The complete mitochondrial genome of short-faced mole (Scaptochirus moschatus, Talpidae)

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Abstract

The short-faced mole (Scaptochirus moschatus) is a unique Chinese mammal that lives in burrows for life. In this study, we used Illumina NovaSeq sequencing to obtain the complete mitochondrial genome of the short-faced mole. The total length of the genome is 16,699 bp, containing 13 protein-coding genes, 22 transfer RNA genes (tRNA), 2 ribosomal RNA genes (rRNA), and 1 control region, with a base composition of 33.82% A, 26.89% T, 25.27% C, and 14.01% G. Phylogenetic analysis of the Talpidae by using complete mitochondrial genome sequences of 14 Talpidae species shows that short-faced mole is closely related to Parascaptor leucura.

Keywords
short-faced mole; mitochondrial genome; Talpidae; phylogenetic analysis

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In order to explore the evolutionary status of the short-faced mole, we used the complete mitochondrial genome sequences of short-faced mole and 13 other species of the Talpidae for phylogenetic analysis. *Erinaceus amurensis* (KX964606.1) was used as the outgroup (Tsuchiya et al. 2000). MEGA X software is used to construct a phylogenetic tree under Tamura–Nei and maximum-likelihood model with 1000 bootstrap replication (Kumar et al. 2018) (Figure 1). The result shows that short-faced mole is closely related to *Parascaptor leucura*, which is similar to the previous studies (He et al. 2017; Xie et al. 2021).

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**Data availability statement**

The genome sequence data that support the findings of this study is openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under the accession number MZ594566.1. The associated BioProject, SRA, and BioSample numbers are PRJNA769832, SRR16494732 and SAMN22419676, respectively.

**References**

Bernt M, Donath A, Juhling F, Externbrink F, Florentz C, Fritzsch G, Putz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69 (2):313–319.

Chen L, Xu D, Zhu J, Wang S, Liu M, Sun MY, Wang GY, Song LY, Liu XY, Xie TY. 2021. Habitat environmental factors influence intestinal microbial diversity of the short-faced moles (*Scaptochirus moschatus*). AMB Express. 11(1):93.

Chen Z, He K, Huang C, Tao W, Lin L, Liu S, Jiang X. 2017. Integrative systematic analyses of the genus Chodsigoa (Mammalia: Eulipotyphla: Soricidae), with descriptions of new species. Zool J Linn Soc. 180(3):1–20.

Gutiérrez J, Lamelas L, Aleix-Mata G, Arroyo M, Marchal JA, Palomeque T, Lorite P, Sánchez A. 2018. Complete mitochondrial genome of the Iberian mole *Talpa occidentalis* (*Talpidae, Insectivora*) and comparison with *Talpa europaea*. Genetica. 146(4-5):415–423.

He K, Shinohara A, Helgen KM, Springer MS, Jiang X, Campbell KL. 2017. Talpid mole phylogeny unites shrew moles and illuminates overlooked cryptic species diversity. Mol Biol Evol. 34 (1):78–87.

He K, Shinohara A, Jiang X, Campbell KL. 2014. Multilocus phylogeny of Talpine moles (*Talpini, Talpidae, Eulipotyphla*) and its implications for systematics. Mol Phylogenet Evol. 70:513–521.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. Mol Biol Evol. 35 (6):1547–1549.

Sansalone G, Colangelo P, Loy A, Raia P, Wroe S, Piras P. 2019. Impact of transition to a subterranean lifestyle on morphological disparity and integration in talpid moles (*Mammalia, Talpidae*). BMC Evol Biol. 19(1):179.

Smith AT, Johnston CH. 2016. *Scaptochirus moschatus* (errata version published in 2017). The IUCN Red List of Threatened Species 2016: e.T41476A115188844.

Tsuchiya K, Suzuki H, Shinohara A, Harada M, Wakana S, Sakaizumi M, Han SH, Lin K, Kryukov AP. 2000. Molecular phylogeny of East Asian moles inferred from the sequence variation of the mitochondrial cytochrome b gene. Genes Genet Syst. 75(1):17–24.

Xie F, Chen D, Qin B, Fu C, Chen S. 2021. The complete mitochondrial genome of white-tailed mole (*Parascaptor leucura*). Mitochondrial DNA B Resour. 6(3):1112–1113.

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**Figure 1.** Maximum-Likehood (ML) phylogenetic analysis based on the complete mitochondrial genome sequences of short-faced mole and 13 other species of the Talpidae. The node numbers represent supported value of the ML bootstraps.