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The complete mitochondrial genome of the *Odorrana schmackeri* (Anura, Ranidae)

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ABSTRACT

The complete mitochondrial genome of *O. schmackeri* has been sequenced and characterized in this study. The mitogenome is a circular molecule of 18 610 bp in length, containing 13 protein-coding genes (PCGs), two ribosomal RNA (rRNA) genes, 21 transfer RNA (tRNA) genes and a non-coding D-loop region (control region). Its gene arrangements are identical to the typical neobatrachian-type except for the loss of $tRNA^{His}$ gene. Our data provide a useful resource for the phylogenetic studies of genus *Odorrana*.

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The Chinese piebald odorous frog (*Odorrana schmackeri*) is widely distributed in southern and south-central China at 200–1400 m elevation (Frost 2015). The specimen of *O. schmackeri* was captured from Huangshan, Anhui province in China (30°06′N, 118°09′E; 595 m elevation) and stored in Anhui Provincial Key Laboratory of the Conservation and Exploitation of Biological Resources from Anhui Normal University. Total genomic DNA was extracted from *O. schmackeri* muscle tissue using the standard phenol–chloroform protocol, as described by Sambrook and

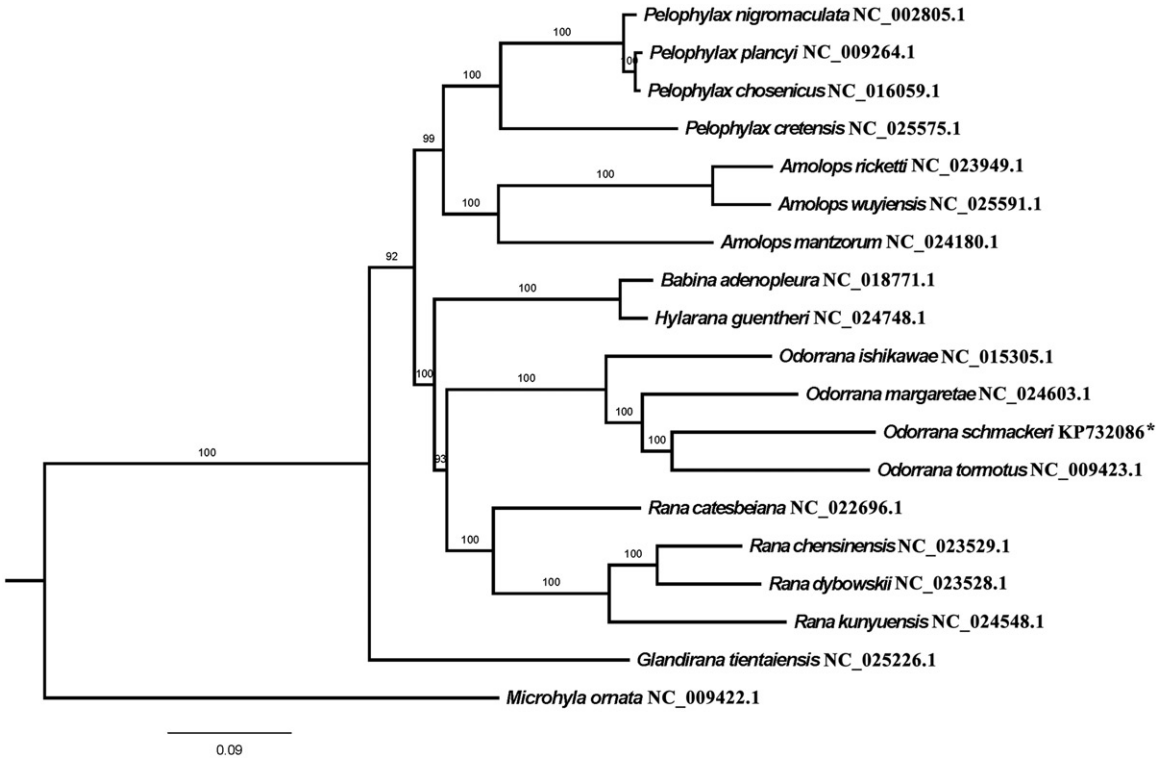

Figure 1. ML phylogeny of Ranidae species based on the complete mitochondrial genomes. The asterisk indicates the sequence generated in this study.

