

MITOGENOME ANNOUNCEMENT

Sequencing and analysis of the whole mitochondrial genome of a variegated racerunner from Taklamakan DesertTianhe Zhou^{1,2}, Xiaoqin Wan³, and Xianguang Guo¹¹Chengdu Institute of Biology, Chinese Academy of Sciences, Chengdu, PR China, ²University of Chinese Academy of Sciences, Beijing, PR China, and ³Hechuan Middle School, Chongqing, PR China**Abstract**

The whole mitochondrial genome of a variegated racerunner (*Eremias vermiculata*) from the Taklamakan Desert was determined using polymerase chain reaction and directly sequenced with a primer walking method. The mitogenome sequence was 19 796 bp in size, containing 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and a control region (D-loop), which is similar to the typical mtDNA of vertebrates. Mitochondrial genomes analyses using maximum parsimony and Bayesian analyses yielded identical phylogenetic trees, indicating a close phylogenetic affinity of the seven *Eremias* species. Monophyly of the genus *Eremias* and *E. vermiculata* was recovered. The mitogenome presented here will contribute to the examination of genetic differentiation for *E. vermiculata* and understanding of the mitochondrial DNA evolution in *Eremias*.

Keywords*Eremias vermiculata*, mitochondrial genome, Taklamakan Desert**History**Received 7 June 2015
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The variegated racerunner, *Eremias vermiculata*, is widespread in Northwest China, southern Mongolia, and Zaissan Depression of Kazakhstan (Szczerbak, 2003). Despite its wide distribution, this lizard is considered to be a monotypic species without subspecies differentiation (Sindaco & Jeremčenko, 2008). To date, little is known about its population structure and genetic relationships with other congeneric species (Guo et al., 2011; Liu et al., 2014).

Recently, two mitochondrial genome sequences of *E. vermiculata* have been reported (Tong et al., 2014; Zhou et al., 2015). In this study, we sequenced a third complete mitogenome of *E. vermiculata*, with specimen number WGXC08403. This lizard was collected from the Taklamakan Desert (83.74777°N, 38.92712°E). Its liver tissue was fixed with 95% ethanol and stored at –20 °C in the herpetological collection at Chengdu Institute of Biology, Chinese Academy of Sciences. We took the same strategy as described previously (Zhou et al., 2015) to get the whole mitogenome of this sample albeit with some specific walking primers.

The complete mitochondrial genome of *E. vermiculata* was 19 796 bp in length, with overall base composition of 31.1% A, 28.9% T, 27.0% C, and 13.0% G. Annotation of the mitogenome revealed 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and a control region (CR or D-loop). The nucleotide composition of CR had a richer A + T content (66.8%) than that of the whole

mitogenome (60.0%). The higher AT content in CR might be a driving force for its high evolutionary rate. The gene organization exhibited a typical vertebrate mitochondrial genome feature. The majority of genes in the mtDNA of *E. vermiculata* were distributed on H-strand, except for the *ND6* and eight tRNAs which were encoded on the L-strand. In 13 protein-coding genes, the shortest one was *ATP8* gene (162 bp) and longest one was the *ND5* gene (1824 bp). Twelve of the 13 protein-coding genes started with a common initiation codon ATG, while *COI* gene utilized GTG. Eleven of the 13 protein-coding genes ended with complete (TAA) or incomplete (T–) stop codons. *COI* and *ND6* genes stopped with AGG. The 22 tRNA genes ranged in size from 62 bp in *tRNA-Cys* to 73 bp in *tRNA-Asn*. The 12S rRNA, 16S rRNA, and D-loop were 1020 bp, 2616 bp, and 4409 bp, respectively. For the whole mitogenome, there were seven regions of gene overlap (ranging from 1 to 10 bp), and 13 intergenic spacer regions (ranging from 1 to 28 bp).

