

MITOGENOME ANNOUNCEMENT

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Complete mitochondrial genome sequence of Arboreal Brown-toothed Shrew, *Episoriculus macrurus*

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ABSTRACT

The Arboreal Brown-toothed Shrew (*Episoriculus macrurus*) belongs to the family *Soricidae*, and distributes in China, Nepal, India, Myanma, and Vietnam. In this study, the complete mitochondrial genome sequence of *E. macrurus* was determined. The mitogenome is 16,943 bp in length. Phylogenetic trees were constructed by the methods of Bayesian inference and maximum likelihood. The results showed that in the family of *Soricidae*, *Crocidae* differentiated earlier than *Soricinae*. *Episoriculus* was more close to *Nectogale* or *Neomys* rather than *Sorex*, and *Blarinella* was close to *Sorex*. This study contributes to illuminating the taxonomic status of *E. macrurus*.

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The Arboreal Brown-toothed Shrew (*Episoriculus macrurus*) is a species in the genus *Episoriculus* of the subfamily *Soricinae*, family *Soricidae*. It mainly appears in China (provinces of Yunnan, Sichuan and Tibet), Nepal, India, Myanma and Vietnam (Smith et al. 2010; Chakraborty et al. 2013; Jiang et al. 2015). This species primarily inhabits temperate broad-leaved forests or scrubs at altitudes of 1500 ~ 3000 m asl and

feeds on invertebrates (Smith et al. 2010; Li et al. 2015). Currently, this species was evaluated and listed as Least Concern by IUCN (ver. 3.1), and its population trend is still unknown.

By now, the complete mitochondrial genome about *E. macrurus* has not been reported, with only partial gene fragments (*Cyt b*, *Rag 2* and *CDS*) data available (Ohdachi et al.

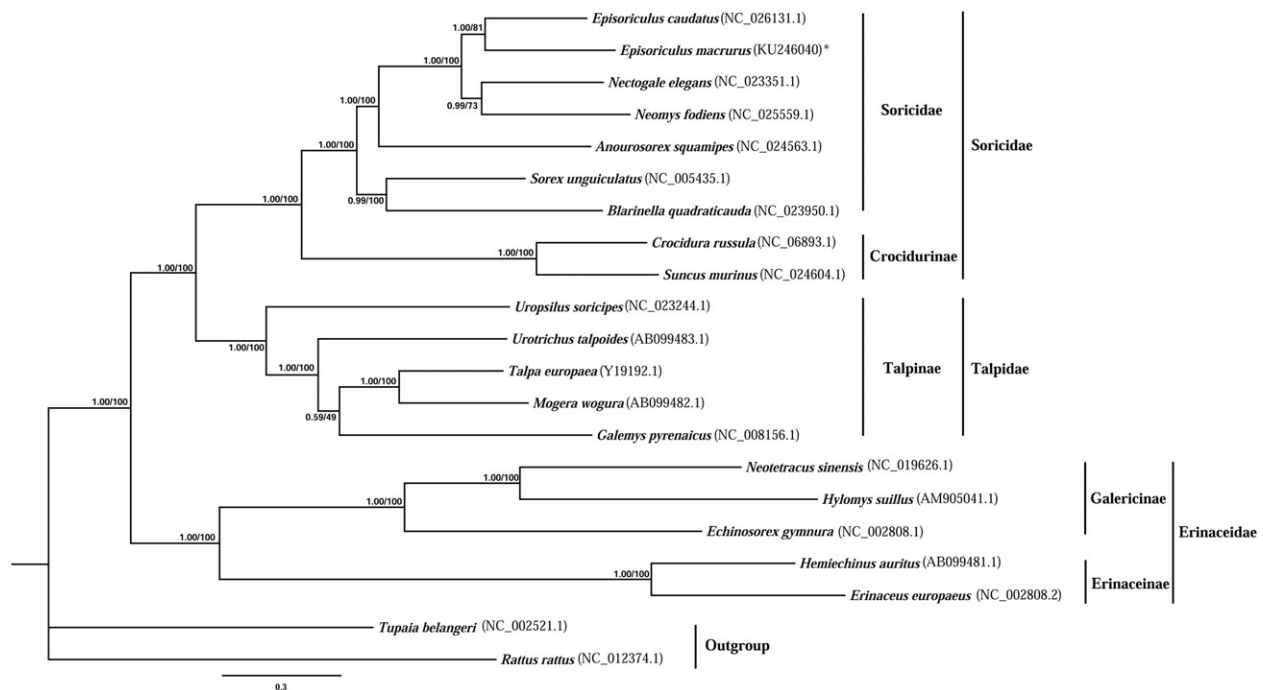


Figure 1. Bayesian 50% majority-rule consensus phylogenetic tree of *Episoriculus macrurus*. The numbers on the internode branches are Bayesian posterior probability and bootstrap percentages for the ML analysis.

2006; He et al. 2010). Here, we sequenced the complete mitochondrial genome and constructed the phylogenetic trees of *E. macrurus*. The specimen was collected in the Longxi–Hongkou National Nature Reserve, Dujiangyan County, Sichuan, China (latitude: 31.1435° N, longitude: 103.5799° E) and was stored in the Nature Museum of Sichuan University.

The complete mitochondrion of the *E. macrurus* was 16,943 bp in length (GenBank accession No. KU246040). Similar to other mitochondrial genomes of insectivores, the complete mitochondrial genome of *E. macrurus* contains 13 typical vertebrate protein-coding genes (PCGs), 22 tRNA genes, two rRNA genes and one control region. The whole base composition of the mitochondrial genome consisted of 33.3% A, 12.8% G, 30.6% T and 23.3% C, with A + T > G + C. The 12S rRNA and 16S rRNA were 960 bp and 1574 bp in length, respectively. The 22 tRNAs ranged from 59 bp (tRNA^{lys}) to 107 bp (tRNA^{ser} and tRNA^{lys}) in length, and was distributed through the whole mitochondrial genome. Among the 13 PCGs, ND5 was the longest (1821 bp in length) and ATP8 was the shortest (205 bp in length). The D-loop region was 1484 bp in length and was found between tRNA^{pro} and tRNA^{phe}.

Twenty-one complete mitochondrial genome sequences were used to construct phylogenetic trees based on the concatenated 13 PCGs. *Rattus rattus* and *Tupaia belangeri* were chosen as outgroups. Based on the previous studies (Tu et al. 2012; Zeng et al. 2013; Yan et al. 2014), Bayesian inference (BI) and maximum-likelihood (ML) frameworks were used to examine the phylogenetic position of *E. macrurus*. Both ML and BI analyses generated similar trees (Figure 1). Our results showed that in the family of *Soricidae*, *Crocidurinae* differentiated earlier than *Soricinae*, which was also supported by He et al. (2012) and Huang et al. (2014). *Episoriculus* was more close to *Nectogale* or *Neomys* rather than *Sorex*, and *Blarinella* was close to *Sorex*. Moreover, *E. macrurus* and *E. caudatus* may have close phylogenetic relationship. These two species are sympatric and inhabit similar habitats (Smith et al. 2010). This study contributes to illuminating the taxonomic status of *E. macrurus* at the molecular level and essential resource for further research on this species. Further studies are still needed to better understand the phylogenetic relationships within the genus of *Episoriculus*.

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Disclosure statement

The authors declare no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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