Complete mitochondrial genome of Stummer’s Racerunner (Eremias stummeri) from Kazakhstan

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Abstract

The whole mitochondrial genome was determined from a viviparous racerunner, Eremias stummeri, which was collected from southeast Kazakhstan. The mitogenome sequence was 19,602 bp in size, containing 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and a control region, 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 sampled taxa in genus Eremias. Monophyly of both Eremias and its viviparous group is recovered. The complete mitogenome sequence of E. stummeri provides fundamental data for resolving phylogenetic and genetic problems related to Eremias viviparity.

The viviparous Stummer’s Racerunner, Eremias stummeri, occurs in Kyrgyzstan (Issyk Kul Basin), extreme Kazakhstan (Tekess-Kegen Depression), and adjoining China (Ily River Valley) (Sindaco & Jeremčenko, 2008). Historically, it was assigned to subspecies status of Eremias velox stummeri or Eremias multioicellata stummeri (Wettstein, 1940; Szczerbak, 1974). However, Eremchenko & Panfilov (1999) confirmed its status as distinct biological species through long term research including hybridization experiments. To date, little is known about its genetic affinities with other viviparous species in genus Eremias albeit with limited understanding of viviparity evolution in racerunner lizards (Guo et al., 2011).

In this study, we reported the whole mitochondrial genome of E. stummeri, with voucher number KZ51. The specimen was collected from Kumtekey Sands, Kazakhstan (N42°57′50.5″, E 79°16′44.4″) in August 2013. This population’s discovery, history and its phenetic character was described by Dujsebayeva et al. (2009). 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 similar strategy as described previously (Zhou et al., 2015) to get the complete mitogenome of E. stummeri albeit with some species-specific genome walking primers.

The mitogenome of E. stummeri was 19,602 bp in length, with overall base composition of 31.27% A, 27.19% C, 13.19% G, and 28.35% T. Annotation of the mitogenome revealed 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and one control region (CR or D-loop). The gene organization and order was used GTG. Ten of 13 protein-coding genes ended with complete (TAA) or incomplete (T) stop codons. ND1, CO1, and ND6 stopped with TAG, AGG, and AGA, respectively. The 22 tRNA genes ranged in size from 62 bp in tRNA-Cys to 73 bp in tRNA-Asn and tRNA-Asp. The 12S and 16S rRNA genes were 952 bp and 1536 bp, respectively. For the whole mitochondrial sequence, there were nine regions of gene overlap totaling 17 bp (ranging from 1 to 5 bp) and 12 intergenic spacer regions totaling 34 bp (ranging from 1 to 10 bp). D-loop was 4214 bp in length. The nucleotide composition of CR had a richer A + T content (67.67%) than that of the whole mitogenome (55.54%).

Mitochondrial genomes analyses using maximum parsimony in PAUP* 4.0b10 (Swofford, 2003) and Bayesian analyses in MrBayes 3.2 (Ronquist et al., 2012) yielded identical phylogenetic trees, indicating a close phylogenetic affinity of the seven racerunner species. The phylogram obtained from Bayesian inference is shown in Figure 1. Monophyly of both genus Eremias and the viviparous group was recovered. The mitogenome sequence of E. stummeri will provide fundamental data for resolving phylogenetic and genetic problems related to viviparity of Eremias.

Keywords

Mitogenome, racerunner lizard, viviparity

History

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Figure 1. A majority-rule consensus tree inferred from Bayesian inference by using MrBayes v.3.2 with GTR + G + I 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 przewalskii, KM507330; Eremias multiocellata, KM257724, KJ664798; Eremias argus, JQ086345; Eremias brenchleyi, EF490071; Eremias velox, KM359148; Eremias vermiculata, KM104865, KP981388, KP981389; Lacerta agilis, KC990830; Lacerta viridis, AM176577; Phoenicolacerta kulzeri, FJ460596; Podarcis muralis, FJ460597; Podarcis siculus, FJ460598; Takydromus wolteri, JX181764; Takydromus sexlineatus, KF425529; Takydromus tachydromoides, AB082037; Takydromus sylvaticus, JX290083; Zootoca vivipara, KM401599.

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Declaration of interest
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Nucleotide sequence accession number
The complete mitochondrial genome sequence of E. stummeri has been assigned GenBank accession number KT372881.

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