

Lovette, I. J., S. M. Clegg, and T. B. Smith. 2003. Limited utility of mtDNA markers for determining connectivity among breeding and overwintering locations in three Neotropical migrant birds. *Conservation Biology* 18: 156-166.

Abstract: For the past two decades, population declines in Neotropical migrant songbirds have been both a flagship conservation issue and the subject of intensive research initiatives. Nonetheless, the design of effective conservation measures for Neotropical migrants has been hindered by a lack of information on where and how migrant populations are regulated. This problem stems in large part from the difficulty of following individual long-distance migrants throughout their annual cycles. As a result, there has been an increasing interest in using genetic markers to determine patterns of connectivity between particular breeding populations and overwintering regions: in species with geographically structured genetic variation during the breeding season, genetic markers can be used to determine the origin of migrating and overwintering individuals. This information on demographic connectivity could be then used to infer the locations or seasons contributing to population trends of currently unknown origin. To date, genetic markers (primarily mitochondrial DNA) have been used to survey only a few species of migratory songbirds, with varying success. To provide examples of the geographic scale at which mtDNA markers are likely to prove most relevant to Neotropical migrant conservation, we surveyed breeding-season variation in North American populations of three long-distance migrant taxa: the Yellow-breasted Chat (*Icteria virens*), Common Yellowthroat (*Geothlypis trichas*), and Nashville Warbler (*Vermivora ruficapilla*). We then used this information to screen individuals sampled at overwintering sites in Mexico and Central America. Genetic structure was only found at the broadest continent-wide scale in all three species, which then allowed us to assign overwintering individuals to eastern or western breeding lineages, but which did not allow us to assign overwintering individuals to breeding populations of origin on a finer scale suitable for assaying local demographic trends. Owing to mitochondrial homogeneity among widely separated breeding locations, mtDNA markers (especially when used alone) are unlikely to provide a panacea for the problem of migrant interseasonal connectivity.