

Chapter Five

The Population History of Bicknell's Thrush and Veery

Introduction

The population history of Bicknell's Thrush and Veery are tied to the biogeographic effects of repeated Pleistocene glaciation. Much of northeastern North America was ice covered as recently as 14 to 13 thousand years ago and it was re-populated by its current flora and fauna in recent geologic times (Pielou 1991). Because Bicknell's Thrush and Veery have very different habitat preferences they likely had widely separated ranges at the glacial maximum and had very different recolonization patterns in the Northeast. Such differences in habitat and range expansion suggest that these birds may have had different population histories and may show different patterns of genetic variation and gene flow between them. The Bicknell's Thrush's habitat is sub-alpine boreal conifers, thus it must have inhabited regions at or near the edge of glacial ice during Pleistocene glaciations. Thus it is plausible that Bicknell's Thrush had a distribution shifted just a few hundred kilometers to the south of its current breeding range. As such the post-glacial range expansion of Bicknell's Thrush may not have involved an especially long-distance range shift. On the other hand, the Veery's association with hardwood forest implies its range was far to the south of its current position. The Veery probably had a much narrower geographic distribution due to the limited distribution of appropriate vegetation at

glacial maxima (e.g. Delcourt and Delcourt 1987), and would have lived a few thousand kilometers south of the bulk of its current range. Thus it appears reasonable to postulate a glacial population bottleneck, and rapid population expansion during the Veery's reoccupation of the north after ice retreated. It is also plausible that the Veery went through multiple founder events along its expanding post-glacial range front (Hewitt 1996).

Aspects of population history that may be inferred from coalescence patterns of genealogical trees derived from molecular data include effective population size (Kuhner *et al.* 1995), population growth (Kuhner *et al.* 1998b), and gene flow, including its rate and net direction (Beerli 1999). Patterns of population history may also be guessed at by examination of more standard measures of population genetic diversity and neutrality indices (Tajima 1989; Templeton 1998). I have used the population genetic analysis programs Arlequin (Schneider *et al.* 1997), Fluctuate (Kuhner *et al.* 1998a), and Migrate (Beerli 1997) on my mtDNA sequence data from Veery and Bicknell's Thrush to examine whether the Veery shows the hallmarks of a bottlenecked population and long-distance range expansion in contrast to Bicknell's Thrush.

Methods

I used Arlequin, developed at the University of Geneva (Schneider *et al.* 1997), to determine a variety of metrics from the data of both species and to test whether the sequences showed signs of exposure to natural selection. Arlequin is a broadly applicable population-genetics program that calculates an array of

population-genetic parameters for a variety of molecular data types including mtDNA sequences. These include measures of genetic diversity, and tests for neutrality of genetic variation (Schneider *et al.* 1997). The metrics I obtained included gene diversity (h), which is roughly equivalent to heterozygosity for diploid data, nucleotide diversity (π), the per site variation among the sequences, and the mean pairwise differences among the sequences. I also used the Arlequin to calculate values of Tajima's D statistic to test the assumption of sequence neutrality (Tajima 1989). Lack of response to natural selection is a valuable trait for determining population genetic parameters because the only force presumably acting on neutral sequences should be random genetic drift, thus reflecting the true patterns of gene flow and drift rather than recent selection.

I defined the samples from each mountain range as sub-populations for gene flow analyses. The metrics calculated by Arlequin shown in Table 5.1 are indicative of the amount of variation contained in each sub-population and allow inferences about the long-term size of populations due to the positive relationship between population size and maintenance of genetic variation. Since many of the parameters estimated by Arlequin assume a population that is not growing or experiencing gene flow, I also used the programs Migrate and Fluctuate from the University of Washington's LaMarc package that attempt to determine if these phenomena were acting on the populations I studied.

I used Fluctuate to measure effective population (N_{ef}) and population growth (g , Kuhner *et al.* 1998b), and Migrate to estimate bi-directional gene flow

among mountain ranges (Beerli and Felsenstein 1999). Fluctuate and Migrate construct gene trees, in essence genealogies, to determine patterns of coalescence in the data. These programs were developed by Joseph Felsenstein's research group and use maximum likelihood techniques to estimate population genetic parameters from genealogies of haplotypes employing a coalescent approach (Kingman 1980; Kingman 1982). Estimates derived from coalescence methods are sensitive to gene tree topology; thus it is important to find the correct intraspecific phylogeny to use these methods (Smouse 1998). Maximum likelihood estimation of parameters using Metropolis-Hastings Markov Chain analysis attempts to answer these objections by using data re-sampling and examination of large numbers of trees to obtain maximum likelihood estimates of effective population, population growth, and migration rate (Kuhner *et al.* 1998b; Beerli and Felsenstein 1999). These programs first establish an initial estimate of θ ($2N_{ef} \mu$) where μ represents the mutation rate per site per generation and N_{ef} the effective number of breeding females (because mtDNA is maternally inherited) by constructing a genealogical tree from the sequence data. This estimate of effective population and mutation rate is then used as a reference to construct further genealogical trees with maximum likelihood estimation. Each maximum likelihood tree is derived via a Markov Chain process using the posterior probability of the initial genealogy in comparison to the probability of each newly constructed genealogy in the chain. Several Markov Chains are run to produce maximum likelihood estimates, from the best genealogies, of the parameters g , the exponential growth rate; θ , in

essence the effective female population at a given mutation rate (Kuhner *et al.* 1998b); and the effective migration rate $4Nm$ (Beerli and Felsenstein 1999).

I executed runs with Fluctuate on the complete DNA sequence data for each species. I ran five short Markov Chains recording 400 genealogies per chain and achieved final maximum likelihood estimates of g and θ with two long Markov Chains recording 2000 genealogies in each chain.

I made pairwise comparisons among all pairs of sub-populations with Migrate to obtain estimates of bi-directional gene flow among sub-populations. To obtain gene flow estimates I ran 10 short chains in Migrate of 25,000 steps recording 500 genealogies, and three long chains of 2,500,000 steps recording 50,000 genealogies.

Results

Genetic Diversity

Bicknell's Thrush

Overall, Bicknell's Thrush shows higher levels of gene diversity, nucleotide diversity, and mean pairwise difference than does Veery (Table 5.1A), in spite of the Veery's higher number of variable sites and haplotypes. The Catskills exhibit the highest values for all genetic diversity indices including gene diversity, nucleotide diversity; and mean pairwise differences among sequences, the Green Mountains have the lowest gene diversity measure and the White Mountains show the lowest nucleotide diversity and mean pairwise differences.

Tajima's D statistics imply that the Bicknell's Thrush sequences have not been subjected to the effects of natural selection (see Table 4.2A). However note that although the values of Tajima's D statistic are not significant at $P < 0.05$, they do approach significance at $P < 0.1$ for the total sample and in the Catskills (see Table 4.2A). This trend suggests that these samples may not be strictly neutral to selection or that the population as a whole, and the Catskill sub-population in particular, may not be in strict equilibrium with respect to population growth or random genetic drift.

Veery

As noted above, the Veery samples show less genetic diversity than Bicknell's Thrush samples. As with Bicknell's Thrush, the Catskills show the highest values for measures of genetic diversity among sub-populations, but unlike Bicknell's Thrush, the Adirondacks exhibited the lowest values (see Table 5.1B).

Most of the Tajima's D statistics indicate that Veery samples do not vary significantly from neutrality (see Table 4.2B). However for all 40 sequences Tajima's D reaches $P < 0.05$. Although it does not reach this level for any single sub-population it trends toward significance at $P < 0.1$ for the Green Mountain sub-population (see Table 4.2B). The significance of Tajima's D for the entire Veery sample indicates that the populations may not be in equilibrium with respect to growth or drift, or that selection may be acting on the mitochondrial genome of the Veery at a regional scale (Tajima 1989). The latter conclusion is doubtful

given the non-coding nature of the control region and the high level of variability of control region III.

Effective Population Size and Estimates of Population Growth

Bicknell's Thrush

The maximum likelihood estimate of θ generated by Fluctuate for Bicknell's Thrush was 0.0320 (SD = 0.0032). If one applies a reasonable estimate of the mitochondrial mutation rate (μ) of ca. 1×10^{-8} substitutions per site per generation (Baker and Marshall 1997) this value of $2N_{ef}\mu$ translates to an effective female population (N_{ef}) of 800,000 (95% confidence interval around the estimate of theta, 640,000 to 960,000) in the region I sampled. At a faster mutation rate the N_{ef} would be smaller (e.g., at 1×10^{-6} it would be 64,000 to 96,000). The estimate of g (Kuhner *et al.* 1998a) was 790.15, indicative of slow growth or a stable population. To dramatize this, consider that at this growth rate the effective population is predicted to grow, assuming a mutation rate of 1×10^{-8} (as defined above), by 60 individuals in 100 generations (approximately 100 years).

Veery

The Veery displays an estimate of θ , 0.2852, almost nine times higher than in Bicknell's Thrush. This translates into an N_{ef} of 7,000,000 (95% confidence interval of theta, 5.6×10^6 to 8.7×10^6) in northeastern New York State, Vermont and New Hampshire assuming $\mu = 1 \times 10^{-8}$ substitutions per site per generation. The growth rate estimator $g = 2598.14$ suggests approximately

three times more rapid population growth than in Bicknell's Thrush. The predicted growth over the next 100 generations would be almost 1900 individuals.

Gene Flow

Bicknell's Thrush

Estimates of gene flow based on Markov Chain Monte Carlo maximum likelihood estimation via Migrate are shown in Figure 5.1A. This shows that all Bicknell's Thrush populations are connected by $N_m \geq 1.0$, that is at least one individual per generation brings its genes into another sub-population. When N_m reaches or exceeds 1.0 migrant per generation a population has sufficient gene flow to counteract random genetic drift. Migrate also allows inference on the direction of gene flow (Figure 5.1A). Note that there is at least some gene flow indicated from the Catskills and Green Mountains to all other sub-populations and that the amount of gene flow inferred is highest between the Catskills and Adirondacks.

Veery

Figure 5.1B shows gene flow estimates for the Veery. As with Bicknell's Thrush, all estimates of N_m exceed or are equivalent to 1.0. Migrate suggests an essentially infinite amount of gene flow between the Green and White Mountains (5.5×10^6), reflecting the predominance of haplotype A in all sub-populations and a lack of population subdivision. Not only is the abundant haplotype A almost evenly distributed across all mountain ranges, the three other haplotypes found in more than one bird (B, C and D) occurred in more than one region (see Figure 4.4). Although the inferred gene flow from the Green to White Mountains appears

far out of line, it is well to remember a value of Nm in excess of one is indicative of panmixia and that levels in excess of four imply essentially infinite gene flow and thus are not qualitatively different from any higher number. This result indicates how artificial it is to define sub-populations for this widespread species. The next highest levels of gene flow, according to Migrate, appear to be from the Catskills to the Adirondacks and from the White to the Green Mountains. The direction of gene flow is from the Green Mountains to all other regions and to the Adirondacks from all other regions. The Catskills and White Mountains show a mix of gene flow direction.

