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MITOGENOME ANNOUNCEMENT

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The complete mitochondrial genome of *Mactra quadrangularis* (Mactridae)

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ABSTRACT

The whole mitochondrial genome sequence of *Mactra quadrangularis* (Reeve, 1854) was determined. It had a total length of 16,848 bp and it contained 12 protein coding genes, 2 ribosome RNA genes, and 22 transfer RNA genes. The base composition was 25.75% A, 20.82% G, 11.53% C, and 41.90% T, respectively. Furthermore, state codon of *ND4* was ATT; *ND1* and *CYTB* were ATA; *COX1* was GTG; *ND5*, *COX2*, *ND4L*, *ND6*, *ND2*, *COX3*, *ATP6*, and *ND3* were ATG. Phylogenetic analysis demonstrated that *M. quadrangularis* was most closely related to *Mactra chinensis*. The mitochondrial genome will provide reference for the further investigation and research of *M. quadrangularis*.

As an important edible seashore clam and seafood resource in the coastal areas of China, Japan, and South Korea, the surf clam *Mactra quadrangularis* (Reeve, 1854), sometimes also referred to as *Mactra veneriformis* (Reeve, 1854), belongs to Bivalvia, Venerida, Mactridae, *Mactra* (Linnaeus, 1767) (Hou et al. 2006; Luan et al. 2011; Nie et al. 2013; Zhu et al. 2019). We reconstructed the complete mitochondrial genome of *M. quadrangularis* based on Illumina paired-end sequencing data.

Samples were collected at Lianyungang, Jiangsu province, China (34.9497°N, 119.1886°E). The specimen is stored at Laboratory of Marine Ecology, Ocean University of China (specimen code OUCMLE09529; chenguan1021@163.com). Total genomic DNA was extracted from muscular tissue according to the CTAB method as detailed in (Mirimin and Roodt-Wilding 2015). We generated 400 bp paired-end reads from total genomic DNA by whole genome shotgun (WGS) sequencing using the Illumina NovaSeq platform (GenomeAnalyzer, Illumina, San Diego, CA). *De novo* assembly was conducted using A5-miseq version 20150522 (Coil et al. 2014) and SPAdes version 3.9.0 (Bankevich et al. 2012; Choi et al. 2020). The annotation was performed using GeSeq software (Tillich et al. 2017).

The complete mitochondrial genome of *M. quadrangularis* was submitted to GenBank and the GenBank accession number was MW691169. The raw data of *M. quadrangularis* were submitted to Sequence Read Archive (SAR) and the accession number was SRR14764610. The complete mitochondrial genome was 16,848 bp in size. The A + T base content (67.65%) was higher than the G + C content (32.35%). The base composition of the complete mitochondrial genome of *M. quadrangularis* was 25.75% for A, 20.82% for G, 11.53% for C, and 41.90% for T, respectively. The newly sequenced mitochondrial genome encodes for a total of 36 genes, including 12 protein-coding genes (PCGs), 2 rRNA genes, and 22 tRNA genes. In PCGs of *M. quadrangularis*, ATP8 gene is missing. Of the 12PCGs, *ND5*, *ND1*, *COX1*, *ND4L*, *COX3*, and *CYTB* had TAA as stop codons; while the other PCGs had TAG as stop codons. The state codon of *ND4* was ATT, that of *ND1* and *CYTB* was ATA, that of *COX1* was GTG, and that of *ND5*, *COX2*, *ND4L*, *ND6*, *ND2*, *COX3*, *ATP6*, and *ND3* was ATG.

To investigate the phylogenetic relationships of *M. quadrangularis*, four complete mitochondrial genomes of Mactridae (*Coelomactra antiquata* [Spengler, 1802], *Mactra chinensis* [Philippi, 1846], *Lutraria maxima* [Jonas, 1844], and *Lutraria rhynchaena* [Jonas, 1844]) and two complete mitochondrial genomes of Veneridae (*Meretrix* [Linnaeus, 1758], *Meretrix lusoria* [Röding, 1798]), one mitochondrial genome of Arcticidae (*Arctica islandica* [Linnaeus, 1767]), as well as one mitochondrial genome of Cyrenidae (*Corbicula fluminea* [Müller, 1774]) were downloaded from GenBank and aligned using complete mitochondrial genome sequences (Figure 1). The maximum likelihood (ML) phylogeny was constructed based on the General Time Reversible + Invariant + gamma sites (GTR + I + G) model of nucleotide substitution with 1000 bootstrap replicates by Mega-X version 10.0.2 (Kumar et al. 2018). The ML tree analysis indicated that *M. quadrangularis* closely related to *M. chinensis* and *Coelomactra antiquata* (Figure 1). This published *M. quadrangularis* mitochondrial genome will provide evolutionary information in the Mactridae.
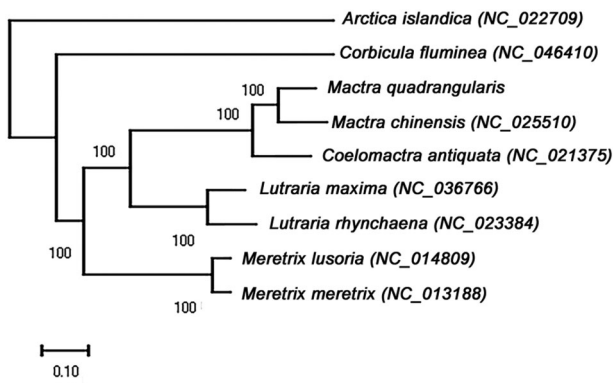

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Figure 1. Maximum likelihood (ML) phylogenetic tree based on 9 complete mitochondrial genome sequences of Venerida. ML bootstrap values are shown above nodes. All the sequences were downloaded from NCBI GenBank.

Disclosure statement

There are no conflicts of interest for all the authors including the implementation of research experiments and writing this article.

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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/MW691169/, reference number MW691169. BioProject accession number was PRJNA736184 at https://www.ncbi.nlm.nih.gov/bioproject/PRJNA736184. BioSample accession number at https://www.ncbi.nlm.nih.gov/biosample/SAMN19611295/ and Sequence Read Archive at https://www.ncbi.nlm.nih.gov/sra/SRR14764610.

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