The complete mitochondrial genome of the freshwater crab *Bottapotamon lingchuanense* Türkay and Dai 1997 (Decapoda: Brachyura: Potamoidea)

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The *Bottapotamon* is a genus of freshwater crab that is unique to mainland China. Up to now, there are eight species under the genus (*Bott* 1967; *Dai* 1999; Gao et al. 2019). In mainland China, the species under the *Bottapotamon* are mainly distributed within the area of the Wuyi Mountain Range, and only the species of *Bottapotamon lingchuanense* have been isolated in the Nanling Mountain Range (Türkay and Dai 1997). The terrain of the habitat of *B. lingchuanense* is geologically stable, as there is hardly affected by the Cenozoic orogeny (Gao et al. 2019). Therefore, we believe that the distribution of *B. lingchuanense* in mainland China is caused by the emergence of the mountains. At present, there is no mitochondrial genome data of the species under the genus *Bottapotamon* in GenBank. Here we present the first mitogenome for the genus *Bottapotamon* by sequencing the mitochondrial genome of the freshwater crab *B. lingchuanense*, which has a new mitogenome protein-coding gene order for the Decapoda, aiming to explore the evolutionary relationship within the genus *Bottapotamon*.

A male adult specimen of *B. lingchuanense* was collected from Yuanpu Village, Guanyin Township, Gongcheng County, Guilin City, Guangxi Province, China (**latitude** 110.9598 and **longitude** 25.1634) in 2017. The sample is *B. lingchuanense*, which was identified by morphological methods. The specimen was deposited at the Laboratory Specimen Library of Freshwater Crustacean Decapoda & Paragonimus, School of Basic Medical Sciences, Nanchang University, Nanchang, PR China.

The complete mitogenome of *B. lingchuanense* is 17,612 bp in length (GenBank accession number: MN117717) with high A + T bias (72.33%), containing 13 protein-coding genes (PCGs), 2 ribosomal RNA (rRNA) genes, 22 transfer RNA (tRNA), and 1 non-coding AT-rich region and known as the D-loop. In addition, the mitogenome has 17 intergenic regions ranging from 1 to 1512 bp in length. The mitochondrial genome of *B. lingchuanense* is the first mitochondrial genome under the genus *Bottapotamon*, providing DNA data for species identification, enriching the species diversity of Brachyura. The maximum-likelihood (ML) tree and Bayesian inference (BI) tree based on the 13 PCGs of mitochondrial genome of Brachyura species showed similar topologies with high confidence, and the analysis results were consistent with the current mainstream classification system. The results indicating that *B. lingchuanense* is closely related to *Neilupotamon sinense*, *Sinopotamon*, and *Tenuilapotamon*, and it is likely to be derived from them.
general tRNA-Met (about 70 bp), it is obvious that the length of tRNA-Met in *B. lingchuanense* is markedly longer. It is suspected that the deletion or replication of the base caused the abnormal of the tRNA genes, which may be caused by the mtDNA copy base deletion mutation.

Using the 48 Brachyura species published by GenBank and the 13 PCGs of mitochondrial genome of *B. lingchuanense* obtained in this study for phylogenetic analysis, *Kiwa tyleri* was selected as the outgroup, building maximum-likelihood (ML) and Bayesian inference (BI) trees, respectively. The ML tree and the BI tree obtained by the phylogenetic analysis showed similar topological structure and supported by a high degree of confidence (Figure 1). The results of phylogenetic analysis showed that, consistent with the results of morphological classification analysis, *B. lingchuanense* with unique gene arrangement and *Neilupotamon sinense* were clustered together, and they were combined with *Sinopotamon* and *Tenuilapotamon*. The composed clades form sister clades, indicating that *B. lingchuanense* is closely related to *Neilupotamon sinense*, *Sinopotamon*, and *Tenuilapotamon*, and it is likely to be derived from them.

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

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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/ under the accession no. MN117717.

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