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Systematics of *Sturnira* (Chiroptera: Phyllostomidae) in Ecuador, with comments on species boundaries

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Abstract

Molecular and morphological analyses of variation often conflict with historical species descriptions based on a few characters and small samples sizes. Here we present a molecular phylogeny together with a quantitative morphological analysis of the species in *Sturnira* in Ecuador. The 438 terminal taxa or organisms included in the analysis occur within a total of 10 ingroup lineages, which contain considerable substructure. Some species, as recognized by their morphological traits, form paraphyletic arrangements with other taxa. We could not distinguish the close species pairs *S. erythromos* / *S. bogotensis* and *S. ludovici* / *S. oporophilum* in morphospace and therefore when distinct lineages were recovered genetically, they initially contained mixed membership of specimens identified using morphological criteria. Similarly, the qualitative character states that diagnose *S. luisi* in its original description are not recovered in a quantitative analysis of morphological variation and thus *S. luisi* cannot be mapped to a single lineage in a molecular phylogeny. We present additional evidence to corroborate the existence of *S. perla* as a species. We found a remarkable geographic structure within some species containing sister pairings, with lineages having a clear eastern or western distribution in relation to the Andes. Our analysis demonstrates the potential for conflict between character-based diagnoses, analysis of morphological variation and molecular phylogenetics in the identification of species and supports a combined approach to this problem.

Key words: *Sturnira*, systematics, morphometry, species boundaries, lineage, ontology

Introduction

A species should be diagnosable; that is, detectable by a sense of discreteness or discontinuity (Dobzhansky 1937). For example, we might expect species to be recognizable by discontinuities in multivariate morphological or ecological canonical spaces. We similarly expect sister species to show relatively large interspecific genetic divergences and strongly supported branches in phylogenetic hypotheses compared to intraspecific divergence. While these criteria are not always met (e.g. cryptic species may not show a morphological discontinuity), it is usually the mechanism by which we observe and measure species. Species can also be considered as hypotheses about the distribution of character states (Hey 2001), where these should show evidence of small within-group variation relative to among-group variation.

In an analysis of morphological variation within the genus *Sturnira* Gray, Jarrín-V. & Kunz (2011) showed a remarkable level of morphological overlap between *S. lilium* Geoffroy Saint-Hilaire and *S. luisi* Davis, both putative species also having comparatively small genetic divergence. This past study (Jarrín-V. & Kunz 2011) also presented a novel argument in bat systematics, that the description of morphological variation can't be achieved through the written description of specific characters, but instead, requires the quantification of variation in these diagnostic traits and estimates of uncertainty. Here, we expand on this by discussing problems in our current understanding of species boundaries in *Sturnira* within Ecuador. We present a new phylogenetic hypothesis and