



First record of *Hylomyscus walterverheyeni* (Rodentia: Muridae) on the north-western side of the Sanaga River (western Cameroon)

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Abstract

We used both molecular and craniometrical data to test the presence of *Hylomyscus walterverheyeni* in the Cameroon Volcanic Line (CVL). Our molecular (cytochrome *b* and 16S gene sequencing) and morphometrical data (discriminant analyses) clearly show the presence of *H. walterverheyeni* in the CVL, north-west of the Sanaga River. *Hylomyscus walterverheyeni* occupies both lowland and mountain forests (up to 2000m asl). In our phylogenetic analyses, the CVL specimens form a monophyletic group. This clade seems to reflect the role of the Sanaga River as a barrier to gene flow within the species.

Key words: Cameroon Volcanic Line, barrier, discriminant analyses, phylogenetic analyses

Introduction

Despite the wide range of studies conducted on African small mammals this last decade, their true species-diversity still remains largely unknown. Moreover, the discovery of a cryptic diversity within murids has considerably increased the interest of this group for systematic and biogeographical studies. Species of *Hylomyscus* (Murinae, Praomyini), all of small body size, are restricted to tropical Africa, where they are abundant in forests and dense second growth (Nicolas *et al.* 2006). Due to the existence of many cryptic species, taxonomy at the species level remains difficult to assess and is still under debate (Carleton & Stanley 2005, Carleton *et al.* 2006; Nicolas *et al.* 2006, 2008; Robbins *et al.* 1980). In 2005, Musser and Carleton recognized 12 species within the genus. Recent studies based on morphological and/or molecular data have revealed several new species, and have underlined the necessity to reassess the systematics and biogeography of *Hylomyscus* (Carleton & Stanley 2005, Carleton *et al.* 2006, Nicolas *et al.* 2006, 2008).

Recently, Nicolas *et al.* (2008) described a new *Hylomyscus* species from lowland forests of Central Africa (*H. walterverheyeni*). This species cannot be easily distinguished from its relatives based on morphology, but it can be identified through molecular DNA sequencing and morphometric analyses of cranial and dental variables. According to this latter work, *H. walterverheyeni* is known from Republic of Congo, Central African Republic, Gabon and South-East Cameroon. The possibility for the Sanaga River to have constrained the westward distribution of *H. walterverheyeni* was suggested by Nicolas *et al.* (2008) pending additional sampling in western Cameroon and the Dahomey gap region.