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# Genetic Diversity of Neotropical *Myotis* (Chiroptera: Vespertilionidae) with an Emphasis on South American Species

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## Abstract

**Background:** Cryptic morphological variation in the Chiropteran genus *Myotis* limits the understanding of species boundaries and species richness within the genus. Several authors have suggested that it is likely there are unrecognized species-level lineages of *Myotis* in the Neotropics. This study provides an assessment of the diversity in New World *Myotis* by analyzing cytochrome-*b* gene variation from an expansive sample ranging throughout North, Central, and South America. We provide baseline genetic data for researchers investigating phylogeographic and phylogenetic patterns of *Myotis* in these regions, with an emphasis on South America.

**Methodology and Principal Findings:** Cytochrome-*b* sequences were generated and phylogenetically analyzed from 215 specimens, providing DNA sequence data for the most species of New World *Myotis* to date. Based on genetic data in our sample, and on comparisons with available DNA sequence data from GenBank, we estimate the number of species-level genetic lineages in South America alone to be at least 18, rather than the 15 species currently recognized.

**Conclusions:** Our findings provide evidence that the perception of lower species richness in South American *Myotis* is largely due to a combination of cryptic morphological variation and insufficient sampling coverage in genetic-based systematic studies. A more accurate assessment of the level of diversity and species richness in New World *Myotis* is not only helpful for delimiting species boundaries, but also for understanding evolutionary processes within this globally distributed bat genus.

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## Introduction

A well-defined perspective of the continental and insular biotic diversity of South and Central America remains difficult to resolve despite years of effort by systematists. An excellent example is the low species-level resolution and current state of knowledge of the mammalian genus *Myotis* (Chiroptera: Vespertilionidae). This poor resolution is largely due to limited genetic studies focused on species-level variation. Moreover, morphological variation within the genus is low (i.e., cryptic variation) [1,2,3] and limits the resolving power of classical morphological studies. For these reasons the taxonomy and systematics of New World *Myotis* is complex and often controversial [1,4–12]. Recent taxonomic syntheses and publications focused on *Myotis* recognize ~ 42 species distributed in the New World, with 26 species in North

America, 11 in Central America, 15 in South America, and five in the Caribbean (Table 1) [12–16].

The most recent DNA sequence-based overview of New World *Myotis* [3] examined one or a few individuals from 32 of the recognized species (those with available tissues). Here, we build on the findings of Stadelmann et al. [3] by generating DNA sequence data from an increased geographic sample of *Myotis* (especially in South America). Collectively, these genetic data serve to elucidate the diversity within *Myotis* (including cryptic species) and provide the basis for understanding the taxonomic boundaries of several wide-ranging species. Our baseline questions included: How many species-level lineages, based on cytochrome-*b*, are there in broadly defined geographic regions (i.e., North America, Central America, Caribbean, South America)? How do these numbers compare among regions? Do these numbers correspond to the currently recognized number of species? What does this mean in the context