Characterization of the complete mitochondrial genome and phylogenetic status of a recently described species of Mountain Dragon, Diploderma vela (Reptilia: Squamata: Agamidae), from the upper Lantsang valley in west China

Yayong Wu, Ke Li, Feng Wang, Qin Liu and Bo Cai

The mountain dragon, Diploderma vela, is an endemic valley lizard that inhabits the upper Lantsang Valley in West China. In this study, we sequenced the complete mitochondrial genome of a male individual of D. vela using next-generation sequencing methodologies. The complete mitogenome is 16,432 bp in length and contains one noncoding control regions, 13 protein-coding, 22 transfer RNA and two ribosomal RNA genes. The mitogenome content and structure of D. vela was consistent with the previously published representatives of the family. A Bayesian phylogenetic analysis using the complete mitochondrial genomes of Agamidae fully resolved D. vela in the Draconinae, a result consistent with previous investigations. This study provides bioinformatic data for better understanding the evolution and the phylogenetic history of the mountain dragon.

The complete mitochondrial genomes of D. vela was 16,432 bp in length, comprising one non-coding control region (CR), 13 protein-coding genes (PCGs), two ribosomal RNA genes, and 22 transfer RNA genes (tRNA), while lacking origin of light-strand replication (OL). The mitogenome base-pair is AT biased (58.8%) with 34.8% for A, 28.1% for C, 13.1% for G and 23.9% for T. Most genes were located on the heavy strand (H-strand) with the exception of ND6 and eight tRNA genes (tRNA-Glu, Ala, Asn, Cys, Tyr, Ser(UJC), Glu, and Pro). The mean length of tRNA genes was 68 bp, the shortest and the longest were tRNA-Cys gene (54 bp) and tRNA-Leu (75 bp), respectively. The mean length of PCGs was 865 bp, the shortest and the longest were ATP8 gene (162 bp) and ND5 (1779 bp), respectively. Most PCGs initiated with ATG except for ND2, ND5, and ATP8, and TAG (ND2 and ND6), while the other six genes ended with the incomplete stop codon, TA/T (COX2, ATP6, COX3, ND3, ND4, and Cytb). The mitogenome content and structure of D. vela was consistent with the previously identified based on Wang et al. (2015). The specimen and the liver tissue using Trelief Animal Genomic DNA Kit (Tsingke, Jia-Tang, lijt@cib.ac.cn). Total genomic DNA was extracted from the herpetological collection, Chengdu Institute of Biology, Chinese Academy of Science (http://herpmuseum.cib.ac.cn, Li Jia-Tang, lijt@cib.ac.cn). Total genomic DNA was extracted from liver tissue using Trelief Animal Genomic DNA Kit (Tsingke, Beijing, China) following the manufacturer’s instruction with minor modification. The complete mitochondrial DNA sequence was analyzed on an Illumina HiSeq 2000 platform. Genes were assembled and annotated with the SPAdes v3.11.0 (Bankevich et al. 2012) and MITOS web server (Bernt et al. 2013), respectively. The mitogenome was submitted to GenBank under the accession number MW788326. All sampling activities were conducted in accordance with the Guidelines of Animal Ethics published by the Chengdu Institute of Biology.

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Phylogenetic analysis based on nucleotide sequences of 13 PCGs of *D. vela* with the other 17 species of Agamidae, both Uromastycinae (*Uromastyx benti*) and Leiolepidinae (*Leiolepis belliana*) were designated as outgroups based on published higher-level phylogenetic studies of squamate reptiles (Pyron et al. 2013). Bayesian phylogenetic tree using the GTR + I + G substitution model indicated that *D. vela* was closely related to its congeners, fully resolved in the subfamily Draconinae (PP 1.00) (Figure 1). The overall phylogenetic relationships among Agamidae were consistent with previous studies (Wang et al. 2019a). This study provides a valuable mitogenome resource for better understanding the molecular evolution and phylogenetic relationships of *D. vela*, and serves as a reference for the establishment of conservation strategies and measures.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**Data availability statement**

The data that support the findings of this study are openly available in NCBI (National Center for Biotechnology Information) with GenBank Accession No. MW788326 (https://www.ncbi.nlm.nih.gov/nuccore/MW788326) and DRYAD (Dryad Digital Repository) with the unique DOI (doi:10.5061/dryad.qj2bvqgb).
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