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Comparative Phylogeography and a Mitochondrial DNA Barcode for Identifying Three Sympatric Lagomorphs in the Northeastern United States

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COMPARATIVE PHYLOGEOGRAPHY AND A MITOCHONDRIAL DNA BARCODE FOR IDENTIFYING THREE SYMPATRIC LAGOMORPHS IN THE NORTHEASTERN UNITED STATES

BY

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ABSTRACT

The New England cottontail (*Sylvilagus transitionalis*), New England's endemic cottontail, has been experiencing dramatic population declines and is estimated to exist in only 14% of its historical range. The New England cottontail is currently a candidate for endangered species listing under the Endangered Species Act of 1973. New England cottontails may be distinguished accurately from eastern cottontails (*S. floridanus*) with the use of non-invasive genetic techniques (e.g., fecal sample collection) that allow sampling of large geographical areas with minimal cost. A restriction enzyme technique has been published based on NlaIII (New England Biolabs Inc, Massachusetts) cut sites within the control region of the mitochondrial genome (mtDNA); this technique assumes that variation among and between species does not interrupt cut patterns and relies on qualitative identification (visual interpretation of gel bands) with no positive control that true mtDNA has been amplified. Phylogenetic analyses of the New England cottontails, eastern cottontails and snowshoe hares (*Lepus americanus*) in northeastern states may indicate the reason for New England cottontail decline. Because eastern cottontails were stocked from several locations they may have increased genetic variability, especially when compared to New England cottontails, which could be an indication of hybrid vigor. Furthermore, phylogeographic patterns may help infer introduction and spread patterns of eastern cottontails. I sequenced 1,773 fecal and tissue samples from CT, MA, NH, NY, and RI. I identified 12 New England cottontail, 101 eastern cottontail, and eight snowshoe hare haplotypes. Eastern cottontails exhibited a larger number of haplotypes compared to New England cottontails; however, there was no geographic

pattern to haplotype occurrences. I analyzed all haplotypes using the restriction enzyme technique to test digestion site reliability and found 19 instances of conflicting cut sites between haplotypes and previously published cut sites. I also found two haplotypes that appeared to be non-mitochondrial in origin and can be preferentially amplified in some samples when the mammalian reverse primer used in the restriction enzyme method was used for amplification. To provide an unambiguous and reliable identification method I created a "barcode" for the mitochondrial control region of these three species and developed a rabbit specific reverse primer. I found 13 diagnostic characters for New England cottontail, 18 diagnostic characters for eastern cottontail, and 36 diagnostic characters for snowshoe hare. I propose that the use of the barcode and the rabbit specific reverse primer described here provides a reliable and inexpensive method for species identification. Furthermore, sequencing Polymerase Chain Reaction (PCR) product provides an opportunity to detect non-mitochondrial sequences and provides information for further analyses such as phylogeographic studies.

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DEDICATION

This thesis is dedicated to the memory of Celeste M. Sullivan.

PREFACE

The following thesis is written in manuscript format following guidelines given by the University of Rhode Island. Chapters one and two are written to follow the guidelines for submission to *Conservation Genetics.*

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MANUSCRIPT I

A Mitochondrial DNA barcode for identifying three sympatric lagomorphs in the Northeastern United States

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Is in preparation for submission to Conservation Genetics

Abstract The New England cottontail (*Sylvilagus transitionalis*) is currently a candidate for endangered species listing under the Endangered Species Act of 1973. External characteristics do not allow New England cottontails to be distinguished accurately in the field from eastern cottontails (*S. floridanus*). Noninvasive techniques (e.g., fecal sample collection) that allow sampling of large geographical areas with minimal cost require genetic identification to distinguish species. A restriction enzyme technique has been published (Kovach et al. 2003) based on NlaIII (New England Biolabs Inc, Massachusetts) cut sites within the control region of the mitochondrial genome (mtDNA); this technique assumes that variation among and between species does not interrupt cut patterns and it relies upon visual interpretation of gel bands, with no positive control that true mtDNA has been amplified. We sequenced over 1,750 fecal and tissue samples from Connecticut, Massachusetts, New Hampshire, New York, and Rhode Island. We identified 12 New England cottontail, 101 eastern cottontail, and eight snowshoe hare (*Lepus americanus*) haplotypes. We found 19 instances of conflicting cut sites between haplotypes and previously published cut sites. We also found two haplotypes that appeared to be non-mitochondrial in origin and could be preferentially amplified in some samples when the mammalian reverse primer used in the restriction enzyme method was used for amplification. To provide an unambiguous and reliable identification method, we created a "barcode" for the mitochondrial control region of these three species and developed a rabbit specific reverse primer. We found 13 diagnostic sites for New England cottontail, 18 diagnostic sites for eastern cottontail, and 36 diagnostic sites for snowshoe hare.

Keywords Barcode, mitochondrial DNA, *Sylvilagus transitionalis*, *Sylvilagus floridanus*, *Lepus americanus,* pseudogenes

Introduction

The distribution of the New England cottontail (*Sylvilagus transitionalis*) in southern New England has declined dramatically over the past century (Litvaitis et al. 2006) with the extent and presence of current populations remaining largely unknown. In addition, the New England cottontail is currently a candidate for listing as an endangered species (U.S. Fish & Wildlife Service 2006), due to the recent dramatic reduction in population sizes, and the apparent lack of connectivity of extant populations (Fenderson et al. 2011; Litvaitis et al. 2006). The current initiative for conservation plans for the New England cottontail has illuminated the need for further research to determine the range, genetic diversity, and population structure for both New England and eastern cottontails (*S. floridanus*). A survey conducted from 2000 through 2004 concludes that the species has seen a range reduction of 86% since 1960 (Litvaitis et al. 2006). This reduction in range may be due to a number of different factors possibly including the decline of early successional habitat and the introduction of eastern cottontails (Litvaitis and Villafuerte 1996; Probert and Litvaitis 1996).

