Genetic variation in a long-distance migrant bird, the Bicknell's Thrush (*Catharus [minimus] bicknellii*).

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Abstract

I hope to assess the genetic relatedness among apparently isolated populations of the Bicknell's Thrush. These birds occur above 900 m in mountains of the northeastern U.S.A., thus there appears to be isolation of breeding populations within and among mountain ranges. I propose to document the amount of gene flow among Bicknell's Thrush populations as a test of the effectiveness of long-distance migration in overcoming the geographic isolation of mountain-top bird populations. To achieve this end I will examine variation of microsatellite DNA loci among thrush populations in the Catskills, Adirondacks, Green and White mountains. Patterns of microsatellite DNA variation from Mt. Mansfield thrushes will be compared with patterns of variation from the other ranges listed above and other peaks in the Green Mountains. Four Bicknell's Thrushes were captured on Mt. Mansfield from 1-6 June 1993. DNA has been extracted from these samples as of February 1994. This study will have important implications for the conservation of migratory birds.

Introduction

Much recent research in conservation biology addresses the effects of habitat fragmentation and isolation (HFI, for birds see references in Hagan and Johnston 1992). It has been postulated that HFI may influence population structure including the possible interruption of gene flow among populations. These demographic processes can be modeled but are hard to examine under field conditions. Recent developments in molecular biology offer potential inferential tools for studying the genetic effects of HFI (Avise 1994). I plan to use a molecular marker system (microsatellite DNA loci) to document the population structure of Bicknell's Thrush which has a fragmented breeding distribution in the mountains of the northeastern U.S.A. I hope to estimate levels of inbreeding (in the population sense), and population isolation within and among mountain ranges. I believe this will enable me to establish the level of interaction between long-distance migration and isolation of breeding populations.

Molecular techniques that have been used to study population structure include protein electrophoresis (allozymes), mitochondrial DNA (mtDNA), and minisatellite DNA fingerprinting. Allozyme studies have limited value for establishing fine-scale population structure in birds due to low enzyme variability (Avise 1994). Although mtDNA can be used to detect population sub-division in birds (e.g., Avise and Nelson 1989), it appears to evolve too slowly for analysis of genetic variation at small geographic scales and time frames of less than one million years. Hypervariable repetitive nuclear DNA might be more appropriate for short-distance and geologically brief population separations. Nonetheless, minisatellite DNA is generally too variable and allows too little certainty in allele scoring to permit any more than crude estimates of population structure. Another hypervariable repetitive nuclear DNA class, microsatellite DNA, allows more precise identification and scoring of alleles combined with a large number of alleles per locus (Ellegren 1992, Queller *et al.* 1993). I propose to use microsatellite DNA to examine patterns of microgeographic variation in Bicknell's Thrush in the northeastern U.S., and compare these patterns with those of the closely related Gray-cheeked Thrush (*Catharus minimus*) of subarctic North America.

Bicknell's Thrush is a breeding endemic of northeastern North America ranging from the St. Lawrence River southward to the Catskill Mountains (Wallace 1939, Ouellet 1993), it is migratory, wintering in the Greater Antilles (Arendt 1992, Ouellet 1993). This bird is currently considered a subspecies of Gray-cheeked Thrush, however recent studies strongly suggest it is a separate species (Ouellet 1993). In its U.S. range Bicknell's Thrush is almost entirely restricted to stunted sub-alpine forest above 900 m elevation. Concern has recently arisen over the conservation status of this bird (Rimmer *et al.* 1993). Some populations have disappeared (e.g., Mt. Greylock, Massachusetts), and subalpine habitat has apparently been degraded by industrial pollution (Vogelmann 1982), and increased recreational pressure. Greater Antillean forest is also disappearing rapidly (Arendt 1992). A pressing question is: does the fragmented distribution of Bicknell's Thrush cause genetic partitioning of its population? It is imperative to separate the influence of

long-distance migration and its potential value in source-sink population dynamics from the influence of natal philopatry on gene flow among this thrushes' isolated mountain populations.

Methods

I capture Bicknell's Thrushes in 6 m nylon mist nets by inducing aggressive behavior with a tape of territorial calls and songs, and a carved thrush model. Once I have a bird in-hand I band and color-mark it (on Mt. Mansfield the right-leg combination is always mauve and USFWS band), make several measurements (e.g., tarsus), and collect 100 µl of blood from a small puncture in the medial wing vein. I collect samples in heparinized capillary tubes and transfer them to microcentrifuge tubes with 1 ml of lysis buffer that prevents degradation of high molecular weight DNA. DNA remains intact for extended periods in lysis buffer even at temperatures up to 25°C, but I have stored samples at 4°C to ensure sample quality.

I obtain DNA from my samples via phenol-chloroform extraction. I have access to microsatellite DNA primers designed for *Aphelocoma* jays that should help me amplify Bicknell's Thrush microsatellite loci with the polymerase chain reaction. I then will use acrylamide gel electrophoresis to visualize alleles at these loci. I will calculate band-sharing indices to assess population variation.

Results

I caught four thrushes on Mt. Mansfield from 1 to 6 June 1993. Two were captured along the Toll Road from the Octagon to the Summit Station, one along the WCAX Access Road west of the Nose, and one near the Forehead Bypass Trail. I collected blood samples ranging from 60-100µl (mean=89.5 µl). I extracted and precipitated DNA from these samples in February 1994.

Future Plans

I plan to obtain five to ten further samples from thrushes on Mt. Mansfield from 24 May to 1 June 1994. I also will search for the birds I color-marked during the previous field season to determine site-faithfulness.

Context

My studies on Mt. Mansfield, as indicated above, are part of a broader study of genetic variation of Bicknell's Thrush among four northeastern U.S. mountain ranges, the Catskills, Adirondacks, Green and White mountains. I also collected blood from nine birds on four mountains in the Catskills, four birds from Whiteface Mt. in the Adirondacks, and from four birds on Shrewsbury Peak in the southern Green Mountains in 1993. I plan to expand sampling in the Adirondacks, and extend sampling to the White Mountains in 1994. I will also collect blood from Gray-cheeked Thrushes in northern Canada during the 1995 field season to compare population structure in this closely related form to Bicknell's Thrush. I am just beginning extraction and analysis of DNA from my samples. I hope to perfect my lab skills during a proposed ten week graduate fellowship at the National Zoo in Washington, D.C. this autumn.

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