

Patterns of morphological and genetic variation in western Indian Ocean members of the *Chaerephon ‘pumilus’* complex (Chiroptera: Molossidae), with the description of a new species from Madagascar

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Abstract

The species delimitations of African, Arabian Peninsula, and western Indian Ocean island members of the Molossidae bat species complex *Chaerephon pumilus* remain largely unresolved. Based on genetic analyses this group is paraphyletic, with *C. leucogaster* nested within *C. pumilus* sensu lato, and the latter is composed of several distinct clades. DNA was isolated from a specimen of *C. p. pumilus* obtained at the type locality (Massawa, Eritrea). Although incomplete, this sequence allowed us to clearly define which clade is referable to nominate *pumilus*, a critical step in resolving the systematics of this species complex. Using morphological and molecular genetic (cytochrome *b* and D-loop sequences) characters, we establish that *C. leucogaster* and *C. ‘pumilus’* on Madagascar represent two different lineages and that the Malagasy population referred to *C. ‘pumilus’* is specifically distinct from those on Africa, the

Arabian Peninsula, the Comoros Archipelago, and the western Seychelles (Aldabra). The Madagascar population is here described as a new species, *Chaerephon atsinanana* sp. nov. This taxon is common in the eastern portion of Madagascar, particularly in synanthropic settings, across an elevational range from near sea level to 1100 m, and there are no immediate conservation concerns. Members of the *C. pumilus* species complex from the western Seychelles are referable to *C. pusillus*, to which populations from the Comoros (Mayotte, Anjouan, Mohéli, and Grande Comore) are also assigned.

Résumé

Les délimitations du complexe d'espèces *Chaerephon pumilus*, membre des chauves-souris Molossidae de l'Afrique, de la Péninsule Arabique et de l'Océan Indien occidental, sont largement non résolues. D'après les données génétiques, ce groupe est paraphylétique, avec *C. leucogaster* inclus dans *C. pumilus* sensu lato, ce dernier taxon étant composé de plusieurs clades distincts. L'ADN a été isolé à partir d'un spécimen de *C. p. pumilus* obtenu dans la localité type (Massawa, en Erythrée). Bien qu'incomplète, la séquence obtenue nous a permis de définir clairement le clade de référence pour la nomination de *pumilus*, une étape cruciale dans la résolution de la systématique de ce complexe d'espèces. L'utilisation des caractères morphologiques et moléculaires (séquences de cytochrome b et de D-loop) nous a permis d'établir que *C. leucogaster* et *C. 'pumilus'* à Madagascar correspondent à deux lignées différentes et que la population malgache désignée comme *C. 'pumilus'* est spécifiquement distincte de celles de l'Afrique, de la péninsule arabique, de l'Archipel des Comores et des Seychelles occidentales (Aldabra). Nous nommons cette nouvelle espèce, *Chaerephon atsinanana* sp. nov. Cette dernière est commune dans la partie orientale de Madagascar, en particulier comme espèce synanthropique, et présente une distribution altitudinale allant du niveau de la mer jusqu'à 1100 m d'altitude. A l'heure actuelle, l'espèce ne semble pas nécessiter une attention particulière en termes de conservation. Les membres du complexe *C. pumilus* des Seychelles occidentales sont désignés sous le nom de *C. pusillus*, ainsi que les populations des Comores (Mayotte, Anjouan, Mohéli et Grande Comore).

Key words: taxonomy, morphology, molecular genetics, *Chaerephon*, Madagascar, Africa, Comoros, Aldabra

Introduction

As currently configured, the small Molossidae bat, *Chaerephon pumilus* (Cretzschmar 1830-1831), has a broad distribution across much of sub-Saharan Africa and on offshore islands of both the Atlantic and Indian Ocean coasts of this continent, East to the Arabian Peninsula, and on islands in the western Indian Ocean (Bouchard 1998; Harrison & Bates 1991; Simmons 2005). The nominate form was described based on specimens collected at Massawa, Eritrea. On the Arabian Peninsula, this taxon appears limited to Yemen, specifically the portion directly across the Red Sea from Eritrea (Harrison & Bates 1991). Animals currently assigned to *C. pumilus* sensu lato show considerable phenotypic variation with bat taxonomists recognizing 12 different forms (Koopman 1994). In contrast, given the considerable levels of dichromatism in certain populations, particularly associated with wing and pelage coloration, it has been suggested that “attempts at subspecific separation based mainly on colour are profitless” (Hayman & Hill 1971, p. 64).

Seven forms of *C. pumilus* sensu lato have been named from the eastern and southern portions of the African continent and western Indian Ocean islands: *limbata* Peters 1852 (type locality: Mozambique Island, Mozambique, but see Turni & Kock 2008); *naivashae* Hollister 1916 (type locality: Naivasha Station, Kenya); *hindei* (Thomas 1904) (type locality: Fort Hall, Kenya); *elphicki* Roberts 1926 (type locality: southeastern Transvaal, South Africa); *langi* Roberts 1932 (type locality: northern Botswana); *leucogaster* (Grandidier 1869) (type locality: Menabe Region, western Madagascar, neotype locality: Belo sur Mer [Ratrimomanarivo *et al.* 2009a]); and *pusillus* (Miller 1902) (type locality: Aldabra Island, western Seychelles). On the basis of phenetic analyses associated with skull morphology, Peterson *et al.* (1995) proposed to elevate three forms (*hindei*, *limbata*, and *naivashae*) to full species. While this suggestion may indeed be valid, the lack of a phylogenetic context and diagnoses to separate these forms renders their taxonomic conclusion difficult to interpret in light of other potential factors to explain the patterns of morphological variation in this species complex (e.g., Ratrimomanarivo *et al.* 2008). Given apparent high levels of morphological polymorphism in *C. pumilus* sensu lato, overlaid on clinal and geographic variation, it has been rather problematic to sort out the systematics of this putative species complex.