Discussion

Comparing the Population Genetics of Veery and Bicknell's Thrush in Northeastern Mountain Ranges

It is noteworthy that Catskills samples of both Veery and Bicknell's Thrush differ from samples from other ranges in their greater sequence diversity. The Catskills sub-populations exhibit the highest levels of gene diversity (h), nucleotide diversity (π), and mean pairwise sequence difference (see Chapter 4 and Table 5.1). The Catskills sub-populations also showed the highest haplotype diversity in both species, five in Bicknell's Thrush, and five in Veery (the Green Mountains also had five Veery haplotypes). I would be more skeptical of this pattern if it were not shown by both species. This may reflect the age of settlement of the Catskills sub-population as rare haplotypes are better represented in older populations (Templeton 1998).

It is also notable that the Catskills appear to show the genetic imprint of being the first settled region in the northeast for both species. A gradient from more variable to less variable populations appears to be a signature of range expansion (Templeton *et al.* 1995). It seems likely based on models of vegetation range expansion from palynological and macrofossil analyses that the Catskills were amenable to Bicknell's Thrush between 14,000 to 13,000 years before present (YBP) (Delcourt and Delcourt 1987). I also suggest that the species arrived thereafter in the Green Mountains 12,000 to 11,000 YBP, the Adirondacks 11,000 to 10,000 YBP, and the White Mountains 10,000 to 9,000 YBP. I base this hypothesis on the pattern of genetic diversity and the historical pattern of range expansion in beech (*Fagus grandifolia*), maple (*Acer* spp.), and hemlock (*Tsuga canadensis*) combined with the retreat of spruce (*Picea* spp.) and fir (*Abies* spp.) (Delcourt and Delcourt 1987). For instance, Davis *et al.* (1980) showed that balsam fir (*Abies balsamea*), an important element of current Bicknell's Thrush habitat (Sabo 1980), appeared in abundance in the White Mountain pollen record ca.9000 YBP. For much of the period from ca.12,000 YBP to 9000 YBP it is likely that Bicknell's Thrush habitat was more widespread and at lower elevations than it is in the present. The retreat to the current distribution along mountain ridges and summits probably took place 8000 to 7000 YBP during the hypsithermal interval (Pielou 1991). It has been demonstrated that white pine (*Pinus strobus*) and hemlock ranged upward to 1000 m in the White Mountains during this period (Davis *et al.* 1980), implying that suitable Bicknell's Thrush habitat was above this elevation at the time.

Similarly, the Veery probably arrived in the Catskills 11,000 to 10,000 YBP, the Green Mountains very soon thereafter, and the Adirondacks and White Mountains 8000 to 7000 YBP. This is based on the patterns of range expansion of beech, maple, oak (*Quercus* spp.), and hemlock (Delcourt and Delcourt 1987; Davis *et al.* 1980).

Patterns of gene flow between the Catskills and other ranges also appear explicable for similar reasons. The direction of gene flow is largely away from the Catskills in the Migrate analysis, indicating the status of the Catskills as a source of genetic variation in other mountain ranges. A notable exception is net gene flow from the Green Mountains in the Veery, and from the White Mountains in Bicknell's Thrush. The former seems biologically reasonable since it is likely that during its post-glacial range expansion the Veery may have reached the southern Green Mountains from the Hudson Lowlands very soon after reaching the Catskill region, thus making detection of a difference in net gene flow between the Catskills and Green Mountains unlikely. These mountain ranges are only 160 kilometers apart and the Veery probably re-settled the lowlands adjacent to them fairly rapidly leading to scant differences in re-settlement time and thus a seemingly inconsistent direction of gene flow between them. The net gene flow from the White Mountains to the Catskills in the Bicknell's Thrush, with its more insular distribution, is less likely to be based on biology than a sampling artifact, perhaps attributable to the makeup of the founder population in northern New Hampshire. Large estimates of gene flow were generated between the Catskills and Adirondacks for both thrushes. Given the close geographic proximity of the

ranges and their positions in a north to south line it is not surprising that the migratory Bicknell's Thrush's and Veery's respective sub-populations should exchange genes regularly across the modest barriers of the Mohawk Valley and intervening low ranges.

It seems probable that the Catskill sub-population of Bicknell's Thrush initially built up to high numbers, enabling it to retain much genetic diversity even after a long-term slow decline set in as the interglacial climate warmed. Alternatively, the current level of gene flow with other mountain ranges is sufficiently high to retain the original level of genetic diversity achieved upon colonization. This explanation seems less likely than the former when one considers the direction of gene flow inferred by 'Migrate'. It is plausible that both mechanisms contribute to the relatively high levels of genetic diversity evinced by Catskills samples of both species.

Comparing Bicknell's Thrush to Veery

The salient difference between Veery and Bicknell's Thrush is the paradoxically higher genetic diversity of Bicknell's Thrush, given its lower number of haplotypes overall, and its small, slowly growing population. Results from 'Fluctuate' reveal a Bicknell's Thrush population far smaller than Veery that is increasing slowly if at all. 'Fluctuate' estimates a very high population for Bicknell's Thrush (ca. 800,000), relative to current field estimates of 25,000 to 50,000 (Rimmer *et al.* 2001). The high and positive Tajima's D (1.8247) in Bicknell's Thrush seems to indicate a population that has declined or one that is stable but not at drift equilibrium. Only the Catskill sub-population produced a

comparably high level of Tajima's D. Given that this sub-population has almost certainly declined since the interglacial temperature maximum ca. 8000 YBP, a high Tajima's D may reflect this decline.

By contrast, in spite of low measures of genetic diversity, the Veery shows all the earmarks of a rapidly growing population, exhibiting many apparently young and scarce haplotypes along with a seemingly older and abundant core haplotype. A similar pattern has been documented for the widespread and common Greenfinch (*Carduelis chloris*) of Europe, attributed by Merilä *et al.* (1997) to growth out of southern European bottlenecked populations in glacial refugia. Hewitt (1996) has also pointed out that genetic diversity might be lost at an expanding range front as a species occupies new territory due to the establishment of many small founder populations at the forefront of the expansion. The significant negative value of Tajima's D (-1.8373) probably indicates a rapid demographic expansion rather than the effect of selection on the control region (Hartl and Clark 1997).

These data appear to reflect the contrasting population histories of these thrush species. The Bicknell's Thrush's range was much closer to the glacial front at its maximum advance and this species has likely always maintained a much smaller, more stable population with greater levels of genetic diversification than Veery (i.e. fewer but more widely diverging haplotypes). They have also been present in the northeast north of the maximum glacial advance at least two to three thousand years longer than Veery (see above). On the other hand, the Veery shows signs of having spent time in a small, bottlenecked population in a

restricted refugium or refugia well south of the current southern boundary of its modern range. Although one cannot pinpoint the location of this refugium, the vegetation maps in Delcourt and Delcourt (1987) suggest that it may have been in the Mississippi Delta region. The rapid demographic expansion has nearly obliterated much indication of the pattern of range expansion in the Veery. However the genetic diversity gradient from the Catskills and Green Mountains to the Adirondacks and White Mountains and the direction of the gene flow indicated in Figure 5.1 sensibly suggest that settlement occurred later in northeastern New York and northern New Hampshire.

Summary

The higher levels of genetic diversity for both Bicknell's Thrush and Veery seen in the Catskill samples sensibly suggest that the Catskills have indeed been longer occupied than the more northerly Adirondack, Green and White mountains. The differing patterns of genetic diversity, and coalescence estimates of population growth and population size point to small populations showing little growth in Bicknell's Thrush versus much larger populations that have grown much faster in the Veery. This result is consistent with presumptive bottlenecks combined with a fairly rapid population increase and post-glacial range expansion in the Veery. Bicknell's Thrush seems to have had a stable population with fairly high levels of dispersal to maintain genetic diversity. The high value of Tajima's D in the Catskill Mountains may indicate a population decline in Bicknell's Thrush at the southern edge of its range. The comparable gene flow

results between the Φ_{ST} based estimates of Chapter Four and the coalescence-based method used in this chapter emphasize the apparent mobility of Bicknell's Thrush among mountain ranges.

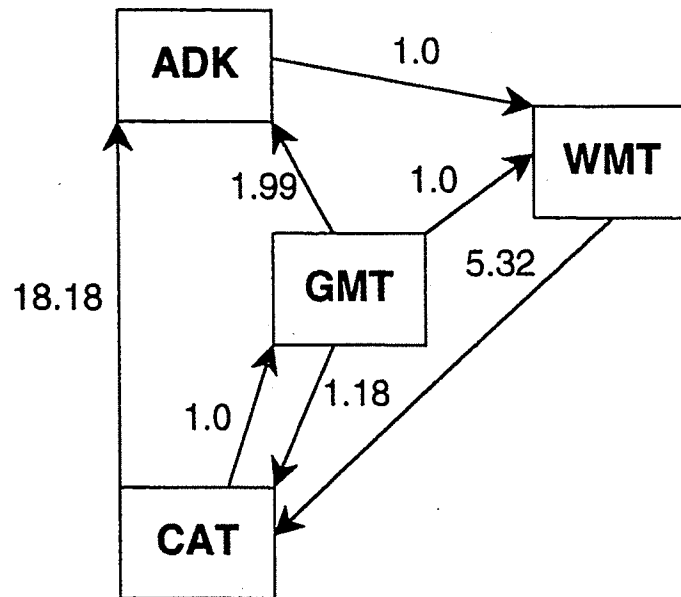
Conservation of Bicknell's Thrush should focus on habitat preservation and the husbanding of its largest source populations (e.g. Mt. Mansfield, Vermont; Mt. Washington, New Hampshire), as well as a major effort to preserve the limited wintering habitat on Hispaniola (C. Rimmer, pers. comm.). The Veery appears to be in less danger than Bicknell's Thrush, but it has gone through an extended decline over the last three decades (Price *et al.* 1995), apparently due to habitat fragmentation and habitat loss on its South American wintering range (Moskoff 1995). If these trends continue the Veery's apparent lack of genetic diversity attributable to Pleistocene population bottlenecks may limit its ability to adapt to global change in the near future.

