



Molecular phylogeny of long-tailed shrews (genus *Sorex*) from México and Guatemala

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Abstract

We present a molecular phylogeny of North American species of long-tailed shrews of the genus *Sorex*. Our focus is on Mexican and Guatemalan species to begin understanding their evolutionary relationships and to test the validity of nominal species. Seventy-seven sequences of the mitochondrial cytochrome *b* gene were analyzed, including 19 specimens representing nine Mexican and one Guatemalan species. Phylogenetic analyses using parsimony, maximum likelihood and Bayesian approaches revealed two major clades of North American species, all within the subgenus *Otisorex*. The first major clade includes *S. trowbridgii* and southern species (*S. macrodon* from Oaxaca; *S. veraecrucis* from Nuevo León, Michoacán, Chiapas, *S. saussurei* from Jalisco and Guatemala; *S. veraepacis* from Guerrero and Guatemala). Relatively deep branches among taxa characterize this clade and suggest that their early divergence from other North American shrews was soon after arrival of the ancestral stock from the Beringian region. The other major clade includes all other North American species of *Sorex* we examined, with two Mexican species, *S. milleri* and *S. emarginatus*, grouped in a subclade with the *S. cinereus* complex. *Sorex veraecrucis* is not, however, a monophyletic taxon because specimens of this nominal species were included in both the major clades. The Isthmus of Tehuantepec has likely played a role as a biogeographic barrier in the evolutionary history of Mexican shrews. This study of mitochondrial variation in southern North American shrews of the genus *Sorex* indicates there is substantial, previously undetected diversity that necessitates a revision of the taxonomy of *S. veraecrucis* and *S. veraepacis*.

Key words: biogeography, mammals, mitochondrial DNA, Soricidae, systematics

Introduction

Approximately 77 species of shrews in the genus *Sorex* (Soricomorpha, Soricidae) are currently recognized (Hutterer 2005). These diminutive species are often among the most abundant members of terrestrial mammalian communities in the boreal and mountainous regions of Europe, Asia, and North America. Phylogenetic relationships among some species have been studied using cranial, dental and other morphological characters (Junge & Hoffmann 1981; Carraway 1990), allozymes (George 1988), and molecular sequence data (Fumagalli *et al.* 1999; Ohdachi *et al.* 2006; Dubey *et al.* 2007). A comprehensive assessment that includes all species will be difficult to complete due to limited availability of specimens for many species within this widely distributed group. Nevertheless, new species are described regularly (e.g., Dokuchaev 1997; Rausch *et al.* 2007; Nagorsen & Panter 2009) as more detailed assessments of geographic variation are completed.

The ancestral lineages of *Sorex* are hypothesized to have arisen in Eurasia (Repenning 1967; Storch *et al.* 1998) and then split between 7.0–18.4 million years ago (mya) into two principal lineages that are recognized as: a) subgenus *Sorex* (most Palearctic species plus Holarctic *S. tundrensis* Merriam 1900 and Nearctic *S. arcticus* Kerr 1792, *S. maritimensis* Smith 1939, and *S. yukonicus* Dokuchaev 1997) and b) subgenus *Otisorex* (chiefly Nearctic or Beringian taxa, Hutterer 2005; and possibly including *S. trowbridgii* Baird 1857,