

Molecular identification and phylogenetic analysis of the mitogenome of *Solenia oleivora* MG

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ABSTRACT

Solenia oleivora, belongs to Bivalvia, Unionidae, and Gonideinae, is a burrowing bivalve uniquely distributed in China. In this study, the complete mitochondrial genome of *S. oleivora* MG was sequenced and determined. The complete mitogenome of *S. oleivora* MG is 16,392 bp in total length, consist of 22 *tRNA* genes, 13 protein-coding genes (PCGs), and 2 *rRNA* genes. The overall base composition of the *S. oleivora* MG mitogenome is 36.90% A, 23.85% T, 27.09% C, and 12.16% G, respectively, exhibits a similar AT bias (60.75%) feature to other invertebrate bivalve mitogenomes. The phylogenetic analysis that *S. oleivora* MG clustered in genus *Solenia*. This result provides useful data to the conservation and sustainable utilization of *S. oleivora* MG and other invertebrate mussels.

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Solenia oleivora, belongs to Bivalvia, Unionidae, Gonideinae, is a burrowing bivalve uniquely distributed in Hunan, Hubei, Jiangxi, Zhejiang, Jiangsu, Anhui, and Henan province of China (Xu et al. 2005, 2006, 2013; Li et al. 2012; Wang et al. 2015; Wu et al. 2018; Bolotov et al. 2019). It is an economically important freshwater mollusk with fast growth, large individuals, and high nutritional value (Xu et al. 2003, 2005, 2008; Yang et al. 2011). However, in recent years, its wild population declines rapidly because of water pollution and increasing capture pressure (Xu et al. 2005; Huang et al. 2015; Zhang et al. 2020). Identification of the complete mitochondrial genome, and make clear its phylogenetic relationships with other closely related species is necessary for the conservation and sustainable utilization of *S. oleivora* and other aquatic species (Tzeng et al. 1992; Liu and Cui 2009; Min and Park 2009; Chen et al. 2013; Huang et al. 2013; He et al. 2014; Wu et al. 2019).

The individual of *S. oleivora* MG was sampled from Chihe River, Mingguang city, Anhui Province of China (32°81'79.6"N, 117°96'74.03"E), and was kept in 99% ethanol in the Aquatic Service Platform of Shaoxing (accession no. SXAF20200219).

The complete mitochondrial genome of *S. oleivora* MG is 16,392bp in length, deposited in GenBank database with an

accession number MT477834. It consists of 22 *tRNA* genes, 13 protein-coding genes (PCGs), and two *rRNA* genes. Its gene structure and arrangements are similar to the typical bivalve mitogenomes (Huang et al. 2013; Huang et al. 2015).

The total length of the protein-coding gene sequences is 11,118 bp. Except for the ND6 is encoded on the L-strand; all the other *PCD* genes (ND1–5 and ND4L, COXI-III, ATP6, ATP8, and CytB) are encoded on the H-strand. The total length of all *tRNA* genes is 1433 bp, varying from 61 bp (*tRNA*^{Gly}) to 71 bp (*tRNA*^{Ala}). The 12S *rRNA* gene (843 bp) and 16S *rRNA* (1287 bp) gene are located between two *tRNA* genes (*tRNA*^{Arg} and *tRNA*^{Leu}), and are separated by *tRNA*^{Lys}, *tRNA*^{Thr}, and *tRNA*^{Tyr} genes. The gene structure and arrangement of *S. oleivora* MG are very similar to other mollusks (Huang et al. 2013). The overall base composition of the *S. oleivora* MG mitogenome is 36.90% A, 23.85% T, 27.09% C, and 12.16% G, respectively, exhibits an obvious and similar AT bias (60.75%) feature to other invertebrate bivalve mitogenomes (Huang et al. 2013; Yang et al. 2015).

The phylogenetic tree was constructed using the neighbor-joining method. The results showed that *S. oleivora* MG is clustered with other *Solenia* mussels including *S. oleivora* (Huang et al. 2015), *S. carinatus* (Huang et al. 2013), and *S. carinatus* (GenBank accession number: NC_039839) (Figure 1).