Diversity Indices

	<u>Gene</u> <u>Diversity (<i>h</i>)</u>	<u>Nucleotide</u> <u>Diversity (π)</u>	<u>Mean Pairwise</u> <u>Difference</u>
A. <u>Bicknell's Thrush</u>			
Total	0.7010	0.005995	2.35
Adirondack	0.6889	0.006122	2.40
Catskill	0.8000	0.006546	2.53
Green Mt.	0.5256	0.005155	2.00
White Mt.	0.6889	0.004138	1.62
B. <u>Veery</u>			
Total	0.6026	0.001699	0.67
Adirondack	0.3778	0.001023	0.40
Catskill	0.7556	0.002444	0.96
Green Mt.	0.6667	0.001538	0.60
White Mt.	0.6444	0.001913	0.76

Table 5.1. Measures of genetic diversity in Bicknell's Thrush and Veery for the complete sample and among sub-populations.

A. Bicknell's Thrush



B. Veery

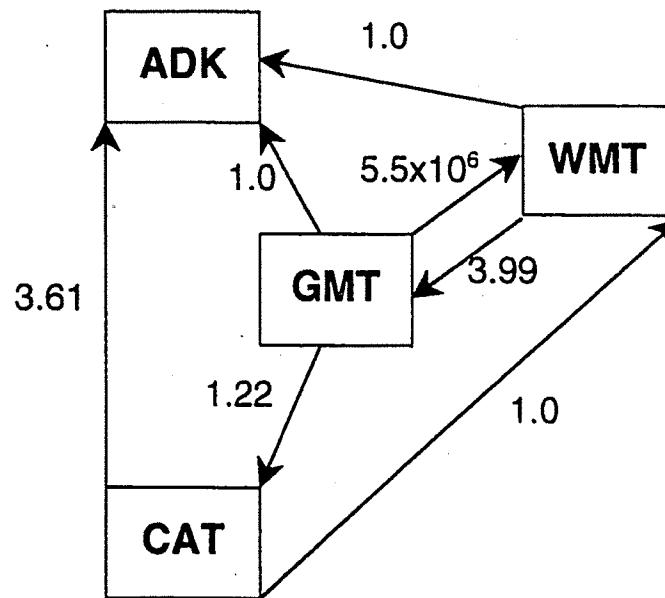


Figure 5.1. Patterns and rates of gene flow among mountain ranges for Bicknell's Thrush (A) and Veery (B). The boxes represent mountain ranges roughly in relation to geographical position (ADK=Adirondacks, CAT=Catskills, GMT=Green Mts., WMT=White Mts.). Lines among boxes represent gene flow with arrow heads indicating the predominant direction of genetic exchange, and the numbers representing the calculated number of breeding individuals exchanged per generation ($4N_m$) by the program Migrate (Beerli and Felsenstein 1999).

Literature Cited

- American Ornithologists' Union (1995) Fortieth supplement to the American Ornithologists' Union *Check-list of North American Birds*. *Auk* 112: 819-830.
- American Ornithologists' Union (1998) Check-list of North American Birds. Washington, D. C.: American Ornithologists' Union.
- Andrle, R. F. and J. R. Carroll (1988) The Atlas of Breeding Birds in New York State. Ithaca, NY: Cornell University Press.
- Arctander, P. (1988) Comparative studies of avian DNA by restriction fragment length polymorphism analysis: Convenient procedures based on blood samples from live birds. *Journal fur Ornithologie* 129: S. 205-216.
- Askins, R. A., J. F. Lynch and R. Greenberg (1990) Population declines in migratory birds in eastern North America. Pp. 1-57 in *Current Ornithology*, Vol 7. Power, D. M., Ed. New York: Plenum.
- Avise, J. C. (1983) Biochemical studies of microevolutionary processes: Commentary. Pp. 262-270 in *Perspectives in Ornithology*. Brush, A. H. and G. A. Clark, Eds. New York: Cambridge University Press.
- Avise, J. C. (1994) *Molecular Markers, Natural History and Evolution*. New York: Chapman and Hall.
- Avise, J. C. (1998) The history and purview of phylogeography: A personal reflection. *Molecular Ecology* 7(4): 371-379.
- Avise, J. C., R. T. Alisauskas, W. S. Nelson and C. D. Ankney (1992) Matriarchal population genetic structure in an avian species with female natal philopatry. *Evolution* 46: 1084-1096.
- Avise, J. C., J. Arnold, R. M. Ball, E. Bermingham, T. Lamb, J. E. Neigel, C. A. Reeb and N. C. Saunders (1987) Intraspecific phylogeography: The mitochondrial DNA bridge between population genetics and systematics. *Annual Review of Ecology and Systematics* 18: 489-522.
- Avise, J. C., J. C. Patton and C. F. Aquadro (1980) Evolutionary genetics of birds. I. Relationships among North American thrushes and allies. *Auk* 97: 135-147.

- Avise, J. C. and D. Walker (1998) Pleistocene phylogeographic effects on avian populations and the speciation process. *Proceedings of the Royal Society of London B: Biological Sciences* **265**: 457-463.
- Avise, J. C. and K. Wollenberg (1997) Phylogenetics and the origin of species. *Proceedings of the National Academy of Sciences of the United States of America* **94**: 7748-7755.
- Baker, A. J., C. H. Daugherty, R. Colbourne and J. L. McLennan (1995) Flightless brown kiwis of New Zealand possess extremely subdivided population structure and cryptic species like small mammals. *Proceedings of the National Academy of Sciences of the United States of America* **92**: 8254-8258.
- Baker, A. J. and H. D. Marshall (1997) Mitochondrial control region sequences as tools for understanding evolution. Pp. 51-82 *in* Avian Molecular Evolution and Systematics. Mindell, D. P., Ed. New York: Academic Press.
- Baker, M. C. (1981) A muscle biopsy procedure for use in electrophoretic studies of birds. *Auk* **98**: 392-393.
- Ball, R. M. and J. C. Avise (1992) Mitochondrial DNA phylogeographic differentiation among avian populations and the evolutionary significance of subspecies. *Auk* **109**: 626-636.
- Ball, R. M., Jr., S. Freeman, F. C. James, E. Bermingham and J. C. Avise (1988) Phylogeographic population structure of Red-winged Blackbirds assessed by mitochondrial DNA. *Proceedings of the National Academy of Sciences of the United States of America* **85**: 1558-1562.
- Barrell, B. G., S. Anderson, A. T. Bankier and J. Drouin (1979) A different genetic code in human mitochondria. *Nature* **282**: 189-194.
- Beerli, P. (1997) MIGRATE: documentation and program, part of LAMARC. 0.4. University of Washington.
- Beerli, P. (1998) Estimation of migration rates and population sizes in geographically structured populations. Pp. 39-53 *in* Advances in Molecular Ecology. Carvalho, G., Ed. Amsterdam: IOS Press.
- Beerli, P. (1999) Analysis of geographically structured populations: (Traditional) estimators based on gene frequencies. Department of Genetics, University of Washington. Web Page.

- Beerli, P. and J. Felsenstein (1999) Maximum likelihood estimation of migration rates and effective population numbers in two populations using a coalescent approach. *Genetics* **152**(2): 763-773.
- Bensch, S. and A. Härlid (2000) Mitochondrial genomic rearrangements in songbirds. *Molecular Biology and Evolution* **17**(1): 107-113.
- Bertin, R. I. (1977) Breeding habitats of the Wood Thrush and Veery. *Condor* **79**: 303-311.
- Bibb, M. J., R. A. V. Etten, C. T. Wright, M. W. Walberg and D. A. Clayton (1981) Sequence and gene organization of mouse mitochondrial DNA. *Cell* **26**: 167-180.
- Bossart, J. L. and D. P. Prowell (1998) Genetic estimates of population structure and gene flow: Limitations, lessons and new directions. *Trends in Ecology & Evolution* **13**(5): 202-206.
- Brown, W. M. (1985) The mitochondrial genome of animals. Pp. 95-130 in *Molecular Evolutionary Genetics*. MacIntyre, R. J., Ed. New York: Plenum Press.
- Brown, W. M., E. M. Prager, A. Wang and A. C. Wilson (1982) Mitochondrial DNA sequences of primates: Tempo and mode of evolution. *Journal of Molecular Evolution* **18**: 225-239.
- Brown, W. M. and J. Vinograd (1974) Restriction endonuclease cleavage maps of animal mitochondrial DNAs. *Proceedings of the National Academy of Sciences of the United States of America* **71**: 4617-4621.
- Buerkle, C. A. (1999) The historical pattern of gene flow among migratory and nonmigratory populations of Prairie Warblers (Aves: Parulinae). *Evolution* **53**(6): 1915-1924.
- Cochran, W. W., G. G. Montgomery and R. R. Graber (1967) Migratory flights of *Hylocichla* thrushes in spring: A radio telemetry study. *Living Bird* **6**: 213-225.
- Collura, R. V. and C.-B. Stewart (1995) Insertions and duplications of mtDNA in the nuclear genomes of Old World monkeys and hominoids. *Nature* **378**: 485-489.
- Davis, M. B., R. W. Spear and L. C. K. Shane (1980) Holocene climate of New England. *Quaternary Research* **14**: 240-250.

- Delcourt, P. A. and H. R. Delcourt (1987) Long-term forest dynamics of the temperate zone. Berlin: Springer-Verlag.
- Diamond, J. (1986) Overview: Laboratory experiments, field experiments, and natural experiments. Pp. 3-22 in *Community Ecology*. Diamond, J. and T. J. Case, Eds. New York: Harper and Row.
- Diehl, R. H. and R. P. Larkin (1998) Wingbeat frequency of two *Catharus* thrushes during nocturnal migration. *Auk* 115(3): 591-601.
- Dilger, W. C. (1956a) Adaptive modifications and ecological isolating mechanisms in the thrush genera *Catharus* and *Hylocichla*. *Wilson Bulletin* 68: 170-199.
- Dilger, W. C. (1956b) Hostile behavior and reproductive isolating mechanisms in the avian genera *Catharus* and *Hylocichla*. *Auk* 73: 312-353.
- Edwards, S. V. (1993) Long-distance gene flow in a cooperative breeder detected in genealogies of mitochondrial DNA sequences. *Proceedings of the Royal Society of London B: Biological Sciences* 252: 177-185.
- Excoffier, L., P. E. Smouse and J. M. Quattro (1992) Analysis of molecular variance inferred from metric distances among DNA haplotypes: Application to human mitochondrial DNA restriction data. *Genetics* 131: 479-491.
- Eyre-Walker, A., N. H. Smith and J. M. Smith (1999) How clonal are human mitochondria? *Proceedings of the Royal Society of London B: Biological Sciences* 266: 477-483.
- Felsenstein, J. (1985) Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* 39: 783-791.
- Fleischer, R. C. (1998) Genetics and avian conservation. Pp. 29-47 in *Avian Conservation*. Marzluff, J. M. and R. Sallabanks, Eds. Washington, D.C.: Island Press.
- Freeland, J. R. and P. T. Boag (1999a) The mitochondrial and nuclear genetic homogeneity of the phenotypically diverse Darwin's ground finches. *Evolution* 53(5): 1553-1563.