Mitochondrial genomes analyses using maximum parsimony in PAUP* 4.0b10 (Sinauer, Sunderland, MA) (Swofford, 2003) and Bayesian analyses in MrBayes 3.2 (Ronquist et al., 2012) yielded identical phylogenetic trees, indicating a close phylogenetic affinity of the five racerunner species. The phylogram obtained from Bayesian inference is shown in Figure 1. Monophyly of both the genus *Eremias* and *E. vermiculata* was

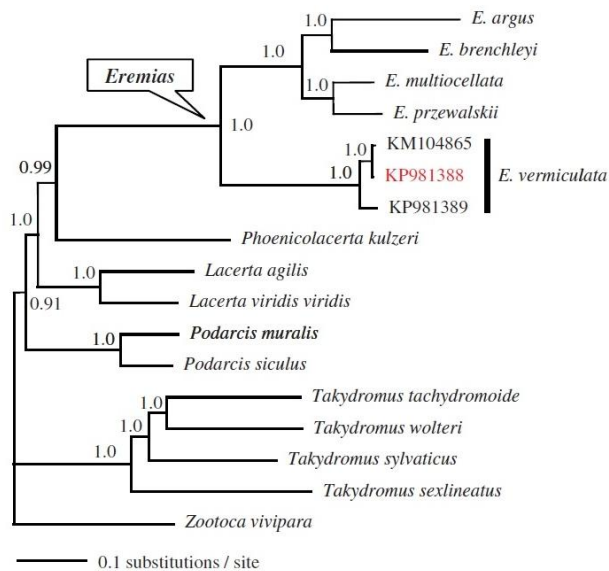


Figure 1. A majority-rule consensus tree inferred from Bayesian inference by using MrBayes v.3.2 with *GTR + I + G* substitution model. The values beside the nodes are Bayesian posterior probabilities. Branch lengths represent means of the posterior distribution. Accession numbers for sequences retrieved from the GenBank: *Eremias vermiculata*, KM104865, KP981389; *Eremias przewalskii*, KM507330; *Eremias multiocellata*, KM257724; *Eremias argus*, JQ086345; *Eremias brenchleyi*, EF490071; *Lacerta agilis*, KC990830; *Podarcis siculus*, FJ460598; *Podarcis muralis*, FJ460597; *Phoenicolacerta kulzeri*, FJ460596; *Zootoca vivipara*, KM401599; *Lacerta viridis*, AM176577; *Takydromus wolteri*, JX181764; *Takydromus sexlineatus*, KF425529.

recovered. The new mitogenome sequence will provide fundamental data for further investigating the phylogeographical pattern of *E. vermiculata*, along with detecting mitochondrial DNA evolution in *Eremias*.

Nucleotide sequence accession number

The complete genome sequence of *E. vermiculata* has been assigned GenBank accession number KP981388.

Declaration of interest

This work was supported by the National Natural Science Foundation of China (31272281). The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

References

- Guo X, Dai X, Chen D, Papenfuss TJ, Ananjeva NB, Melnikov DA, Wang Y. (2011). Phylogeny and divergence times of some racerunner lizards (Lacertidae: *Eremias*) inferred from mitochondrial 16S rRNA gene segments. *Mol Phylogenet Evol* 61:400–12.
- Liu J, Yuan X, Zhou T, Li D, Dujsebayaeva TN, Guo X. (2014). *Eremias vermiculata* was discovered in the north of Tianshan Mountains in Xinjiang Uygur Autonomous Region. *Chin J Zool* 49:423–7 (in Chinese with English abstract).
- Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, et al. (2012). MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst Biol* 61: 539–42.
- Sindaco R, Jeremčenko VK. (2008). The reptiles of the Western Palearctic. 1. Annotated checklist and distributional Atlas of the turtles, crocodiles, amphisbaenians and lizards of Europe, North Africa, Middle East and Central Asia. Latina, Italy: Edizioni Belvedere.
- Swofford DL. (2003). PAUP*. Phylogenetic analysis using parsimony (* and other methods), Version 4. Sunderland, MA: Sinauer.
- Szczerbak NN. (2003). Guide to the Reptiles of the Eastern Palearctic. Malabar (FL): Krieger Publishing Company.
- Tong Q-L, Yao Y-T, Lin L-H, Ji X. (2014). The complete mitochondrial genome of *Eremias vermiculata* (Squamata: Lacertidae). *Mitochondrial DNA*. [Epub ahead of print]. doi: 10.3109/19401736.2014.953086.
- Zhou T, Liu J, Guo X. (2015). Complete mitogenome of a variegated racerunner, *Eremias vermiculata*, from north of Tianshan Mountains, Xinjiang, China. *Mitochondrial DNA*. [Epub ahead of print]. doi: 10.3109/19401736.2015.1053055.