



Next-generation sequencing yields a nearly complete mitochondrial genome of the Variegated Racerunner (*Eremias Vermiculata*) from Dunhuang Basin

Dali Chen, Xiuliang Su, Jinlong Liu & Xianguang Guo

To cite this article: Dali Chen, Xiuliang Su, Jinlong Liu & Xianguang Guo (2019) Next-generation sequencing yields a nearly complete mitochondrial genome of the Variegated Racerunner (*Eremias Vermiculata*) from Dunhuang Basin, Mitochondrial DNA Part B, 4:1, 1626-1627, DOI: [10.1080/23802359.2019.1604102](https://doi.org/10.1080/23802359.2019.1604102)

To link to this article: <https://doi.org/10.1080/23802359.2019.1604102>



© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



Published online: 17 Apr 2019.



Submit your article to this journal [↗](#)



Article views: 70



View Crossmark data [↗](#)

Next-generation sequencing yields a nearly complete mitochondrial genome of the Variegated Racerunner (*Eremias Vermiculata*) from Dunhuang Basin

Dali Chen^a, Xiuliang Su^b, Jinlong Liu^b and Xianguang Guo^b

^aWest China School of Basic Medical Sciences and Forensic Medicine, Sichuan University, Chengdu, China; ^bChengdu Institute of Biology, Chinese Academy of Sciences, Chengdu, China

ABSTRACT

The Variegated Racerunner, *Eremias vermiculata*, is widespread in Northwest China, southern Mongolia, and Zaisan Basin of Kazakhstan. In this study, a nearly complete mitochondrial genome (17,972 bp in length) of *E. vermiculata* from the Dunhuang Basin in Northwest China was determined by next-generation sequencing. Similar to the typical mtDNA of vertebrates, it contained two ribosomal RNA genes, 13 protein-coding genes (PCGs), 22 transfer RNA genes, and one control region (CR). With exception to the CR, all of the 37 genes were completely recovered. The concatenated PCGs were used to conduct Bayesian phylogenetic analyses together with mitogenome data of lacertids in GenBank. The resulting phylogenetic tree confirmed the monophyly of genus *Eremias* and its viviparous species as well as *E. vermiculata*, respectively. The mitogenome presented here will contribute to the examination of phylogeographic structure for *E. vermiculata* and understanding of mitochondrial DNA evolution in *Eremias*.

ARTICLE HISTORY

Received 18 March 2019
Accepted 23 March 2019

KEYWORDS

Mitochondrial genome;
next-generation sequencing;
Eremias; phylogenetic tree

The Variegated Racerunner, *Eremias vermiculata*, is widespread in Northwest China, southern Mongolia, and Zaisan Basin of Kazakhstan (Szczerbak 2003). Despite its wide distribution, this lizard is considered to be a monotypic species without subspecies differentiation (Sindaco and Jeremčenko 2008). To date, little has been known regarding its population structure and genetic relationships with other congeneric species (Guo et al. 2011).

Recently, three mitochondrial genome sequences of *E. vermiculata* have been reported (Tong et al. 2016; Zhou et al. 2016a, 2016b). In this study, we determined a nearly complete mitochondrial genome of this species by using next-generation sequencing through Roche 454 GS-FLX technology (Roche, Basel, Switzerland). The lizard was collected from Dunhuang Basin (N39.94°, E94.11°) in July 2013. The Basin is situated on the western end of Northwestern China's Hexi Corridor and is bounded by the Mingsha, Sanwei, and Beijie Mountains to the southeast, the Mazong and Bei Mountains to the north, and the Kumtag Desert to the west. The specimen (field number Guo2628) was deposited at the herpetological collection in Chengdu Institute of Biology, Chinese Academy of Sciences. We took a similar strategy as described previously (Chen et al. 2019) to assemble and annotate the mitogenome by using published sequence (GenBank accession number KP981388) as queries for the reference. A nearly complete mitogenome of 17,972 base pairs (bp) was obtained and deposited in GenBank with accession number MK261078.

The mtDNA sequence comprised two ribosomal RNA genes, 13 protein-coding genes (PCGs), 22 transfer RNA

genes (tRNAs), and one control region (CR or D-loop). The gene content, arrangement, and composition exhibited a typical vertebrate mitochondrial genome feature. The majority of the genes in the mtDNA of *E. vermiculata* was distributed on H-strand, except for the *ND6* gene and 8 tRNAs (*tRNA-Gln*, *Ala*, *Asn*, *Cys*, *Tyr*, *Ser[UGA]*, *Glu*, and *Pro*). In 13 PCGs, the shortest was *ATP8* gene (162 bp) and the longest was *ND5* gene (1824 bp). Eleven of 13 PCGs were initiated with the typical ATG codon, except for *COI* and *ND3* with GTG. Most PCGs were terminated with the typical TAA/AGG codons, except for *ND2*, *COII*, *COIII*, *ND3*, and *ND4* with the incomplete termination codon T. The 22 tRNA genes ranged in size from 62 bp for *tRNA-Cys* to 73 bp for *tRNA-Leu* and *tRNA-Asn*. The *12S* and *16S rRNA* genes were 953 bp and 1530 bp in length, respectively. As for the CR, 1538 bp were already determined adjacent to *tRNA-Pro*, along with 1047 bp prior to *tRNA-Phe*.

The concatenated PCGs of *Eremias* available in GenBank plus 14 other lacertids as outgroups were used to reconstruct the Bayesian phylogenetic tree for assessing mitochondrial sequence authenticity of *E. vermiculata* and its phylogenetic placement. As shown in Figure 1, the monophyly of both *Eremias* and the viviparous group were recovered. Four individuals of *E. vermiculata* clustered together and formed sister taxon to all other sampled members of the genus. The new mitogenome sequence will provide fundamental data for further investigating the phylogeographic structure of *E. vermiculata* along with detecting mitochondrial DNA evolution in *Eremias*.