- Freeland, J. R. and P. T. Boag (1999b) Phylogenetics of Darwin's finches: Paraphyly in the tree-finches, and two divergent lineages in the Warbler Finch. *Auk* **116**(3): 577-588.
- Gemmel, N. J. and S. Akiyama (1996) An efficient method for the extraction of DNA from vertebrate tissues. *Trends in Genetics* **12**: 338-339.
- Godfrey, W. E. (1986) *The Birds of Canada*. Ottawa: National Museums of Canada.
- Greenwood, P. J. (1987) Inbreeding, philopatry and optimal outbreeding in birds. Pp. 207-222 in *Avian Genetics: A population and Ecological Approach*. Cooke, F. and P. A. Buckley, Eds. New York: Academic Press.
- Gyllensten, U., D. Wharton, A. Josefsson and A. C. Wilson (1991) Paternal inheritance of mitochondrial DNA in mice. *Nature* **352**: 255-257.
- Hagelberg, E., N. Goldman, P. Lió, S. Whelan, W. Schiefenhövel, J. B. Clegg and D. K. Bowden (1999) Evidence for mitochondrial DNA recombination in a human population of island Melanesia. *Proceedings of the Royal Society of London B: Biological Sciences* **266**: 485-492.
- Hall, G. A. (1983) *West Virginia Birds*. Carnegie Museum of Natural History Special Publication No. 7. Pittsburgh, PA: Carnegie Museum of Natural History.
- Hanski, I. (1998) Metapopulation dynamics. *Nature* **396**: 41-49.
- Hartl, D. L. and A. G. Clark (1997) *Principles of Population Genetics*. Sunderland, MA: Sinauer Associates, Inc.
- Hastings, A. and S. Harrison (1994) Metapopulation dynamics and genetics. *Annual Review of Ecology and Systematics* **25**: 167-188.
- Hewitt, G. M. (1996) Some genetic consequences of ice ages, and their role in divergence and speciation. *Biological Journal of the Linnean Society* **58**: 247-276.
- Hobson, K. A., K. P. McFarland, L. I. Wassenaar, C. C. Rimmer and J. E. Goetz (2001) Linking breeding and wintering grounds of Bicknell's Thrushes using stable isotope analyses of feathers. *Auk* **118**(1): 16-23.

- Holder, K., R. Montgomerie and V. L. Friesen (1999) A test of the Glacial Refugium Hypothesis using patterns of mitochondrial and nuclear DNA sequence variation in Rock Ptarmigan (*Lagopus mutus*). *Evolution* **53**(6): 1936-1950.
- Holmes, R. T. and S. K. Robinson (1988) Spatial patterns, foraging tactics, and diets of ground-foraging birds in a northern hardwoods forest. *Wilson Bulletin* **100**: 377-394.
- Holmes, R. T. and R. H. Sawyer (1975) Oxygen consumption in relation to ambient temperature in five species of forest-dwelling thrushes (*Hylocichla* and *Catharus*). *Comparative Biochemistry and Physiology* **50A**: 527-531.
- Ingman, M., H. Kaessmann, S. Pääbo and U. Gyllensten (2000) Mitochondrial genome variation and the origin of modern humans. *Nature* **408**: 708-713.
- Johns, M. B. and J. E. Paulus-Thomas (1989) Purification of human genomic DNA from whole blood using sodium perchlorate in place of phenol. *Analytical Biochemistry* **180**: 276-278.
- Kingman, J. F. C. (1980) *Mathematics of Genetic Diversity*. Philadelphia: Society for Industrial and Applied Mathematics.
- Kingman, J. F. C. (1982) The coalescent. *Stochastic Processes and their Applications* **13**: 235-248.
- Klicka, J. and R. M. Zink (1997) The importance of recent ice ages in speciation: A failed paradigm. *Science* **277**: 1666-1669.
- Kocher, T. D., W. K. Thomas, A. Meyer, S. V. Edwards, S. Pääbo, F. X. Villablanca and A. C. Wilson (1989) Dynamics of mitochondrial DNA evolution in animals: amplification and sequencing with conserved primers. *Proceedings of the National Academy of Sciences of the United States of America* **86**: 6196-6200.
- Kuhner, M. K., J. Yamato and J. Felsenstein (1995) Estimating effective population size and mutation rate from sequence data using Metropolis-Hastings sampling. *Genetics* **140**: 1421-1430.
- Kuhner, M. K., J. Yamato and J. Felsenstein (1998a) FLUCTUATE - Metropolis-Hastings Markov Chain Monte Carlo genealogy sampler. 1.3. University of Washington.

- Kuhner, M. K., J. Yamato and J. Felsenstein (1998b) Maximum likelihood estimation of population growth rates based on the coalescent. *Genetics* **149**: 429-434.
- Kumar, S., P. Hedrick, T. Dowling and M. Stoneking (2000) Questioning evidence for recombination in human mitochondrial DNA. *Science* **288**: 1931a.
- Lanyon, S. M. (1985) Detecting internal inconsistencies in distance data. *Systematic Zoology* **34**: 397-403.
- Levine, E., Ed. (1998) Bull's birds of New York State. Ithaca, NY: Cornell University Press.
- Li, S.-H. (2000) The phylogeography of a sedentary species, the Mexican Jay (*Aphelocoma ultramarina*). *submitted*.
- Lovette, I. J. and E. Bermingham (1999) Explosive speciation in the New World *Dendroica* warblers. *Proceedings of the Royal Society of London B: Biological Sciences* **266**: 1629-1636.
- Lynch, M. and T. J. Crease (1990) The analysis of population survey data on DNA sequence variation. *Molecular Biology and Evolution* **7**(4): 377-394.
- Marshall, H. D. and A. J. Baker (1998) Rates and patterns of mitochondrial DNA sequence evolution in Fringilline finches (*Fringilla* spp.) and the Greenfinch (*Carduelis chloris*). *Molecular Biology and Evolution* **15**(6): 638-646.
- Mayr, E. (1963) Animal Species and Evolution. Cambridge, MA: Harvard University Press.
- Mayr, E. and L. L. Short (1970) Species Taxa of North American Birds: A Contribution to Comparative Systematics. Cambridge, MA: Nuttall Ornithological Club.
- McLaren, I. A. (1995) Field identification and taxonomy of Bicknell's Thrush. *Birding* **27**: 358-366.
- Merilä, J., M. Björklund and A. J. Baker (1997) Historical demography and present day population structure of the greenfinch, *Carduelis chloris* - An analysis of mtDNA control-region sequences. *Evolution* **51**(3): 946-956.

- Miller, S. A., D. D. Dykes and H. F. Polesky (1988) A simple salting out procedure for extracting DNA from human nucleated cells. *Nucleic Acids Research* 16(3): 1215.
- Moore, W. S. (1995) Inferring phylogenies from mtDNA variation: Mitochondrial-gene trees versus nuclear-gene trees. *Evolution* 49(4): 718-726.
- Moskoff, W. (1995) Veery (*Catharus fuscescens*). Pp. 16 in *The Birds of North America*, No 142. Poole, A. and F. Gill, Eds. Philadelphia, PA and Washington, D.C.: The Academy of Natural Sciences and The American Ornithologists' Union.
- Nei, M., T. Maruyama and R. Chakraborty (1975) The bottleneck effect and genetic variability in populations. *Evolution* 29: 1-10.
- Neigel, J. E. (1996) Estimation of effective population size and migration parameters from genetic data. Pp. 329-346 in *Molecular Genetic Approaches in Conservation*. Smith, T. B. and R. K. Wayne, Eds. New York: Oxford University Press.
- Neigel, J. E., R. M. Ball, Jr. and J. C. Avise (1991) Estimation of single generation migration distances from geographic variation in animal mitochondrial DNA. *Evolution* 45(2): 423-432.
- Noon, B. R. (1981) The distribution of an avian guild along a temperate elevational gradient: The importance and expression of competition. *Ecological Monographs* 51: 105-124.
- O'Brien, S. J., M. E. Roelke, L. Marker, A. Newman, C. A. Winkler, D. Meltzer, L. Colly, J. F. Evermann, M. Bush and D. E. Wildt (1985) Genetic basis for species vulnerability in the cheetah. *Science* 227: 1428-1434.
- Ouellet, H. (1993) Bicknell's Thrush: Taxonomic status and distribution. *Wilson Bulletin* 105: 545-572.
- Peterson, R. T. (1980) A field guide to the birds east of the Rockies. Boston: Houghton Mifflin Company.
- Petren, K., B. R. Grant and P. R. Grant (1999) A phylogeny of Darwin's finches based on microsatellite DNA length variation. *Proceedings of the Royal Society of London B: Biological Sciences* 266: 321-329.
- Phillips, A. R. (1991) *The Known Birds of North and Middle America, Part II*. Denver, CO: A. R. Phillips.

- Pielou, E. C. (1991) *After the Ice Age: The Return of Life to Glaciated North America*. Chicago: University of Chicago Press.
- Price, J., S. Droege and A. Price (1995) *The Summer Atlas of North American Birds*. New York: Academic Press.
- Price, T., H. L. Gibbs, L. d. Sousa and A. D. Richman (1998) Different timing of the adaptive radiations of North American and Asian warblers. *Proceedings of the Royal Society of London B: Biological Sciences* **265**: 1969-1975.
- Questiau, S., M.-C. Eybert, A. R. Gaginskya, L. Gielly and P. Taberlet (1998) Recent divergence between two morphologically differentiated subspecies of bluethroat (*Aves: Muscicapidae: Luscinia svecica*) inferred from mitochondrial DNA sequence variation. *Molecular Ecology* **7**(2): 239-245.
- Quinn, T. W. (1997) Molecular evolution of the mitochondrial genome. Pp. 3-28 in *Avian Molecular Evolution and Systematics*. Mindell, D. P., Ed. New York: Academic Press.
- Ridgely, R. S. and G. Tudor (1989) *The Birds of South America: Oscine passerines*. Austin: University of Texas Press.
- Ridgway, R. (1882) Descriptions of two new thrushes from the United States. *Proceedings of the United States National Museum* **4**: 374-379.
- Rimmer, C. C., J. L. Atwood and L. R. Nagy (1993) Bicknell's Thrush: A northeastern songbird in trouble? *Bird Observer* **21**: 84-89.
- Rimmer, C. C. and K. P. McFarland (1999) Sky island songbirds. *Natural History* **108**(7): 34-39.
- Rimmer, C. C., K. P. McFarland, W. G. Ellison and J. Goetz (2001) Bicknell's Thrush (*Catharus bicknelli*). Pp. in *The Birds of North America*. Poole, A. and F. Gill, Eds.: The Academy of Natural Sciences, Philadelphia, PA, and The American Ornithologists' Union, Washington, D.C.
- Robinson, S. K., F. R. I. Thompson, T. M. Donovan, D. R. Whitehead and J. Faaborg (1995) Regional forest fragmentation and the nesting success of migratory birds. *Science* **267**: 1987-1990.

