

PHYLOGENETIC AND BIOGEOGRAPHIC RELATIONSHIPS OF *AKODON* (RODENTIA, MURIDAE)

KEYWORDS: *Akodon*, South America, Systematics, Biogeography, *cyt-b*, IRBP, DMP1.

The genus *Akodon* (Rodentia, Muridae) is among the most speciose groups of rodents in South America where its 63 extant named forms occur from northern Venezuela to southern Argentina (Fig. 1). The genus stands “at the nexus of a host of specific- and generic-level taxonomic problems,”¹ as its species limits have remained unstable and ambiguous with a number of revisions increasing or decreasing the number of recognized species, subspecies, and supraspecific groups as taxonomists, systematists, and ecologists tease apart the morphotypical genus.

Despite this taxonomic diversity, only 30 taxa have been used in molecular studies represented by 43 individuals for the complete cytochrome-*b* (*cyt-b*) gene and 12 individuals for the interphotoreceptor binding protein gene (IRBP) of the nuclear genome^{2,3}. These studies concluded species of *Akodon* (*sensu stricto*) form a strongly supported monophyletic clade with four commonly recovered species groups (*aerosus* group, *boliviensis* group, *cursor* group, and *varius* group) along with a number of ambiguous lineages^{2,3}. The four groups can be separated based on geographic distributions, but levels of support and phylogenetic resolution vary greatly among studies.

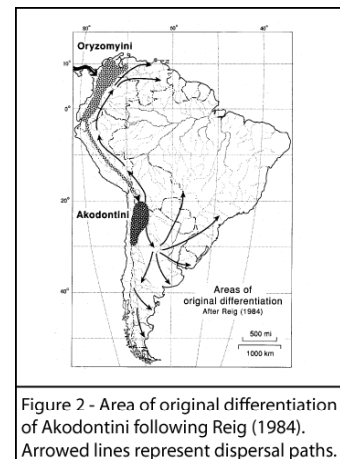
Thorough taxonomic, geographic, and gene sampling is required to provide greater resolution of the phylogenetic relationships within the genus and to clarify the systematics, taxonomy, and biogeography. By resolving interspecific relationships of *Akodon*, major steps can be made in understanding the diversity of forms at higher taxonomic levels.

AKODONTINE BIOGEOGRAPHY – A solid understanding of the historical biogeography of the genus *Akodon* will enhance current knowledge of the diversity of extant forms. Although proposed nearly 20 years ago, the most commonly cited biogeographic hypothesis involving the genus *Akodon* is Reig’s scenario⁴ for the sigmodontine colonization of South America (Fig. 2). Recently, it was found that this hypothesis needs revision regarding the locations and timings of differentiations⁵. A few recent studies³ have attempted, with limited success, to evaluate Reig’s scenario. Based on these studies, preliminary conclusions included sister taxa speciations being allopatric and the possibility that diversifications took place across ecological gradients. It was clear to these authors that a more resolved phylogeny is necessary to assess adequately Reig’s scenario.

HYPOTHESES – To assess intraspecific relationships within *Akodon*, null and alternative systematic and biogeographic hypotheses will be considered regarding the monophyly and current distributions of taxa at all levels, with the primary null hypotheses being:

H₀Systematic: All species of *Akodon* are monophyletic.

H₀Biogeographic: All current *Akodon* species distributions are due to vicariant events.



¹D.E. Wilson and D.M. Reeder. 1993. *Mammal Species of the World*. ²M.F. Smith and J.L. Patton. 1999. *J. Mamm. Evol.* 6:89-128. ³G. D’Elia. *Clad.* 19:307-323 (2003). ⁴O.A. Reig. 1986. Pp. 404-440 in *High altitude tropical biogeography* (F. Vuilleumier and M. Monasterio, eds.).

STATEMENT OF OBJECTIVES – With the lack of resolution in current *Akodon* phylogenies, it is difficult to verify or falsify previously hypothesized biogeographical and evolutionary scenarios. Therefore, the ultimate purpose of this study is to obtain a well-resolved phylogeny for the genus *Akodon* (*sensu stricto*) based upon the mitochondrial *cyt-b* gene and the nuclear IRBP and dentin matrix protein (DMP1) genes. This study also will address the following secondary objectives.

- Evaluate the status of the supraspecific taxa *Chalcomys*, *Hypsimys*, and *Microxus*.
- Investigate the validity of informal groups (e.g. *aerosus* group, *cursor* group, *varius* group).
- Examine the historical biogeography of *Akodon* using phylogenetic results and determine their correspondence to historical changes in climate, geology, and vegetation.

METHODS – Previous studies have attempted to explain *Akodon* diversity and made conclusions based on partially unresolved trees. Because sampling imposed many of the limitations on these conclusions, dense geographic and taxonomic sampling will be key to the elucidation of the phylogenetic and biogeographic relationships. Sixty-three named species and subspecies and three unnamed species of *Akodon*, along with 36 taxa outside of *Akodon*, have been identified for inclusion in this study. For each species of *Akodon*, tissues from 5-10 individuals will be selected to maximize geographic and morphologic diversity. Each individual will be amplified and sequenced for *cyt-b*, IRBP, and exon 6 of DMP1. For taxa that occur outside of *Akodon*, a single individual will be sequenced for all three genes. The three genes represent two independent genomes and were chosen based on their observed and expected utility at the taxonomic levels of interest in this study^{2,3,6}. Although each gene has inherent limitations when answering systematic questions, the combination of the three independent genes should provide a more complete phylogeny for the genus *Akodon* than each gene can independently.

Upon completion of sequencing, each gene data set will be aligned and analyzed using maximum parsimony, minimum evolution, maximum likelihood, Bayesian, and DIVA analyses to assess the phylogenetic and biogeographic relationships between and among the species of *Akodon* based on each gene dataset separately and on the concatenated dataset.

EXPECTED RESULTS AND SIGNIFICANCE – This research marks the first large-scale, sample-rich study of the genus *Akodon*. The expected results are a well-resolved phylogeny of the genus *Akodon*, which will clarify species distinctness, species validity, and the phylogenetic validity of informal supraspecific groupings. Because approximately 1/16th of all mammalian species occurring in South America are assigned to the genus *Akodon*, a well-resolved phylogeny for *Akodon* will assist in understanding the diversity, evolution, and historical biogeography of extant South American rodents.

Species of *Akodon* are known reservoirs of Hanta and Junín viruses and hosts to a variety of ectoparasites implicated in human diseases^{7,8}. By understanding the systematics, biogeography, and evolution of the genus *Akodon*, an understanding of the spread and evolution of its pathogens can be obtained and future outbreaks of such pathogens can be predicted, treated and controlled more efficiently and even perhaps be completely prevented.

STATEMENT OF ORIGINALITY – This work has not previously been submitted for a degree or diploma at any university. To the best of my knowledge, this proposal contains no material previously published or written by another person except where due reference is made in the proposal itself.

⁵U.F.J. Pardiñas, G. D'Elia, and P.E. Ortiz. 2002. *Mast. Neotrop.* 9:209-252. ⁶Jansa, S. A. J. F. Forsman, and R. S. Voss. Submitted. *Mol. Phylog. Evol.* ⁷S. Levis et al. 1998. *J. Inf. Dis.* 177:529-538. ⁸J.N. Mills et al. 1991. *Amer. J. Trop. Med. Hyg.* 44:589-597.