

ABSTRACTS FOR *CONDOR* 103(3) AUGUST 2001

FEATURE ARTICLES

GENETIC STRUCTURING AMONG MIGRATORY POPULATIONS OF THE BLACK-WHISKERED VIREO, WITH A COMPARISON TO THE RED-EYED VIREO

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Abstract. The Black-whiskered Vireo (*Vireo altiloquus*) breeds from coastal southern Florida in the United States through the islands of the West Indies, and thus consists of several populations separated by large regions of uninhabitable space. I examined genetic variation within and among six migratory populations in the Florida Keys, Jamaica, and Puerto Rico, using random amplified polymorphic DNA (RAPD) markers and analysis of molecular variance (AMOVA). Calculations of variance components revealed that over 90% of the variance was among individuals; a significant portion also occurred among regional groups (Florida, Jamaica, and Puerto Rico). Variance between subpopulations within the regional groups was not significantly different from zero. This contrasts with the closely related Red-eyed Vireo (*V. olivaceus*) of continental North America, in which analyses of three widely separate geographic localities revealed that over 99% of the genetic variance was among individuals, with no significant variance detectable among localities. The greatest differences in *V. altiloquus* were detected between the Florida Keys populations and the populations from Jamaica and Puerto Rico; the latter two showed no significant differentiation. Estimates of gene flow from the AMOVA analog to Wright's *F*-statistics suggest that there is enough gene flow among regions to prevent differentiation by genetic drift. Although not strongly isolated, the Florida population of *V. altiloquus* is sufficiently differentiated to suggest reduced genetic exchange with the populations on Puerto Rico and Jamaica.

Key words: Black-whiskered Vireo, genetic structure, island populations, RAPD, Red-eyed Vireo, *Vireo altiloquus*, *Vireo olivaceus*.

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