Molecular identification and phylogenetic analysis of the mitogenome of Solenaia oleivora MG

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ABSTRACT

Solenaia 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 Solenaia. This result provides useful data to the conservation and sustainable utilization of S. oleivora MG and other invertebrate mussels.

Solenaia oleivora, belongs to Bivalvia, Unionidae, and 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 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. It is 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^{Asp} and tRNA^{Leu}), and are separated by tRNA^{Gly}, tRNA^{Thr}, and tRNA^{Pro} 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 Solenaia mussels including S. oleivora (Huang et al. 2015), S. carinatus (Huang et al. 2013), and S. carinatus (GenBank accession number: NC_039839) (Figure 1).
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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References

Bolotov IN, Konopleva ES, Vikhrev IV, Lopes-Lima M, Bogan AE, Lunn Z, Chan N, Win T, Aksenova OV, Gofarov MY, et al. 2019. Eight new freshwater mussels (Unionidae) from tropical Asia. Sci Rep. 9(1):12053.

Chen X, Zhou ZM, Chen ZJ, Ai WM. 2013. Complete mitochondrial genome of Sarcocheilichthys parvus (Cypriniformes, Cyprinidae). Mitochondrial DNA. 24(2):97–98.

He L, Yang S, Zheng D, Li C, Tao G, Wei M, Wang H. 2014. Complete mitochondrial genome of Pseudorasbora elongata (Cypriniformes: Cyprinidae): sequencing and analysis. Mitochondrial DNA. 25(6):433–434.

Huang XC, Zhou CH, Ouyang S, Wu XP. 2015. The complete F-type mitochondrial genome of threatened Chinese freshwater mussel Solenaia oleivora (Bivalvia: Unionidae: Gonideinae). Mitochondrial DNA. 26(2):263–264.

Huang XC, Rong J, Liu Y, Zhang MH, Wan Y, Ouyang S, Zhou CH, Wu XP. 2013. The complete maternally and paternally inherited mitochondrial genomes of the Endangered freshwater mussel Solenaia carinatus (Bivalvia: Unionidae) and implications for Unionidae taxonomy. PLOS One. 8(12):e84352.

Li QK, Zhang GR, Wei KJ, Wang YN, Guo XZ, Chen ZL, Yan GX. 2012. A preliminary study on morphology and phagocytic ability of hemocytes from Solenaia oleivora (Bivalvia: Unionidae). J Hydroecol. 33(3):116–121.

Liu Y, Cui Z. 2009. The complete mitochondrial genome sequence of the cutlassfish Trichiurus japonicus (Perciformes: Trichiuridae): genome characterization and phylogenetic considerations. Mar Genomics. 2(2):133–142.

Min GS, Park JK. 2009. Eurotatorian paraphyly: revisiting phylogenetic relationships based on the complete mitochondrial genome sequence of Rotaria rotatoria (Dinoflagellata; Rotifera: Syndermata). BMC Genomics. 10(533):533–513.

Tzeng CS, Hui CF, Shen SC, Huang PC. 1992. The complete nucleotide sequence of the Crossostoma lacustre mitochondrial genome: conservation and variations among vertebrates. Nucleic Acids Res. 20(18):4853–4858.

Wang YN, Zhang GR, Wei KJ, Gardner JPA. 2015. Reproductive traits of the threatened freshwater mussel Solenaia oleivora (Bivalvia: Unionidae) from the middle Yangtze River. J Mollusk Stud. 81(4):522–526.

Wu RW, Liu XJ, Wang S, Roe KJ, Ouyang S, Wu XP. 2019. Analysis of mitochondrial genomes resolves the phylogenetic position of Chinese freshwater mussels (Bivalvia, Unionidae). Zookeys. 812:23–46.

Wu RW, Liu YT, Wang S, Liu XJ, Zanatta DT, Roe KJ, Song XL, An CT, Wu XP. 2018. Testing the utility of DNA barcodes and a preliminary phylogenetic framework for Chinese freshwater mussels (Bivalvia: Unionidae) from the middle and lower Yangtze River. PLOS One. 13(8):e0200956.

Xu QQ, Liu J, He LR. 2003. Flesh content and nutrition component of Solenaia oleivora. Freshw Fish. 33(4):28–29.

Xu QQ, Liu J, Huang HW. 2005. Effects of temperature on oxygen consumption and ammonia excretion by Solenaia oleivora. Acta Hydrobiol Sin. 30(6):697–701.

Xu QQ, Wu Y, Yuan HW. 2006. Studies on 4 kinds of trace elements in the soft tissue of Solenaia oleivora. Reserv Fish. 26(6):29–100.

Xu QQ, Zhang Q, Li B. 2008. Electrophoresis analysis on LDH and MDH in different tissues of Solenaia oleivora. J Yangcun. 5(1):39–41, 46.

Xu Y, Zhang GR, Guo SS, Guo XZ, Wei KJ, Ge TM. 2013. Isolation and characterization of fifteen polymorphic microsatellite loci in the threatened freshwater mussel Solenaia oleivora (Bivalvia: Unionidae). Biochem Syst Ecol. 47:104–107.

Yang SB, Mi ZX, Tao G, Liu XF, Wei M, Wang H. 2015. The complete mitochondrial genome sequence of Margaritaria dahurica Middendorff. Mitochondrial DNA. 26(5):716–717.

Yang XL, Li HC, Song L. 2011. Gonadal development and growth of freshwater mussel Solenaia oleivora. Fish Sci. 30(9):580–582.

Zhang GF, Zhang WF, Fang AP, Yang SB. 2020. Path analysis of quantitative traits of shellfish Solenaia oleivora population in Ganjiang River. Fish Sci. 39(2):271–276.