

The complete mitochondrial genome sequence of *Rana dabieshanensis* (Anura: Ranidae)

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ABSTRACT

Rana dabieshanensis is a species of frog within the family Ranidae. In this study, we assembled a complete mitochondrial genome (mito-genome) for *R. dabieshanensis* by high-throughput sequencing technology. It is 18,291 bp and includes 13 protein-coding genes, 22 tRNA genes, two rRNA genes and one control region. The nucleotide composition is A: 27.0%, T: 28.6%, C: 29.3% and G: 15.2%. Two overlaps among the 13 protein-coding genes were found: *ATP8/ATP6*, *ND4L/ND4*. The study of phylogenetic analysis based on complete mitochondrial genome showed that there was close genetic relationship between *R. dabieshanensis* and *R. omeimontis* and it is useful for systematic analyses of genus *Rana*.

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The Dabie mountain brown frog (*Rana dabieshanensis*) belongs to the family Ranidae, which is distributed in Dabie Mountains regions, Anhui Province, China (Wang et al. 2017). It is controversy about the classification of species within the genus *Rana* in the Dabie Mountains (Wang 2018). To better understand the mitochondrial genomic characteristics, phylogeny and evolution of the *R. dabieshanensis*, we determined and described the mitogenome sequence of *R. dabieshanensis* in order to obtain basic genetic information about this species.

A specimen of *R. dabieshanensis* was collected from Sucheng County, Anhui Province, China (31°31'13.61"N, 116°32'44.87"E) and stored in Anhui University Museum, Research Center for Biology (Voucher number: DBS202001). The genomic DNA extraction, library preparation and Illumina sequencing were done by Novogene Bioinformatics Technology Co. Ltd. (Tianjin, China).

We obtained the complete mitochondrial genome of *R. dabieshanensis* is 18,291 bp and submitted to the GenBank with the accession number MW526989. It included 13 protein-coding genes, two ribosomal RNAs genes, 22 transfer RNAs genes and one control region. The overall nucleotide composition is A: 27.0%, T: 28.6%, C: 29.3% and G: 15.2%, with a total A + T content of 55.6%. The mitogenome of *R. dabieshanensis* shows the typical gene observed in Ranidae mitogenomes (Liu et al. 2017; Fang et al. 2020; Jiang et al.

2020). Within 37 mitochondrial genes, the *ND6* gene and 8 tRNA genes (*tRNA^{Ser}*, *tRNA^{Glu}*, *tRNA^{Pro}*, *tRNA^{Gln}*, *tRNA^{Ala}*, *tRNA^{Asn}*, *tRNA^{Cys}* and *tRNA^{Tyr}*) were encoded on the light strand and other genes were encoded by the H-strand. In 13 mitochondrial protein-coding genes, except *COX1*, *ATP6* and *ND4L* begin with GTG, *ND6* begin with TCT, the other nine genes begin with ATG as start codon. In all six types of stop codon were annotated, TAT for *ND2*, AGG for *COX1* and *ND5*, TAG for *ATP8*, TAA for *ND4L* and *CYTb*, CAT for *ND6* and an incomplete stop codon T for the remaining six PCGs (*COX2*, *ATP6*, *COX3*, *ND3*, *ND4* and *ND1*), which is presumably completed as TAA by posttranscriptional polyadenylation (Ojala et al. 1981). With regard to the codon of *ND6* and *ND2*, it is consistent with the *Rana omeimontis* submitted on NCBI (Jiang et al. 2020). Two overlaps among the 13 protein-coding genes were found: *ATP8/ATP6* and *ND4L/ND4*. The two rRNA genes were 930 bp (*rrnS*) and 1576 bp (*rrnL*), respectively.

