


Complete mitochondrial genome of the spiny rock crab *Thalamita crenata* (rüppell, 1830) (Crustacea: Decapoda: Portunidae) from China coast and its phylogeny

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ABSTRACT

To understand the evolution of the swimming crab *Thalamita crenata*, the complete mitochondrial genome of *T. crenata* from China was sequenced and analyzed. The circular mitogenome sequence was 15,787 bp in length, made up of 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes and a control region. The overall mitogenome composition was 34.40% for A, 11.55% for G, 35.31% for T, and 18.74% for C, respectively, with a high A + T content of 69.71%. Phylogenetic analysis showed that *T. crenata* was closest to the genus *Charybdis*.

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The spiny rock crab, *Thalamita crenata*, under the Family Portunidae is mainly distributed in Western Pacific and Indian Ocean (Dai et al. 1986; Dai and Yang 1991; Stephenson 1972). It inhabits the rocky and muddy intertidal regions of mangrove forests (Vezzosi et al. 1994). Unlike other big-size economic portunids, such as the mud crab *Scylla paramamosain* and the red crab *Charybdis feriatus*, *T. crenata* has less economic value (Manickaraja and Balasubramanian 2009). However, its natural population is under threat from local fishing pressure (Manickaraja and Balasubramanian 2009). In order to gain a deep understanding of the phylogeny and species evolution, we described, in this study, the complete mitochondrial genome of *T. crenata* from China.

Specimens of *T. crenata* were collected from Weizhou Island (21.0234°N, 109.0940°E), Guangxi province, China and preserved in pure ethanol in Marine Biology Institute of Shantou University. Total genomic DNA was extracted from muscle tissues and the complete mitogenome sequence was obtained by long and conventional PCR. Additionally, the complete mitochondrial genomes of 17 brachyuran species and one shrimp (*Haplosquilla harpax*) were downloaded from NCBI. The ND6 gene showed a high degree of heterogeneity and caused poor phylogenetic performance (Miya and Nishida 2000), so it was omitted in next analysis. The maximum-likelihood (ML) phylogenetic tree was constructed by MEGA7 software based on 12 protein-coding genes.

The complete mitochondrial genome of *T. crenata* was 15,787 bp in length (GenBank accession number: MH425338),

including 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes, and a control region. The overall mitogenome composition was 34.40% for A, 11.55% for G, 35.31% for T, and 18.74% for C, respectively, with a high A + T content of 69.71%. The phylogenetic analysis showed that *T. crenata* was closest to the genus *Charybdis* (Figure 1). The control region (D-loop) was 898 bp long and between the genes tRNA^{Pro} and tRNA^{Phe}, with a high similarity of 95% to the corresponding region of *T. crenata* collected from Australia (Tan et al. 2016).

Disclosure statement

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

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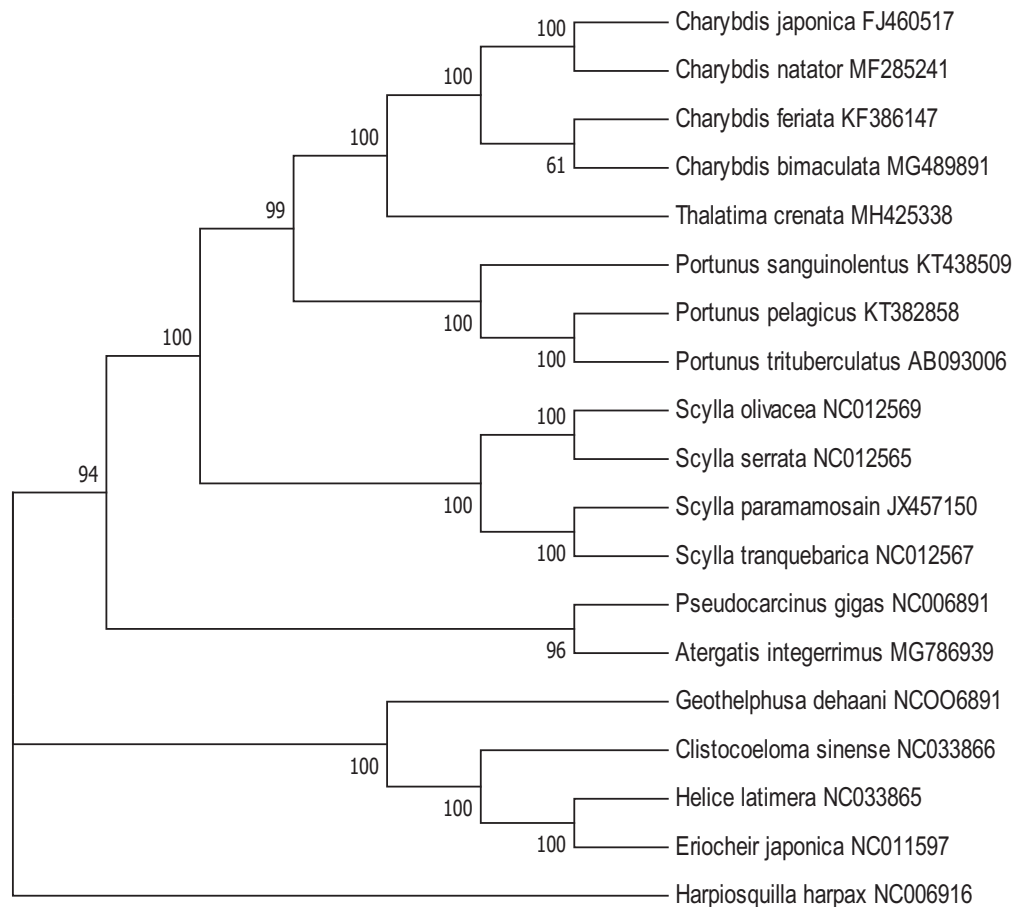


Figure 1. Molecular phylogeny of *T. crenata* and other related species based on 12 protein-coding genes. The complete mitochondrial genomes of 18 species were downloaded from NCBI, with *Haplosquilla harpax* as an outgroup.

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