MITOGENOME ANNOUNCEMENT

Sequencing and analysis of the whole mitochondrial genome of a variegated racerunner from Taklamakan Desert

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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

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The variegated racerunner, Eremias vermiculata, is widespread in Northwest China, southern Mongolia, and Zaiissan 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 WGXG08403. This lizard was collected from the Taklamakan Desert (83.74777\textdegree N, 38.92712\textdegree E). Its liver tissue was fixed with 95\% ethanol and stored at −20\textdegree 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 rich 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 (TTA) 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 12 intergenic spacer regions (ranging from 1 to 28 bp).

Mitochondrial genomes analyses using maximum parsimony in PAUP\textsuperscript{4} 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

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Nucleotide sequence accession number

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

Declaration of interest

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References


