

Taxonomic status of *Brucepattersonius albinasus* (Rodentia: Sigmodontinae)

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Abstract

Molecular (cytochrome *b*) comparisons between topotypical specimens of *Brucepattersonius griserufescens* and the holotype of *B. albinasus*, both described from the same locality in southeastern Brazil, reveal a very low estimate of genetic distance, equivalent to those obtained in comparisons between haplotypes of *B. griserufescens*. Only six variable sites, five transitions and one transversion, were found among the 1040 bp of all haplotypes. These findings, together with a re-evaluation of the morphological characters on which the distinction between the two nominal forms was based, indicate that only one evolutionary lineage is represented, which must bear the name *B. griserufescens*, with *B. albinasus* as a junior synonym.

Key words: *Brucepattersonius*, molecular phylogeny, cyt-*b*, morphology, taxonomy, systematics

Introduction

The genus *Brucepattersonius* was described by Hershkovitz (1998) as a member of the tribe Akodontini, to include *B. iheringi* (Thomas 1896) and four new species then described from other Brazilian localities: *B. sorcinus* (type species), *B. igniventris*, *B. griserufescens* and *B. albinasus*. Subsequently, Mares and Braun (2000) described *B. paradisius*, *B. misionensis* and *B. guarani* from the province of Misiones, Argentina. The genus *Brucepattersonius* has a restricted distribution in the Atlantic Forest, with its northern limit in the State of Espírito Santo, Brazil, its southern limit in the State of Rio Grande do Sul, Brazil, and its western limit in the province of Misiones, Argentina.