Rockwell, R. F. and G. F. Barrowclough (1987) Gene flow and the genetic structure of populations. Pp. 223-255 in *Avian Genetics: A Population and Ecological Approach*. Cooke, F. and P. A. Buckley, Eds. New York: Academic Press.

Rowley, J. S. and R. T. Orr (1964) The status of Frantzius' Nightingale Thrush. *Auk* **81**: 308-314.

Sabo, S. R. (1980) Niche and habitat relations in subalpine bird communities of the White Mountains of New Hampshire. *Ecological Monographs* **50**: 241-257.

Sabo, S. R. and R. T. Holmes (1983) Foraging niches and the structure of forest bird communities in contrasting montane habitats. *Condor* **85**: 121-138.

Saccheri, I., M. Kuussaari, M. Kankare, P. Vikman, W. Fortelius and I. Hanski (1998) Inbreeding and extinction in a butterfly population. *Nature* **392**: 491-494.

Sambrook, J., E. F. Fritsch and T. Maniatis (1989) *Molecular Cloning: A Laboratory Manual*: Cold Spring Harbor Laboratory.

Schneider, S., J.-M. Kueffer, D. Roessli and L. Excoffier (1997) Arlequin version 1.0: A software package for population genetic data analysis. 1.0. Genetics and Biometry Laboratory, University of Geneva.

Seutin, G., B. N. White and P. T. Boag (1991) Preservation of avian blood and tissue samples for DNA analysis. *Canadian Journal of Zoology* **69**: 82-90.

Shields, G. F. and A. C. Wilson (1987) Calibration of mitochondrial DNA evolution in geese. *Journal of Molecular Evolution* **24**: 212-217.

Sibley, C. G. and B. L. Monroe, Jr. (1990) *Distribution and Taxonomy of the Birds of the World*. New Haven, CT: Yale University Press.

Slatkin, M. (1987) Gene flow and the geographic structure of natural populations. *Science* **236**: 787-792.

Slatkin, M. and W. P. Maddison (1989) A cladistic measure of gene flow inferred from the phylogenies of alleles. *Genetics* **123**: 603-613.

Smouse, P. E. (1998) To tree or not to tree. *Molecular Ecology* **7**(4): 399-412.

- Stupka, A. (1963) Notes on the Birds of Great Smoky Mountains National Park. Knoxville, TN: The University of Tennessee Press.
- Swofford, D. L. (2001) PAUP*. Phylogenetic Analysis Using Parsimony (* and Other Methods). Version 4. Sinauer Associates.
- Swofford, D. L., Gary J. Olsen, Peter J. Waddell, and David M. Hillis (1996) Phylogenetic inference. Pp. 407-514 in *Molecular Systematics*. Hillis, D. M., Craig Moritz, and Barbara K. Mable, Ed. Sunderland, MA: Sinauer Associates, Inc.
- Tajima, F. (1989) Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. *Genetics* 123: 585-595.
- Takahata, N. and S. R. Palumbi (1985) Extranuclear differentiation and gene flow in the finite island model. *Genetics* 109: 441-457.
- Tarr, C. L. (1995) Primers for amplification and determination of mitochondrial control-region sequences in oscine passerines. *Molecular Ecology* 4(4): 527-529.
- Tarr, C. L. and R. C. Fleischer (1993) Mitochondrial-DNA variation and evolutionary relationships in the Amakihi complex. *Auk* 110: 825-831.
- Templeton, A. R. (1998) Nested clade analyses of phylogeographic data: testing hypotheses about gene flow and population history. *Molecular Ecology* 7(4): 381-397.
- Templeton, A. R., E. Routman and C. A. Phillips (1995) Separating population structure from population history: A cladistic analysis of the geographical distribution of mitochondrial DNA haplotypes in the tiger salamander, *Ambystoma tigrinum*. *Genetics* 140: 767-782.
- Todd, W. E. C. (1963) Birds of the Labrador Peninsula and Adjacent Areas: A Distributional List. Toronto: University of Toronto Press.
- Wallace, G. J. (1939) Bicknell's Thrush, its taxonomy, distribution, and life history. *Proceedings of the Boston Society of Natural History* 41: 211-402.
- Weary, D. M., R. E. Lemon and E. M. Date (1987) Neighbour-stranger discrimination by song in the veery, a species with song repertoires. *Canadian Journal of Zoology* 65: 1206-1209.

- Winker, K. and J. H. Rappole (1988) The relationship between *Hylocichla* and *Catharus* (Turdinae). *Auk* 105: 392-394.
- Wright, S. (1931) Evolution in mendelian populations. *Genetics* 127: 97-159.
- Wright, S. (1969) Evolution and the Genetics of Natural Populations. II. The Theory of Gene Frequencies. Chicago: University of Chicago Press.
- Wright, S. (1978) Evolution and the Genetics of Natural Populations. IV. Variability Within and Among Natural Populations. Chicago: University of Chicago Press.
- Yong, W. and F. R. Moore (1997) Spring stopover of intercontinental migratory thrushes along the northern coast of the Gulf of Mexico. *Auk* 114(2): 263-278.
- Zink, R. M. and R. C. Blackwell (1998) Molecular systematics and biogeography of aridland gnatcatchers (genus *Polioptila*) and evidence supporting species status of the California gnatcatcher (*Polioptila californica*). *Molecular Phylogenetics and Evolution* 9(1): 26-32.
- Zink, R. M. and D. L. Dittmann (1993) Gene flow, refugia, and evolution of geographic variation in the song sparrow (*Melospiza melodia*). *Evolution* 47: 717-729.

Appendix I

Thrushes Sampled in this Study

Complete band numbers, location information, and morphometric data for Bicknell's Thrushes, Veeries and Gray-cheeked Thrushes captured in this study.

Date format includes Roman numeral to represent month;
Age codes: SY=Second (calendar) Year, AHY=After Hatch Year;
Sex codes: M=Male, F=Female, U=Unknown sex

Bicknell's Thrush

Band Number	Locality	Latitude Longitude	Elevation (m)	Date	Age-Sex	Wing (mm)	Tail (mm)	Culmen (mm)	Tarsus (mm)	Mass (g)
ADIRONDACK MOUNTAINS, NY										
1161-17732	Whiteface Mt.	44°22', 73°53'	1250-1300	30 VI 1993	SY-M	91	73	8.6	28.2	28.8
1161-17733	Whiteface Mt.	44°22', 73°53'	1250-1300	30 VI 1993	AHY-M	95	72	8.5	27.0	30.0
1161-17734	Whiteface Mt.	44°22', 73°53'	1250-1300	1 VII 1993	SY-M	92	68	8.9	27.6	27.1
1161-17735	Whiteface Mt.	44°22', 73°53'	1250-1300	7 VII 1993	AHY-M	92	74	9.8	29.6	29.0
1161-17748	Phelps Mt.	44°00', 73°50'	1200-1250	22 VI 1994	AHY-M	95	72	9.1	27.6	26.5
1161-17749	Phelps Mt.	44°00', 73°50'	1200-1250	22 VI 1994	AHY-M	97	74	9.5	28.8	30.0
1161-17750	Phelps Mt.	44°00', 73°50'	1200-1250	22 VI 1994	AHY-M	96	72	9.6	28.5	29.0
1161-17751	Phelps Mt.	44°00', 73°50'	1200-1250	22 VI 1994	AHY-M	95	73	9.5	28.2	29.0
1161-17755	Wright Peak	44°08', 73°58'	950	31 V 1995	AHY-M	95	71	9.5	28.2	26.2
1161-17756	Wright Peak	44°08', 73°58'	950	31 V 1995	AHY-M	94	70	9.0	27.5	27.2
1161-17757	Cascade Mt.	44°13', 73°51'	1170	1 VI 1995	AHY-M	94	70	9.5	27.5	26.0
1161-17758	Cascade Mt.	44°13', 73°51'	1170	1 VI 1995	AHY-M	93	67	8.5	27.5	27.5
1161-17759	Hurricane Mt.	44°10', 73°40'	1100	2 VI 1995	AHY-M	95	72	8.9	27.0	26.4
CATSKILL MOUNTAINS, NY										
1161-17718	Hunter Mt.	42°10', 74°15'	1210	9 VI 1993	SY-M	88	64	8.3	27.0	24.7
1161-17719	Slide Mt.	42°00', 74°25'	1180-1210	11 VI 1993	AHY-M	96	70	9.2	27.0	29.2
1161-17720	Slide Mt.	42°00', 74°25'	1180-1210	14 VI 1993	AHY-F	88	65	9.9	26.5	29.5
1161-17726	Black Dome	42°15', 74°07'	1180	26 VI 1993	AHY-M	91	66	9.7	28.5	26.9
1161-17727	Black Dome	42°15', 74°07'	1180	26 VI 1993	SY-M	88	67	9.3	28.6	27.0

