

## The complete mitochondrial genome of an Asian warty newt, *Paramesotriton aurantius* (Caudata: Salamandridae)

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### ABSTRACT

*Paramesotriton aurantius* (Caudata: Salamandridae) is a new species that found in southeastern China. Its complete mitochondrial genome (mitogenome) sequence was 16,313 bp in length with with A + T contents of 60.9%, and contained 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, one control region (D-loop), and one non-coding region. Our molecular tree showed that *P. aurantius* was positioned near *P. hongkongensis*, and formed a clade with other *Paramesotriton* species. The first complete mitogenome sequence of *P. aurantius* could provided fundamental data for resolving phylogenetic and genetic problems related to genus *Paramesotriton*.

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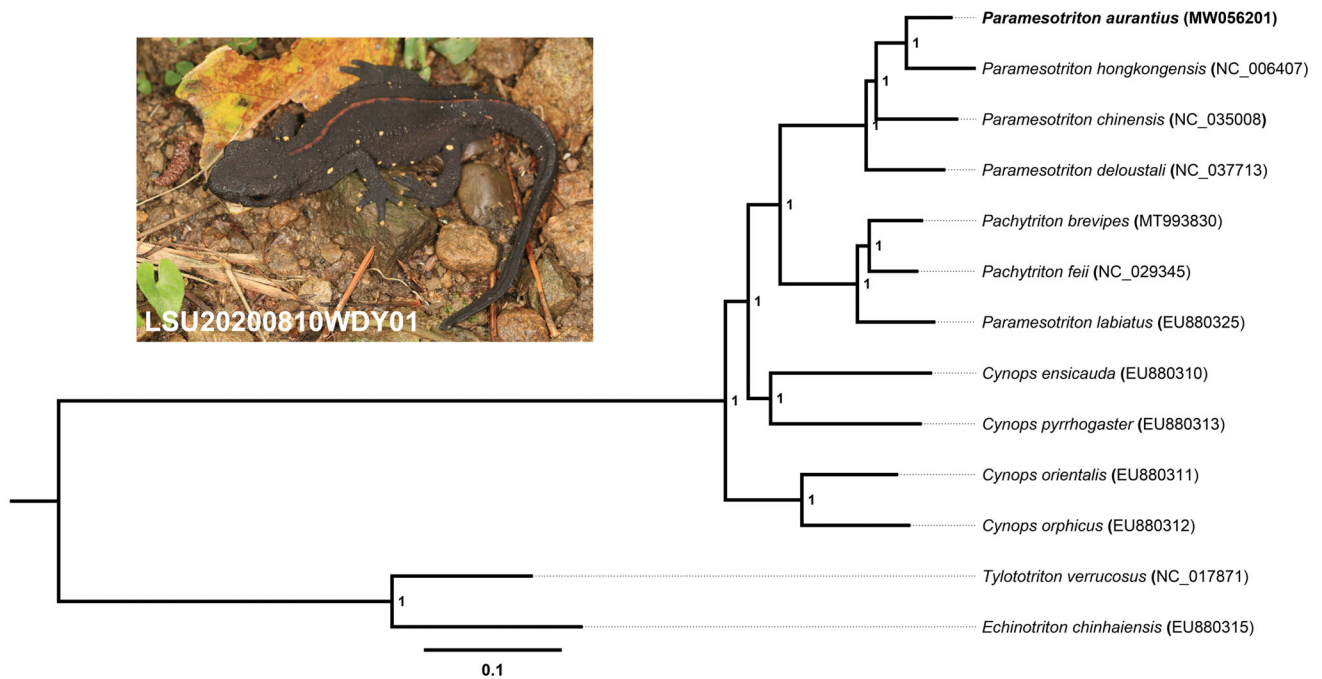
There are 14 species in the genus of *Paramesotriton* in the world, and they are distributed in Northern Vietnam and southwest-central and southern China (Frost 2020). The main adult external morphological traits of *Paramesotriton* species are skin rough, dorsal warts small and scattered evenly wart on the sides of body relatively large and distinct (Fei and Ye 2016). This genus consists of two species groups (*P. caudopunctatus* group and *P. chinensis* group) (Yuan et al. 2014), but the phylogenetic relationship between the two groups has not been well solved. In 2016, *Paramesotriton aurantius* (Yuan et al. 2016) is a new species of the genus *Paramesotriton* that found in southeastern China (Yuan et al. 2016). Until now, four geographical populations of this species were known (Yuan et al. 2016; Liu et al. 2019). The mitochondrial genome (mitogenome) as the molecular marker could utilized to examine the phylogeny of *Paramesotriton* species. In Genbank, three complete mitogenome of *Paramesotriton* species are available (Zhang et al. 2005; Yang et al. 2017; Zhang et al. 2018), but not containing *P. aurantius*. In this study, we determined the complete mitogenomes via next-generation sequencing, and compared the sequence with those of other species of Salamandridae to analyze the phylogenetic relationship among them.