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Russell (2001), and the complete mtDNA of *O. schmackeri* was amplified and sequenced using 17 primer pairs.

In this study, we determined the complete mitochondrial genome sequence of *O. schmackeri*, which is 18 610 bp in size (GenBank accession no. KP732086). The circular mitogenome contains 36 genes, including 13 typical protein-coding genes, 21 tRNA genes (*tRNA^{His}* gene lacked), two rRNA (*12S rRNA* and *16S rRNA*) genes and a control region. Most genes were encoded on the heavy strand (H-strand) except for *ND6* gene and eight tRNA genes (*tRNA^{Pro}*, *tRNA^{Gln}*, *tRNA^{Ala}*, *tRNA^{Asn}*, *tRNA^{Cys}*, *tRNA^{Tyr}*, *tRNA$^{Ser(UCN)}$* and *tRNA^{Glu}*) which were encoded on the L-strand.

The non-coding regions in the *O. schmackeri* mtDNA included the control region and some intergenic spacers. The control region was located between *Cyt b* and *tRNA$^{Leu\ (CUN)}$* genes, with a 2769 bp length. Two long (167 bp and 229 bp) and several short (1–67 bp) non-coding sequences are dispersed in the *O. schmackeri* mtDNA. The putative origin of light-strand replication (OL) (30 bp) is situated between the *tRNA^{Ala}* and *tRNA^{Asn}* genes instead of between *tRNA^{Asn}* and *tRNA^{Cy}* as in most vertebrates in the WANCY tRNA cluster (Su et al. 2007; Jiang et al. 2015; Sun et al. 2015; Yan et al. 2016).

The 13 identified PCGs were 11 299 bp in total length (168–1794 bp). Nine of the 13 protein-coding genes initiated with ATG as the start codon, while *COI* and *ATP6* began with ATA, and *ND2* and *ND4L* started with ATT. Stop codons were variable for all protein-coding genes. Six genes (*ATP8*, *ND4L*, *ND4*, *Cyt b*, *ND2* and *ND5*) used the common TAA and TAG as the stop codon, whereas, *COI* and *COII* ended with AGA, and *ND6* stopped with AGG. Incomplete stop codons (T– –) were found in *ND1*, *ATP6*, *ND3* and *COIII*.

The 21 tRNA genes ranged in size from 64 bp (tRNA^{Cys}) to 73 bp (tRNA^{Asn} and *tRNA$^{Leu\ (UUR)}$*). In the new mitogenome, the notable feature is the loss of *tRNA^{His}*, we were unable to find the potential *tRNA^{His}* gene at any other location in the mitogenome of *O. schmackeri*. In contrast to the PCGs, loss of tRNA genes is relatively more frequent during the evolution of animal mtDNAs (Zhang et al. 2009). Nevertheless, the loss of *tRNA^{His}* gene was discovered for the first time in anurans. The predominant explanation for the mitochondrial gene loss is the gene replacement hypothesis (Adams & Palmer 2003).

The complete mitogenomes sequences of *O. schmackeri* and other individuals belonging to Ranidae were used for phylogenetic analysis, with setting *Microhyla ornata* as outgroup (Figure 1). Maximum-likelihood method (ML) was used to examine the phylogenetic position of *O. schmackeri* applying RAxML (7.2.6) (Stamatakis 2007). It appeared that *O. schmackeri*, *O. tormotus*, *O. margaretae* and *O. ishikawae* formed a monophyletic group. These data provide a powerful tool for systematic analysis of genus *Odorrana* and family Ranidae.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the article. This work was supported by Anhui Provincial Natural Science Fund under Grant no. 1508085MC56; the Research Foundation for Outstanding Young Scholars in Higher Education Institutions of Anhui Province under Grant no. 2011SQRL027; Doctoral scientific research fund project of Anhui Normal University under Grant no. 161-070089 and the Key Laboratory of Biotic Environment and Ecological Safety of Anhui Province.

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