

Population structure and gene flow in a long-distance migrant bird,
the Bicknell's Thrush (*Catharus bicknelli*).

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Abstract

Isolation of populations may lead to interruption of gene flow among them. I plan to assess how much gene flow occurs among apparently isolated populations of Bicknell's Thrush. This bird nests above 900 m in several mountain ranges in upstate New York and northern New England. I will use microsatellite DNA variation to determine genetic distances among Bicknell's Thrush populations of the Catskills, Adirondacks, Green and White mountains. I hope to test the effectiveness of long-distance migration in bridging geographic and habitat gaps in this bird's range. Patterns of microsatellite DNA variation from Mt. Mansfield thrushes will be compared with patterns from other ranges and other peaks in the Green Mountains. As a control I plan to examine population structure of the continuously distributed and more numerous Gray-cheeked Thrush (*C. minimus*) in northern Québec and Labrador. Eleven thrushes were captured on Mt. Mansfield in June of 1993 (4) and 1994 (7). All four birds caught in 1993 were seen in 1994 demonstrating strong site faithfulness. DNA has been extracted from most samples and three polymerase chain reaction (PCR) primer sets amplify Bicknell's Thrush DNA. My study should have important implications for models of gene flow in mobile organisms, and conservation of migratory birds.

Introduction

The geographic isolation of fragments of habitat may interrupt gene flow among populations of organisms spread out among such fragments (Milligan et al. 1994). These processes can be modeled but are generally difficult to demonstrate under field conditions. Developments in molecular biology such as polymerase chain reaction (PCR) amplification of specific genetic loci have provided inferential tools for attacking problems in evolutionary biology including the genetic effects of habitat fragmentation and isolation (Avice 1994).

Short motif repetitive segments of nuclear DNA called microsatellites show promise for measuring fine-scale geographic variation among populations (Queller et al. 1993, Bowcock et al. 1994, Morin et al. 1994). I propose to use microsatellite DNA variation to examine patterns of microgeographic differentiation in a bird with a highly fragmented breeding range and small overall population, Bicknell's Thrush, and to compare these results with a control sample from the closely related, but more common and continuously distributed, subarctic Gray-cheeked Thrush.

The breeding range of Bicknell's Thrush is confined to southeastern Canada, northern New England and upstate New York (Ouellet 1993, Rimmer et al. 1993). In its United States range it is almost entirely found at high elevations in stunted subalpine spruce-fir forest. It is migratory, wintering in the Greater Antilles (Wallace 1939, Ouellet 1993). Concern has recently been expressed over the conservation status of this bird (Rimmer et al. 1993). Does the fragmented distribution of Bicknell's Thrush cause genetic partitioning of its populations? Long-distance migration might provide an important avenue for gene exchange among seemingly isolated populations. On the other hand, many migratory animals exhibit a high degree of natal philopatry, it is therefore necessary to assess the importance of migration in promoting gene flow among isolated populations of very mobile organisms such as Bicknell's Thrush.

Methods

I capture thrushes in 6 m nylon mist nets by inducing aggressive behavior with a tape of territorial songs and calls. I band and take several morphometric measurements from each bird. I then remove 100 μ l of blood from the humeral wing vein before releasing the bird. I transfer the blood to a lysis buffer solution to preserve DNA (Seutin et al. 1991). I obtain DNA from my samples with phenol-chloroform extraction (Kirby 1991). Three sets of PCR primers that amplify microsatellite loci in Long-tailed Manakins (*Chiroxiphia linearis*) (McDonald and Potts 1994, Shou-hsien Li, pers. comm.) also amplify Bicknell's Thrush loci, therefore I can use these to examine allelic variation among thrush populations. I will calculate population structure (F_{ST} ; Wright 1978), and gene flow (Nm ; Slatkin 1987) indices from polyacrylamide gels showing band patterns from the thrush populations I have sampled.

Results

I have captured and sampled 11 total Bicknell's Thrushes on Mt. Mansfield. Four were caught in June 1993, and a further seven were netted in June 1994 in joint netting with Christopher Rimmer of the Vermont Institute of Natural Science. At present I have met my minimum sample needs for Mt. Mansfield, however if variances in allele frequencies prove high I may need to add more individuals to aid in analyses of population structure, inbreeding coefficients, and gene flow. All four birds banded in 1993 were encountered in 1994 indicating site faithfulness. However three of the four were at new locations in 1994. Birds moved from 0 to 595 m between years. The bird that moved over one-half km was a one-year-old in June 1993. I have extracted DNA from six of the eleven Mt. Mansfield samples and I intend to complete extracting these samples in August 1995.

Context

My Mt. Mansfield work is a portion of my broader study of population structure in Bicknell's and Gray-cheeked thrushes in northeastern North America. I still need to increase my samples in the Adirondacks (n=8), and White Mountains (n=5) in 1995. I also will be collecting blood samples from Gray-cheeked Thrushes in northern Canada from late June through July 1995. I am hoping to use a short-term visitor award at the National Zoological Park Genetics Laboratory to develop more primers for microsatellite loci in Bicknell's Thrush by working with Dr. Robert Fleischer who is developing primers for the closely related Omao (*Phaeornis obscurus*).

Literature Cited

- Avise, J. C. 1994. *Molecular markers, Natural History, and Evolution*. Chapman and Hall, New York.
- Bowcock, A. M., A. Ruiz-Linares, J. Tomfohrde, E. Minch, J. R. Kidd, and L. L. Cavalli-Sforza. 1994. High resolution of human evolutionary trees with polymorphic microsatellites. *Nature* 368:455-457.
- Kirby, L. T. 1991. *DNA Fingerprinting*. Stockton Press, New York
- McDonald, D. B. and W. K. Potts. 1994. Cooperative display and relatedness among males in a lek-mating bird. *Science* 266:1030-1032.
- Milligan, B. G., J. Leebens-Mack, and A. E. Strand. 1994. Conservation genetics: Beyond maintenance of marker diversity. *Molec. Ecol.* 3:423-435.
- Morin, P. A., J. J. Moore, R. Chakraborty, Li J., J. Goodall, and D. S. Woodruff. 1994. Kin selection, social structure, gene flow, and the evolution of chimpanzees. *Science* 265:1193-1201.
- Ouellet, H. 1993. Bicknell's Thrush: Taxonomic status and distribution. *Wilson Bull.* 105:545-572.

- Queller, D. C., J. E. Strassman, and C. R. Hughes. 1993. Microsatellites and kinship. *Trends Ecol. Evol.* 8:285-288.
- Rimmer, C. C., J. L. Atwood, and L. R. Nagy. 1993. Bicknell's Thrush: A northeastern songbird in trouble? *Bird Observer* 21:84-89.
- Seutin, G., B. N. White, and P. T. Boag. 1991. Preservation of avian blood and tissue samples for DNA analyses. *Can. J. Zool.* 69:82-90.
- Slatkin, M. 1987. Gene flow and the geographic structure of natural populations. *Science* 236:787-792.
- Wallace, G. J. 1939. Bicknell's Thrush, its taxonomy, distribution, and life history. *Proc. of the Boston Soc. Nat. Hist.* 41:211-402.
- Wright, S. 1978. *Evolution and the genetics of natural populations. IV. Variability within and among natural populations.* University of Chicago Press, Chicago.