

## The mitochondrial genome of broad-folded frog (*Hylarana latouchii*)

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### ABSTRACT

The broad-folded frog, *Hylarana latouchii*, is an endemic freshwater frog in southern China. In the present study, the mitochondrial DNA sequence of the *H. latouchii* was first determined. The genome was 17,291 bp in length, which contains 37 genes (13 protein-coding genes, 2 ribosomal tRNAs, 22 transfer RNAs) and a putative CR (D-loop). The phylogenetic tree was constructed based on the 13 protein-coding genes of *H. latouchii* and 11 closely species.

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The broad-folded frog, *Hylarana latouchii*, is an endemic freshwater frog in southern China (Fei 1999). There are only a few mitochondrial genomes (mitogenome) have been reported in *Hylarana*, and the phylogenetic relationship and classification of this genera still remains controversial (Oliver et al. 2015). Recent advances in next-generation sequencing (NGS) technologies have facilitated to obtain the whole mitogenome (Yuan et al. 2016). In this study, the nearly complete mitogenome of *H. latouchii* was determined by using NGS and described for the first time. The frog was collected from Jinggangshan, Jiangxi province in China (N26.56580°, E114.12456°). The voucher specimens (YSQ284) were deposited in the Herpetological Museum of Chengdu Institute of Biology, Chinese Academy of Sciences. It was deposited in GenBank with accession number MN241431.

The Genomic DNA were shipped to Novogene Bioinformatics Technology (Beijing, China) for library construction and sequencing with Illumina MiSeq (SRA accession numbers: SRR5248584) (Xia et al. 2018). Then, the contaminant sequences and the low-quality regions were removed. We used SOAPdenovo2 (Luo et al. 2012) and Trinity v2.1.0 (Haas et al. 2013) to assembly mitogenome. After assembly, the mitogenome of *Hylarana krefftii* (GenBank number: KM247362.1) was used as queries for the reference mitogenome. The reference mitogenomes were BLASTed against assembly using BLASTn (BLAST + v2.2.30) to search for contigs with mitochondrial protein-coding and RNA genes. The mitogenome was annotated by using tRNAscan-SE v.1.21 (<http://lowelab.ucsc.edu/tRNAscan-SE>; Lowe and Eddy 1997; Schattner et al. 2005) and the MITOS webserver (<http://mitos.bioinf.uni-leipzig.de/index.py>; Bernt et al. 2013)

The mitogenome of *H. latouchii* is a closed-circular molecule of 17,291 bp in length, which contains the typical set of

37 genes, including protein-coding genes (PCGS) (*ATP6*, *ATP8*, *COI-III*, *ND1-6*, *ND4L*, and *Cytb*), 22 tRNA genes, 2 genes for ribosomal RNAs (16S and 12S), and 1 D-loop control regions. For the 13 PCGS, the longest one is *ND5* (1776 bp), the shortest one is *ATP8* (159 bp). All PCGS start with an ATG codon except *ND2* and *COI* start with ATT, and *ND6* start with CCT. The most frequent stop codon is T—, although *ND4L* and *ATP8* end with TAG, *ND4* and *Cytb* stop with TAA, *COI* end with AGG and *ND5* stop with AGA. The overall base composition for mtDNA sequence is as follows: A 29.2%, C 14.2%, G 27.3%, and T 29.3%.

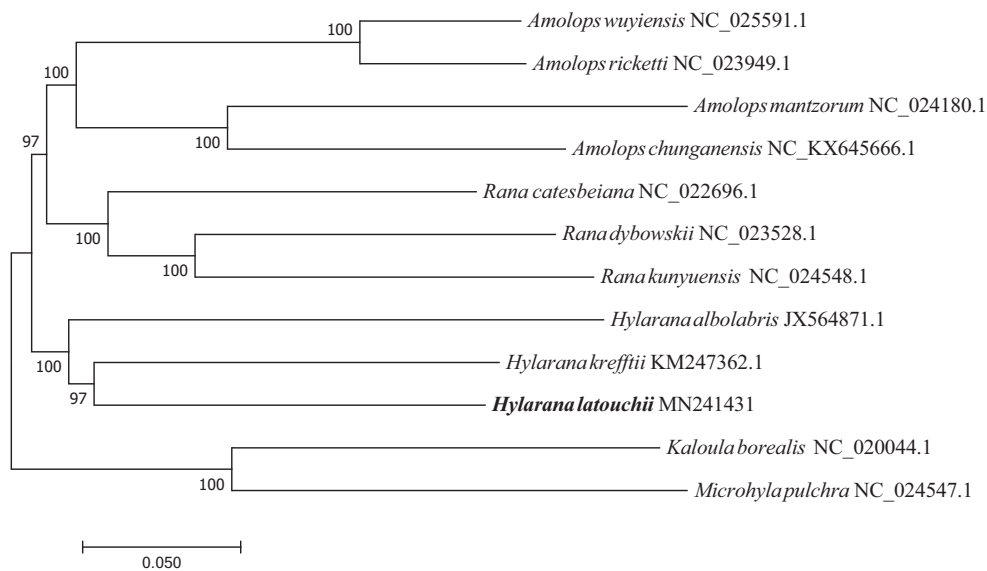
The phylogenetic tree (Figure 1) was estimated based on the 13 protein-coding genes of *H. latouchii* and 11 closely related species by using the neighbour-joining method of MEGA 7.0 (Kumar et al. 2016) with 1000 bootstrap replicates. The phylogenetic tree indicated that the mitogenome of *H. latouchii* and *H. krefftii* clustered together and closely related to *H. albolabris*. Although there are not enough published mitogenomes of *Hylarana* to compare or analyze phylogenetically, more information about related species at the level of family, as well as genus, could be useful for a more detailed study of mitogenome evolution and phylogenetic relationships in *Hylarana*.

### Disclosure statement

No potential conflict of interest was reported by the authors.

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**Figure 1.** Neighbour-joining phylogenetic tree based on the mitochondrial genome sequences of *Hylarana laouthii* and other 11 closely species using MEGA 7.0.

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