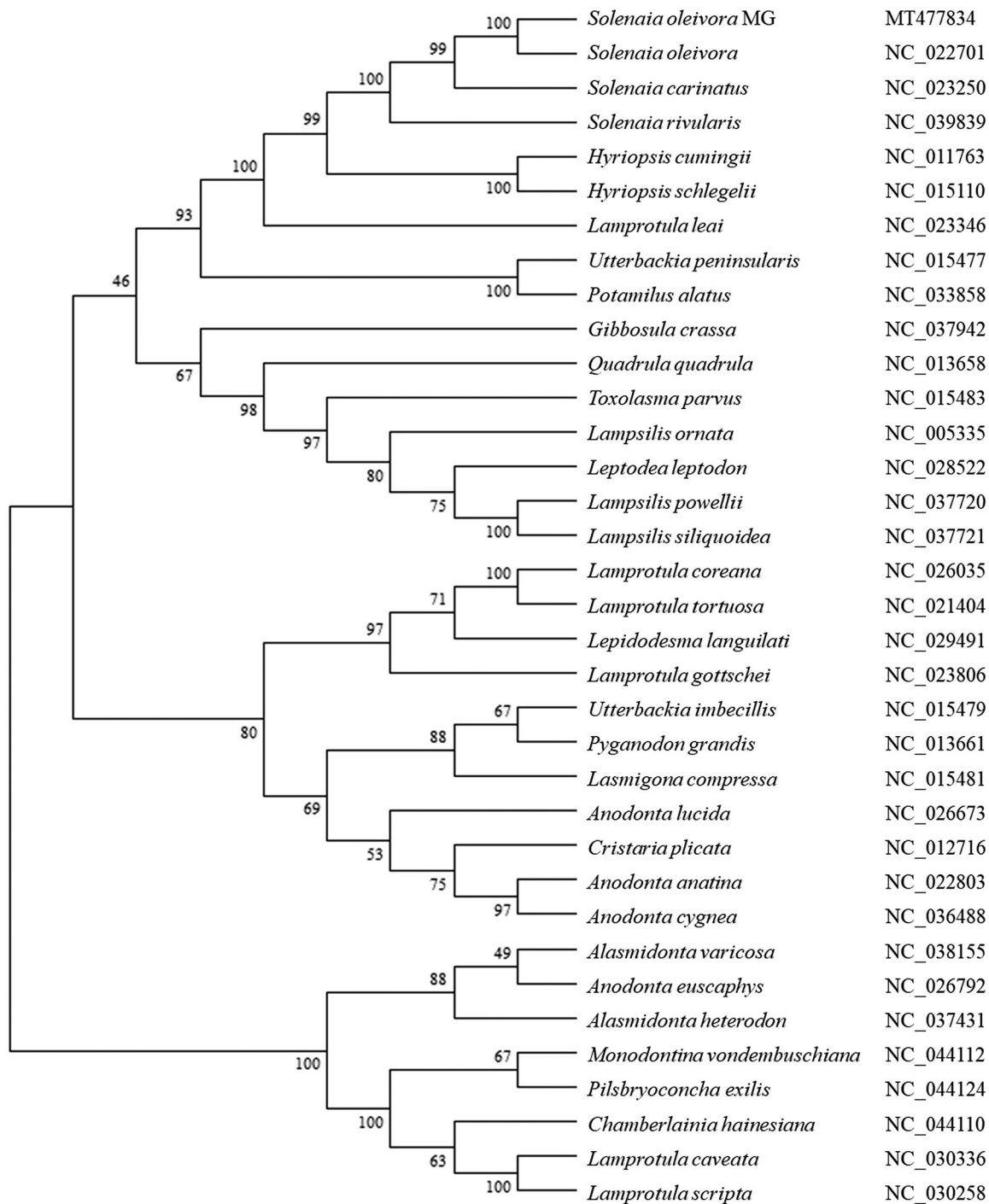


Figure 1. The phylogenetic analysis of *Solenaia oleivora* MG and other shellfishes based on the mitogenome sequences.

While it showed distant kinship with other shellfishes like *Lamprotula caveata* (GenBank accession number: NC_030336) and *Alasmidonta varicosa* (GenBank accession number: NC_038155). This study provides useful data to the conservation and sustainable utilization of *S. oleivora* MG and other invertebrate bivalves.

Disclosure statement

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

Data availability statement

The data that support the findings of this study are openly available at NCBI (<https://www.ncbi.nlm.nih.gov>), GenBank accession no. MT477834. And the data that support the findings of this study are also available from the corresponding author, Dr. Yang, upon reasonable request.

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