Characterization of the complete mitogenome of *Gammarus lacustris* (G.O. Sars, 1863) (Amphipoda: Gammaridae) and its phylogenetic position within Amphipoda

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**ABSTRACT**

*Gammarus lacustris* is native to the Qinghai-Tibet Plateau (QTP), widely distributed in alpine lakes. The complete mitochondrial DNA sequence of *G. lacustris* was 15,349 base pairs in length and comprised 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and 1 control region. The BI tree showed that *G. lacustris* was most closely related to *Gammarus duebeni*, and indicated that *Gammarus*, *Gmelinoides*, *Brachyurupus*, *Pallaseopsis*, and *Eulimnogammarus* evolved from a common ancestor. The mitogenome of *G. lacustris* provides new molecular data for further taxonomic and phylogenetic studies of Amphipoda.

**ARTICLE HISTORY**

Received 19 June 2021
Accepted 14 July 2021

**KEYWORDS**

*Gammarus lacustris*; mitochondrial genome; phylogenetic relationships
The BI tree indicated that *G. lacustris* shared a close relationship with *Gammarus duebeni* (Figure 1). In addition, *Gammarus* species together with *Gmelinoides fasciatus*, *Brachyuropus grewingkii*, *Pallaseopsis kessleri*, and *Eulimnogammarus vittatus* formed a clade, representing these species evolved from a common ancestor (Figure 1). The complete mitogenome of *G. lacustris* presents here provides valuable resources for investigating the phylogenetic relationships within Amphipoda.

**Disclosure statement**

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

**Funding**

The present work was financially supported by Projects of Agricultural Intelligence Introduction of Tibet [2020WZ006]; National College Students’ Innovative Entrepreneurial Training Plan; College Students in Zhejiang Province Science and Technology Innovation Activities Plan; The national College of Life Science Competition.

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**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/nuccore/MZ029704) under the accession number: MZ029704.

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