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Phylogeny and classification of the New World suboscines (Aves, Passeriformes)

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Abstract

Here we present a phylogenetic hypothesis for the New World suboscine radiation, based on a dataset comprising of 219 terminal taxa and five nuclear molecular markers (ca. 6300 bp). We also estimate ages of the main clades in this radiation. This study corroborates many of the recent insights into the phylogenetic relationships of New World suboscines. It further clarifies a number of cases for which previous studies have been inconclusive, such as the relationships of Conopophagidae, Melanopareiidae and Tityridae. We find a remarkable difference in age of the initial divergence events in Furnariida and Tyrannida. The deepest branches in Furnariida are of Eocene age, whereas the extant lineages of Tyrannida have their origin in the Oligocene. Approximately half of the New World suboscine species are harboured in 5 large clades that started to diversify around the Mid Miocene Climatic Optimum (16–12 Mya). Based on our phylogenetic results we propose a revised classification of the New World suboscines. We also erect new family or subfamily level taxa for four small and isolated clades: Berlepschiinae, Pipritidae, Tachurididae and Muscigrallinae.

Key words: Furnariida, Tyrannida, phylogeny, classification

Introduction

With more than 1200 extant species, the New World suboscines (NWS) are one of the largest endemic vertebrate radiations on the South American continent. Phylogenetic relationships are comparatively well studied. The studies with the most comprehensive taxon sampling have either relied on the RAG1 and RAG-2 protein coding regions (Moyle *et al.* 2009; Tello *et al.* 2009) or nuclear introns, primarily myoglobin intron 1, G3PDH intron 11 and ODC introns 6 and 7 (e.g. Irestedt *et al.* 2009; Ohlson *et al.* 2008), in some cases complemented by mitochondrial DNA. These two sets of molecular markers have yielded phylogenetic hypotheses that are generally congruent but also differ at several points. Partially conflicting tree topologies have previously been observed between the RAG genes and nuclear introns (Irestedt & Ohlson 2008) or between RAG genes and other nuclear protein-coding markers (e.g. ZENK, Treplin *et al.* 2008).

The last decade has seen a drastic overturning of the traditional view of systematic relationships in nearly every larger group of passerines. However, adjustments in classification often lag, creating a discrepancy between classification and current hypotheses of phylogenetic relationships. Moyle *et al.* (2009) and Tello *et al.* (2009) proposed several changes to the classification of Furnariida and Tyrannida respectively, whereas the studies by Irestedt *et al.* (2009) and Ohlson *et al.* (2008) have not been synthesized into a comprehensive proposal for a new classification. At this point we have a sufficiently clear picture of the NWS radiation to propose a consensus classification that reflects the results of these combined analyses. The NWS are among the most comprehensively sampled bird radiations and there are no taxa left unstudied that are likely to have any impact on classification at the subfamily level. A few taxa of uncertain affinities at the generic level still remain to be included in molecular studies and a few large radiations of rather recent origin remain to be disentangled to settle generic limits.

In this study we aim to explore the effects of increased data on the topology of the NWS tree. We compare the phylogenies obtained using RAG-1 and RAG-2 with those obtained from intron data (G3PDH intron 11,

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