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Complete mitochondrial genome and the phylogenetic position of the Jenkins whipray *Himantura jenkinsii* (Myliobatiformes, Dasyatidae)

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ABSTRACT

We determined the complete mitochondrial genome of the Jenkins whipray *Himantura jenkinsii*. The total length of the mitogenome was 17, 670 bp, consisted of 37 genes with typical gene order in vertebrate mitogenome. The nucleotide composition was: 30.5% A, 29.1% T, 26.5% C and 13.9% G. It had 70 bp short intergenic spaces and 22 bp overlaps. Two start codons (GTG and ATG) and two stop codons (TAG and TAA/T) were used in the protein-coding genes. The 22 tRNA genes were ranged from 67 bp (tRNA-*Ser2*) to 75 bp (tRNA-*Leu1*). The phylogenetic result showed that *H. jenkinsii* was clustered with the Hortle's whipray *H. hortlei*.

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The Jenkins whipray *Himantura jenkinsii* (Myliobatiformes, Dasyatidae), a widely distributed but with patchy occurrence species, mainly found in the Indo-Pacific, from southern Africa and India to Australia and Papua New Guinea (Last & Compagno 1999). It was ovoviviparous and mainly inhabited shallow coastal waters (Dulvy & Reynolds 1997; Kapoor et al. 2002). In this study, we determined the complete mitochondrial genome of *H. jenkinsii* for the first time and analyzed its phylogenetic relationship within Myliobatiformes.

One specimen of *H. jenkinsii* was captured from Andaman Sea and landed in Ranong, Thailand. Its tissue sample (voucher RN2012122427) was preserved in 95% alcohol. The whole specimen failed to be saved for its huge size. The experimental protocol and data analysis methods followed Chen et al. (2015). Including *H. jenkinsii*, all fifteen species of Myliobatoformes with the complete mitogenomes available in the Genbank were selected to construct the phylogenetic tree using the Bayesian method. The outgroup was *Plesiobatis daviesi* (Myliobatoformes, Plesiobatidae).

The complete mitochondrial sequence of *H. Jenkinsii* was 17,670 bp (GenBank accession no. KU873081), consisting of 13 protein-coding genes, two rRNAs, 22 tRNAs and a non-coding control region, with the gene order identical to that of typical vertebrates. The nucleotide composition was: 30.5% A, 29.1% T, 26.5% C and 13.9% G. The A + T content (59.6%) was higher than the G + C content (40.4%). Its whole mitogenome had 70 bp short intergenic spaces located in 19 gene junctions and 22 bp overlaps located in four gene junctions. The 13 protein-coding genes used two start codons (GTG and ATG) as well as two stop codons (TAG and TAA/T), and most of them shared common initial codon ATG and terminal codon TAA/T. The *COI* gene owned a nonstandard initial codon GTG, which was common in vertebrates (Slack et al. 2003). The *COII* and *ND4* genes were terminated with a single T, which could be extended to complete TAA through polyadenylation in transcriptions (Ojala et al. 1981). Both 12S rRNA (963 bp) and 16S rRNA (1695 bp) genes were between tRNA-*Phe* and tRNA-*Leu1* genes, separated by tRNA-*Val* gene. A non-coding sequence (34 bp) associated with the putative L-strand replication origin (OL) located between tRNA-*Asn* and tRNA-*Cys* in the WANCY [tryptophan (W), alanine (A), asparagine (N), cysteine (C) and tyrosine (Y) cluster]. The control region was 1924 bp, presenting a high A + T content (59.0%).

Himantura jenkinsii was clustered with the Hortle's whipray *H. hortlei*, and all five *Himantura* species clustered together with strong support value (100%). Three *Dasyatis* species also clustered together. It suggested that these two genuses were monophyletic (Figure 1). However, the genus *Taeniura* was polyphyletic. *Taeniura lymma* clustered with *Neotrygon kuhlii* while *T. Meyeni* clustered with the (*Pteroplatytrygon violacea* + *Dasyatis*) clade.

