the Australian Government's National Environmental Research Program (NERP). Researcher PF was partly supported by the North Australia Marine Research Alliance (NAMRA). Researcher PMK was partly supported by the NERP Northern Australia Hub.The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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