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PHYLOGEOGRAPHY AND ADAPTIVE PLUMAGE EVOLUTION IN CENTRAL AMERICAN SUBSPECIES OF THE SLATE-THROATED REDSTART (*MYIOBORUS MINIATUS*)

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Abstract.—The Slate-throated Redstart (*Myioborus miniatus*) is a common warbler of montane forests from northern Mexico to Argentina. We examined phylogenetic structure and plumage pattern in relation to subspecific taxonomy across the broad geographic range of this species. Phylogenetic analysis of two complete mitochondrial protein-coding genes (subunits 2 and 3 of NADH dehydrogenase) from 36 individuals, representing 10 of the 12 subspecies, revealed four clades, three of which showed general concordance with subspecific classification. However, in a Central American clade, four subspecies (*hellmayri*, *connectens*, *comptus*, and *aurantiacus*) could not be resolved by the molecular phylogenetic analysis, even though populations of *hellmayri* and *connectens* are currently geographically isolated from those of *comptus* and *aurantiacus* by the Nicaraguan lowlands. The genetic homogeneity within this clade suggests a late Pleistocene range expansion at a time when today's montane forest types existed at lower elevations. The Pleistocene hypothesis is supported by both paleoecological reconstructions of Central America and the mismatch distribution of pairwise nucleotide differences among haplotypes in our data set. Despite the genetic homogeneity within the Central American clade, the four subspecies are differentiated in plumage pattern, particularly in the extent of white in the tail. Subspecific variation in the tail pattern is of particular interest because the tails are used in animated displays to startle potential insect prey that are pursued and captured in flight. Field experiments conducted with birds of the Costa Rican subspecies *comptus* and their key prey indicated (1) that a contrasting black-and-white tail is critical to flush-pursuit foraging success and (2) that subspecific variation in the extent of white in the tail reflects evolutionary adaptation to regional prey or habitat characteristics that maximizes flush-pursuit foraging performance. Thus, even though the subspecies of the Central American clade are genetically homogeneous with respect to the mitochondrial genes, analysis of tail pattern and its effect on foraging performance suggests a recent adaptive evolutionary divergence. Our findings serve as a reminder that mitochondrial DNA (mtDNA) gene trees will not always succeed in capturing all evolutionarily significant genetic change, and that manipulative field experiments can provide crucial information on the selective factors that lead to evolution of subspecies-specific morphological traits even in the absence of mtDNA diversification.

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