To best understand its phylogenetic position within the genus *Rana*, we reconstructed the phylogenetic tree of some species in *Rana* with maximum-likelihood method (ML) (<http://iqtree.cibiv.univie.ac.at/>), which is based on 13 complete mitochondrial genome sequences for *Rana* species. Another species (*Pelophylax nigromaculatus*) is included as the outgroup (Figure 1). The result showed that phylogenetic

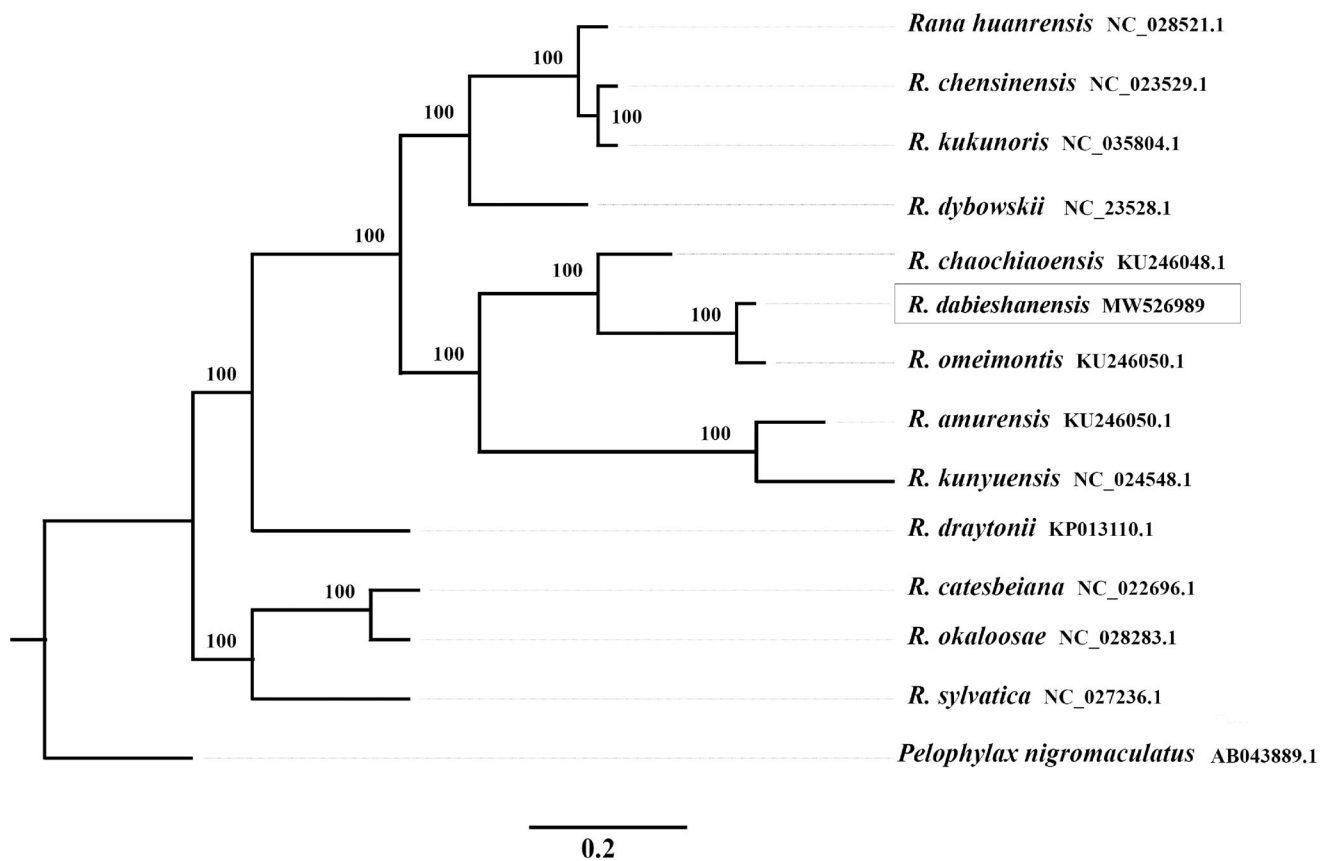


Figure 1. Phylogenetic tree of the relationships of *Rana dabieshanensis* with maximum-likelihood method (ML) based on complete mitochondrial sequences. The bootstrap support values for ML analyses are shown orderly on the nodes.

relationship of Dabie mountains wood frog is very close to *R. omeimontis*.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The data that support the findings of this study are openly available in NCBI at <https://www.ncbi.nlm.nih.gov/> (MW526989).

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