Bicknell's Thrush, continued

Band Number	Locality	Latitude Longitude	Elevation (m)	Date	Age Sex	Wing (mm)	Tail (mm)	Culmen (mm)	Tarsus (mm)	Mass (g)
CATSKILL MOUNTAINS, NY, continued										
1161-17728	Plateau Mt.	42°07', 74°12'	1130-1150	27 VI 1993	AHY-M	95	75	8.9	30.1	31.9
1161-17729	Plateau Mt.	42°07', 74°12'	1130-1150	27 VI 1993	SY-M	89	67	8.9	28.9	29.0
1161-17730	Plateau Mt.	42°07', 74°12'	1130-1150	27 VI 1993	AHY-M	90	71	9.4	28.9	24.7
1161-17731	Plateau Mt.	42°07', 74°12'	1130-1150	27 VI 1993	AHY-M	89	74	9.5	30.0	28.5
1161-17737	Blackhead	42°10', 74°00'	1180	5 VI 1994	AHY-M	95	69	9.0	29.2	27.9
1161-17738	Blackhead	42°10', 74°00'	1180	5 VI 1994	AHY-M	96	72	9.1	29.5	30.0
1161-17739	Plateau Mt.	42°07', 74°12'	1130-1150	8 VI 1994	AHY-M	90	66	9.8	30.2	29.2
1161-17740	Plateau Mt.	42°07', 74°12'	1130-1150	8 VI 1994	AHY-M	92	67	9.9	30.0	30.9
1161-17741	Plateau Mt.	42°07', 74°12'	1130-1150	8 VI 1994	AHY-M	92	65	8.6	28.5	27.6
1161-17752	Blackhead	42°10', 74°00'	1180	25 V 1995	AHY-U	93	68	9.1	29.9	25.6
1161-17753	Blackhead	42°10', 74°00'	1180	25 V 1995	AHY-M	93	69	9.3	29.0	-
1161-17754	Black Dome	42°15', 74°07'	1180	25 V 1995	SY-M	93	71	9.3	27.4	29.1
GREEN MOUNTAINS, VT										
1161-17715	Mt. Mansfield	44°30', 72°50'	1090-1150	3 VI 1993	AHY-M	95	69	8.9	29.8	28.0
1161-17716	Mt. Mansfield	44°30', 72°50'	1090-1150	4 VI 1993	AHY-M	89	65	9.6	28.3	26.7
1161-17717	Mt. Mansfield	44°30', 72°50'	1090-1150	5 VI 1993	AHY-F	92	68	8.9	28.2	30.3
1161-17722	Shrewsbury Pk.	42°32', 72°50'	1060-1090	17 VI 1993	AHY-F	87	66	8.4	24.5	29.5
1161-17723	Shrewsbury Pk.	42°32', 72°50'	1060-1090	17 VI 1993	AHY-M	94	72	9.2	27.9	28.9
1161-17724	Shrewsbury Pk.	42°32', 72°50'	1060-1090	19 VI 1993	AHY-M	97	73	9.5	27.3	29.1

Bicknell's Thrush, continued

<u>Band Number</u>	<u>Locality</u>	<u>Latitude</u> <u>Longitude</u>	<u>Elevation</u> <u>(m)</u>	<u>Date</u>	<u>Age</u> <u>Sex</u>	<u>Wing</u> <u>(mm)</u>	<u>Tail</u> <u>(mm)</u>	<u>Culmen</u> <u>(mm)</u>	<u>Tarsus</u> <u>(mm)</u>	<u>Mass</u> <u>(g)</u>
<i>GREEN MOUNTAINS, VT, continued</i>										
1161-17725	Shrewsbury Pk.	42°32', 72°50'	1060-1090	19 VI 1993	AHY-M	94	72	9.7	26.8	28.2
1161-17736	Stratton Mt.	43°00', 72°50'	1200	29 V 1994	AHY-M	90	67	9.1	27.4	28.1
1471-47932	Mt. Mansfield	44°30', 72°50'	1090-1150	1 VI 1994	AHY-F	94	60	10.5	28.7	28.8
1471-47901	Mt. Mansfield	44°30', 72°50'	1090-1150	2 VI 1994	ASY-M	95	61	9.6	29.4	27.7
1471-47916	Mt. Mansfield	44°30', 72°50'	1090-1150	2 VI 1994	AHY-U	90	65	9.6	28.4	28.6
1471-47937	Mt. Mansfield	44°30', 72°50'	1090-1150	2 VI 1994	AHY-M	97	67	9.5	27.0	29.4
1471-47938	Mt. Mansfield	44°30', 72°50'	1090-1150	3 VI 1994	SY-M	93	68	8.9	29.5	28.8
1471-47904	Mt. Mansfield	44°30', 72°50'	1090-1150	3 VI 1994	ASY-M	91	66	9.2	27.9	26.8
1161-17742	Shrewsbury Pk.	42°32', 72°50'	1060-1090	10 VI 1994	SY-M	90	65	9.2	29.4	26.5
1481-27602	Haystack Mt.	42°55', 72°55'	1050	5 VII 1994	AHY-M	91	70	8.1	29.2	25.2
1481-27603	Haystack Mt.	42°55', 72°55'	1050	5 VII 1994	AHY-F	86	65	9.4	28.5	29.5
<i>WHITE MOUNTAINS, NH</i>										
1161-17743	Mt. Jefferson	44°10', 71°10'	950-1200	14 VI 1994	AHY-M	94	70	8.5	26.5	28.2
1161-17744	Mt. Jefferson	44°10', 71°10'	950-1200	14 VI 1994	AHY-M	92	68	9.2	28.3	28.5
1161-17745	Mt. Jefferson	44°10', 71°10'	950-1200	14 VI 1994	AHY-M	96	68	9.2	27.5	29.1
1161-17746	Mt. Washington	44°10', 71°10'	1320-1400	15 VI 1994	AHY-M	96	72	8.9	26.2	27.5
1161-17747	Mt. Washington	44°10', 71°10'	1320-1400	15 VI 1994	AHY-M	90	67	9.5	27.9	27.9
1161-17760	Mt. Jefferson	44°10', 71°10'	950-1200	7 VI 1995	AHY-M	92	68	9.0	26.3	24.9
1161-17761	Mt. Jefferson	44°10', 71°10'	950-1200	7 VI 1995	AHY-U	94	69	9.2	31.0	27.1

Bicknell's Thrush, continued

<u>Band Number</u>	<u>Locality</u>	<u>Latitude, Longitude</u>	<u>Elevation (m)</u>	<u>Date</u>	<u>Age-Sex</u>	<u>Wing (mm)</u>	<u>Tail (mm)</u>	<u>Culmen (mm)</u>	<u>Tarsus (mm)</u>	<u>Mass (g)</u>
1161-17762	Mt. Jefferson	44°10', 71°10'	950-1200	8 VI 1995	AHY-M	95	73	9.5	26.6	28.1
1161-17763	Mt. Jefferson	44°10', 71°10'	950-1200	8 VI 1995	AHY-F	88	65	9.9	26.7	26.8
1161-17764	Mt. Jefferson	44°10', 71°10'	950-1200	8 VI 1995	AHY-M	95	72	9.6	28.1	27.9
1161-17765	Mt. Osceola	44°00', 71°30'	1060	10 VI 1995	SY-M	92	66	9.1	29.0	27.4

Veery

Band Number	Locality	Latitude Longitude	Elevation (m)	Date	Age Sex	Wing (mm)	Tail (mm)	Culmen (mm)	Tarsus (mm)	Mass (g)
ADIRONDACK MOUNTAINS, NY										
1161-17793	Lincoln Pd., Elizabethtown	44°00', 73°30'	390-450	17 VI 1997	AHY-M	98	75	9.2	27.8	33.2
1161-17794	Lincoln Pd., Elizabethtown	44°00', 73°30'	390-450	17 VI 1997	AHY-M	100	74	8.8	26.8	31.5
1161-17795	Lincoln Pd., Elizabethtown	44°00', 73°30'	390-450	17 VI 1997	AHY-M	97	70	9.4	29.4	31.0
1161-17796	Lincoln Pd., Elizabethtown	44°00', 73°30'	390-450	17 VI 1997	AHY-M	101	74	9.7	29.0	32.4
1161-17797	High Falls Gorge, Wilmington	44°20', 73°50'	390-450	18 VI 1997	SY-U	99	71	8.4	28.4	31.0
1161-17798	Wilmington Notch Campground, Wilmington	44°20', 73°50'	390-450	18 VI 1997	SY-M	96	68	9.2	28.2	31.2
1161-17799	Hearn Swamp, Forestdale Rd., Black Brook	44°20', 73°40'	450	19 VI 1997	AHY-M	101	74	9.6	28.5	31.5
1431-98210	Taylor Pond Campground, Black Brook	44°20', 73°40'	450	30 VI 1997	SY-M	98	74	9.8	29.5	30.5

Veery, continued

<u>Band Number</u>	<u>Locality</u>	<u>Latitude, Longitude</u>	<u>Elevation (m)</u>	<u>Date</u>	<u>Age, Sex</u>	<u>Wing (mm)</u>	<u>Tail (mm)</u>	<u>Culmen (mm)</u>	<u>Tarsus (mm)</u>	<u>Mass (g)</u>
<i>ADIRONDACK MOUNTAINS, NY, continued</i>										
1431-98211	Hearn Swamp, Forestdale Rd., Black Brook	44°20', 73°50'	450	30 VI 1997	AHY-M	101	72	8.9	28.8	31.4
1431-98212	Hearn Swamp, Forestdale Rd., Black Brook	44°20', 73°50'	450	30 VI 1997	SY-U	97	72	9.1	28.3	30.0
<i>CATSKILL MOUNTAINS, NY</i>										
1161-17770	Mink Hollow, Hunter	42°00', 74°00'	680-695	24 V 1997	SY-M	97	70	8.9	25.2	30.0
1161-17771	Mink Hollow, Hunter	42°00', 74°00'	680-695	24 V 1997	AHY-U	100	73	10.5	27.3	32.2
1161-17772	Mink Hollow, Hunter	42°00', 74°00'	680-695	24 V 1997	AHY-M	102	77	8.5	27.5	31.6
1161-17773	Mink Hollow, Hunter	42°00', 74°00'	680-695	24 V 1997	AHY-M	98	76	8.6	28.6	31.8
1161-17774	Stony Clove, Hunter	42°00', 74°10'	575	26 V 1997	AHY-M	100	75	8.2	29.8	31.9
1161-17775	Stony Clove, Hunter	42°00', 74°10'	575	27 V 1997	AHY-M	101	75	8.8	27.5	31.5

Veery, continued

Band Number	Locality	Latitude, Longitude	Elevation (m)	Date	Age-Sex	Wing (mm)	Tail (mm)	Culmen (mm)	Tarsus (mm)	Mass (g)
CATSKILL MOUNTAINS, NY, continued										
1161-17776	Stony Clove, Hunter	42°00', 74°10'	575	27 V 1997	SY-M	99	74	9.7	28.5	29.6
1161-17777	McKenley Hollow, Big Indian	42°00', 74°20'	545	27 V 1997	SY-M	100	76	10.0	28.5	29.8
1161-17778	McKenley Hollow, Big Indian	42°00', 74°20'	545	27 V 1997	AHY-M	100	76	8.9	27.0	30.6
1161-17779	Dutcher Notch Trail, Roundtop	42°10', 74°00'	360	28 V 1997	SY-M	95	70	8.9	28.5	31.1
GREEN MOUNTAINS, VT										
1161-17780	Searsburg Res., Searsburg	42°50', 72°50'	540	31 V 1997	SY-M	100	73	10.1	29.7	30.6
1161-17781	Harbour Rd., Woodford	42°50', 73°00'	425-450	2 VI 1997	AHY-M	102	76	9.0	27.2	29.0
1161-17782	Roaring Brook, Stamford	42°46', 73°05'	515	3 VI 1997	AHY-M	100	75	8.6	26.5	30.1
1161-17783	Burgess Rd., Woodford	42°50', 73°10'	425-450	3 VI 1997	AHY-M	99	73	9.2	27.4	29.9
1161-17784	Burgess Rd., Woodford	42°50', 73°10'	425-450	3 VI 1997	AHY-M	97	73	9.0	28.0	33.0

