

Understanding neotropical diversification: Implications from phylogenetic patterns in two avian genera

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Abstract (Summary)

In this study, phylogenetic analyses using molecular data and present-day patterns of species distributions were used to uncover historical relationships among Neotropical areas of endemism for two widespread co-distributed genera, *Platyrinchus* spadebills (Aves: Tyrannidae) and *Cercomacra* antbirds (Aves: Thamnophilidae). All phylogenetic hypotheses were developed using a combination of three protein-coding mitochondrial genes (NADH dehydrogenase subunit 2, NADH dehydrogenase subunit 3, and cytochrome *b*) and one nuclear intron (β -Fibrinogen intron 5). Molecular phylogenetic analyses uncovered 19 independent evolutionary lineages in *Platyrinchus* and 22 in *Cercomacra* distributed across 29 Neotropical areas of endemism, which suggest that diversity in these taxa is highly underestimated. Phylogenetic analyses also found *Cercomacra* to be paraphyletic (composed of two non-sister clades, "*nigricans*" and "*tyrannina*"). The origin and patterns of major diversification differed among the three study clades (*Platyrinchus*, "*nigricans*", and "*tyrannina*"), ranging from a peak of diversification at the late Pliocene in *Platyrinchus* to a peak of diversification occurring during the Pleistocene in the "*nigricans*" clade. Area relationships, inferred from phylogenetic patterns of these clades showed both concordant and discordant spatial and temporal origins of lineages in these three clades. Temporal discordance of spatial patterns was not expected, owing to the overall similarity in distribution of the species in the study clades. However, this discordance may be explained by origin of the patterns of distribution under different scenarios. The results of this study suggest that the history of diversification of Neotropical organisms is complex and ongoing. For the first time, these extensive data sets allow us to contrast the patterns of lineage diversification with the spatial distribution of lineages to understand the historical relationships of areas of endemism in the Neotropical region.