The complete mitogenome of the *Chionoecetes opilio* (Crustacea: Decapoda: Oregoniidae) and its unique characteristics

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**ABSTRACT**

The complete mitochondrial genome of *Chionoecetes opilio* is a 16,067 bp long, circular molecule which contains 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), and 2 ribosomal RNA genes (rRNAs). Its gene contents and organization are generally similar to other majoide mitogenomes. However, the mitogenome shows unique characteristics; long terminal amino acids, loss or addition of 3 PCGs, a 1216 bp long putative D-loop region, and peculiar secondary structures of 5 tRNAs. The concatenated amino acid sequences of 13 PCGs were used to analyze the phylogenetic tree, which well supported the monophyly of brachyuran clades of Majoidea, Heterotremata, Thoracotremata, and Eubrachyura.

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C. japonicus and Damithrax spinosissimus show the almost identical synteny, there is a gene order rearrangement from Maja crispata and Maja squinado genomes (putative translocation of nd6-cytb-trns2 segment between trnE and nd1).

The complete mitogenomes of 10 Brachyura species (4 Majoids, 2 non-majoid Heterotremes, 2 Thoracotremes, 2 Raninoids), and one outgroup (Clibanarius infraspinatus) were downloaded from the GenBank and used to reconstruct their phylogenetic relationships. The concatenated amino acid sequences of 13 PCGs were analyzed by RAxML 8.2.12 (Stamatakis 2006) using the maximum-likelihood (ML) method and MrBayes 3.2.7 (Ronquist et al. 2012) using Bayesian inference (BI) analysis. The consensus tree based on both ML and BI analyses results supports the monophyly of the Majoidea, Heterotremata, Thoracotreamata, Eubrachyura, and Raninoidea with 100% bootstrap values and 1.00 posterior possibilities (Figure 1).

**Figure 1.** The phylogenetic tree showing relationships between Chionoecetes opilio and 11 brachyuran species with an outgroup taxon (Clibanarius infraspinatus). The tree was reconstructed from the concatenated amino acid sequences of 13 PCGs using RAxML 8.2.12 and MrBayes 3.2.7 applications based on the ML method. The bootstrap value above 50% in the ML analysis and posterior probability above 0.90 from the BI analysis are indicated at the bases of the each node. The distance based on the BI analysis is indicated above each node. GenBank accession number for each species is indicated with its respective scientific name. The species of interest of this study, C. opilio is marked with a reversed triangle.

**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/nuccore/MT335860.

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**Disclosure statement**

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

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