

MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the green odorous frog *Odorrana margaretae* (Anura: Ranidae)

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Abstract

The complete mitochondrial genome (mitogenome) of the green odorous frog *Odorrana margaretae* (Anura: Ranidae) has been studied. The 17,903 bp circular genome contains the typical complement of 13 protein-coding genes, 2 ribosomal RNAs, 22 transfer RNAs, and a control region. The AT content of the overall base composition of H-strand is 56% and the length of control region is 2501 bp with 63.8% AT content. The arrangement of the protein-coding and ribosomal RNA genes was the same as that found in other anurans. The cluster of rearranged LTPF tRNA genes and the translocation of *tRNA^{His}* gene into the D-loop region are observed.

Keywords

Mitochondrial genome, *Odorrana*, *Odorrana margaretae*, ranidae

History

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The green odorous frog, *Odorrana margaretae* (Anura: Ranidae), is the type species of the genus *Odorrana* (Fei et al., 1990) and an ideal environmental indicator. It lives mostly in swift boulder-strewn streams in the mountains of Gansu, Guangxi, Sichuan, Hubei, Hunan, Guizhou, Shaani provinces in China and northern Vietnam (Fei et al., 2010). The taxonomy and phylogeny of the genus *Odorrana* remain unresolved and contentious (Chen et al., 2013; Fei et al., 2010; Matsui et al., 2005). Mitogenome has been successfully applied to resolve the phylogenetic relationships among various groups at different taxonomic ranks (Xiong et al., 2009; Zhang et al., 2009). To improve our understanding of the *Odorrana* radiation, we determined the complete mitogenome sequences of *O. margaretae*.

The sample of *O. margaretae* (Voucher: HNNU1207003) was preserved in 95% ethanol at Henan Normal University. Thirteen DNA fragments were amplified using three pairs of highly conserved primers (Chen et al., 2014) and ten new pairs of primers designed in this study. The primer information is available upon request. All PCR amplifications were conducted using a BioRAD PTC-200 (BioRad Laboratories, Hercules, CA) with 2×EasyTaq PCR SuperMix (TransGen Biotech, Beijing, China) or LA-Taq Kits (Takara, Dalian, China). Both strands of each amplification were sequenced.

The complete sequence of the mitogenome of *O. margaretae* is 17,903 bp in length with 56% AT content (Table 1). The genome contains the typical component of 13 protein-coding genes, 2 ribosomal RNA genes, 22 tRNA genes, and non-coding regions. The arrangement of the protein-coding and ribosomal RNA genes was the same as that found in other anurans except *tRNA^{His}*. The *tRNA^{His}* gene was typically located between the ND4 gene and the *tRNA^{Ser}* in other anurans, however, it was translocated into the D-loop region in the *O. margaretae* mitogenome.

Table 1. Location of features in the mtDNA of *Odorrana margaretae*.

Gene/region	Position		Spacer (+), Overlap (–)	Length (bp)	Codon		
	From	To			Start	Stop	Strand
<i>tRNA^{Leu}</i>	1	72	+3	72			H
<i>tRNA^{Thr}</i>	76	144		69			H
<i>tRNA^{Pro}</i>	145	213	+1	69			L
<i>tRNA^{Phe}</i>	215	284		70			H
<i>12S rRNA</i>	285	1219		935			H
<i>tRNA^{Val}</i>	1220	1288		69			H
<i>16S rRNA</i>	1289	2872	+2	1584			H
<i>tRNA^{Leu (UUR)}</i>	2875	2948	+1	74			H
<i>ND1</i>	2950	3910		961	GTG	T	H
<i>tRNA^{Ile}</i>	3911	3981		71			H
<i>tRNA^{Gln}</i>	3982	4052	–1	71			L
<i>tRNA^{Met}</i>	4051	4120		69			H
<i>ND2</i>	4121	5153		1033	ATT	T	H
<i>tRNA^{Trp}</i>	5154	5221		68			H
<i>tRNA^{Ala}</i>	5222	5291		70			L
<i>tRNA^{Asn}</i>	5292	5364		73			L
<i>OL</i>	5365	5393	–3	29			L
<i>tRNA^{Cys}</i>	5391	5454		64			L
<i>tRNA^{Tyr}</i>	5455	5521	+1	67			L
<i>COI</i>	5523	7076	–9	1554	GTG	AGG	H
<i>tRNA^{Ser (UCN)}</i>	7068	7138	+1	71			L
<i>tRNA^{Asp}</i>	7140	7208		69			H
<i>COII</i>	7209	7896		688	ATG	T	H
<i>tRNA^{Lys}</i>	7897	7965		69			H
<i>ATP8</i>	7966	8133	–4	168	ATG	TAA	H
<i>ATP6</i>	8130	8805		676	ATA	T	H
<i>COIII</i>	8806	9589		784	ATG	T	H
<i>tRNA^{Gly}</i>	9590	9658		69			H
<i>ND3</i>	9659	9998		340	GTG	T	H
<i>tRNA^{Arg}</i>	9999	10,067		69			H
<i>ND4L</i>	10,068	10,352	–7	285	ATG	TAG	H
<i>ND4</i>	10,346	11,713	+30	1368	ATG	TAG	H
<i>tRNA^{Ser (AGY)}</i>	11,744	11,808	+32	65			H
<i>ND5</i>	11,841	13,635	+50	1795	ATG	TAA	H
<i>ND6</i>	13,685	14,185		501	ATG	AGA	L
<i>tRNA^{Glu}</i>	14,186	14,254	+2	69			L
<i>Cytb</i>	14,257	15,402		1146	ATG	TAA	H
<i>D-loop</i>	15,403	17,903		2501			H
<i>tRNA^{His}</i>	17,682	17,750		69			H

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Protein-coding genes begin with ATG as start codon except *ND2* with ATT, *ATP6* with ATA, *ND1*, *ND3* and *COI* with GTG. *ATP8*, *ND5* and *Cytb* are terminated with TAA as stop codon, *COI* end with AGG, *ND6* end with AGA, *ND4L* and *ND4* end with TAG, and the other six protein-coding genes end with an incomplete stop codon (a single stop nucleotide T).

Within the mitogenome of *O. margaretae*, there are five reading frame overlaps (*tRNA^{Gln}* and *tRNA^{Met}* share one nucleotides; *OL* and *tRNA^{Cys}* share three nucleotides; *COI* and *tRNA^{Ser(UCN)}* share 9 nucleotides; *ATP8* and *ATP6* share 4 nucleotides; *ND4L* and *ND4* share 4 nucleotides). The non-coding regions of *O. margaretae* include the control regions (*D-loop*) and a few intergenic spacers (Table 1). The control regions are 2501 bp in length, and the AT content of this region is 63.8% (T, 32.9%; C, 23.6%; A, 30.9%; G, 12.6%). The 5'-side of the control region possesses a few repeat regions consisting of 5 tandem repeat units of 127 bp (5'-CATATTATGTCTAATCAGC- -ATTCATATTTATATTTGATCTTAAGACGTACATATCCATCCTTAAGAACATATTATGCTTAATCAGCATTTCATATATATGTGCATTTCCCCATATTATGTGTAGTTAC-3'), 9 tandem repeat units of 42 bp (5'-TATATATGCATTTCCCCATACTATGTATAATC- -ACCATATATG-3') and 3 tandem repeat units of 20 bp (5'-CATATATATGTGC- -ATTTCCC-3'). However, no significant repeat regions were found in the 3'-side of the control region.

Nucleotide sequence accession number

The complete mitogenome sequence of *O. margaretae* has been assigned GenBank accession number KJ815050.

Declaration of interest

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