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Molecular phylogenetic position of endangered *Wilfredomys* within Sigmodontinae (Cricetidae) based on mitochondrial and nuclear DNA sequences and comments on Wiedomyini

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Abstract

Wilfredomys, a monotypic genus of endangered sigmodontine rats, was historically related to the tribe Thomasomyini or considered “incertae sedis”. Given no molecular data is available for *Wilfredomys*, the phylogenetic position of this taxon is uncertain in relation to modern, molecular hypotheses of sigmodontine relationships. We investigate the phylogeny of *Wilfredomys* to provide a hypothesis of its position within Sigmodontinae based on nuclear and mitochondrial DNA sequences. Bayesian and maximum likelihood phylogenetic analyses recovered *Wilfredomys oenax* as sister to *Wiedomys pyrrhorhinos*, and *Wie. cerradensis* fell out sister to this clade. At the genus level, *Phaenomys* is sister to *Wilfredomys* + *Wiedomys*, forming a novel and well-supported sigmodontine clade. Our results suggest that tribe Wiedomyini should encompass *Wilfredomys* in addition to *Wiedomys* and *Cholomys*, thus the hypothesis that *Wiedomys* is paraphyletic should be investigated further. Another plausible classification scheme consistent with our results would be to expand Wiedomyini to encompass the clade composed of *Phaenomys* + *Wilfredomys* + *Wiedomys*. Last, our recovery of an “Atlantic clade” composed of lineages restricted to eastern South America supports the idea that this region has likely played an important role in sigmodontine diversification.

Key words: phylogeny, new clade, South America, Sigmodontinae, cytochrome *b* gene (*cyt-b*), Interphotoreceptor Retinoid-Binding Protein gene (IRBP)

Introduction

Subfamily Sigmodontinae is a highly diverse lineage of New World rodents found within the family Cricetidae (Musser & Carleton 2005). Recent estimates suggest Sigmodontinae is composed of around 400 living species distributed from southern North America to southern South America (Patterson & Costa 2012). Sigmodontine rat species are found in nearly all biomes of the Neotropics, ranging from sea level to the top of the Andes mountains, and display numerous morphological variants and adaptations (Musser & Carleton 2005). The morphological complexity of this subfamily has historically led to a plethora of classification schemes at supra-generic taxonomic levels (e.g. Hershkovitz 1966; Carleton 1973; Reig 1980; Stepan 1995; Smith & Patton 1999), as well as the levels of relationships within tribes (e.g. Weksler 2003, 2006) and genera (e.g. Voss 1993).

Groups of related sigmodontine genera have traditionally been classified into tribes (Vorontsov 1959; Reig