Phylogenetic relationships of the short-faced mole, *Scaptochirus moschatus* (Mammalia: Eulipotyphla), among Eurasian fossorial moles, as inferred from mitochondrial and nuclear gene sequences

Akio Shinohara¹,*, Shin-ichiro Kawada², Masashi Harada³, Kazuhiro Koyasu⁴, Sen-ichi Oda⁵ and Hitoshi Suzuki⁶

¹ Department of Bio-resources, Division of Biotechnology, Frontier Science Research Center, University of Miyazaki, Kiyotake, Miyazaki 889-1692, Japan
² Department of Zoology, National Museum of Nature and Science, Tokyo 1609-0073, Japan
³ Laboratory Animal Center, Graduate School of Medicine, Osaka City University, Osaka 545-8585, Japan
⁴ The Second Department of Anatomy, School of Dentistry, Aichi-Gakuin University, Nagoya 464-8650, Japan
⁵ Laboratory of Animal Management and Resources, Graduate School of Bio-Agricultural Sciences, Nagoya University, Nagoya 464-8601, Japan
⁶ Laboratory of Ecology and Genetics, Graduate School of Environmental Earth Science, Hokkaido University, Sapporo, Hokkaido 060-0810, Japan

The East Asian region is rich in species of the family Talpidae, represented by moles, shrew-moles, and shrew-like moles. The ecological, genetic, and morphological diversity of these species provides valuable information on the historical background of talpid evolution in this area. To date, we have performed molecular phylogenetic analyses of Eurasian moles of the modern mole lineage that are distributed in the lowland areas of East Asia (*Mogera*) and Europe (*Talpa*), as well as an East Asian primitive lineage distributed fragmentarily in highland regions (*Euroscaptor*) (Tsuchiya et al. 2000; Shinohara et al. 2004a, 2004b, 2005). However, these molecular studies have not covered all the genera, so that the full details of the evolution of the family Talpidae are still unclear (Shinohara et al. 2005). In particular, East and Southeast Asian fossorial moles of the genera *Scaptochirus* and *Parascaptor*, both of which are distributed in China, are unanalyzed taxa represented by little known species, so that these species do offer the prospect of providing further insights into the evolution of the talpids.

The short-faced mole, *Scaptochirus moschatus* (Eulipotyphla, Talpidae), is endemic to China; its genus is among those that hold unclear phylogenetic positions. This mole is thought to be marginally adapted to dry range areas (Allen 1938), but other details, including its ecological traits, life cycle, habits, and phylogenetic status, are still unknown. In contrast to this paucity of ecological information, we do know that this species has specific morphological and karyotypic characteristics. The dental formula of *S. moschatus* (I 3/3 + C 1/1 + P 3/3 + M 3/3 = 40) is unique among the lineage of moles of the Eurasian continent, that is, *Talpa*, *Mogera*, *Euroscaptor*, and *Parascaptor* (Allen 1938; Abe 1991; Table 1). In addition, *S. moschatus* has the largest diploid number of chromosomes (*2n* = 48: Kawada et al. 2002); other mole genera have a restricted range of chromosome numbers (*2n* = 32 to 38; Table 1, summarized in Kawada et al. 2002). Therefore, *S. moschatus* has been classified as a monospecific genus (Hutterer 2005), and there has been much interest in its phylogenetic positions to the talpids. We therefore determined the gene sequences of mitochondrial cytochrome *b* (*cyt* *b*: 1140 bp), 12S rRNA (12S: about 800 bp) and nuclear recombination activating gene-1 (*RAG1*: 1010 bp) in this species and executed molecular phylogenetic analyses to elucidate the phylogenetic relationships among *S. moschatus* and Eurasian fossorial moles.

Materials and methods

The animal was collected from western Jilin, China (44°35′N, 123°30′E) in July 1991 and identified on the basis of morphology of the skull data provided by Abe et

*To whom correspondence should be addressed. E-mail: akioshi@med.miyazaki-u.ac.jp