Distinguishing native New England cottontails from non-native eastern cottontails is often difficult and traditional identification techniques involve species confirmation through skull characteristics or genetic analysis (Kovach et al. 2003; Litvaitis and Litvaitis 1996). Furthermore, species identification using genetic techniques allows for non-invasive sampling, which is a cost effective and efficient method for determining absence or presence of a species in a given area. However, the mtDNA analysis technique developed by Kovach et al. (2003) is flawed because it is dependent upon conserved cut sites of a single restriction enzyme and is vulnerable to variation in the four nucleotide recognition site. An enzyme digestion method for distinguishing New England and eastern cottontails that was developed in the past, for unknown reasons, has been found unreliable (Synder 1998). Management efforts for the New England cottontail are critically dependent upon reliable survey and identification methods that accurately detect species' occupancy and distribution.

The task of properly identifying a species using fecal pellet analysis has undoubtedly been made more difficult by the introduction of hundreds of thousands of eastern cottontails, and possibly other *Sylvilagus* species including *S. auduboni*, to New England beginning in the early and mid-1800s Johnson et al. 1972. These introductions were largely unregulated until the 1950s when most states enforced regulation by permit only and often were not recorded (McAninch 1976). Dice (1927) and Johnson (1972) report introductions to southern New England from Kansas, Minnesota, Missouri, West Virginia, possibly Oklahoma, as well as, several instances of stocking from "the Midwest" and "western states." Proper testing of identification techniques is contingent upon a thorough investigation into eastern cottontail haplotypes.

Kovach et al. (2003) describes a molecular technique for identifying species based on a restriction enzyme digest of the mitochondrial control region to produce consistent banding patterns for the three lagomorph species. Specifically, New England cottontails will have three digestion sites, eastern cottontails will have two, and snowshoe hares (*Lepus americanus*) will have one digestion site. However, 20 samples were used in their study to confirm the identification method and the number of haplotypes tested is not mentioned, leaving room for error due to variation in nucleotide haplotypes possibly producing inconsistent cut sites within and between species. Furthermore, error resulting from polymerase chain reaction (PCR) amplification of nuclear mitochondrial DNA or NUMTs (Lopez et al. 1994) instead of true mtDNA was not considered.

The analysis of mtDNA is used for a wide variety of applications including the construction of phylogenetic trees and species identification. Although mtDNA analysis can be an extremely useful method for answering many biological questions, it is not without problems and requires careful testing. In particular, NUMTs are of concern and may be wrongly included in a dataset leading to misleading results and possible species misidentifications (Zhang and Hewitt 1996). Furthermore, because mtDNA is maternally inherited, hybridization cannot be determined. Despite these drawbacks, the much greater abundance of mtDNA compared to nuclear DNA (Birky et al. 1989) provides greater success rates when using non-invasive sampling techniques (Frantzen et al. 1998; Kohn et al. 1999; Waits and Paetkau 2005).

Mitochondrial DNA barcodes are used for many purposes including the identification of new or cryptic species (Amato et al. 1999) and as a tool for identifying species that have been well documented (DeSalle et al. 2005; DeSalle 2006). The two main methods that are used to interpret mtDNA barcodes are the use of diagnostic characters (Amato et al. 1999) and distance methods (Hebert et al. 2003). Diagnostic characters are used to identify a species of origin based on unique characters in the sequenced portion of the mtDNA. Herbert et al. (2003) proposed using a distance method with the cytochrome oxidase I mitochondrial gene, where a divergence value greater than 3% is used as a cut-off threshold for distinguishing species; however, some distinct species show divergence below this cut-off threshold. While Rubinoff (2006) discourages the use of barcodes as a method for identifying cryptic species, especially when a divergence cut-off threshold is used, using a diagnostic character based method for species confirmation for described species is uncontested (DeSalle 2006; Rubinoff et al. 2006). The objectives of our study were to: 1) construct a diagnostic character barcode identification method to distinguish among three sympatric taxa in the Family Leporidae found in northeastern United States; 2) test the reliability of the Kovach et al. (2003) method against all mtDNA control region haplotypes found in a survey of Leporidae samples in five northeastern states (Rhode Island, Massachusetts, Connecticut, New Hampshire, and New York); and 3) test for the presence of non-mtDNA haplotypes in mtDNA control region sequences.

Methods

Sample collection, extraction, amplification, and sequencing

Between 2010 and 2012 (2011 and 2012 winter field seasons) we obtained Leporidae tissue and fecal samples from five Northeastern states: Rhode Island, Massachusetts, Connecticut, New Hampshire, and New York. Fecal samples were collected and stored in either 100% ethanol or tubes containing silica beads that were separated from the sample with Kim wipes (Fisher Scientific, Georgia). Tissue samples were collected and stored in 100% ethanol. Fecal and tissue samples were initially stored at -20°C and then subsequently stored at -80°C until DNA was extracted from the sample. Blood samples were collected on FTA cards (Whatman, Buckinghamshire) and stored at room temperature in desiccant pouches (Whatman, Buckinghamshire).

