

Complete mitochondrial genome of Perny's long-nosed squirrel *Dremomys pernyi* (Rodentia: Sciuridae)

Haiyan Cong^a, Lingming Kong^a, Masaharu Motokawa^b, Masashi Harada^c, Tatsuo Oshida^d, Yi Wu^e and Yuchun Li^a

^aMarine College, Shandong University, Weihai, China; ^bThe Kyoto University Museum, Kyoto University, Kyoto, Japan; ^cGraduate School of Medicine, Osaka City University, Osaka, Japan; ^dLaboratory of Wildlife Biology, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan; ^eSchool of Life Sciences, Guangzhou University, Guangzhou, China

ABSTRACT

The complete mitochondrial genome of Perny's long-nosed squirrel (*Dremomys pernyi*) was firstly sequenced and characterized. The genome was 16,573 bp in length, and its composition and arrangement of genes were analogous to other rodents. The sequences of 13 protein-coding genes were used to construct phylogenetic tree for *D. pernyi* and other 13 sciurid species available on GenBank. To date, this is the first species whose complete mitochondrial genome sequence was sequenced in genus *Dremomys*. Our results will provide information for further molecular studies.

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Genus *Dremomys* contains six species (Thorington & Hoffmann 2005), among them five species are distributed in China (Smith et al. 2008). The recent research demonstrates that *Dremomys* is not monophyletic, the species *D. everetti* is not clustered with other *Dremomys* species (Hawkins et al. 2016). To date, there are no complete mitochondrial genome data of species in this genus. In order to provide more molecular information for species in this genus, we first sequenced and characterized the complete mitochondrial genome of *D. pernyi* collected from Kangding of Sichuan province, China. The voucher specimen (G10138) was stored in School of Life Sciences, Guangzhou University.

According to our result, the mitogenome of *D. pernyi* was 16,573 bp in length and has been deposited in GenBank under the accession number KP708711. It contains 37 genes arranged in the same order with other reported vertebrate mitogenomes, including 22 tRNA genes, 13 protein-coding genes (PCGs), 2 rRNA genes and 2 non-coding regions. Among these genes, 28 are transcribed on the heavy-coding strand (H-strand), whereas the other nine genes on the light-coding strand (L-strand). The nucleotide composition is biased towards A and T with 59.1% A+T content (A=31.9%, C=27.9%, G=13.0%, T=27.2%). All PCGs are encoded on the H-strand except *ND6*. ATG is most preferred for most PCGs as the initial codon, whereas *ND3* and *ND5* start with ATA, and *ND2* starts with ATT. *ND6* and *Cytb* end with AGG and AGA, respectively, and other PCGs end with TAA or TAG,

COX3 and *ND4* end with TA- and T-, respectively, which can be completed by post-transcriptional polyadenylation (Ojala et al. 1981). The two rRNA genes (12S rRNA and 16S rRNA) are separated by gene tRNA-Val.

A set of 22 tRNA genes which arrange from 63 to 73 bp are found in the mitochondrial genome. All the tRNA genes could be folded into canonical cloverleaf structure except for tRNA-Ser(AGY) in which its dihydrouridine (DHU) simply forms a loop. The mitochondrial genome contains two non-coding regions, the 1098 bp control region and the 30 bp *O_L* region. The control region was flanked by genes tRNA-Pro and tRNA-Phe, the *O_L* region is located between tRNA-Asn and tRNA-Cys in a cluster of five tRNA genes (WANCY region).

The phylogenetic tree constructed by the Maximum Likelihood (ML) method using RAXML v7 (Stamatakis 2006) included mitochondrial genomes of 13 PCGs of 13 species in family Sciuridae and two sequences of Gliridae downloaded from GenBank, and *Ochotona curzoniae* was used to root the phylogenetic tree. The result shows that *D. pernyi* is a sister lineage to genus *Tamiops* (Figure 1). *D. pernyi*, *T. maritimus*, *T. swinhoei* and *Callosciurus erythraeus* form a well-supported lineage which belongs to tribe Callosciurini (Thorington & Hoffmann 2005).

Molecular studies show good resolution on phylogenetic analysis and species identification in *Dremomys* (Hawkins et al. 2016; Li et al. 2008). The complete mitochondrial genome of *D. pernyi* reported in this study firstly provides the complete

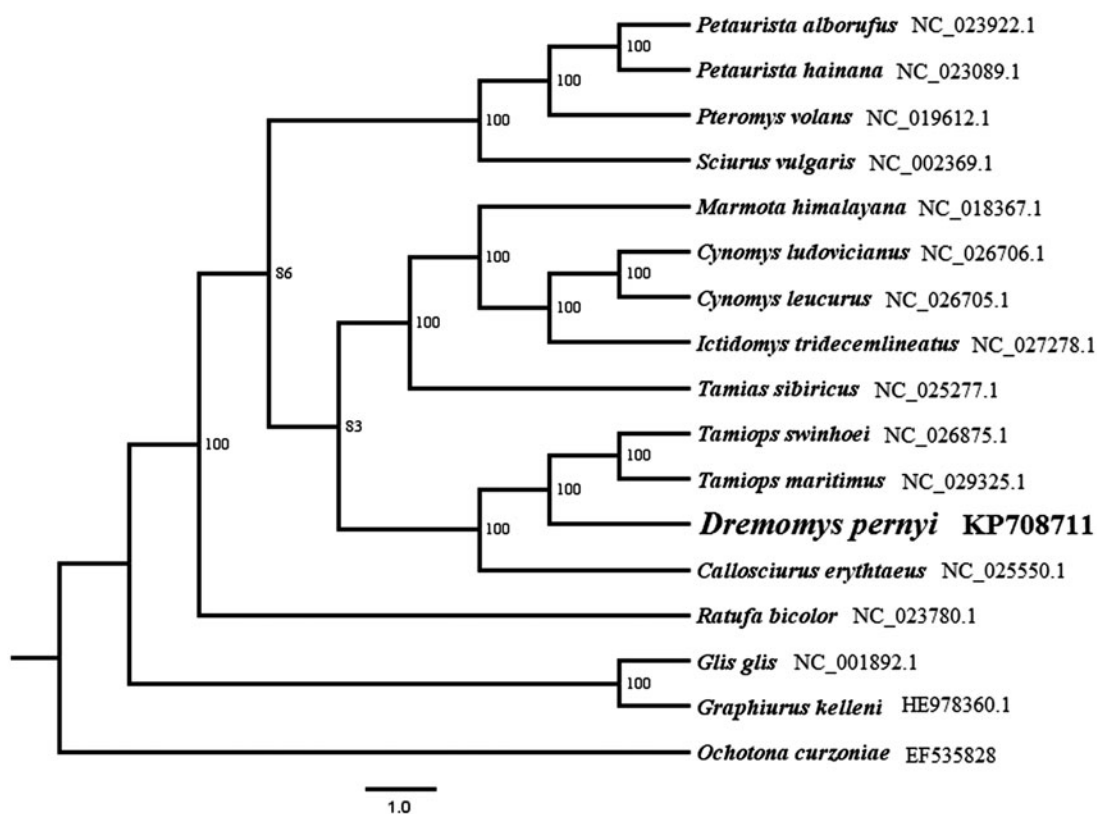


Figure 1. Maximum likelihood (ML) phylogenetic tree based on complete mitochondrial genome under GTR + G model. ML bootstrap values are shown above nodes.

mitochondrial genome of this genus, it will be useful for molecular studies regarding this species in the future.

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Disclosure statement

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