



Mitochondrial DNA and morphometrical identification of a new species of *Hylomyscus* (Rodentia: Muridae) from West Africa

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Abstract

In this paper we describe a new species of *Hylomyscus* based on molecular (Cyt *b* and 16S rDNA gene sequencing) and morphometrical analyses. This new species occurs in Benin and Nigeria, and probably also in Togo. It differs by 8.29 to 10.40 % of sequence divergence (K2P distance for the Cyt *b* gene) from all other species of the *H. alleni* species complex, and can be distinguished from these species through morphometrical multivariate analyses. It differs significantly from its closest relative, *H. simus*, by four external and nine cranio-dental measurements. The role of rivers and Pleistocene forest refugia in the diversification of the *H. alleni* species complex is discussed.

Key words: 16S rDNA, Benin; Cytochrome *b*, Nigeria, sibling species, taxonomy, traditional morphometrics, tropical African forests, woodmice

Introduction

Woodmice of the genus *Hylomyscus* Thomas, 1926 are small-sized rodents belonging to the family Muridae (Musser & Carleton, 2005). They are geographically restricted to tropical Africa, where they are abundant in forest and dense vegetation (Nicolas & Colyn, 2003; Rosevear, 1969). Based on external and cranio-dental morphology, *Hylomyscus* species were separated into six species groups: *aeta*, *alleni*, *anselli*, *baeri*, *denniae* and *parvus* (Carleton *et al.*, 2006). Within these species groups, *Hylomyscus* species are morphologically similar and, as a result, the taxonomy of each species is a subject of debate (Carleton *et al.*, 2006; Robbins *et al.*, 1980; Rosevear, 1969; Rosevear, 1966).

Before we attempt to recognize species, we need a clear concept of what species are. De Queiroz (1998) suggested that despite the long history of dispute over species concepts, most species concepts agree fundamentally that species are lineages. What previous authors have generally disagreed about are the best criteria for recognizing these lineages (de Queiroz, 1998). In this paper we will use two lines of evidence to delimit species: phenetic distinguishability and reciprocal monophyly. During the past decade, the development of multivariate morphometrical analyses allowed to clarify the taxonomy within the genus *Hylomyscus* (Carleton *et al.*, 2006; Carleton & Stanley, 2005; Missoup *et al.*, 2009; Nicolas *et al.*, 2008). Moreover, a number of studies have demonstrated the utility of mitochondrial DNA (mtDNA) sequence variation in illuminating potential species boundaries between morphologically similar taxa (Avice, 2000). A major problem with this approach is that processes unrelated to speciation (e.g. deep coalescence) may be responsible for patterns such as reciprocal monophyly of mtDNA haplotype lineages within a species as well as for patterns of non-monophyly in reproductively isolated taxa (Avice *et al.*, 1983; Maddison, 1997). While we recognize the