The specimen of *P. aurantius* (specimen voucher: LSU20200810WDY01) was captured from Wangdongyang (27.702646°N 119.626208°E; elevation: 1045 m), Lishui City, Zhejiang Province, China, and stored at the Museum of Laboratory of Amphibian Diversity Investigation at Lishui University by 75% alcohol in specimen bottle. Genomic DNA extraction and next-generation sequencing were described in previous publication (Chen et al. 2020). The mitogenomes

were sequencing by Illumina NovaSeq 6000 platform. Raw data (22.09 G) was deposited in the NCBI's Sequence Read Archive database, and clean data (21.35 G) subjected to *de novo* assembled by the NOVO Plasty 3.7 (Dierckxsens et al. 2017) to produce a closed circular form of complete mitogenome.

The complete mitogenome sequence of *P. aurantius* is 16,313 bp in length with with A + T contents of 60.9% (32.9% A, 28.0 T%, 14.9% G, and 24.2% C). The mitogenome was annotated by MITOS WebServer (<http://mitos2.bioinf.uni-leipzig.de/>) (Matthias et al. 2013) and tRNAscan-SE version 2.0 (<http://trna.ucsc.edu/tRNAscan-SE/>) (Lowe and Chan 2016), and included 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA (12S rRNA and 16S rRNA) genes, one control region (D-loop), and one non-coding region. Twenty-eight out of 37 genes were encoded on the H-strand, while 9 were located on the L-strand. The 12S rRNA (929 bp) and 16S rRNA genes (1,559 bp) were located between tRNA<sub>Phe</sub> and tRNA<sup>Val</sup>, and between tRNA<sup>Val</sup> and tRNA<sup>Leu</sup>, respectively. Except COI gene which was began with GTG, other 12 PCGs were initiated with ATG as start codon. The stop codon of the PCGs was TAA (ND2, ND3, ND4L, ND5, ATP6, ATP8, and COI), TAG (ND1), AGA (ND6), TA (ND4 and CYTB), and T (COII and COIII). The complete mitogenome of *P. aurantius* had the same gene arrangement and similar compositions according with other *Paramesotriton* species (Zhang et al. 2005; Yang et al. 2017; Zhang et al. 2018).

We used MrBayes v3.2.2 software to construct a Bayesian tree (with 1,000,000 generations, sampling every 1000 generations and discarded 1000 trees as burn-in) containing complete mitogenomes of 13 species to further explore



**Figure 1.** The Bayesian tree base on 13 concatenated mitochondrial PCGs of 13 species from the family Salamandridae. *Echinotriton chinhaiensis* and *Tylotriton verrucosus* were chosen as the outgroups. Numbers at the nodes represent Bayesian posterior probabilities. Samples sequenced in the present study are highlighted in bold.

taxonomic status of *P. aurantius* and the phylogenetic relationship within *Paramesotriton*. The phylogenetic tree showed that *P. aurantius* is sister to *P. hongkongensis* and that the *Paramesotriton* genus is monophyletic (Figure 1). This result was supported by previous phylogenetic studies (Yuan et al. 2014, 2016). The first complete mitogenome sequence of *P. aurantius* from our study will contribute to the further understanding of the genus *Paramesotriton*.

## Disclosure statement

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

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## Data availability statement

Mitogenome data supporting this study are openly available in GenBank at: <https://www.ncbi.nlm.nih.gov/nuccore/MW056201>. SRA and BioSample accession numbers are <https://www.ncbi.nlm.nih.gov/sra/SRR12750572>, <https://www.ncbi.nlm.nih.gov/biosample/SAMN16326665>, respectively.

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