Fecal samples were extracted using the Qiagen QIAamp DNA Stool Mini Kit (Qiagen Sciences, Maryland) according to the manufacturer's instructions. Tissue samples were extracted using the Qiagen DNeasy blood and tissue kit according to the manufacturer's instructions. Each sample was handled using spatulas that were cleaned with a 10% Clorox bleach (Clorox, California) and then autoclaved, fresh disposable weigh boat, and placed on a clean work surface to reduce the possibility of sample cross-contamination. Each tissue sample was manipulated using a new disposable razor blade. FTA blood samples were punched out of each card using a new disposable hole punch and were either purified using Whatman purification kits, according to the manufacturer's instructions for direct use in PCR, or extracted using a Qiagen DNeasy blood and tissue kit according to the manufacturer's instructions for blood extractions. Negative controls were included in each set of DNA extractions to test for contamination of reagents.

All PCRs were run with reagent negative controls and prepared in a UV-equipped hood to avoid cross contamination. We PCR amplified a 565 base pairs (bp) portion of the mitochondrial control region using published primers for samples collected in the 2011 field season. The forward primer (L15934), which is *Sylvilagus* sp. specific, anneals to the threonone tRNA gene (Litvaitis et al. 1997). The reverse primer (H16498) is a general mammalian primer and anneals to a conserved region of the D-loop (Shields and Kocher 1991). Because many samples did not amplify with these primers we developed a new primer specifically for *S. transitionalis* and *S.*

floridanus (H16443). Although this primer amplifies a smaller portion of mtDNA (480 bp), the new primer was designed to ensure proper amplification in both species with minimal loss of sequence information. PCR products were electrophoresed on 1% agrose gels (Invitrogen, California) to determine if the expected band was present. Correctly amplified product was then purified using Agencourt Ampure purification beads (Beckman Coulter, Massachusetts) according to the manufacture's instructions and submitted for sequencing to the University of Rhode Island Genomic Sequencing Center according to their instructions (http://www.uri.edu/research/gsc/submitins.html), which they sequenced using an Applied Biosystems 3130xl Genetic Analyzer (Life Technologies, California).

Polymerase chain reactions were executed in 25 µl reactions consisting of 12.5 µl TopTaqmaster mix kit (Qiagen Sciences, Maryland), 0.4 µM forward primer, 0.4 µM reverse primer, 2500 ng Bovine Serum Albumin (BSA), 1 µl of DNA extracted from tissue samples or 4 µl of DNA extracted from fecal or FTA samples, and the appropriate amount of water for a total volume of 25 µl. Three PCR programs were used. The first program was used for fecal samples and primer pairs L15934 and H16498; this PCR program consisted of an initial temperature of 94°C for 3 minutes, 30 cycles of 94°C for 30 seconds, 45°C for 30 seconds, and 72°C for 45 seconds, followed by an extension step of 72°C for 10 minutes. The second program was used for primers L15934/H16498 with tissue and blood samples or for primer pairs L15934/H16443 for all sample types except those samples that produced multiple bands during electrophoresis or ambiguous chromatograms after sequencing. This program consisted of an initial temperature of 94°C for 3 minutes, 10 cycles of 94°C for 30 seconds, 66°C for 30 seconds (with a 1°C temperature reduction every cycle) and 72°C for 45 seconds, followed by 30 cycles of 94°C for 30 seconds, 56°C for 30 seconds, and 72°C for 45 seconds, and a final elongation step of 72°C for 10 minutes. For samples amplified with primer pairs L15934/H16443 and that either produced multiple bands during electrophoresis or ambiguous chromatograms with the second PCR program, a third program was used. This program consisted of an initial temperature of 94°C for 3 minutes, 30 cycles of 94°C for 30 seconds, 70°C for 30 seconds, and 72°C for 45 seconds, followed by an extension step of 72°C for 10 minutes.

Barcode construction, haplotype testing, and phylogenetic analysis

We used known mtDNA samples to create an initial consensus sequence for each species and identified diagnostic characters manually. We considered samples known if there was an accompanying skull or if the sequence had been deposited in the NCBI database. For New England cottontails, we used one sequence found on the NCBI database (accession: AF002244) and three tissue samples with accompanying skulls. For eastern cottontails we used one sequence from the NCBI database (accession: AF002243) and five tissue samples with accompanying skulls. Because sequences from several eastern cottontail voucher samples matched very closely to sequences from *S. robustus* found on NCBI, we included three additional sequences (accession: HQ143431.1, HQ143444.1, HQ143445.1) as eastern cottontail haplotypes. For snowshoe hare, we used two sequences found on the NCBI database (accession: HM771307 and HM771308). We used ClustalW 2.011 cost matrix (Larkin et al. 2007) and aligned sequences using Geneious Pro 5.4.6 (Biomatters, New Zealand) to create an initial barcode and for all alignment analyses. We identified samples to the species based on this initial barcode and manually checked each diagnostic character against each haplotype; if a character was not constant for all haplotypes, we discarded the character.

We tested 101 eastern cottontail haplotypes, 14 New England cottontail haplotypes, and seven snowshoe hare haplotypes against the Kovach et al. (2003) restriction enzyme method using SeqBuilder (DNASTAR, Wisconson) to find NlaIII (New England Biolabs Inc, Massachusetts) digestion sites in sequences for each haplotype. We followed the Kovach et al. (2003) protocol for 65 eastern cottontail haplotypes, 7 New England cottontail haplotypes, and one snowshoe hare haplotype to test the banding pattern produced compared to the expected banding pattern predicted by Kovach et al. (2003).