Veery, continued

<u>Band Number</u>	<u>Locality</u>	<u>Latitude Longitude</u>	<u>Elevation (m)</u>	<u>Date</u>	<u>Age Sex</u>	<u>Wing (mm)</u>	<u>Tail (mm)</u>	<u>Culmen (mm)</u>	<u>Tarsus (mm)</u>	<u>Mass (g)</u>
GREEN MOUNTAINS, VT, continued										
1161-17785	Plymsbury Unit, Coolidge S.F., Plymouth	43°30', 72°40'	410-485	10 VI 1997	AHY-M	101	72	9.4	28.5	34.2
1161-17786	Plymsbury Unit, Coolidge S.F., Plymouth	43°30', 72°40'	410-485	10 VI 1997	AHY-M	99	75	9.0	29.1	32.2
1161-17787	Plymsbury Unit, Coolidge S.F., Plymouth	43°30', 72°40'	410-485	10 VI 1997	SY-M	98	69	9.1	29.2	32.1
1161-17788	Little River S.P., Waterbury	44°20', 72°40'	410-425	15 VI 1997	AHY-U	96	76	8.4	27.1	31.1
1161-17789	Little River S.P., Waterbury	44°20', 72°40'	410-425	15 VI 1997	AHY-M	97	74	8.4	28.2	32.0
1161-17790	Little River S.P., Waterbury	44°20', 72°40'	410-425	15 VI 1997	AHY-M	100	74	10.1	29.8	32.1
1161-17791	Little River S.P., Waterbury	44°20', 72°40'	410-425	15 VI 1997	AHY-M	97	74	9.2	26.9	30.3
1161-17792	Little River S.P., Waterbury	44°20', 72°40'	410-425	16 VI 1997	AHY-U	100	77	9.4	26.5	30.0

Veery, continued

Band Number	Locality	Latitude, Longitude	Elevation (m)	Date	Age-Sex	Wing (mm)	Tail (mm)	Culmen (mm)	Tarsus (mm)	Mass (g)
WHITE MOUNTAINS, NH										
1161-17800	Mossilauke e. shoulder, Rt. 118, Woodstock	43°50', 71°40'	450-515	22 VI 1997	AHY-M	97	73	9.2	28.2	29.9
1431-98201	Jackman Brook, Rt. 118, Woodstock	44°00', 71°40'	450-515	22 VI 1997	AHY-M	100	73	9.2	29.2	33.1
1431-98202	Tripoli Rd., Thornton	43°50', 71°30'	425-485	23 VI 1997	AHY-M	100	77	8.6	28.4	31.8
1431-98203	Tripoli Rd., Thornton	43°50', 71°30'	425-485	23 VI 1997	SY-M	95	70	9.3	28.3	30.1
1431-98204	Tripoli Rd., Thornton	43°50', 71°30'	425-485	23 VI 1997	AHY-M	98	74	8.8	29.3	30.0
1431-98205	s. of Zealand Campground, Ammonoosuc R., Carroll	44°10', 71°30'	450	24 VI 1997	SY-M	95	72	9.2	26.5	26.2
1431-98206	s. of Zealand Campground, Ammonoosuc R., Carroll	44°10', 71°30'	450	24 VI 1997	AHY-M	100	73	9.9	28.4	30.0

Veery, continued

<u>Band Number</u>	<u>Locality</u>	<u>Latitude, Longitude</u>	<u>Elevation (m)</u>	<u>Date</u>	<u>Age-Sex</u>	<u>Wing (mm)</u>	<u>Tail (mm)</u>	<u>Culmen (mm)</u>	<u>Tarsus (mm)</u>	<u>Mass (g)</u>
<i>WHITE MOUNTAINS, NH, continued</i>										
1431-98207	Gale River trailhead,	44°10', 71°40'	450	24 VI 1997	SY-M	100	77	8.5	29.3	31.8
1431-98208	Bethlehem Bear Notch, Bartlett	44°00', 71°10'	425	24 VI 1997	AHY-M	102	79	8.9	28.5	33.0
1431-98209	Bear Notch, Bartlett	44°00', 71°10'	425	24 VI 1997	SY-M	97	74	9.0	28.2	30.0

Gray-cheeked Thrush

<u>Band Number</u>	<u>Locality</u>	<u>Latitude, Longitude</u>	<u>Elevation (m)</u>	<u>Date</u>	<u>Age-Sex</u>	<u>Wing (mm)</u>	<u>Tail (mm)</u>	<u>Culmen (mm)</u>	<u>Tarsus (mm)</u>	<u>Mass (g)</u>
1161-17766	Miron River, Trans Labrador Hwy	53°15', 66°00'	500-550	25 VI 1995	AHY-M	107	75	10.8	29.7	35.0
1161-17767	Miron River, Trans Labrador Hwy	53°15', 66°00'	500-550	27 VI 1995	AHY-M	107	79	11.0	26.7	34.1
NEWFOUNDLAND										
1161-17768	east shore, Pistolet Bay, N. Peninsula	51°29', 55°39'	50	23 VI 1996	SY-M	102	74	9.0	28.6	32.9
1161-17769	Viking Trail, Sainte Lunaire, N. Peninsula	51°28', 55°35'	50	23 VI 1996	SY-M	100	73	9.9	29.5	29.8

Appendix II

Control Region III Sequences of *Catharus* thrushes

Aligned 395 bp sequence from control region III of Bicknell's Thrush, Veery, Gray-cheeked Thrush, Hermit Thrush, and Swainson's Thrush.

Sample ID codes are derived from a single letter locality designation [G=Green Mt; C=Catskill Mt; A=Adirondack Mt; W=White Mt (for Bicknell's and Veery); L=Labrador; N=Newfoundland (for Gray-cheeked)], a single letter species code (B=Bicknell's Thrush; V=Veery; G=Gray-cheeked Thrush; H=Hermit Thrush; S=Swainson's Thrush), a three digit (four in Swainson's) numerical code for each bird, and the single letter within-species haplotype code.

Bicknell's Thrush

	10	20	30	40	50
CB718a	GATGCACTTT	GACCCCATTC	ACGAGGGGGA	GGCTATTTAC	CTCTTAAGTA
CB719c
CB720d?
CB727b
CB728f	?
CB730b?
CB737b
CB741a	?????
CB753b	?????
CB754a	?
GB602a?
GB603b	..??
GB715a
GB717g
GB724a?	?
GB725a	...?????
GB736a
GB901b
GB904d
GB916a
GB932a
GB937a
GB938a
AB732e
AB733a??
AB734a
AB735a
AB748a
AB749e	?????
AB755b	?????
AB757b	?????
AB758b	?
AB759a	?????
WB743b	..?
WB744b	?
WB745b	?
WB746c	?
WB747a
WB760c
WB761c	?????
WB762b	??????
WB764a
WB765b	..?

ery.

on Mt;
 abrador;
 ll's
 Thrush)
 letter

	60	70	80	90	100
CB718a	TGCAGATAGT	GTAATGGTCA	CCGCACATAT	TTAGATTGTT	TCCCCTTCT
CB719c
CB720d
CB727b
CB728f
CB730b
CB737b
CB741a
CB753b
CB754a
GB602a?
GB603b
GB715a
GB717g
GB724a
GB725a
GB736a
GB901b
GB904d
GB916a
GB932a
GB937a
GB938a
AB732e
AB733a?
AB734a
AB735a
AB748a
AB749e
AB755b
AB757b
AB758b
AB759a
WB743b
WB744b
WB745b
WB746c
WB747a
WB760c
WB761c
WB762b
WB764a
WB765b

Bicknell's Thrush (continued)

	110	120	130	140	150
CB718a	AGGAATTTCC	ATCTAAACCC	CTAAAAATCA	TCATTTTTTT	CGTTCGTTTA
CB719c
CB720d
CB727b
CB728f
CB730b
CB737b
CB741a
CB753b
CB754a
GB602a
GB603b
GB715a
GB717gC.....
GB724a
GB725a
GB736a
GB901b
GB904d
GB916a
GB932a
GB937a
GB938a
AB732e
AB733a?
AB734a
AB735a
AB748a
AB749e
AB755b
AB757b
AB758b
AB759a
WB743b
WB744b
WB745b
WB746c
WB747a
WB760c
WB761c
WB762b
WB764a
WB765b

Bicknell's Thrush (continued)

	160	170	180	190	200
CB718a	TTTTTATCAT	GACATTTTCG	TTTAAAATTG	ACCAAATATT	CTTAGACATC
CB719c
CB720d?
CB727b?
CB728f?
CB730b
CB737b
CB741a
CB753b
CB754a
GB602a?
GB603b
GB715a
GB717g
GB724a
GB725a?
GB736a
GB901b
GB904d
GB916a
GB932a
GB937a
GB938a
AB732e
AB733a?
AB734a?
AB735a
AB748a
AB749e
AB755b
AB757b
AB758b
AB759a
WB743b
WB744b
WB745b
WB746c
WB747a
WB760c
WB761c
WB762b
WB764a
WB765b

Bicknell's Thrush (continued)

	210	220	230	240	250
CB718a	TCCCTACCTT	TAACCAAAGC	ATTCATCATC	ACAAAACATA	CGAACAAACT
CB719c
CB720d?
CB727b
CB728f
CB730b
CB737b
CB741a
CB753b
CB754a
GB602a	...?.....?
GB603b
GB715a
GB717g
GB724a
GB725a
GB736a
GB901b
GB904d
GB916a
GB932a
GB937a
GB938a
AB732e
AB733a?..??
AB734a
AB735a
AB748a
AB749e
AB755b
AB757b
AB758b
AB759a
WB743b
WB744b
WB745b
WB746c
WB747a
WB760c
WB761c
WB762b
WB764a
WB765b

Bicknell's Thrush (continued)

	260	270	280	290	300
CB718a	TCCTCTATTT	TCCCCCTATT	TATCAGAACC	GAAAATACAA	CAAACCTTTC
CB719cG...C.....
CB720d?	A.....
CB727bG...
CB728f	C.....	A.....
CB730bG...?
CB737bG...
CB741a
CB753bG...
CB754a
GB602a
GB603bG...	?.....?
GB715a
GB717g	C.....	A.....
GB724a
GB725a
GB736a
GB901bG...
GB904d	A.....
GB916a
GB932a
GB937a
GB938a
AB732e	C.....	A.....
AB733a
AB734a
AB735a
AB748a
AB749e	C.....	A.....
AB755bG...
AB757bG...
AB758bG...
AB759a
WB743bG...
WB744bG...
WB745bG...
WB746cG...C.....
WB747a
WB760cG...C.....
WB761cG...C.....
WB762bG...
WB764a
WB765bG...

