

## Complete mitochondrial genome of *Andrias davidianus* (Caudata: cryptobranchidae): sequencing and analysis

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### ABSTRACT

In this study, the total mitochondrial genome sequence of *Andrias davidianus* (Caudata: Cryptobranchidae) was determined. The genome is 16,519 bases in length. It consists of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and 2 non-coding regions. These results will contribute to the natural resources conservation and species identification of *A. davidianus*.

### ARTICLE HISTORY

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### KEYWORDS

Analysis; mitochondrial genome; *Andrias davidianus*; sequencing

The Chinese giant salamanders (*Andrias davidianus*), belonging to the Order Caudata and the Family Cryptobranchidae, is one of the world's largest amphibian species (Dong et al. 2011). *Andrias davidianus* may represent the transition steps from aquatic to terrestrial life in the evolution history of vertebrate system (Wang et al. 2013), it has an important value in scientific research of phylogeny relationship of land vertebrate evolution.

Because of its maternal mode of inheritance and relative lack of recombination (Saccone et al. 1999; Arnason et al. 2002). The complete mitochondrial genome sequence is a useful tool for the analysis of genetic diversity of endangered species (Chen et al. 2012; Min & Park 2009; Peng et al. 2006).

In this study, an individual *A. davidianus* was sampled in Shaoxing, Zhejiang province, China (29.77°N, 120.58°E) and was collected in the Animal specimen room of Shaoxing University (No. 405). The complete mitochondrial genome sequence of the sample was sequenced and characterized. The PCR amplification was performed using total DNA as

template, and the parameters are initial denaturation at 95 °C for 4 min, followed by 35 cycles of amplification (94 °C for 45 s, 52 °C or 58 °C for 30 s and 72 °C for 90 s), and one final cycle of 10 min at 72 °C.

The complete mitochondrial genome was determined to be 16,519 bp in length (GenBank accession no. KT119359). It consists of 22 tRNA genes, the large and small rRNA unit genes, 13 protein-coding genes (PCGs), and 2 non-coding regions: origin of light-strand replication (OL) and control region (CR).

Except for *ND6* and eight tRNA genes (*tRNA<sup>Gln</sup>*, *tRNA<sup>Ala</sup>*, *tRNA<sup>Asn</sup>*, *tRNA<sup>Cys</sup>*, *tRNA<sup>Tyr</sup>*, *tRNA<sup>Ser</sup>*(UCN), *tRNA<sup>Glu</sup>*, and *tRNA<sup>Pro</sup>*), all of the other mitochondrial genes are encoded on the heavy strand (H-strand). Total base composition of the mitochondrial genome of *A. davidianus*: 31.91% A, 32.81% T, 20.97% C, and 14.31% G, respectively.

Except for *COX I* with a GTG start codon, the remaining protein-coding genes initiate with ATG. Six protein-coding genes end with TAA (*COX I*, *ATP8*, *ATP6*, *ND3*, *ND4L*, and *ND6*).

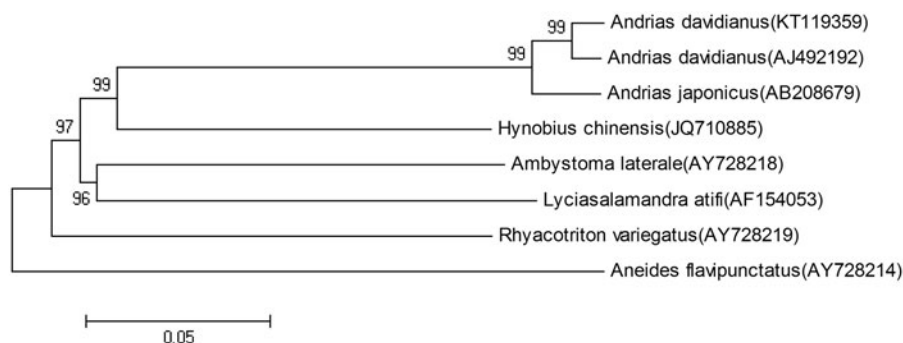


Figure 1. The phylogenetic analysis of *A. davidianus* and other salamanders based on the mitogenome sequences.

Incomplete stop codons are found in *ND5*, *ND4(TA-)*, as well as *ND1*, *ND2*, *COX II*, *COX III*, and *Cyt b* (T-), respectively.

A phylogenetic tree was constructed based on the complete mitochondrial genome sequences of *A. davidianus* and other salamanders using the neighbour-joining method (Figure 1). The results showed that *A. davidianus* and *A. japonicus* are clustered together, and showed close relationship with other salamanders including *Hynobius chinensis* (Tang et al. 2015) and *Lyciasalamandra atifi*, while it showed distant kinship with other salamanders.

### Disclosure statement

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

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