We aligned all New England and eastern cottontail haplotypes to a draft mtDNA genome sequence from each taxon that was provided by Dr. Timothy King (unpublished data) using Geneious's BLAST search option to determine how similar the haplotypes were to the full mitochondrial sequence of each taxon. We used a mtDNA extraction kit (Wako, Virginia) to attempt to extract only mtDNA from five tissue samples for haplotype testing. We followed the manufacturer's instructions, except for the first step that recommends using a glass homogenizer; instead, we used a Qiagen TissueLyser (Qiagen Sciences, Maryland) with one 5 mm stainless steal bead per sample.

We used Geneious Pro 5.4.6 "design new primers" tool to develop primers, Lnumt and Hnumt, specifically to amplify haplotypes that we considered odd because they could not be identified to species and suspected did not originate from the mitochondrial genome. The PCR reaction was carried out with the same concentrations as mentioned above; however, a different program was used consisting of an initial temperature of 95°C for 2 minutes, 35 cycles of 95°C for 45 seconds, 55°C for 45 seconds, and 72°C for 45 seconds, followed by an extension step of 72°C for 8 minutes. Microsatellite markers were used to test for the presence of nuclear DNA in the mtDNA extraction. PCRs were executed in 25 µl reactions consisting of 12.5 µl TopTaqmaster mix kit, 0.16 µM forward primer, 0.16 µM reverse primer, 2500 ng/µl BSA, and 1 µl of DNA extracted using mtDNA extraction kit. Two programs were used for microsatellite amplification. The first was used for markers Sfl001, Sfl013, Sfl014, and Sfl015 and consisted of an initial temperature of 94°C for 3 minutes, 12 cycles of 94°C for 30 seconds, 65°C (decreasing by 0.5°C per cycle) for 45 seconds, and 72°C for 45 seconds, followed by 22 cycles of 94°C for 30 seconds, 53°C for 45 seconds, and 72°C for 45 seconds, followed by 10 cycles of 94°C for 30 seconds, 55°C for 45 seconds, and 72°C for 45 seconds, followed by an extension step of 72°C for 8 minutes. The second program was used for Sfl006 and consisted of an initial temperature of 94°C for 3 minutes, 35 cycles of 94°C for 30 seconds, 60°C for 45 seconds, and 72°C for 45 seconds, followed by an extension step of 72°C for 10 minutes.

We aligned the haplotypes using ClustalW cost matrix in Geneious and included a sequence from *Ochotona curzoniae* (NCBI accession: NC_011029) as the outgroup. We trimmed the sequence length using Geneious to reflect our sequence length. We used MrModelTest 2.3 (Nylander 2004) to identify the best model for

Bayesian tree construction based on Akaike Information Criterion (AIC) (Akaike 1973) and MrBayes 2.3 (Huelsenbeck and Ronquist 2001; Ronquist and Huelsenbeck 2003) for tree construction. For the MrBayes phylogenetic analyses, we increased the number of generations until the average standard deviation of split frequency was below 0.01 for three independent runs. Phylogenetic trees were visualized using FigTree 1.4 (Rambaut 2012).

Results

We sequenced a total of 1,773 samples (Table 1.2) from five Northeastern states (Fig. 1.1). We identified 101 eastern cottontail haplotypes (NCBI gene bank accession: numbers will be here), 14 New England cottontail haplotypes (Sth008 and Sth009 were not considered true mtDNA haplotypes; NCBI gene bank accession: numbers will be here), and 8 snowshoe hare haplotypes (NCBI gene bank accession: numbers will be here). We considered all haplotypes in barcode construction except for Sth008 and Sth009. We identified 18 diagnostic characters for eastern cottontail identification, 13 for New England cottontail identification, and 38 for snowshoe hare identification (Table 1.3).

Several New England and eastern cottontail haplotypes showed different digestion sites when analyzed using SeqBuilder compared to those predicted by Kovach et al. (2003). Fourteen of 101 eastern cottontail haplotypes, or 238 out of 1577 eastern cottontail samples sequenced (15%), produced different bands than expected with an extra band of varying size. Five of 14 New England cottontail haplotypes, or 7 out of 178 samples sequenced (4%), produced an unexpected banding patterns. Two of the New England cottontail haplotypes contained an extra digestion site (Sth006 and Sth011 accession: number will be here); two did not contain two digestion sites (Sth008 and Sth009, accession: number will be here); one did not contain one digestion site (sth012 accession: number will be here). Ninety-seven percent of eastern cottontail haplotypes that were tested using the Kovach et al. (2003) method matched the banding pattern from digestion sites identified using SeqBuilder, including patterns that would not give a correct identification. Eighty-six percent of New England cottontail haplotypes that were tested using the Kovach et al. (2003) method matched banding pattern from digestion sites identified using SeqBuilder, including patterns that would not give the correct identification, which may be an issue stemming from visualizing banding patterns using gel electrophoresis.

Two New England cottontail haplotypes (GenBank accession: numbers will be here, Sth008 and Sth009) did not align well to known New England cottontail mtDNA sequences. These haplotypes had an 84% and 83% pairwise identity, respectively, when aligned to the full New England cottontail mitochondrial genome. All other haplotypes aligned with a 94-100% pairwise identity when we aligned them to the New England or eastern cottontail full mitochondrial genome. The extraction product from the mtDNA specific extraction kit amplified fragments when both rabbit specific primer sets and pseudogene specific primer sets were used. The extraction product also amplified fragments when used with microsatellite markers.

Haplotypes Sth008 and Sth009 were not amplified when the species-specific primer (H16442) developed in this study was used on the same DNA extraction that amplified these abnormal sequences when the non species-specific primer (H16498) was used. Specifically, the sample that amplified Sth008 when H16498 was used amplified Sth001 when H16442 was used and the sample that amplified Sth009 when H16498 was used amplified Sth015 when H16442 was used. The pseudogene specific primer set was able to amplify identical or closely identical haplotypes to Sth008 and Sth009 on other New England cottontail samples and on eastern cottontail samples.

