There are currently 17 species of *Hyla* (Anura: Hylidae) distributed in Eurasia (Frost 2020). Eight species of *Hyla* are currently known in China, and six of which are endemic to China (AmphibiaChina 2020). The Sanchiang Tree Toad (*H. sanchiangensis*) is an endemic Chinese arboreal frog, which is distributed in southeastern China (AmphibiaChina 2020). At GenBank, only three mitochondrial genomes (mitogenomes) are available for *Hyla* species. Here, we attempted to sequence the complete mitogenome of *H. sanchiangensis* via next-generation sequencing, and retrieved successfully the genetic information about partial mitogenome of the above mentioned species.

The specimen (LSU20200425002JL) of *H. sanchiangensis* was collected in Jiulongshan National Nature Reserve (28.37°N, 118.90°E), Zhejiang, China, and deposited in the Museum of Laboratory of Amphibian Diversity Investigation (ADI) at Lishui University. Total DNA was extracted from muscle tissue of *H. sanchiangensis* using EasyPure Genomic DNA Kit (TransGen Biotech Co, Beijing, China). The mitogenome of *H. sanchiangensis* was acquired by Illumina NovaSeq 6000 (Novogene Bioinformatics Technology Co. Ltd., Tianjin, China) for PE 2 x 150 BP sequencing. Raw sequence data (16.25 G) was deposited in NCBI’s Sequence Read Archive (SRA; accession: SRR11921085). We used the NOVO Plasty 3.7 to de novo assembled the clean data without sequencing adapters (Dierckxsens et al. 2017).

This study reported a 15,664 bp long sequence of *H. sanchiangensis* partial mitogenome (GenBank accession: MT561180), which containing 13 PCGs (COX1-3, ND1-6, ND4L, ATP6, ATP8 and CYTB), 2 ribosomal RNA (rRNA) genes, 22 transfer RNA (tRNA) genes, and 2 non-coding regions of a L-strand replication origin and a partial loop region. The overall base composition of the sequence is 29.91% A, 29.86% T, 14.58% G, and 25.65% C, with a total A + T content of 59.77%. The result of phylogenetic analysis showed that *H. sanchiangensis* formed a clade with other species belonging to the genus of *Hyla*. This mitogenome data could help in evolutionary biology and population genetics of the Hylid species.

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**genus Pseudis** was a basal clade relative to others within Hylidae (Figure 1). This partial mitogenome sequence of *H. sanchiangensis* could help in evolutionary biology, population genetics of the Hylid species.

**Disclosure statement**

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

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**Data availability statement**

The data that support the findings of this study are openly available in NCBI at [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov) reference number [MT561180].

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