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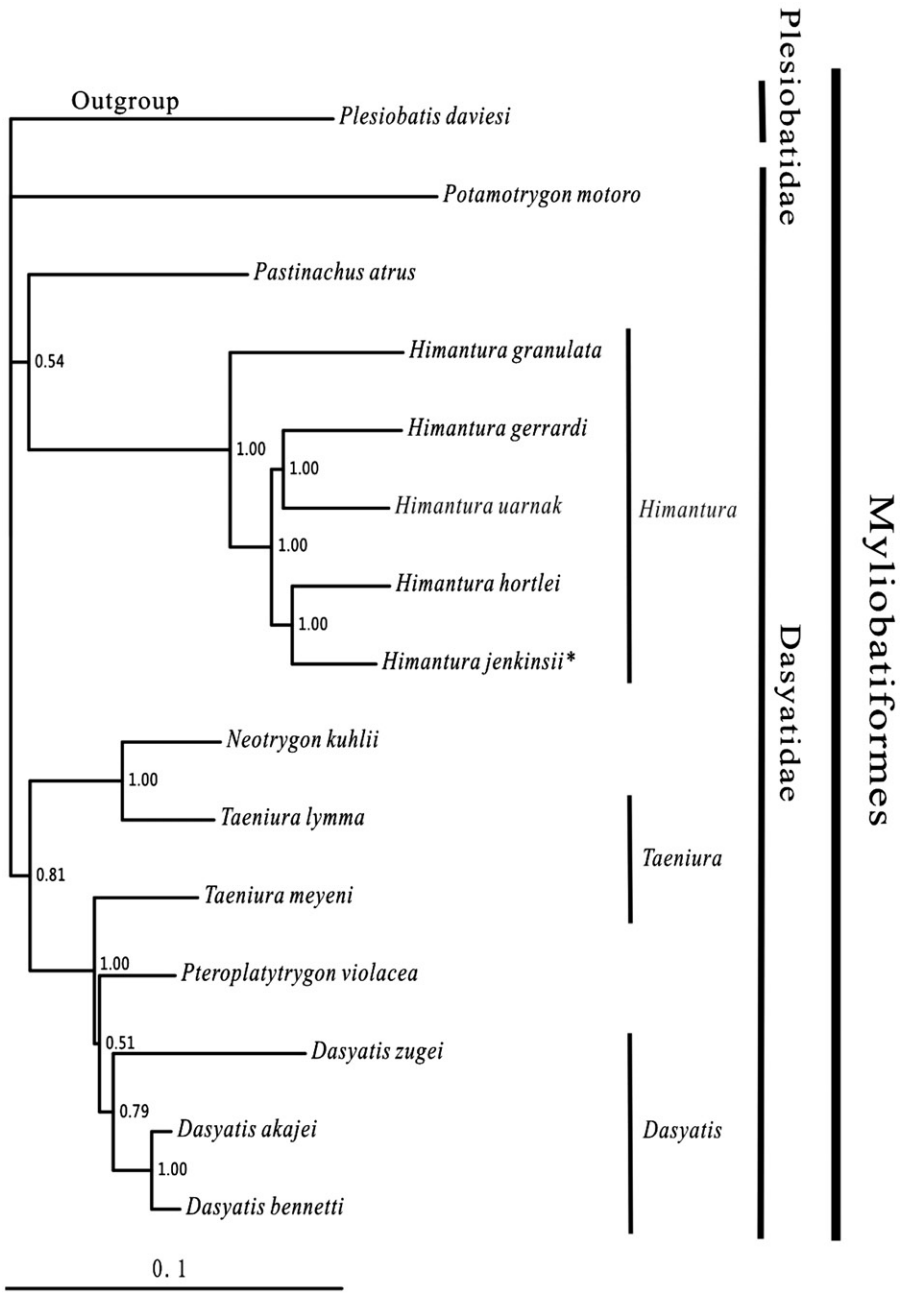

Figure 1. Phylogenetic position of *Himantura jenkinsii*. *Plesiobatis daviesi* (AY597334.1) was selected as the outgroup. The fourteen species of Dasyatidae were: *Potamotrygon motoro* (NC_023116.1), *Pastinachus atrus* (NC_023808.1), *Himantura granulata* (NC_023525.1), *H. gerrardi* (NC_026208.1), *H. uarnak* (NC_028325.1), *H. hortlei* (NC_027497.1), *H. Jenkinsii* (KU873081), *Neotrygon kuhlii* (KR019777.1), *Taeniura lymma* (NC_026210.1), *T. meyeni* (NC_019641.1), *Pteroplatytrygon violacea* (NC_024570.1), *Dasyatis akajei* (NC_021132.1), *D. zugei* (NC_019643.1) and *D. bennetti* (KC633222.1).

Disclosure statement

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

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