Ornithological Monographs
Volume (2006), No. 61, 29–78
© The American Ornithologists' Union, 2006.
Printed in USA.

CHAPTER 2

INTEGRATED ANALYSIS OF GENETIC, STABLE ISOTOPE, AND BANDING DATA REVEAL MIGRATORY CONNECTIVITY AND FLYWAYS IN THE NORTHERN YELLOW WARBLER (*DENDROICA PETECHIA; AESTIVA* GROUP)

Marylène Boulet,[1,3] H. Lisle Gibbs,[1,4] and Keith A. Hobson[2]

[1]*Department of Biology, McMaster University, 1280 Main Street West, Hamilton, Ontario L8S 4K1, Canada;*
[2]*Prairie and Northern Research Center, Canadian Wildlife Service, 115 Perimeter Road, Saskatoon, Saskatchewan S7N 0X4, Canada*

Abstract.—Population-specific genetic tags and stable isotope ratios are markers that can be used to track migratory birds throughout their annual cycle and determine their degree of migratory connectivity or the geographic linking of individuals or populations between different stages of the annual cycle. Until recently, few data had been obtained on the connectivity of small-bodied migrant birds such as warblers. Here, we combined geographic differences in mitochondrial DNA (mtDNA), stable hydrogen isotope (δD) analysis, and banding records to assess migratory connectivity in the northern yellow warbler (*Dendroica petechia*; *aestiva* group) populations and describe their migration patterns.

To use mtDNA variation to identify the geographic breeding region from which birds originated (eastern lineage: eastern and central North America; western lineage: western and central North America; southern lineage: southwest United States), we genotyped 133 wintering birds obtained from 23 sites in Mexico, Central America, and Venezuela; 438 spring migrants from 32 stopovers in North America; and 428 fall migrants from 30 stopovers in North America. There was strong segregation between lineages throughout the annual cycle: the eastern lineage was present in eastern and central North America during migration, and in Yucatan (Mexico), Panama, and Venezuela during the wintering season; the western lineage was present in central and western North America during migration and in Mexico and Panama during the wintering season; the southern lineage was restricted to western Mexico during the wintering season. The distributions of eastern and western lineages indicated strong continental-scale connectivity and a parallel migration system.

We conducted δD analysis on 94 feather samples collected from wintering birds captured on eight wintering areas and on 347 feather samples taken from migrants captured on six spring stopovers and five fall stopovers located in the United States and Mexico. For a large portion of these samples (n = 407), genotypic information was also available, and we combined these two types of information to create lineage-specific isotopic subregions to which birds were then assigned. The addition of the isotopic marker suggested weak connectivity between Mexican states along the Pacific coast and the west coast of North America, as well as between southeastern Mexican states along the Gulf Coast and central North America. Overall, the combined genetic and isotopic information identified the following migratory routes: in spring, there were three main flyways: a trans-Gulf route taken by eastern migrants passing through New York and Louisiana; a circum-Gulf route taken by eastern and western migrants passing through Veracruz, Mexico; and a western route taken by western birds passing through Nevada. In fall, there were two main flyways: the trans-Gulf route taken by eastern migrants passing through Alabama and the western–circum-Gulf routes taken by western migrants passing through California and possibly through New Mexico.

[3]Present address: Department of Biological Anthropology and Anatomy, Box 90383, 08 Bio Science Building, Duke University, Durham, North Carolina 27708, USA. E-mail: marylene.boulet@duke.edu

[4]Present address: Department of Evolution, Ecology and Organismal Biology, The Ohio State University, 300 Aronoff Laboratory, 318 West 12th Avenue, Columbus, Ohio 43210, USA.