Genetic diversity in an Andean forest bird: the Rufous Antpitta (Grallaria rufula)

Spencer Galen and R. Terry Chesser

1Division of Birds, Department of Vertebrate Zoology, National Museum of Natural History, Washington DC, USA
2USGS Patuxent Wildlife Research Center, National Museum of Natural History, Washington DC, USA

Introduction

The Rufous Antpitta (Grallaria rufula) is a suboscine passerine bird found in high elevation Andean forest from Colombia to Bolivia. Seven subspecies of G. rufula are currently recognized. Many subspecies differ qualitatively in vocalizations and some subspecies appear to consist of multiple vocal types. Thus, it has been suggested that this complex may consist of multiple biological species (Graves 1987, Krabbe and Schulenberg 2003). Graves (1987) separated Grallaria blakei as a cryptic species that occurs sympatrically with G. rufula in Peru. However, as he noted, it is more difficult to determine the species status of allopatric populations.

Methods

Forty tissue samples and one blood sample of G. blakei and three tissue samples of G. blakei were obtained from six tissue collections (see Acknowledgments). DNA was extracted from these samples using Qiagen extraction kits, and the mitochondrial gene NADH dehydrogenase 2 (ND2) was amplified using standard polymerase chain reaction (PCR). The PCR products were sequenced and the sequences were edited using Sequencher. Maximum parsimony (MP) and maximum likelihood (ML) analyses of the sequence data were performed using PAUP*. To assess nodal support, 1,000 MP and 100 ML bootstrap replicates were performed.

Results

Complete ND2 sequence was obtained for 32 individuals, including 30 individuals of G. rufula and two individuals of G. blakei. Both phylogenetic analyses revealed eight genetically distinct groups, which were 2.7-10.2% divergent (Figs. 1, 2).

Samples of G. r. cochabambae, G. r. rufula, and G. blakei all formed single, genetically distinct groups. Samples of G. r. obscura formed three genetic groups, which comprised a clade. Samples of G. r. occabambae formed two groups that were not sister taxa; instead the single individual of G. r. cochabambae was sister to the southern samples of G. r. occabambae. Samples of G. blakei fell within the clade formed by G. r. rufula and G. r. obscura in both analyses.

MP and ML analyses differed only in the placement of a group of subspecies G. r. occabambae from Cuzco, Peru (clade 3). MP analysis placed this group as sister to the clade consisting of G. r. rufula, G. r. obscura, and G. blakei. ML analysis placed this group as sister to the clade consisting of G. r. cochabambae and the remaining G. r. occabambae samples (Fig. 2). With this placement, the deepest division of the ML phylogeny separates ‘southern’ groups consisting of birds from southern Peru and Bolivia from ‘northern’ groups consisting of specimens from central Peru, northern Peru, and Ecuador.

Discussion

Whereas species limits in North American birds are relatively well known, there is still much to be learned about the South American avifauna (e.g., Sanin et al. 2009). Analysis of sequences of the mitochondrial gene ND2 revealed significant genetic variation within the G. rufula complex. Notably, all genetic groups identified by the ND2 data differ substantially in vocalizations (later et al. unpub. data) and are likely valid biological species in addition to being valid evolutionary and phylogenetic species.

When data for populations in Colombia are considered (Cadena unpub. data), there may be a dozen or more biological species within the G. rufula complex. Further analyses of intraspecific variation in South American birds will undoubtedly uncover many other cryptic species and enhance our understanding of the patterns of biodiversity in the Neotropics.

Acknowledgements

We thank the National History Research Experience internship program of the National Museum of Natural History, museum director Cristian Sampaio, and the Department of Vertebrate Zoology for their generosity and support of this research. We thank Robert Fleischer, Jesus Malinado, and Nancy Rozai for access to the genetics lab at the Center for Conservation and Evolutionary Genetics, as well as all lab members who helped along the way. We thank the following institutions for contributing tissue samples to this project: Louisiana State University Museum of Natural Science, Baton Rouge; Field Museum of Natural History, Chicago; University of Kansas Natural History Museum; J.J. Jankowski, University of Florida; Academy of Natural Sciences, Philadelphia.

Literature Cited


Figure 1. Geographic range of G. rufula (shaded red) with specimen locations for each subspecies. Numbers correspond to genetic groupings in Figure 2.