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# Complete mitochondrial genome and the phylogenetic position of the White-spotted guitarfish *Rhynchobatus australiae* (Rajiformes, Rhinobatidae)

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**ABSTRACT**

We first determined the complete mitochondrial genome of the White-spotted guitarfish *Rhynchobatus australiae* (Rajiformes, Rhinobatidae). The complete mitogenome was 16,804 bp, with a base composition of 32.3% A, 27.5% T, 26.9% C and 13.3% G, containing 13 protein-coding genes, two rRNAs, 22 tRNAs and a control region (D-loop). It had 35 bp short intergenic spaces and 39 bp overlaps between genes. The gene order and composition of *R. australiae* was similar to most other fishes. The codon usage followed the typical vertebrate mitochondrial pattern (ATG or GTG for start codon and TAA or T for stop codon). The phylogenetic result showed that *R. australiae* was clustered with the Rhinobatos.

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The White-spotted guitarfish *Rhynchobatus australiae* (Rajiformes, Rhinobatidae) was a locally common species found in the Western Pacific from the Gulf of Thailand and the Philippines to Queensland in Australia, mainly inhabiting inshore waters (Compagno & Last 1999; White et al. 2006). The molecular and genetic research of this species were rare. In this study, we first determined the complete mitochondrial genome of *R. Australiae* with GenBank accession no. KU746824 and analyzed the phylogenetic relationship in Rajiformes.

One specimen of *R. australiae*, which was captured from the Gulf of Thailand, was landed on a pier in Songkhla, Thailand. Tissue of *R. Australiae* was preserved in Wenzhou Medical University by 95% alcohol with voucher THSK20121613. The whole specimen of *R. Australiae* could not be preserved for its great size. The experimental protocol and data analysis methods followed Chen et al. (2015). We constructed the phylogenetic tree using the Bayesian method. Thirteen species of Rajiformes (including *R. Australiae*) with the complete mitogenomes available in the Genbank were selected. The outgroup was *Dasyatis akajei* (Myliobatoformes).

The complete mitogenome of *R. Australiae* was 16,804 bp, containing 13 protein-coding genes, two rRNAs, 22 tRNAs and a control region identical to other skates (Chen et al. 2015). The mitogenome of *R. Australiae* had 35 bp short intergenic spaces located in 13 gene junctions and 39 bp overlaps located in six gene junctions. The nucleotide composition of the genome was strongly A–T skewed, with A + T content of 59.8% for the entire sequence (32.3% A, 27.5% T, 26.9% C and 13.3% G). Except for *ND6* gene and eight tRNA genes (tRNA-*Gln*, *Ala*, *Asn*, *Cys*, *Tyr*, *Ser*1(UGA), *Glu* and *Pro*), all other genes were encoded on the H-strand. Twelve out of 13 mitochondrial protein-coding genes used ATG as the start codon (*COI* gene started with GTG). Two types of stop condons were used, except for *COII* and *ND4* ending with the incomplete stop condon T, the rest protein-coding genes all ending with TAA. The 22 tRNA genes were ranged from 66 bp (tRNA-*Ser*2) to 75 bp (tRNA-*Leu*1), and all tRNAs could be folded into the typical cloverleaf secondary structures except the tRNA-*Ser*2, which replaced the dihydrouridine arm by a simple loop. Both 12S rRNA (967 bp) and 16S rRNA (1, 690 bp) genes were between tRNA-*Phe* and tRNA-*Leu*1 genes, separated by tRNA-*Val* gene. The origin of light-strand replication (39 bp) was located between tRNA-*Asn* and tRNA-*Cys* genes. The control region was 1106 bp in length, rich in A + T (64.8%) and poor in G (13.3%).

All 13 mitogenomes available in Rhinobatidae, representing three families, were used to analyze the phylogenic position of *R. australiae* in this study. These three families formed a (Rhinobatidae + (Rajidae + Arhynchobatidae)) rela-