MrModelTest 2.3 identified HKY+I+G as the appropriate model with the lowest AIC value (8017.74). The next model with the lowest AIC value had a delta of 4.09. The Bayesian phylogenetic tree placed haplotypes from the three species together, except for haplotypes Sth008 and Sth009, with moderate clade credibility values. Haplotypes Sth008 and Sth009 were grouped together and appeared on the tree basal to all other New England and eastern cottontail haplotypes (Fig. 1.2).

Discussion

Because of the history of *S. floridanus* importation into New England from various states, it is important to consider a large sample group when developing an identification technique to ensure consistency across all haplotypes. Here we tested a total of 1,750 samples for three species and found 123 haplotypes. The mtDNA species identification method for *S. transitionalis*, *S. floridanus*, and *L. americanus* developed here employs a barcode with diagnostic characters to compare to mtDNA control region sequences of samples in question. The lack of digestion site consistency demonstrates that the restriction enzyme method (Kovach et al. 2003) for distinguishing among these three species is flawed due to haplotype variation. The barcode method developed here provides decisive, accurate species identification, with a number of diagnostic characters for all three species (Table 1.3), as well as, the opportunity to identify whether pseudogenes have been mistakenly amplified to avoid confounded results. Furthermore, a rabbit-specific reverse primer developed during this study shows no evidence of preferentially amplifying non-mtDNA, whereas the mammalian specific primer used in the previous method by Kovach et al. (2003) may do so in some samples.

Unintended amplification of pseudogenes has been recorded for many species and may be amplified preferentially when ‘universal’ primers are used during PCR (Sorenson and Fleischer 1996; Mirol et al. 2000). Not only does the restriction enzyme method employ the use of a non-specific reverse primer (Kovach et al. 2003), but also PCR product is not sequenced to determine if the amplified haplotype originated from the mitochondrial genome. Thus, unknown to the researcher, the PCR product being digested may consist of some or mostly pseudogenes, especially if the amplified pseudogenes are the same length as true mtDNA, which was the case in this study. We found that PCR with the mammalian specific reverse primer, along with the rabbit specific forward primer described in Kovach et al. (2003), produced different sequences for some samples compared to when rabbit-specific forward and reverse primers were used.

While a mtDNA specific extraction kit can be used in an attempt to isolate mtDNA for amplification (Thalmann et al. 2004), we found that the mtDNA specific extraction kit employed in this study extracted nuclear DNA as well as mtDNA. Thalmann et al. (2004) found that reliable amplification of mtDNA using species specific primers differs among species of apes and recommends long-range PCR amplification of mtDNA be used as a reference for comparison and confirmation that true mtDNA was amplified. Instead of long-range PCR, we were able to compare all haplotypes to a full mtDNA genome for eastern and New England cottontails and found two haplotypes produced when using the mammalian reverse primer had a reduced pairwise identity value compared to all the other haplotypes. Furthermore, when a rabbit specific reverse primer was used for amplification on the same samples, a haplotype that aligned well to the full mtDNA genome and that had been found in other samples was produced.

Because the D-loop is a non-coding region of mtDNA, detection of stop codons, insertions-deletions, or frame-shift mutations are not indicators that NUMT sequences have been amplified (Triant and DeWoody 2007). However, due to the slower mutation rate often found in nuclear DNA (Brown et al. 1979) pseudogenes may appear more basal on a phylogenetic tree, therefore, the position of suspected pseudogenes on a phylogenetic tree can be used as an indication of the sequence's origin (Bensasson et al. 2001; Triant and DeWoody 2007). We found that haplotypes Sth008 and Sth009 did not group with other haplotypes found in *S. transitionalis* and both haplotypes appear more basal on a phylogenetic tree.

While we do not have conclusive evidence that haplotypes Sth008 and Sth009 originate from the nucleus, our results suggests that these haplotypes are not true mtDNA haplotypes and further investigation is necessary to determine their origin. We do not suspect that Sth008 and Sth009 are occurrences of mtDNA polymorphism within an individual (heteroplasmy). While heteroplasmy has been reported in rabbit mtDNA, these reports are limited to length variation due to tandem repeats (Biju-Duval et al. 1991; Casane et al. 1997; Casane and Guéride 2002) and we do not suspect that haplotypes Sth008 and Sth009 are the result of heteroplasmy.

We propose the use of the rabbit specific reverse primer and the barcode described here as the standard method for identifying accurately the species among these three sympatric members of Leporidae. The costs of generating DNA sequence data continue to decrease, which is progressively diminishing the cost savings benefit of using the Kovach et al. (2003) restriction enzyme technique to identify the species of an unknown sample. Not only can mtDNA sequences be used for phylogenetic analysis, but sequencing PCR product also is important to analyze for the possibility of pseudogene amplification, which is difficult to detect using the restriction enzymes method. Furthermore, many mtDNA haplotypes do not follow the expected digestion site pattern described by Kovach et al. (2003) and yield ambiguous results that do not allow for accurate species identification. Considering these factors, and the current status of New England cottontail as a candidate species for listing as an endangered species, the barcode identification technique described here should be used for future identification, especially for surveys that concern management decisions.