Bicknell's Thrush (continued)

	310	320	330	340	350
CB718a	CATCTTT--A	CACACACACA	CAAACAGCAA	CCCCCCTGAC	AAACCACCCC
CB719c--.
CB720d--.
CB727b--.
CB728fAC.
CB730b	...?....--.
CB737b--.
CB741a--.
CB753b--.
CB754a--.
GB602a--.
GB603b	...?....--.
GB715a--.
GB717g--.
GB724a--.
GB725a--.
GB736a--.
GB901b--.
GB904d--.
GB916a--.
GB932a--.
GB937a--.
GB938a--.
AB732e--.
AB733a--.
AB734a--.
AB735a--.
AB748a--.
AB749e--.
AB755b--.
AB757b--.
AB758b--.
AB759a--.
WB743b--.
WB744b--.
WB745b--.
WB746c--.
WB747a--.
WB760c--.
WB761c--.
WB762b--.
WB764a--.
WB765b--.

Bicknell's Thrush (continued)

	360	370	380	390	395
CB718a	AACTAAAACC	AAACAAAAAC	ACAACGCATG	TTCTTGTAGC	TTAAC
CB719c
CB720d
CB727b
CB728f
CB730b	..?.....
CB737b
CB741a
CB753b
CB754a
GB602a
GB603b	..?.....
GB715a
GB717g
GB724a	??????????	?????
GB725a
GB736a
GB901b
GB904d
GB916a
GB932a
GB937a
GB938a
AB732e
AB733a	..?.....
AB734a
AB735a
AB748a
AB749e
AB755b
AB757b
AB758b
AB759a
WB743b
WB744b
WB745b
WB746c
WB747a
WB760c
WB761c
WB762b
WB764a
WB765b

Bicknell's Thrush (continued)

Veery

	10	20	30	40	50
CV773a	GATGCACTTT	GACCCCATTC	ACGAGGGGGA	GGCTATTTAC	CTCTTAAGTA
CV770a	?????.?...?.....
CV771cT?.....
CV772bG.
CV774e
CV775a
CV776a
CV777d	???????..C.....
CV778a
CV779c	??.....T
GV780a
GV781i	?????????
GV783a	??.....?.....
GV785a	???????..
GV786j	?.....
GV787a
GV788a
GV790a
GV791h?
GV792g	?.....
AV793bG.
AV794d	?????C.....
AV795a	?????
AV796a	?.....
AV797a
AV798a
AV799a
AV210a	?.....
AV211a
AV212a
WV800a
WV201cT
WV202a?.....
WV203bG.
WV204f
WV205b	?????G.
WV206a	?.....
WV207a
WV208a
WV209a

	60	70	80	90	100
CV773a	TGCAGATAGT	GTAATGGTCA	CCGCACATAT	TTAGATTGTT	TCCCCTTTCT
CV770a
CV771c
CV772b
CV774e
CV775a
CV776a
CV777d
CV778a
CV779c
GV780a
GV781i
GV783a
GV785a
GV786j
GV787a
GV788a
GV790a
GV791h
GV792g
AV793b
AV794d
AV795a
AV796a
AV797a
AV798a
AV799a
AV210a
AV211a
AV212a
WV800a
WV201c
WV202a
WV203b
WV204f
WV205b
WV206a
WV207a
WV208a
WV209a

Veery (continued)

	110	120	130	140	150
CV773a	AGGAATTTCC	ATCTAAACCC	CTAAAAATCA	TCATTTTTTT	CGTTCGTTTA
CV770a
CV771c
CV772b
CV774eC.....
CV775a
CV776a
CV777d
CV778a
CV779c
GV780a
GV781i
GV783a?
GV785a
GV786j
GV787a
GV788a
GV790a
GV791h
GV792g
AV793b
AV794d
AV795a
AV796a
AV797a
AV798a
AV799a
AV210a
AV211a
AV212a
WV800a
WV201c
WV202a
WV203b
WV204f
WV205b
WV206a
WV207a
WV208a
WV209a

Veery (continued)

	160	170	180	190	200
CV773a	TTTTTATCAT	GACATTTTCG	TTTAAAATTA	ACCAAATATT	CTTAGACATC
CV770a
CV771c
CV772b
CV774e
CV775a
CV776a
CV777d
CV778a
CV779c
GV780a
GV781i
GV783a
GV785a
GV786j
GV787a
GV788a
GV790a
GV791h
GV792g
AV793b
AV794d
AV795a
AV796a
AV797a
AV798a
AV799a
AV210a
AV211a
AV212a
WV800a
WV201c
WV202a
WV203b
WV204f
WV205b
WV206a
WV207a
WV208a
WV209a

Veery (continued)

	210	220	230	240	250
CV773a	TCCCTACCTT	TAACCAAAGC	ATTCATCATC	ACAAAACCTAA	CGAACAAACT
CV770a
CV771c
CV772b
CV774e
CV775a
CV776a
CV777d
CV778a
CV779c
GV780a
GV781i
GV783a
GV785a
GV786j
GV787a
GV788a
GV790a
GV791h?
GV792g
AV793b
AV794d
AV795a
AV796a
AV797a
AV798a
AV799a
AV210a
AV211a
AV212a
WV800a
WV201c
WV202a
WV203b
WV204f
WV205b
WV206a
WV207a
WV208a
WV209a

Veery (continued)

	260	270	280	290	300
CV773a	TCCTCTATTT	TCCCCCTATT	TATCAGAACC	GAAAATACAA	CAAACCTTCTC
CV770a
CV771c?
CV772b
CV774e
CV775a
CV776a	?
CV777d
CV778a
CV779c?..?
GV780a?
GV781i
GV783a
GV785a
GV786j
GV787a
GV788a
GV790a
GV791h	..?A..
GV792gC..
AV793b
AV794d
AV795a
AV796a
AV797a
AV798a
AV799a
AV210a
AV211a
AV212a
WV800a
WV201c
WV202a?
WV203b
WV204f	C.....
WV205b
WV206a
WV207a
WV208a
WV209a

Veery (continued)

	310	320	330	340	350
CV773a	CATCTTT--A	CACACACACA	CAAACAGCAA	CCCCCCTGAC	AAACTACCCC
CV770a--.
CV771c--.
CV772b--.
CV774e--.
CV775a--.
CV776a--.
CV777d--.
CV778a--.
CV779c	...?.....
GV780a--.
GV781i--.	T.....
GV783a--.
GV785a--.
GV786j--.
GV787a--.
GV788a--.
GV790a--.
GV791h--.?
GV792g--.
AV793b--.
AV794d--.
AV795a--.
AV796a--.
AV797a--.
AV798a--.
AV799a--.
AV210a--.
AV211a--.
AV212a--.
WV800a--.
WV201c--.
WV202a	...?.....
WV203b--.
WV204f--.
WV205b--.
WV206a--.
WV207a--.
WV208a--.
WV209a--.

Veery (continued)

	360	370	380	390	395
CV773a	AACTAAAACC	AAACAAAAAC	ACAACGCATG	TTCTTGTAGC	TTAAC
CV770a
CV773c
CV772b
CV774e
CV775a
CV776a
CV777d
CV778a
CV779c
GV780a
GV781i
GV783a
GV785a
GV786j	..T.....
GV787a
GV788a
GV790a?
GV791h
GV792g
AV793b
AV794d
AV795a
AV796a
AV797a
AV798a
AV799a
AV210a
AV211a
AV212a
WV800a
WV201c
WV202a	..?
WV203b
WV204f
WV205b
WV206a
WV207a
WV208a
WV209a

Veery (continued)

Gray-cheeked Thrush, Hermit Thrush, Swainson's Thrush

	10	20	30	40	50
NG744a	GATGCACTTT	GACCCCATTTC	ACGAGGGGGA	GGCTATTTAC	CTCTTAAGTA
NG769a
LG766a
LG767b	.G.....?.....
H214a	??????????
H213b	??????????
S9001a
S4002a
	60	70	80	90	100
NG744a	TGCAGATAGT	GTAATGGTCA	CCGCACATAT	TTAGATTGTT	TCCCCTTTCT
NG769a
LG766a
LG767b
H214aA.	.C.....	..G.....
H213bA.	.C.....	..G.....
S9001aA.	.C.....	..G.....
S4002aA.	.C.....	..G.....
	110	120	130	140	150
NG744a	AGGAACTTCC	ATCTAAACCC	CTAAAAATCA	TCATTTTTTT	CGTTCGTTTA
NG769a
LG766a
LG767b
H214aC.....-	.A.....
H213bC.....-	.A.....
S9001aA	.C.....	TA.....
S4002aA	.C.....	TA.....
	160	170	180	190	200
NG744a	TTTTTATCAT	GACATTTTCG	TTTAAAATTA	ACCAAATATT	CTTAGACATC
NG769a
LG766a
LG767b	?.....
H214aT.....T.....	T.A.T.....
H213bT.....T.....	T.A.T.....
S9001aA	.AC.....	G.T.....	T.A.T.....
S4002aA	.AC.....	G.T.....	T.A.T.....

	210	220	230	240	250
NG744a	TCCCTACCTT	TAACCAAAGC	ATTCATCATC	ACAAAACATA	CGAACAAACT
NG769a
LG766a
LG767b
H214aACC.....	...G.....	..A.....
H213bACC.....	...G.....	..A.....
S9001aCG.T...	.TT.C.T.T.	..A.....
S4002aCG.T...	.TT.C.T.T.	..A.....
	260	270	280	290	300
NG744a	TTCTCTATTT	TCCCCCTATT	TATCAGAACC	GAAAATACAA	CAAACCTCTC
NG769a
LG766a
LG767b
H214aT.....	A.CT.....T	...C.....
H213bT.....	A.CT.A...T	...C.....
S9001a	A.A.-...T	A.....	...A-...T
S4002a	A.A.-...T	A.....	...A-...T
	310	320	330	340	350
NG744a	CATCTTT--A	CACACACACA	CAAACAGCAA	TCCCCCTGAC	AAACCACCCC
NG769a--
LG766a--
LG767b--	...T.....
H214a	...C.C--A...T
H213b	...C.C--A...T
S9001a	T.C..CCAC.	...GT...	...T...T	...T.....	...T.....
S4002a	T.C..CCAC.	...GT...	...T...T	...T.....	...T.....
	360	370	380	390	395
NG744a	AACTAAAACC	AAACAAAAC	ACAACGCATG	TTCTTGTAGC	TTAAC
NG769a
LG766a?
LG767b
H214aT...C
H213bT...C
S9001aA...C.CT
S9001aA...C.CT

Gray-cheeked Thrush, Hermit Thrush, Swainson's Thrush (continued)