

The complete mitochondrial genome sequence of *Vanmanenia stenosoma* (Teleostei: Gastromyzontidae)

Xi Chen and Jing Hong Li

College of Forestry, South China Agricultural University, Guangzhou, China

ABSTRACT

Vanmanenia stenosoma belongs to the order Cypriniformes, and it is a typical torrent loach in China. In this study, we successfully determined the complete mitochondrial genome sequence of *V. stenosoma* (type species of *Vanmanenia*), which is 16,560 base pairs (bp) and contains 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes, and a putative control region. The genome has the same gene order as that found in other species of the family Gastromyzontidae. This suggests those genera share a common ancestral mitogenome. Nevertheless, phylogenetic reconstructions did not support the monophyly of the genus *Vanmanenia*.

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Vanmanenia stenosoma, a balitorid loach, occurs mainly in Qiantang-jiang and Yong-jiang basin of China. It is rheophilic, living in swift flowing streams and associated rivers in the mountain regions (Boulenger 1901; Chen 1980). In the current study, the sample of *V. stenosoma* (SCAU 0926783) obtained from Lianhuazhen River (29°4'51"N, 119°0'49"E) in Zhejiang Province, China, has been deposited in the collection of South China Agricultural University (SCAU). Total DNA was extracted from alcohol-preserved caudal fin tissue. The entire mitogenome of *V. stenosoma* were determined by the PCR-based approaches. The PCR products were sequenced and analyzed using Ai et al.'s method (Ai et al. 2013).

The complete mitochondrial genome of *V. stenosoma* was 16,560 bp in length (GenBank accession no. KX786161). Similar to other vertebrate mitochondrial genome structure, it was composed of 22 transfer RNA genes, 13 protein-coding genes, 2 ribosomal RNA genes, and a control region.

Most of the genes were encoded on the H-strand except one protein-coding gene (*ND6*) and eight tRNA genes (tRNA-Gln, tRNA-Ala, tRNA-Asn, tRNA-Cys, tRNA-Tyr, tRNA-Ser1 (UGA), tRNA-Glu and tRNA-Pro). The overall base composition of *V. stenosoma* was 28.0% for A, 29.2% for C, 24.8% for T and 18.0% for G, with a higher A+T content of 52.8%. All protein-coding genes shared the initiation codon ATG, except for *CO1* gene, which started with GTG. With the exception of *ND2*, *CO2*, *ND4* and *Cyt b*, all protein-coding genes were terminated by complete stop codons: TAG was used for *ND1*, *ND3* and *ND5*, TAA was used for *CO1*, *ATP8*, *ATP6*, *CO3*, *ND4L* and *ND6*. The remaining genes, *ND2*, *CO2*, *ND4* and *Cyt b*, were terminated by incomplete stop codon T. Likewise, numerous balitorid loaches used the similar codon structure to restrain the process of protein translation as well

(Chen et al. 2015; Que et al. 2016; Xu & Hu 2016). The longest one was *ND5* gene (1839 bp) in all protein-coding genes, whereas the shortest was *ATP8* gene (168 bp). The two ribosomal RNA genes, 12S rRNA gene (953 bp) and 16S rRNA gene (1680 bp), were located between tRNA-Phe and tRNA-Leu1(UAA) and separated by tRNA-Val. The position of Control region (895 bp) was located between tRNA-Pro and tRNA-Phe.

Vanmanenia Hora, 1932 has long been treated as a senior synonym of *Praeformosania* Fang (1935); loaches of the genus *Vanmanenia* are currently represented by ~20 nominal species in China and Southeast Asia (Chen 1980; Pan et al. 1991; Tang & Chen 2000; Sato et al. 2011; Kottelat 2012; Chen 2013; Yi et al. 2014; Liang et al. 2016). However, based on this study, the molecular phylogeny reveals *V. stenosoma* (type species of *Vanmanenia*) and '*V.*' *pingchowensis* (type species of *Praeformosania*) as separate clades, with the former more closely related to *Formosania lacustris* (type species of *Formosania* Oshima, 1919) than to the latter (Figure 1; the methods returned very similar tree topologies). Such result is qualitatively similar to classification schemes of Fang (1935), in which *Praeformosania* was sister to both *Formosania* and *Vanmanenia*. The *p*-distances between *V. stenosoma* and '*V.*' *pingchowensis* examined here were 18.3% in *CO1*, 13.9% in *Cyt b* and 11.4% in the whole mitogenomes, which were more than those among morphologically distinct species of the same genus within the family Gastromyzontidae. Yet, some molecular phylogenetic analyses did not support the monophyly of *Vanmanenia* (Liu et al. 2012; Tang et al. 2016; Wu et al. 2016). On these grounds, we recommend the exhaustive molecular and morphological studies for clarifying the relationships within or between *Vanmanenia* and *Praeformosania*.

