Copyright © 2008 · Magnolia Press



Akodon cursor Winge, 1887 (Rodentia: Sigmodontinae): one or two species? New evidences based on molecular data

CRISTINA D. A. NOGUEIRA & VALÉRIA FAGUNDES¹

Departamento de Ciências Biológicas, Centro de Ciências Humanas e Naturais, Universidade Federal do Espírito Santo, Av. Marechal Campos 1468, Maruípe, 29.043-900, Vitória, ES, Brazil ¹Corresponding author: vfagunde@npd.ufes.br or vfagunde@cnpq.br

Abstract

Akodon cursor Winge, 1887 (Rodentia, Muridae) occurs in dense rainforest in the Atlantic coast of Brazil, from northern (8°S, Pernambuco and Paraíba) to southern (23-26°S, São Paulo and Paraná) states. This species reveals high karyotype variability, ranging from 2n=16 to 14, and FN (number of autosomal arms) from 26 to 18. Previous cytogenetics studies suggested that each form (2n=14, 15 and 16) are distributed in a clinal pattern and represent polymorphisms in populations, with 2n=15 as an intermediate status (data from crossbreeding in laboratory). However, previous molecular analysis from literature revealed two reciprocal monophyletic clades, each of them composed by 2n=14-15 or 2n=16, suggesting the distinction of A. cursor (2n=14 and 15) from A. aff. cursor (2n=16). In this paper, we verified if the karyotype is the one-step characteristic to separate A. cursor and A. aff. cursor. We evaluated the divergence among northern and southern populations which accomplish 2n=14, 15 and 16 specimens in simpatry. Thus, we employed karyotype information and restriction fragment length polymorphisms analysis (PCR-RFLP) of mitochondrial gene cytochrome b in specimens with 2n=14, 15 and 16 from both northern and southern areas of occurrence. We observed two major clades $(\Phi_{sT}>0.72)$, one including northern and the other southern populations, and all three karyotypes were clustered on both of them, revealing that the distinction of the populations are based on geographical level and not on karyotype structure. Previous contrasting molecular data were interpreted as a biased sample composition, since those samples included exclusively 2n=14 and 15 from southern and 2n=16 from northern populations. Thus, we proposed that 2n=14, 15 and 16 karyotypes belong to a single species, Akodon cursor.

Key words: Akodon, Rodentia, population divergence, genetic variability, cytochrome b, RFLP, Atlantic Forest

Introduction

Akodontini Vorontsov, 1959 comprise the second most diverse tribe in Muridae family in the Neotropics, with 19 genera and 109 described species. Within Akodontini, *Akodon* Meyen, 1833 is widespread throughout South America and is one of the most specious akodont genera among subfamily Sigmodontinae, represented by 41 described species (Musser & Carleton 2005).

Akodon cursor Winge, 1887 occurs in the dense rainforest in the Atlantic coast of Brazil, from northernmost states (Paraíba, Pernambuco) throughout Bahia, Espírito Santo, Rio de Janeiro, São Paulo, Minas Gerais until northern of Paraná state (Yonenaga-Yassuda 1979; Maia & Langguth 1981; Liaschovich & Reig 1989; Rieger et al. 1995; Sbalqueiro & Nascimento 1996; Fagundes et al. 1998; Geise et al. 2001). This species presents high karyotype variability, ranging from 2n=16 to 14, and FN (number of autosomal arms) from 26 to 18 (Fagundes et al. 1998). The differences in the diploid number are caused by a complex mechanism involving pericentric inversions and centric fusion of pairs 1 and 3, resulting in a large pair of metacentrics in 2n=14karyotype, a large metacentric and two different submetacentrics in 2n=15, and two submetacentric pairs in