

The complete mitogenome of Smith's shrew (*Chodsigoa smithii*)

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ABSTRACT

The Smith's shrew (*Chodsigoa smithii*) belongs to subfamily Soricinae, which is an endemic shrew to China. In this study, we obtained the complete mitochondrial genome of the *C. smithii*. This mitogenome is a circular molecule with 17,108 bp in length, containing 13 protein-coding genes, 22 transfer RNA genes, two ribosome RNA genes, one light strand replication origin (OL), one non-coding region, and with a base composition of 32.5% A, 29.3% T, 24.8% C, and 13.4% G. The nucleotide sequence data of 13 protein-coding genes of *C. smithii* and other 19 Soricomorpha species were used for phylogenetic analyses. Phylogenetic tree shows that Soricinae includes two major phylogenetic lineages. *Chodsigoa smithii* is located as a basal position in tribe Nectogalini.

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Chodsigoa smithii belongs to subfamily Soricinae, and is an endemic shrew to China, named by Thomas (1911) based on a specimen from Kangding, Sichuan Province, China. It typically occurs in montane broad-leaved forests at elevations of 900–3000 m of Southwest China (Hoffmann and Lunde 2008; Chen et al. 2017). *Chodsigoa smithii* used to include *C. parca* as subspecies (Allen 1923). Subsequently, based on its smaller size and different shape of rostrum (Allen 1923; Hoffmann 1985), Hoffmann (1985) recognized *C. parca* as a distinct species. Due to continuous loss of habitats, this species was classified as Near Threatened on The IUCN Red List (www.iucnredlist.org). Here, we sequenced the whole mitogenome of *C. smithii* (17,108 bp; GenBank accession number: MN038168) and examined its phylogenetic position with other 19 Soricomorpha species.

The individual was captured in Mount Emei, Sichuan Province, China (Latitude: 29°32'38"N, Longitude: 103°20'0"E; H: 2360 m). The specimen was deposited at Sichuan Academy of Forestry (SNU00039). The mitogenome of *Episorculus macrurus* (NC_029840) was used to design primers for polymerase chain reaction (PCR) and used as template for gene annotation.

The whole mitogenome of *C. smithii* is 17,108 base pairs (bp), including 13 protein-coding genes, 22 transfer RNA genes (tRNA), two ribosome RNA genes (rRNA), one light strand replication origin (OL), and one non-coding region (D-Loop). The entire base composition is as follows: 32.5% A, 29.3% T, 13.4% G, and 24.8% C, with an A + T-rich pattern of the vertebrate mitochondrial genomes. The gene order and gene content of the mitogenome of *C. smithii* is identical to

that observed in most other Soricidae (Chen et al. 2015; Kim et al. 2017; Wang et al. 2018).

In order to explore the evolution of subfamily Soricinae, we used 13 protein-coding genes data of mitogenome in *C. smithii* and other 19 Soricomorpha species for the phylogenetic analysis, *Mogera wogura* and *Mogera robusta* were used as outgroups. We used BEASTv1.7 (Drummond et al. 2012) for Bayesian phylogenetic reconstructions, and the best-fit GTR + I + G model of DNA substitution was selected using Akaike Information Criterion (AIC) test in JModelTest 2 (Darriba et al. 2012). The phylogenetic tree is shown in Figure 1, which shows that Soricinae include two distinct phylogenetic lineages (BPP = 1.00). First lineage is containing six species from tribe Nectogalini and Anourosoricini. The second lineage is containing eight species from tribe Blarinellini and Soricini. *C. smithii* is located as a basal position in tribe Nectogalini.

We expect the study may be useful for phylogenetic and evolution studies of Soricinae, facilitate further investigation of the molecular evolution of genus *Chodsigoa*, and contribute to the conservation of this species.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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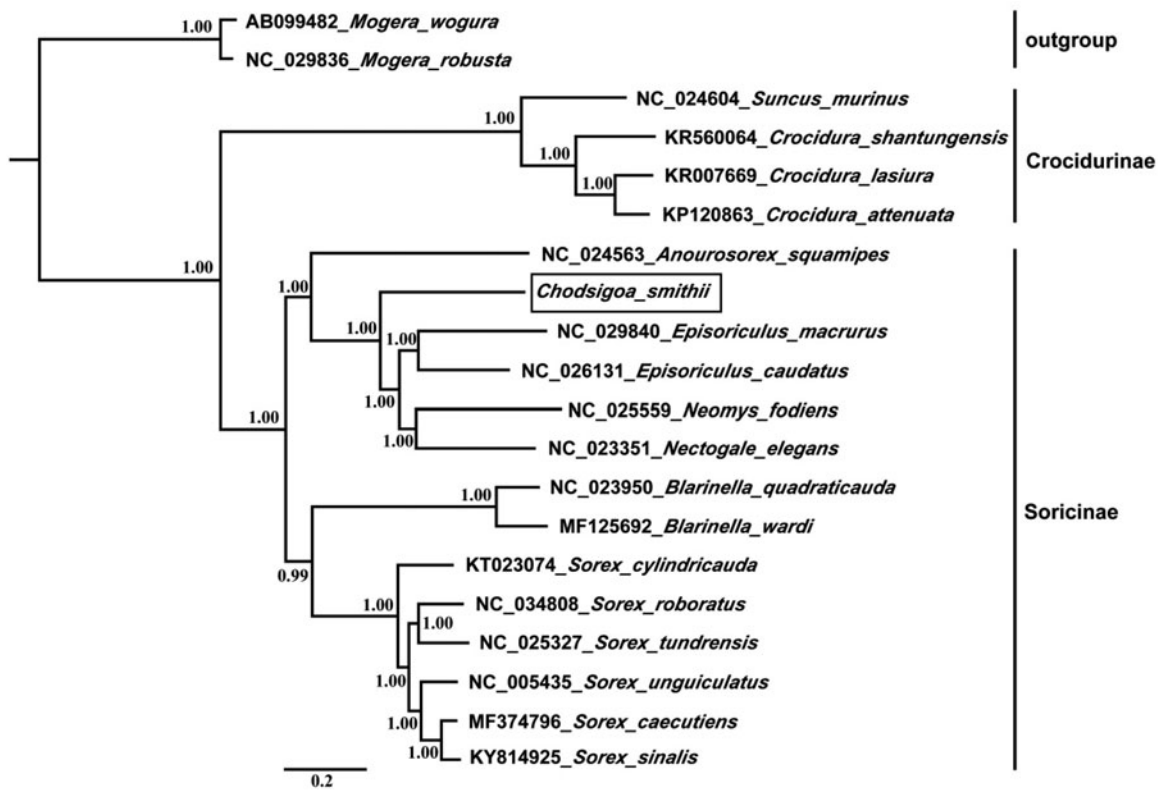


Figure 1. Phylogenetic tree derived from 13 protein-coding gene sequences using BI analysis. Numbers by the nodes indicate Bayesian posterior probabilities.

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