

The complete mitochondrial genome sequence of the mountain crab *Indochinamon bhumibol*

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ABSTRACT

Indochinamon bhumibol has been found as the biggest freshwater crab in Thailand. In this study, we report the first complete sequence of mitochondrial genome from *I. bhumibol* encoding 13 protein-coding genes, 22 transfer RNAs, and 2 ribosomal RNAs. The nucleotide composition of *I. bhumibol* mitogenome showed a strong AT bias (70.4%) with a low GC content (29.6%). Comparative phylogenetic analysis with 28 crustaceans based on nine conserved genes demonstrated that *I. bhumibol* was closely related to members of the Potamidae family.

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Indochinamon spp. is a giant mountain crab, which is broadly found in Myanmar, Vietnam, and northern Thailand especially in waterfall and mountain areas (Van et al. 2016; Ng & Mar 2018). *Indochinamon bhumibol* was reported as the biggest freshwater crab in Thailand that has a significant role as a non-polluted water indicator in the freshwater ecosystem and has been considered as one of the endangered species (Thaewnon-Ngiw and Suthamrit 2020). Taxonomical identification of *I. bhumibol* can be difficult due to large morphological variations; therefore, the genetic information of *Indochinamon* spp. is necessary for this aspect. Here, we assembled the first complete mitochondria genome of *I. bhumibol* and created the phylogenetic tree for taxonomy classification.

The specimens of *I. bhumibol* were collected from Phu Nang National Park, Phayao Province, Thailand (19°08'47.76"N, 100°12'03.46"E). The collected specimen was transported and stored at the Museum of Agricultural University of Phayao with voucher number AUP02360. Genomic DNA was extracted from pereopods muscle by QIAamp Tissue Kit (Qiagen, Germany) and sequenced by Illumina MiSeq sequencer (2 × 150 bp ends) (Illumina, USA). After getting the cleaned read, the mitochondrial genome was assembled using NOVOPlasty 3.8.2 (Dierckxsens et al. 2016) and annotated by the MITOS web server (Bernt et al. 2013). Protein-coding genes (PCGs), ribosomal RNA genes (rRNAs), and transfer RNA genes (tRNAs) were confirmed

using the NCBI Basic Local Alignment Search Tool (BLAST) (Altschul et al. 1990).

The *I. bhumibol* mitogenome was 16,351 bp consisting of 13 PCGs, 22 tRNAs, and 2 rRNAs. The mitogenome sequence was submitted to GenBank under accession number MT872370. Among them, 11 PCGs were initiated by ATN as a start codon with an exception of *ND1* and *ATP8*, starting with GTC and GTG, respectively. The incomplete stop codons (T--) were found in three (*COI*, *ND5*, and *CYT8*) genes while the remaining showed the canonical stop codons (TAA or TAG). Twenty-two tRNAs were ranged from 61 bp (*tRNA^{Thr}*) to 71 bp (*tRNA^{Val}*). The asymmetric composition of nucleotide sequence was found with a high AT ratio (A: 34.8%, T: 35.6%, G: 10.9%, C: 18.7%).

A phylogenetic tree of *I. bhumibol* with other 28 crustaceans species was carried out using *Drosophila melanogaster* as an outgroup (Figure 1). Nine conserved genes (*COI*, *COII*, *COIII*, *ND1*, *ND3*, *ND4*, *ND4L*, *ND5*, *ND6*, and *CYT8*) were selected to perform multiple alignments by MUSCLE 3.8.1 (Edgar 2004). Using MEGA X 10.1 (Kumar et al. 2018) with 1000 bootstrap replications, the maximum likelihood phylogenetic tree was generated. The result indicated that *I. bhumibol* is closely related to other freshwater crab species of family Potamidae forming a separate clade. In conclusion, the mitogenome sequence of *I. bhumibol* reveals a piece of valuable genetic information to fill the gap in phylogenetic knowledge of the Potamidae family.

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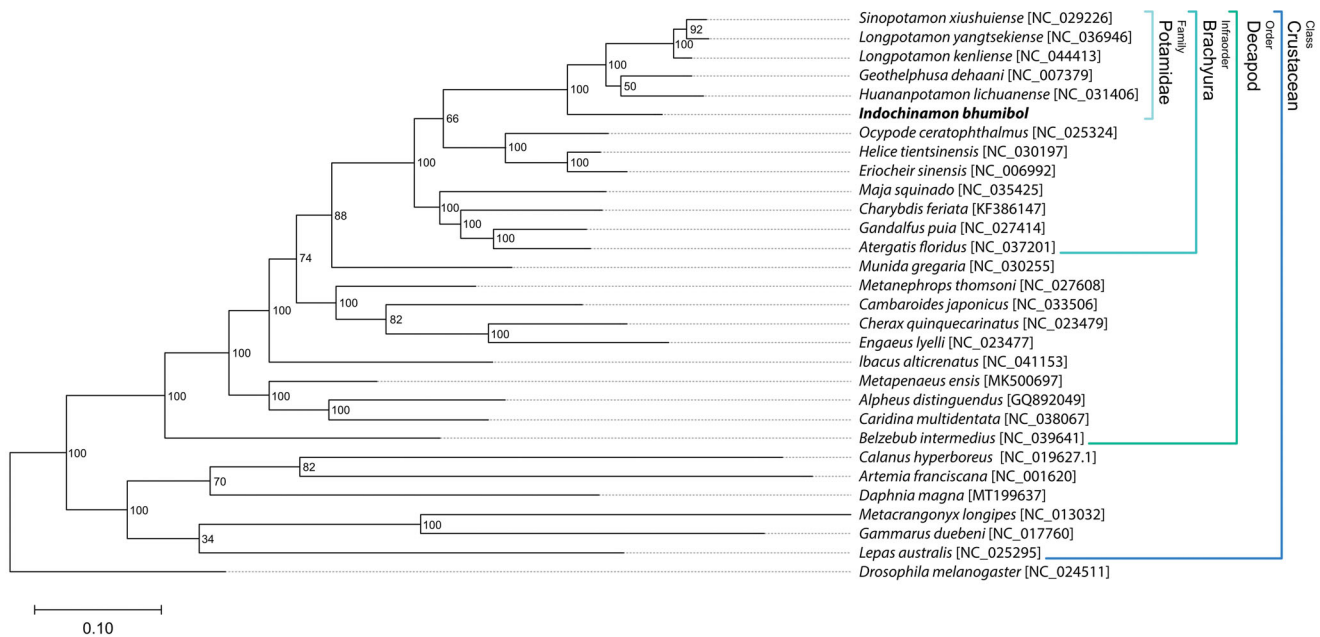


Figure 1. Maximum likelihood phylogenetic tree of *I. bhumibol* with other 28 crustaceans. Bootstrap probability values are displayed on the phylogenetic tree. The vertical line at the right side indicated specific family and order of crab in the Crustacean class.

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Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov/>, accession number: MT872370.

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