



Mitochondrial diversity of the white-toothed shrews (Mammalia, Eulipotyphla, *Crocidura*) in Vietnam

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Abstract

We explored the patterning of genetic diversity within white-toothed shrews of the genus *Crocidura* from 14 localities across Vietnam. An analysis of cytochrome oxidase *c* subunit I (COI) and cytochrome *b* (*cytb*) gene fragments from 185 specimens of white-toothed shrews of the genus *Crocidura* from 14 localities across Vietnam revealed six deeply divergent (p-distance for both COI and *cytb* >10%) lineages, corresponding to the morphological species *C. sokolovi*, *C. zaitsevi*, *C. phuquocensis*, *C. indochinensis*, *C. tanakae* and, *C. phanluongi*. *Crocidura sokolovi* was distinct from all other Vietnamese white-toothed shrews (~13% on average for both *cytb* and COI). In addition to demonstrating the genetic separation of previously described species, substantial cryptic genetic diversity was revealed. *Crocidura zaitsevi* and *C. tanakae* each included two subgroups that corresponded to geographically remote localities, while *C. indochinensis* contained two distinct subgroups that exhibited co-varying patterns of morphological and ecological differentiation, suggesting that the individuals from Sa Pa represent a separate species (provisionally named *Crocidura* sp. AB1). Mitochondrial data generated for the type specimens of *C. phanluongi* from Yok Don and Bu Gia Map supported the validity of the species while an additional specimen from Binh Chau, South Vietnam originally referred to *C. phanluongi* exhibited a deep genetic split (*cytb*: 8.4%; COI: 8.7%) from a neighbouring population in Yok Don. We propose that the specimen from Binh Chau also represents an undescribed species (provisionally named *Crocidura* sp. AB2). Our *cytb* data were then compared to the sequences of 28 species of *Crocidura* from Southeast Asia available in GenBank, suggesting that three more species occur in northern Vietnam, namely *C. wuchihensis*, *C. attenuata* and *C. fuliginosa/C. dracula*. The discovery of fairly deep genetic divergences among Vietnamese *Crocidura* illustrates that the understudied and largely undescribed diversity of white-toothed shrews in Southeast Asia requires deeper scrutiny. It also shows the useful insights of mitochondrial markers as to the taxonomic resolution of this enigmatic group of mammals.

Key words: DNA barcodes, molecular biodiversity, Soricidae, Southeast Asia, molecular diagnostics, cryptic species

Introduction

The white-toothed shrews (*Crocidura*) have a broad distribution across the Old World tropics and are one of the most speciose genera of mammals (Hutterer 2005). Despite their remarkable alpha-taxonomic diversity, these shrews are morphologically rather uniform, which contributes to their extreme taxonomic complexity. The evolutionary relationships of the species within this genus are the subject of serious debate. Most studies involving protein, chromosomal, and recent molecular data suggest the evolutionary division of *Crocidura* into Afrotropical and Asian lineages (Maddalena 1990; Maddalena & Ruedi 1994; Ruedi 1998; Bannikova *et al.* 2006; Dubey *et al.* 2008; Lavrenchenko *et al.* 2009); however, the monophyly of these clades is still insufficiently supported. Yet both karyological and molecular data strongly suggest that East Asian *Crocidura* comprise a mixture of southern and