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Molecular evidence of the taxonomic status of western Mexican populations of *Phaethornis longirostris* (Aves: Trochilidae)

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Abstract

Species diversity is largely underestimated by current taxonomy, precluding a precise understanding of evolutionary processes. Genetic data have increased our understanding of that cryptic diversity, and multilocus studies are now desirable. In this study, we used mitochondrial and nuclear DNA sequences to evaluate the taxonomic status of the western Mexico's populations of *Phaethornis longirostris*. We found differences of 4.2 % in mtDNA and different alleles for one nDNA locus between western and eastern Mexican populations. Molecular and morphological evidence support the separation of these populations (*P. l. mexicanus* and *P. l. griseoventer*) as the species *Phaethornis mexicanus* Hartert 1897. *Phaethornis mexicanus* is endemic to western Mexico and sister to the remaining populations of *P. longirostris*. The speciation of *P. mexicanus* probably occurred around 880,000 years ago by a vicariant event involving climatic-vegetational changes.

Key words: Hummingbirds, Mesoamerica, niche conservatism, speciation, species limits, tropical dry forest

Introduction

The Neotropics host the world's most diverse avifauna (Newton 2003), but their species richness is largely underestimated by current taxonomy (Navarro-Sigüenza & Peterson 2004; Peterson & Navarro-Sigüenza 2009; Tavares *et al.* 2011; Milá *et al.* 2012). For Mesoamerica (*i.e.*, Mexico and Central America), several phylogenetic and phylogeographic studies of birds have indicated marked genetic differentiation of allopatric populations that also show morphological differences or are isolated by geographic barriers (*e.g.*, Navarro-Sigüenza *et al.* 2008; Weir *et al.* 2008; Arbeláez-Cortés *et al.* 2010; Barber & Klicka 2010; Bonaccorso *et al.* 2011; González *et al.* 2011; Arbeláez-Cortés *et al.* 2012). Those studies have been mainly based on information from mitochondrial DNA (mtDNA), but it is now possible and desirable to add nuclear DNA (nDNA) loci to facilitate the detection of patterns derived from species-level processes rather than from single locus histories (Backström *et al.* 2008; Edwards & Bensch 2009). The combination of molecular information, phenotypic traits, and ecological data can be instrumental in recognizing species-level cryptic diversity (Padiá *et al.* 2010; Milá *et al.* 2012). Moreover, the recognition of an appropriate taxonomic rank for a particular lineage has consequences both for conservation purposes (Peterson & Navarro-Sigüenza 1999; Rojas-Soto *et al.* 2009) and for the understanding of evolutionary processes.

The hummingbirds (Aves: Trochilidae) are endemic to the Americas and comprise 342 species (Gill & Donsker 2013). The hermits (subfamily Phaethorninae) are both phylogenetically and morphologically well differentiated from the remaining species (Hinkelmann 1996; Hinkelmann & Schuchmann 1997; Stiles 2004; McGuire *et al.* 2007). Hermits are relatively dull-colored with little or no brilliant iridescence, are non-territorial trap-liners, and are lekking species (Hinkelmann 1996; Stiles 2004). This group, which is restricted to Neotropics, contains 35 species in six genera; 26 of these are in the genus *Phaethornis* (Gill & Donsker 2013).

Phaethornis longirostris (De Lattre 1843), a widespread species ranging from western Mexico to northwestern Peru, comprises six subspecies. This taxon was considered as part of the long-tailed hermit (*P. superciliosus*) until the morphological works of Hinkelmann (1996) and Hinkelmann & Schuchmann (1997), who recognized all