Molecular systematics of the genus Chaetura (Aves: Apodidae)

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Introduction

Swifts are among the most aerial of birds. Various morphological features, many related to the shape of their wings, are likely adaptations to a lifestyle that regularly involves prolonged flight (Chantler 1999, Lentink et al. 2007). Swift morphology is notoriously conservative and species in this genus are difficult to identify both in the field and in the specimen drawer.

Until 1970, Chaetura contained all species that constitute the present tribe Chaeturini and included numerous Old World species, but the genus is currently considered to consist of nine species endemic to the New World (Brooke 1970, Chantler 1999). Marín (1997, 2000) used morphological characteristics to divide Chaetura into two groups, the brown-rumped and the gray-rumped swifts, and to further divide the gray-rumped group into gray-rumped and pale-rumped species (Table 1). Not surprisingly, given the lack of morphological variation, some species limits with Chaetura are controversial.

In this project we used molecular data to:
- determine whether Chaetura is a monophyletic (natural evolutionary) group
- establish whether the brown- and gray-rumped groups, and pale- and gray-rumped subgroups, are monophyletic
- assess the monophyly of each species of Chaetura
- evaluate the generic status of putative species richmondi, viridipennis, famosus, and egregia relative to their proposed conpecifics vauxi, chapmani, spinicauda, and cineriventer/spinicauda, respectively

Materials and Methods

- Tissue samples were obtained for 32 individuals representing eight of the nine Chaetura species and three outgroups (Table 1). Two outgroup species were representatives of other genera within the Chaeturini (Neafrapus and Hirundapus) and the third outgroup species (Apus apus) was a representative of the broader Apodidae.
- DNA was extracted using Qiagen extraction kits, and the mitochondrial gene NADH dehydrogenase 2 (ND2) and intron 5 of the nuclear gene muscle specific receptor tyrosine kinase (MUSK) were amplified using standard PCR protocols.
- Sequences were obtained using an ABI PRISM 3100 automated sequencer, edited using Sequencer 4.9, and analyzed using maximum likelihood (ML) and maximum parsimony (MP) as implemented in RAxML (Stamatakis et al. 2008) and PAUP* 4.0 (Swofford 2003).

Results

- Complete mitochondrial sequence (1041 bp) was obtained for 27 individuals and complete nuclear data (1027 bp) for 22 individuals.
- Most trees (all ML trees and the nuclear MP tree), Fig. 1 indicated that the genus Chaetura was monophyletic. The brown- and gray-rumped groups and the pale- and gray-rumped subgroups were monophyletic in all trees.
- Individual species were monophyletic with the exception of C. spinicauda, which in most trees was paraphyletic with respect to C. egregia. Mean mitochondrial divergence between sister species ranged from 1.5% (between andrewi and brachyura) and 5.5% (between cineriventer and spinicauda/egregia).
- Putative conpecifics vauxi vauxi and c. richmondi were sister taxa in all trees; mean mitochondrial divergence was 0.5%. Nominate chapmani and c. viridipennis formed a clade and were sister taxa in some trees; mean sequence divergence between these taxa was only 0.1%. Nominate spinicauda and s. famosus formed part of a clade that also included the other representative of spinicauda (aetherodroma) and C. egregia. Mean mitochondrial divergence was 0.5% between s. spinicauda and s. famosus and 1.0% between c. spinicauda and c. egregia. Chaetura egregia was not sister to or nested within C. cinereiventris and differed from it by 5.5% mean sequence divergence.

Discussion

- Our results indicate that the genus Chaetura is likely monophyletic, consistent with the restricted definition of the genus (Brooke 1970). However, Neafrapus is closely related and some analyses (mitochondrial MP) place it within Chaetura.
- The basic structure of our phylogenetic tree is consistent with previous views based on morphological variation in Chaetura. Martin’s division of the genus into brown- and gray-rumped groups and pale- and gray-rumped subgroups is supported by all of our trees. Our results also support a close relationship between egregia and spinicauda (cf. Marín 2000), in contrast to previous views suggesting that egregia is conpecific with cinereiventris. Chaetura egregia is nested within C. spinicauda in most trees.
- Morphology and vocalizations are frequently used to distinguish avian species. However, such characters are of limited utility in swifts, and views on species status in the group have often been based on one or a few characters subject to varying interpretations. Under the biological species concept, genetic data on allopatric taxa are insufficient to determine species limits; however, they can provide additional perspective in cases of equivocal morphological and behavioral data. We found low levels of genetic divergence separating richmondi, viridipennis, and famosus from their conspecifics, relative to levels of divergence between sister species in Chaetura. These findings are more consistent with treatment of these taxa as conspecifics than as different species.

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References


