



# Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

**The complete mitochondrial genome of *Eremias vermiculata* (Squamata: Lacertidae)**

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**Abstract**

In this paper, we report the complete mitochondrial genome of *Eremias vermiculata* (Squamata: Lacertidae), which is a circular molecule of 19,914 bp in size and consists of 13 protein-coding genes, 2 ribosomal RNAs, 22 transfer RNAs, and 1 putative control region. The A + T content of overall base of the composition of H-strand is 59.8% (T: 28.9%, C: 27.2%, A: 30.9%, G: 13.0%). All of the results provide powerful data to further study of the molecular systematics, species identification and conservation genetics.

**Keywords**

*Eremias vermiculata*, Lacertidae, mitogenome

**History**

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The variegated racerunner, *Eremias vermiculata* is a small (up to 63 mm in length from snout to vent), oviparous lacertid lizard found in sand dunes or Gobi desert (Zhao, 1999). This lizard is widely distributed in Northwest China (Inner Mongolia, Xinjiang, Gansu, Qinghai and Ningxia) and Mongolia (Zhao, 1999). Despite its wide geographical distribution, the ecology and biology of *E. vermiculata* are poorly known. Incidental information on this species is obtained from studies addressing the phylogenetic relationship among *Eremias* lizards in China as well as intraspecific differentiation of *E. vermiculata* based on mitochondrial DNA sequences (Guo et al., 2011; Wan et al., 2007). In order to obtain more basic genetic information about this vulnerable species, we determined to sequence the complete mitochondrial genome of *E. vermiculata*.

Experimental procedures and results analysis referred to Tong et al. (2014). The tissue (tail muscle) sample of *E. vermiculata* was stored at  $-70^{\circ}\text{C}$  in laboratory at Nanjing Normal University. Some DNA fragments were amplified using highly conserved primers (Kumazawa & Endo, 2004). After obtaining most part of the mitogenome, we designed species-specific primers for the remaining part with reference to previously determined sequences.

The organization of mitochondrial genome was shown in Table 1. Similar to the typical mtDNA of vertebrates, the complete mtDNA sequence of *E. vermiculata* (19,914 bp in length) had 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes (12S rRNA and 16S rRNA) and 1 control region (Table 1). All the genes in *E. vermiculata* were distributed on the H-strand, except for the ND6 subunit gene and eight tRNA genes which were encoded on the L-strand. The overall base composition of H-strand is as follows: T (28.9%), C (27.2%), A (30.9%), G (13.0%), and the

Table 1. Location of features in the mtDNA of *E. vermiculata*.

Gene/region	Start position	Stop position	Spacer(+), overlap(-)	Length (bp)	Start codon	Stop codon	Strand
<i>tRNA<sup>Phe</sup></i>	1	68		68			H
<i>12S rRNA</i>	69	1019	-1	951			H
<i>tRNA<sup>Val</sup></i>	1019	1084		66			H
<i>16S rRNA</i>	1085	2616		1532			H
<i>tRNA<sup>Leu(UUR)</sup></i>	2617	2689		73			H
<i>ND1</i>	2690	3658	+5	969	ATG	TAA	H
<i>tRNA<sup>Ile</sup></i>	3664	3734		71			H
<i>tRNA<sup>Gln</sup></i>	3735	3805	-1	71			H
<i>tRNA<sup>Met</sup></i>	3805	3872		68			H
<i>ND2</i>	3873	4905		1033	ATG	T	H
<i>tRNA<sup>Trp</sup></i>	4906	4975	+2	70			H
<i>tRNA<sup>Ala</sup></i>	4978	5046	+1	69			L
<i>tRNA<sup>Asn</sup></i>	5048	5120		73			L
<i>OL</i>	5121	5151		31			L
<i>tRNA<sup>Cys</sup></i>	5152	5211	+4	60			L
<i>tRNA<sup>Tyr</sup></i>	5216	5279	+1	64			L
<i>COI</i>	5281	6825		1545	GTG	AGG	H
<i>tRNA<sup>Ser(UCN)</sup></i>	6826	6889	+3	64			L
<i>tRNA<sup>Asp</sup></i>	6893	6964		72			H
<i>COII</i>	6965	7652		688	ATG	T	H
<i>tRNA<sup>Lys</sup></i>	7653	7715	+1	63			H
<i>ATP8</i>	7717	7878	-10	162	ATG	TAA	H
<i>ATP6</i>	7869	8549	-1	681	ATG	TAA	H
<i>COIII</i>	8549	9332		784	ATG	T	H
<i>tRNA<sup>Gly</sup></i>	9333	9402		70			H
<i>ND3</i>	9403	9748		346	GTG	T	H
<i>tRNA<sup>Arg</sup></i>	9749	9815	+1	67			H
<i>ND4L</i>	9817	10,113	-7	297	ATG	TAA	H
<i>ND4</i>	10,107	11,487		1381	ATG	T	H
<i>tRNA<sup>His</sup></i>	11,488	11,556	-1	69			H
<i>tRNA<sup>Ser(AGY)</sup></i>	11,556	11,615	+10	60			L
<i>tRNA<sup>Leu(CUN)</sup></i>	11,626	11,696	+3	71			H
<i>ND5</i>	11,700	13,523	-5	1824	ATG	TAA	H
<i>ND6</i>	13,519	14,040		522	ATG	AGG	L
<i>tRNA<sup>Glu</sup></i>	14,041	14,110	+1	70			L

(continued)

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Table 1. Continued

Gene/region	Start position	Stop position	Spacer(+), overlap(-)	Length (bp)	Start codon	Stop codon	Strand
<i>Cyt b</i>	14,112	15,254		1143	ATG	TAA	H
<i>tRNA<sup>Thr</sup></i>	15,255	15,314	+8	60			L
<i>tRNA<sup>Pro</sup></i>	15,323	15,388		66			L
<i>D-loop</i>	15,389	19,914		4526			H

A + T content 59.8%. Eleven of the 13 protein-coding genes require ATG as the start codon, while CO1 and ND3 utilize GTG (Table 1). Six of 13 protein-coding genes use TAA as stop codons. The ND6 and CO1 end with AGG, and five genes (ND2, CO2, CO3, ND3 and ND4) use T as an incomplete stop codon, which is presumably completed as TAA by posttranscriptional polyadenylation. The noncoding regions include a control region (D-loop) and nine intergenic spacers (range from 1 to 10 bp).

We expect the present study to provide a useful database for analyzing the phylogenetic relationship of *Eremias*.

### Nucleotide sequence accession number

The complete genome sequence of *E. vermiculata* has been assigned GenBank accession number KM104865.

### Declaration of interest

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