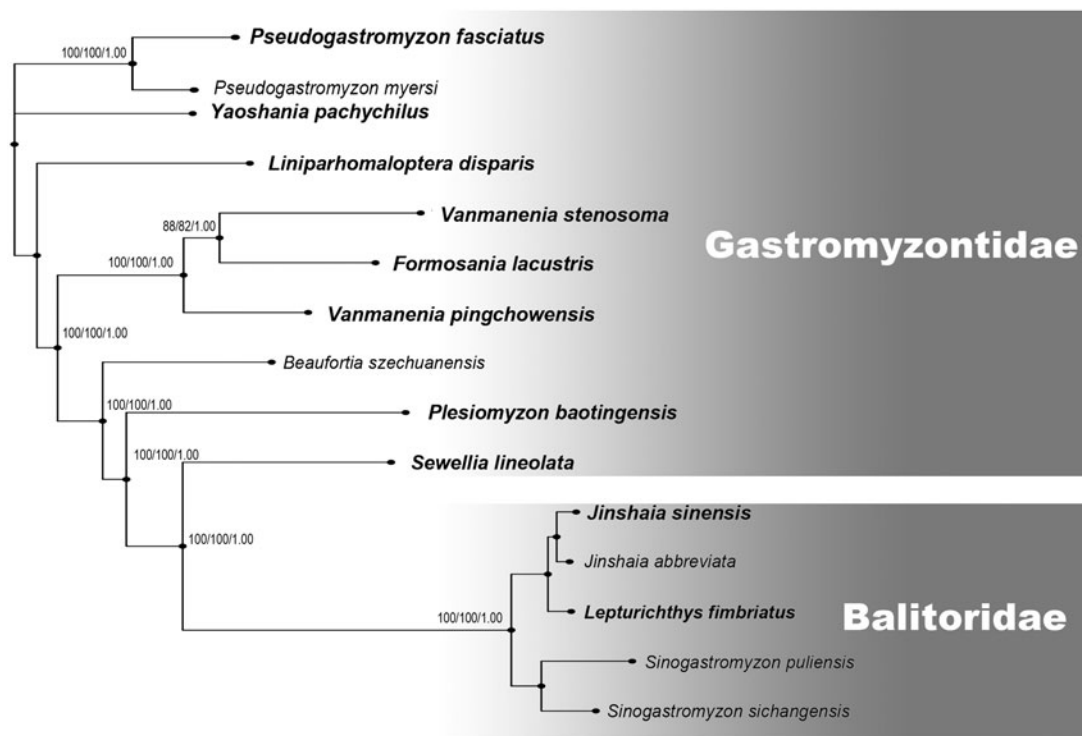


Figure 1. Phylogenetic relationships among *Vanmanenia stenosoma* and other hillstream loaches with complete mitogenome sequences on GenBank were inferred using the Maximum Likelihood (ML), Neighbour-Joining (NJ) and Bayesian (BA) phylogenetic analyses, respectively. Numbers above branches are bootstrap support of the ML, NJ analysis higher than 75 and posterior probabilities of the Bayesian analysis higher than 95%, for the combined analysis. Type species are in bold. The gene's accession numbers for tree construction are listed as follows: *Pseudogastromyzon fasciatus* (KX101229.1), *Pseudogastromyzon myersi* (AP013300.1), *Yaoshania pachyichilus* (KT031050.1), *Liniparhomaloptera disparis* (AP013301.1), *Vanmanenia pingchowensis* (KP005457.1), *Formosania lacustris* (AP010774.1), *Beaufortia szechuanensis* (KP716708.1), *Plesiomyzon baotingensis* (KF732713.1), *Sewellia lineolata* (AP011292.1), *Jinshaia sinensis* (JX155733.1), *Jinshaia abbreviata* (KJ754936.1), *Lepturichthys fimbriata* (KJ830772.1), *Sinogastromyzon sichangensis* (KF711948.1), *Sinogastromyzon puliensis* (FJ605359.1).

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this paper.

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