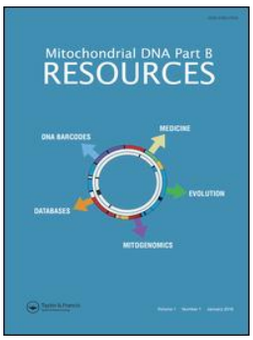

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MITOGENOME ANNOUNCEMENT

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Next-generation sequencing yields a nearly complete mitochondrial genome of the Multiocellated Racerunner (*Eremias multiocellata*) in Northwest China

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ABSTRACT

The viviparous Multiocellated Racerunner, *Eremias multiocellata*, is widespread in North China, Mongolia, and the Tuva Republic of Russia. A nearly complete mitochondrial genome of one individual from the suburb of Jingyuan County in Northwest China was determined by next-generation sequencing. The mitogenome is 17,333 bp in size, comprising 2 ribosomal RNA genes, 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), and one control region. The gene arrangement and composition is similar to the typical mitochondrial DNA of vertebrates. With exception to the control region, all of the 37 genes were completely recovered. The concatenated PCGs were used to conduct Bayesian phylogenetic analyses together with several related lizards with mitogenome data in GenBank. The resulting phylogenetic tree confirmed the monophyly of both genus *Eremias* and its viviparous group. The mitogenome sequence will provide fundamental data for resolving phylogenetic and genetic problems related to *Eremias* viviparity.

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KEYWORDS
Mitochondrial genome; next-generation sequencing; *Eremias*; phylogenetic tree; viviparity

The viviparous Multiocellated Racerunner, *Eremias multiocellata* Günther, 1872, is widely distributed in North China, Mongolia and the Tuva Republic of Russia (Sindaco and Jeremčenko 2008). The advancement of sequencing technology including the next-generation sequencing (NGS) has facilitated rapid obtainment of mitochondrial genome of animals from various groups (Hahn et al. 2013). In this study, we determined a nearly complete mitochondrial genome of *E. multiocellata* by using NGS reads through Roche 454 sequencing platform. The lizard was collected from Jingyuan County (N36.55°, E104.68°), Gansu Province, China. The specimen with field number Guo2760 was deposited in the herpetological collection at Chengdu Institute of Biology, Chinese Academy of Sciences. We took the similar strategy as described previously (Chen et al. 2019) to assemble and annotate the mitogenome, by using a published sequence of *E. multiocellata* (GenBank accession number KM257724; Tong et al. 2016) as queries for the reference. A nearly complete mitogenome of 17,333 bp was obtained and deposited in GenBank with accession number MK261077.

The nearly complete mtDNA sequence consists of two ribosomal RNA genes, 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs) and a control region (CR or D-loop). The gene organization and order exhibited a typical vertebrate mitochondrial genome feature. The majority of genes in the mtDNA of *E. multiocellata* was distributed on H-strand, except for the *ND6* gene and eight tRNAs (*tRNA-Gln*, *Ala*, *Asn*, *Cys*, *Tyr*, *Ser*[*UGA*], *Glu*, and *Pro*). In 13 PCGs, the shortest one was *ATP8* gene (162 bp) and the longest one was *ND5* gene (1824 bp). Twelve of 13 PCGs were initiated with the typical ATG codon, except for *COI* with GTG. Meanwhile, *ND1*, *ATP8*, *ATP6*, *ND4L*, *ND5*, and *Cytb* genes were terminated with TAA as stop codon; *COI* and *ND6* genes end with AGG, and the remaining five PCGs end with the incomplete termination codon T. The 22 tRNA genes ranged in size from 62 bp in *tRNA-Cys* to 73 bp in five tRNAs (*tRNA-Phe*, *Leu*, *Asn*, *Asp*, and *Glu*). The *12S* and *16S rRNA* genes were 952 bp and 1545 bp in size, respectively. As for the D-loop, 1767 bp were already determined adjacent to *tRNA-Pro*, albeit with only 156 bp prior to *tRNA-Phe*.

The concatenated PCGs of *Eremias* available in GenBank plus three lacertids as outgroups were used to reconstruct the Bayesian phylogenetic trees for assessing mitochondrial sequence authenticity of *E. multiocellata* and its phylogenetic placement. As shown in Figure 1, in support of Guo et al. (2011), the monophyly of both *Eremias* and the viviparous group were recovered. Three individuals of *E. multiocellta* clustered together and were closely related to *E. przewalskii*.

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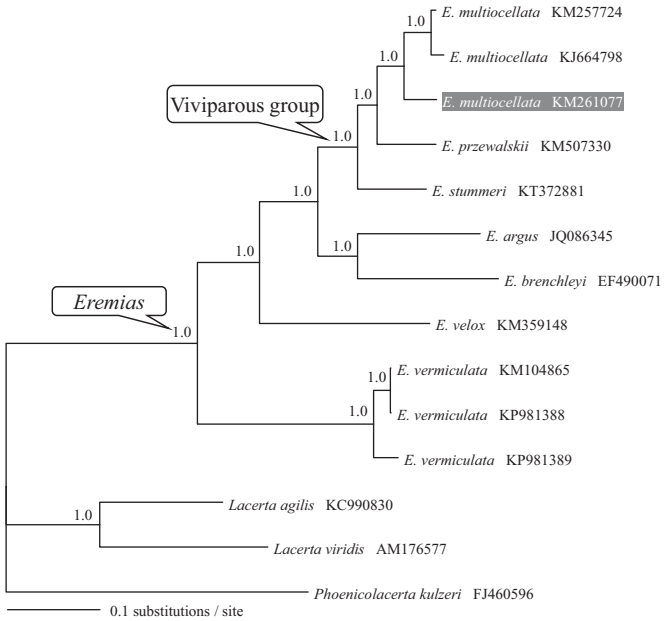

Figure 1. A majority-rule consensus tree inferred from Bayesian inference using MrBayes v.3.2.2 (Ronquist et al. 2012) under the GTRGAMMA model, based on the concatenated PCGs of 11 individuals of racerunner lizards and three outgroups. The novel sequencing sample is highlighted. GenBank accession numbers are given with species names. DNA sequences were aligned in MEGA v.6.06 (Tamura et al. 2013). The PCGs were translated to amino acids sequences, and were manually concatenated all sequences into a single nucleotide dataset (in total 11,393 bp). Node numbers show Bayesian posterior probabilities. Branch lengths represent means of the posterior distribution.

The newly determined mitogenome sequence will provide fundamental data for resolving phylogenetic and genetic problems related to viviparity of *Eremias*.

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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.

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