The complete mitochondrial genome of *Pseudohelice subquadrata* (Dana, 1851) *(Crustacea: Decapoda: Varunidae)*

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**ABSTRACT**

The full-length mitochondrial genome of *Pseudohelice subquadrata* (Dana, 1851) was analyzed by the primer walking method. Its mitogenome is 16,884 bp in length, comprising 13 protein-coding genes, 2 ribosomal RNA genes, and 22 transfer RNA genes. The phylogenetic tree confirmed that *P. subquadrata* belonged to the subsection Thoracotremata within the Crustacea. This is the first record of the complete mitogenome for the genus *Pseudohelice*.
Thoracotremata, with 100% bootstrap value in ML analysis and 1.00 posterior probability in BI analysis against the outgroups (i.e. two species belonging to the family Potamidae). Overall topology among the major families of the phylogenetic tree was mostly congruent with that of Basso et al. (2017). Among them, all species belonging to the family Varunidae consistently formed a monophyletic group with high statistical supports. Within the clade, _P. subquadrata_ placed at the most basal position and the other varunid species were further subdivided into three clades in accordance to their generic taxonomy, that is, _Eriocheir_, _Helicana_, and _Helice_. The latter two genera clustered more closely together and clearly separated from the former genus. The phylogenetic relationship of _P. subquadrata_ based on its complete mitochondrial genome sequence was clearly different from that of Sun et al. (2009) based on partial mitochondrial sequences and supported the taxonomic distinction of the genus _Pseudohelice_ of Sakai et al. (2006).

**Disclosure statement**

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

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**Figure 1.** The phylogenetic tree of maximum-likelihood (ML) based on 13 protein-coding genes in the complete mitochondrial genome sequences from the species belonging to the subsection Thoracotremata. The matrix included the first, second, and third codon positions of their protein-coding genes. Two species belonging to the family Potamidae were used as outgroups. A bootstrap value above 50% in the ML analysis and posterior probability above 0.90 in the Bayesian analysis are indicated at each node. The varunid _Pseudohelice subquadrata_ investigated in this study is shown in bold.