Table 1. 1. Primers used for PCR with New England cottontails, eastern cottontails, and snowshoe hares in Connecticut, Massachusetts, New Hampshire, New York, and Rhode Island

mtDNA Primers	5'-3'	Source
L15934	CCCTGGTCTTGTAAGCCAGAAATGG	Litvaitis and Litvaitis 1996
H16498	CCTGAAGTAGGAACCAGATG	Shields and Kocher 1991
H16442	ATGGGCCCGGAGCGAGAAGA	This study
Pseudogene specific primers		
Hnumt	CCACTGAGGGAAGGGGATAGTCATA	This study
Lnumt	TCTCTGTTTTTCTACTTTAATCTA	This study
Microsatellite Markers		
Sfl006for	TGTAAAACGACGGCCAGTCTTCTGCTCTGTTGATCTGTTACCC	Berkman et al. 2009
Sfl006rev	GTTCCTGGCTTTGGTCTGGTCC	Berkman et al. 2009
Sfl011for	TGTAAAACGACGGCCAGTGCACAGCAGCATATTCCATGC	Berkman et al. 2009
Sfl011rev	GTTTCCATGAATCAATACAGGTTAATGCC	Berkman et al. 2009
Sfl013for	TGTAAAACGACGGCCAGTGAATAGCTTTGAGCATAGAAGATT C	Berkman et al. 2009
Sfl013rev	GTTGGCACTGCATGTAGTGGCTC	Berkman et al. 2009
Sfl014for	TGTAAAACGACGGCCAGTGGGTGCTGGGGATACAGAGATAG	Berkman et al. 2009
Sfl014rev	GTTTGAATGAACCAAC AGATGGAAAAGC	Berkman et al. 2009
Sfl015for	TGTAAAACGACGGCCAGTGCTTCTGGTTTCCATCCG	Berkman et al. 2009
Sfl015rev	GTTTCTACCCACTCATTGTTTGC	Berkman et al. 2009

Microsatellite marker sequences have attached M13 (5'-TGTAAAACGACGGCCAGT-3'; Schuelke 2000) or pigtail (5'-GTT-3') both are underlined.

Table 1. 2. Number of samples sequenced from five northeastern states, Connecticut (CT), Massachusetts (MA), New Hampshire (NH), New York (NY), Rhode Island (RI) and identified as eastern cottontails (EC), New England cottontails (NEC), or snowshoe hares (SSH), collected between 2010 and 2012

State	Total number of samples	Number of EC identified	Number of NEC identified	Number of SSH identified
CT	165	122	43	0
MA	286	160	122	4
NH	34	10	10	14
NY	50	49	1	0
RI	1238	1236	2	0
Total	1773	1577	178	18

Table 1. 3. Diagnostic character Barcode using the mitochondrial control region for species identification distinguishing three lagomorph species, eastern cottontail (*Sylvilagus floridanus*), New England cottontail (*S. transitionalis*), and snowshoe hare (*Lepus americanus*), in Connecticut, Massachusetts, New Hampshire, New York, and Rhode Island. Highlighted nucleotides are diagnostic characters (DC).

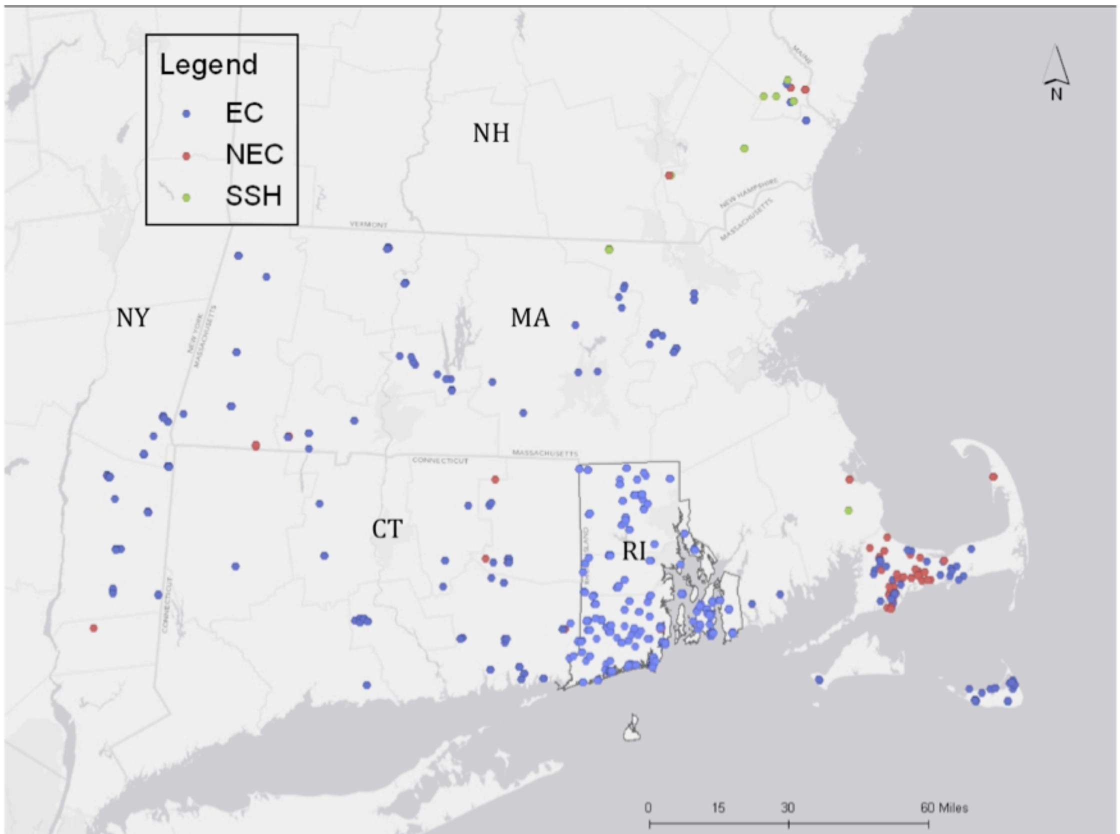
Species	70	71	90	98	99	103	110	111	115	116	117	125	129	133	136	137	138	143	145	149	175	187	189	194	198	201	202	205	223
Reference *S. floridanus*	A	C	T	T	T	T	C	A	A	T	C	G	T	A	C	T	A	A	G	C	C	T	-	T	G	T	A	A	A
S. floridanus Consensus	•	•	•	•	•	•	•	•	•	T	C	•	•	•	•	•	R	•	R	•	C	•	-	Y	•	T	•	•	•
S. transitionalis Consensus	•	•	•	•	•	•	T	G	•	C	Y	•	•	•	T	•	W	•	C	•	Y	•	C	M	•	C	•	•	•
L. americanus Consensus	C	T	A	A	A	A	•	•	G	C	T	C	C	G	A	A	C	T	T	G	T	A	-	A	C	C	T	C	T

