



An assessment of morphometric and molecular variation in *Monodelphis dimidiata* (Wagner, 1847) (Didelphimorphia: Didelphidae)

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Abstract

This study aims to clarify the taxonomic status of *Monodelphis dimidiata* and *M. sorex*, using molecular and morphometric data. Cytochrome-*b* sequences were obtained from specimens morphologically assignable to those taxa from the vicinity of type localities, but also representing their presumptive area of sympatry and extremes in their known distributions. These sequences were compared to GenBank downloaded sequences of select *Monodelphis* spp. and also of *Marmosa lepida*, *Micoureus demerarae*, and *Didelphis albiventris*, used as outgroups. Genetic distances and maximum likelihood analyses were performed to recover phylogenetic affinities among taxa. To assess morphometric variation, univariate and multivariate statistical methods (Principal Component Analysis and Canonical Variate Analysis) were applied to the covariance matrix of 25 craniometric measurements obtained from a total of 108 specimens sampled across the geographic ranges of the species. The molecular analyses revealed a clade composed by haplotypes assignable to *Monodelphis dimidiata* and *M. sorex* (*sensu* Pine and Handley 2007) as distinct from the remaining *Monodelphis* species sampled to date, with 100% bootstrap support. Within this clade, one haplotype from Itatiaia was the sister clade to the remaining 11 specimens from Montevideo (Uruguay), Rio Grande do Sul and Santa Catarina states (Brazil), which formed an assemblage without clear geographic arrangement. In the morphometric analyses, the first two principal components of morphometric data separated variables associated with general latent size comparably expressed in all samples, and a group of variables including molars widths, molar tooththrow length, and postorbital constriction breadth, which separates the geographic samples in a sequence coincident, to a large extent, with their latitudinal distributions. The sample from Itatiaia, Rio de Janeiro State, was again revealed as clearly distinct from the remaining samples, suggesting that it may represent a peripheral isolated population. With the study of original descriptions and published information on the type material of *M. sorex*, including photographs of syntypes, our analyses point to the recognition of *M. sorex* as a subjective junior synonym of *M. dimidiata*, which is then regarded as a widespread taxon ranging from the latitudes of southern Buenos Aires Province and Córdoba in Argentina to at least Minas Gerais State in southeastern Brazil, through the Pampas and the Atlantic Forest domains.

Key words: geographic variation, molecular systematics, multivariate statistics, cranial morphometrics, taxonomy, *Monodelphis sorex*, *Monodelphis henseli*, *Monodelphis dimidiata itatiae*, *Monodelphis brevicaudis*, *Monodelphis tricolor paulensis*, semelparity

Introduction

The genus *Monodelphis* (Burnett 1830) is the most diverse among South American marsupials, comprising at least 22 recognized species (Gardner 2005, Pine & Handley 2008, Voss & Jansa 2009). A major endemic zone for this New World genus is the Atlantic Forest, which includes more than half of the species in *Monodelphis*. Historically, this diversity has been tentatively sorted among different genera, subgenera, or species groups based on pelage color and patterns (Thomas 1888a, Cabrera 1919, Gilmore 1941, Gomes 1991). Original descriptions have been primarily based on size and pelage colors and patterns, and a number of different