SPECIATION IN THE WHITE-BREASTED NUTHATCH (SITTA CAROLINENSIS): A MULTILOCUS STUDY OF DIVERSIFICATION IN NORTH AMERICAN PINE AND OAK WOODLANDS

V.W. Walstrom*, G. M. Spellman, and J. Klicka
Department of Biology
Integrative Genomics Program
Black Hills State University
Spearfish, SD 57799
*veryl.walstrom@yellowjackets.busu.edu

ABSTRACT

Pine and oak woodlands are common North American floral communities with distinct regional species composition. The origination of these distinct communities was the once continentally distributed Tertiary forest. The orogeny of the late Miocene and Pliocene and Quaternary glacial cycles fragmented the Tertiary forest into separate regional communities. The White-breasted Nuthatch (Sitta carolinensis) is a common avian resident of these highly disjunct woodlands. One prior study has presented evidence for four distinct and well-supported clades that evolved in situ in these refugia. This study used one mitochondrial gene (ND2) to elucidate the phylogeography of this species. I am adding to these data the use of five known nuclear loci and fifteen anonymous nuclear loci. Multilocus data are pertinent when determining the accuracy of gene coalescence and divergence times of populations. The stochastic variance related to the creation of gene trees can be reduced only by increasing the number of loci sampled as opposed to the number of samples of the same gene. Analysis using the Genealogical Sorting Index, principle component analysis, and Structure agree with the former mtDNA study. It is very likely that when looking at differences in morphology, song, mtDNA and nuclear DNA, we have four distinct species of the White-breasted Nuthatch.