Species	226	232	233	260	286	296	304	307	313	314	317	318	326	329	332	333	335	339	340	355	360	365	368	374	377	384	385	387	395
Reference *S. floridanus*	-	T	-	T	C	C	G	-	T	A	T	C	A	T	A	C	C	T	T	T	A	A	T	G	T	A	-	T	T
S. floridanus Consensus	-	T	-	•	•	C	G	-	T	A	Y	•	•	•	W	•	Y	T	Y	Y	•	A	Y	R	•	•	-	T	Y
S. transitionalis Consensus	-	C	T	Y	•	A	A	-	A	C	•	T	C	•	•	-	G	Y	A	A	•	C	A	T	•	W	-	G	A
L. americanus Consensus	T	C	T	G	A	A	A	A	A	C	G	•	•	A	C	•	T	A	A	A	C	C	A	A	-	C	C	G	T

Species	339	340	355	360	365	368	374	377	384	385	387	395	397	399	406	459	464	540	541	Total # of DC
Reference *S. floridanus*	T	T	T	A	A	T	G	T	A	-	T	T	C	A	T	C	T	A	A	
S. floridanus Consensus	T	Y	Y	•	A	Y	R	•	•	-	Y	Y	•	R	T	•	Y	•	•	18
S. transitionalis Consensus	Y	A	A	•	C	A	T	•	W	-	G	A	T	A	G	•	T	•	•	13
L. americanus Consensus	A	A	A	C	C	A	A	-	C	C	G	T	•	T	A	A	G	G	T	38

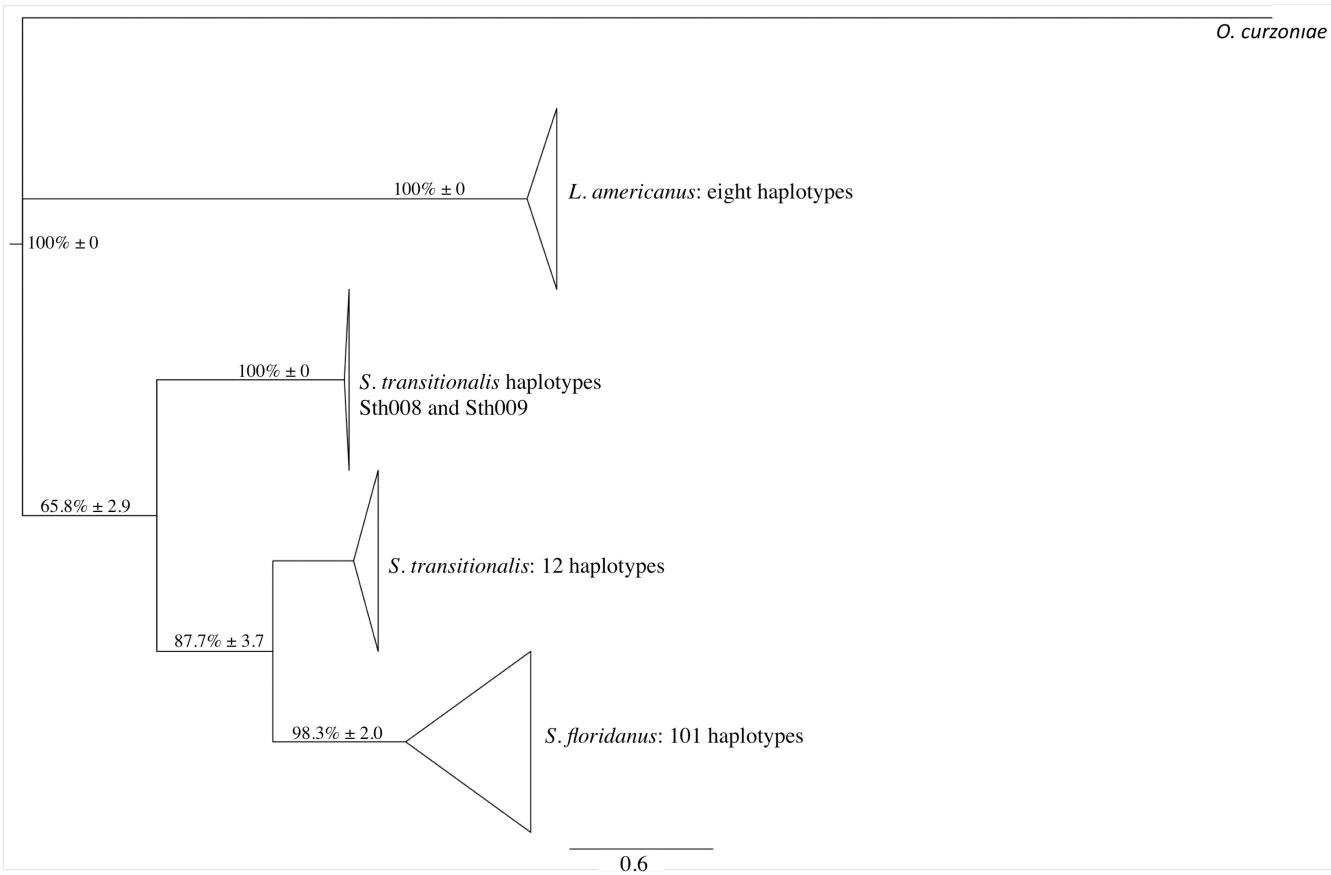
Reference *S. floridanus* is haplotype Sfh079 (accession: Will be added to NCBI genbank). A – indicates a gap in the alignment and a • indicates nucleotides that are equal to nucleotides in the reference sequence. Numbers above base pairs indicate their position in the sequence alignment.

