**The analysis for mitochondrial genome sequencing of** *Triplophysa lewanggensis*

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**ABSTRACT**

*Triplophysa lewanggensis* revealed that the complete length of its mitochondrial genome was 16,568 bp, composed of A (31.7%), T (27.1%), G (15.9%), C (25.4%), and A + T (58.8%). Its genetic constitution and arrangement were consistent with other *Triplophysa*, including 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and 1 control area (D-loop). All genes were encoded by the H-strand, except for one protein-coding gene (ND6) and eight tRNA genes (tRNAGln, tRNAAla, tRNACys, tRNAAsn, tRNATyr, tRNASer(UCC), tRNAGlu, tRNAPro) are encoded on the L-strand. The nucleotide sequence consists of A (31.7%), T (27.1%), G (15.9%), C (25.4%), A + T (58.8%) shows a certain degree of A-T bias, the content of A-T in D-loop area was highest (68.8%).

**Results and discussion**

The overall length of *T. lewanggensis* mitochondrial genome is 16,568 bp, including a total of 22 tRNA genes, two rRNA genes, 13 PCGs and a control region (D-loop). Twenty-eight genes are encoded on the H-strand, the remain nine genes including ND6 and eight tRNA genes (tRNAGln, tRNAAla, tRNACys, tRNAAsn, tRNATyr, tRNASer(UCC), tRNAGlu, tRNAPro) are encoded on the L-strand. The phylogenetic tree was divided into two main clades: one just including *Triplophysa* and the other including *Oreonectes, Homatula, Schistura, Nemacheilus, Traccatichthys*. *T. lewanggensis* is distributed in Southwest Guizhou Province attached to Yunnan–Guizhou Plateau, *T. xiangxiensis* is distributed in Hunan Province, they are near relatives, but their kinship with *Triplophysa* distributed in Tibetan Plateau is farther.

**Keywords**

Mitochondrial genome; phylogenetic tree; *Triplophysa lewanggensis*

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**INTRODUCTION**

*Triplophysa* genera affiliated to Cobitidae family, Nemacheilinae subfamily, and it was known that there are about 100 species and subspecies in *Triplophysa*, mainly distributed in the Tibetan plateau (Zhu 1989). *Triplophysa lewanggensis* is distributed in Southwest Guizhou Province attached to Yunnan–Guizhou Plateau. In the present study, the specimen was collected from Lewang town, Wangmo County of China (25°17.7873’ N, 106°18.7548’ E) in 2015. Now the specimen is deposited in the animal specimen room of the School of Life Sciences, Guizhou Normal University, Guiyang, China.

**METHODS**

Total DNA was extracted from the fish muscle tissues, and 26 pairs of primers were used to amplify genomic DNA. Then, complete mitochondrial genome was submitted to the GenBank (Accession no. KU987438).

Complete mitochondrial DNA sequences of 30 species of Nemacheilinae were obtained from GenBank, from which Cytochrome-b genes were extracted. The nucleic acids of cytochrome-b genes were then compared using the ClustalW method of MEGA version 6.0 software, the terminal irregular regions were removed manually. Subsequently, the phylogenetic tree was established using the neighbour-joining (NJ) method in MEGA 6.0, while reliability was tested using the Kimma2-Pamparameter distance model and bootstrap method by repeating 1000 times.

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Province attached to Yunnan–Guizhou Plateau, T. xiangxiensis is distributed in Hunan Province, they are near relatives, but their kinship with Triplophysa distributed in Tibetan Plateau is farther.

Since mitochondrial genomic information for Triplophysa of Nemacheilinae is relatively rare, it is necessary to obtain mitochondrial genomes of more Triplophysa and other genus of Nemacheilinae in order to clarify the historical development of the Nemacheilinae. To further improve the reliability of the phylogenetic tree, a combination of information on the mitochondrial and nuclear genome is desirable to elucidate the phylogenetic relationships of the Nemacheilinae.

**Disclosure statement**

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

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