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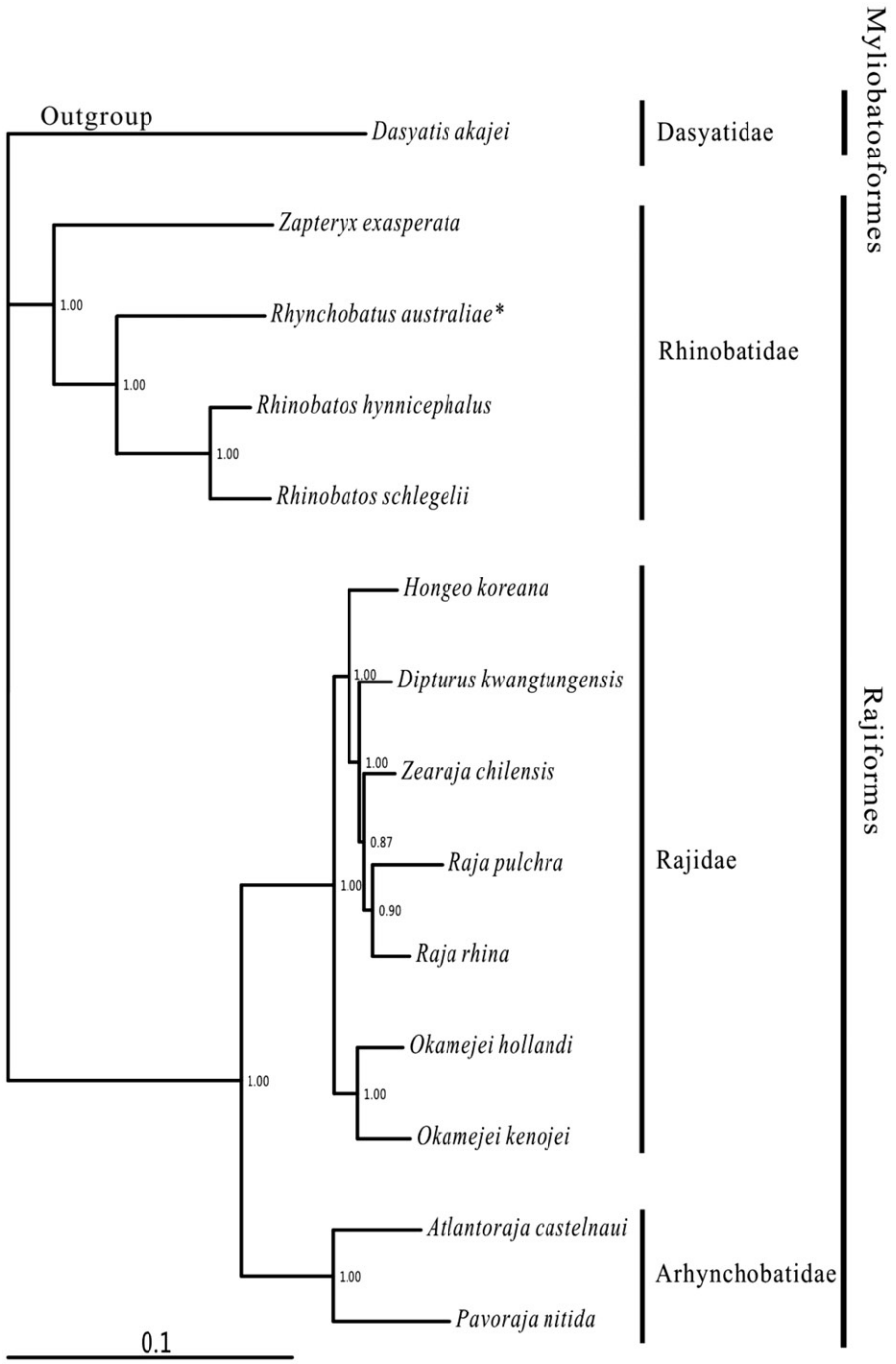


**Figure 1.** Phylogenetic position of *Rhynchobatus australiae*. *Dasyatis akajei* (NC_021132.1) was selected as the outgroup. The 13 species of Rajiformes were *Zapteryx exasperata* (NC_024937.1), *Rhynchobatus australiae* (KU746824), *Rhinobatos hynnicephalus* (NC_022841.1), *R. schlegelii* (NC_023951.1), *Hongeo koreana* (NC_021963.1), *Dipturus kwangtungensis* (NC_023505.2), *Zearaja chilensis* (KJ913073.2), *Raja pulchra* (NC_025498.1), *Raja rhina* (KC914434.1), *Okamejei hollandi* (KP756687.1), *O. kenojei* (NC_007173.1), *Atlantoraja castelnaui* (NC_025942.1) and *Pavoraja nitida* (NC_024599.1).

tionship (Figure 1), which was consistent to the morphological result (McEachran & Dunn 1998). *Rhynchobatus australiae* was sister to the Rhinobatos clade, then this clade was clustered to *Zapteryx exasperata*, which showed Rhynchobatus were closer with Rhinobatos than Zapteryx in phylogeny.

## Disclosure statement

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

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