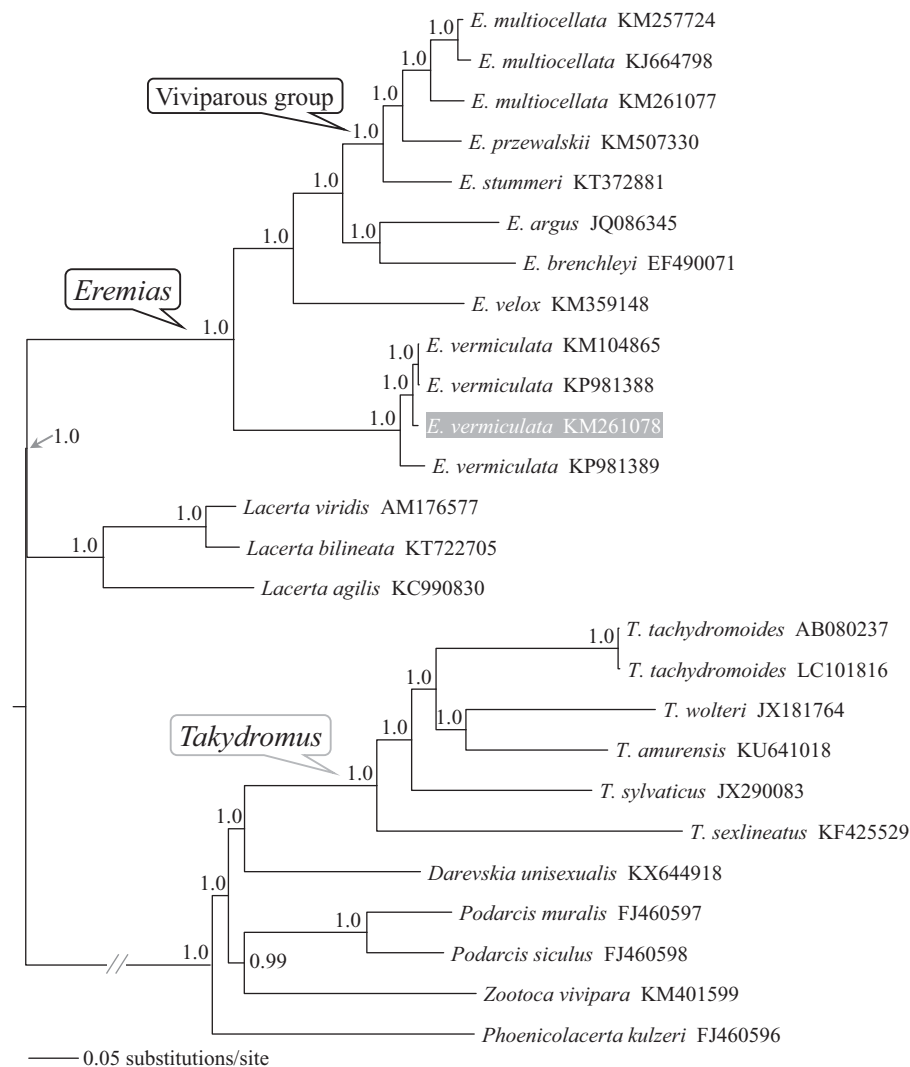


Figure 1. A majority-rule consensus tree derived from Bayesian inference using MrBayes v.3.2.2 (Ronquist et al. 2012) with GTR + GAMMA substitution model, based on the concatenated PCGs of 12 individuals of *Eremias* lizards and 14 outgroups. The tree was rooted using midpoint rooting method and the newly sequenced sample was highlighted in gray. GenBank accession numbers are given with species names. DNA sequences were aligned in MEGA v.7.0.14 (Kumar et al. 2016). The PCGs were translated into amino acid sequences and were manually concatenated into a single nucleotide dataset (in total 11,403 bp). Node numbers show Bayesian posterior probabilities. Branch lengths represent means of the posterior distribution.

Disclosure statement

No potential conflict of interest was reported by the authors. The authors alone are responsible for the content and writing of this article.

Funding

This work was supported by the National Natural Science Foundation of China [31560591, 31672270, 31872959]. XS was supported by grant from the Undergraduate Training Program for Innovation and Practice in University of Chinese Academy of Sciences.

References

- Chen D, Li J, Guo X. 2019. Next-generation sequencing yields a nearly complete mitochondrial genome of the Forsyth's toad-headed agama, *Phrynocephalus forsythii* (Reptilia, Squamata, Agamidae). *Mitochondrial DNA B*. 41:817–819.
- 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*. 61:400–412.
- Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol*. 33: 1870–1874.
- Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst Biol*. 61:539–542.
- Sindaco R, Jeremčenko VK. 2008. The reptiles of the Western Palearctic. Vol. 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.
- Szczerbak NN. 2003. Guide to the reptiles of the Eastern Palearctic. Malabar, Florida: Krieger Publishing Company.
- Tong QL, Yao YT, Lin LH, Ji X. 2016. The complete mitochondrial genome of *Eremias vermiculata* (Squamata: Lacertidae). *Mitochondrial DNA A*. 27:1447–1448.
- Zhou T, Liu J, Guo X. 2016a. Complete mitogenome of a Variegated Racerunner, *Eremias vermiculata*, from north of Tianshan Mountains, Xinjiang, China. *Mitochondrial DNA A*. 27:2765–2766.
- Zhou T, Wan X, Guo X. 2016b. Sequencing and analysis of the whole mitochondrial genome of a variegated racerunner from Taklamakan Desert. *Mitochondrial DNA A*. 27:3041–3042.