Figure 1. 1. Sample distribution of New England cottontails (NEC), eastern cottontails (EC) and snowshoe hares (SSH) across five northeastern states, Connecticut (CT), Massachusetts (MA), New Hampshire (NH), and Rhode Island (RI), collected between 2010 and 2012.



Only samples provided with GPS locations are shown here.

Figure 1. 2. Bayesian phylogenetic tree of eastern cottontail (*Sylvilagus floridanus*), New England cottontail (*S. transitionalis*), and snowshoe hare (*Lepus americanus*) haplotypes samples in Connecticut, Massachusetts, New Hampshire, New York, and Rhode Island between 2010 and 2012 with *O. curzoniae* as the outgroup.



Analysis was repeated three times, average clade credibility values shown with ± standard deviation. Clades are collapsed; see supplementary material for full phylogenetic tree.

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MANUSCRIPT II

Comparative phylogeography of three sympatric lagomorphs in the Northeastern United States

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Abstract The endemic New England cottontail (*Sylvilagus transitionalis* has been experiencing dramatic population declines and is estimated to exist in only 14% of its historical range, making it a candidate for endangered species listing under the Endangered Species Act of 1973. Although the exact cause for New England cottontail decline remains unknown, Eastern cottontails (*S. floridanus*) were stocked in northeastern states as a game species and may be an influencing factor due to the potential for increased habitat occupancy from hybrid vigor. Phylogenetic analyses of the New England cottontails, eastern cottontails, and snowshoe hares (*Lepus americanus*) in the northeastern United States may shed light on the New England cottontail's decline. Because eastern cottontails were stocked from several locations, they may have enhanced genetic variability, especially when compared to New England cottontails. Furthermore, phylogeographic patterns may help infer introduction and spread patterns of eastern cottontails. We sequenced 1,773 fecal, tissue, and blood samples from CT, MA, NH, NY, and RI. We identified 12 New England cottontail haplotypes, 101 eastern cottontail haplotypes, and eight snowshoe hare haplotypes. Eastern cottontails exhibited a greater number of haplotypes compared to New England cottontails; however, there was no geographic pattern to haplotype occurrences.

Keywords invasive species, *Lepus americanus*, mitochondrial DNA control region, *Sylvilagus transitionalis*, *Sylvilagus floridanus*

Introduction

The New England cottontail (*Sylvilagus transitionalis*) was once considered the same species as the Appalachian cottontail (*S. obscurus*) with a distribution from southeastern New England to Alabama (Chapman 1975). However, the New England and the Appalachian cottontail are now considered two different species with the Hudson river seperating their distributions (Chapman et al. 1992). New England cottontails are found north of the Hudson River with a diploid chromosome number (2N) of 52 (Holden and Eabry 1970; Ruedas et al. 1989), whereas those below the Hudson River are now considered Appalachian cottontails with a 2N of 46 (Robinson 1983; Ruedas et al. 1989). The management implications of the reduced habitat range due to the separation of New England and Appalachian cottontails has been recognized since 1992 (Chapman et al. 1992).

The New England cottontail is currently a candidate for listing as an endangered species under the Endangered Species Act of 1973 (U.S. Fish & Wildlife Service 2006) and a survey conducted from 2000 through 2004 indicates a habitat reduction of 86% since 1960 (Litvaitis et al. 2006). The loss of scrub-shrub habitat has been hypothesized as a primary reason for this drastic population decline (Litvaitis 1993; Litvaitis and Villafuerte 1996). The introduced eastern cottontail (*S. floridanus*) has spread throughout northeastern states (Johnston 1972) and is sympatric with New England cottontail, potentially playing a role in its decline. A study conducted by Probert and Litvaitis (1996) showed that eastern cottontails may not be able to expunge New England cottontails from habitat that they already occupy. However, eastern cottontails may be a better disperser, and once established in a patch, may exclude New England cottontail occupation (Probert and Litvaitis 1996).

Eastern cottontails were introduced to the Northeast from various other states by hunting clubs and state wildlife departments. While records of introductions are far from complete, efforts made by Dice (1927) and Johnston (1972) to determine where introduced eastern cottontails originated from have yielded some indications of source populations. In Connecticut, introductions from Kansas, Minnesota, and West Virginia have been documented. Massachusetts has documented introductions from Kansas, as well as "Midwest" and unknown. While New York has reported stocking eastern cottontails, records do not indicate the origin of the introduced rabbits. Rhode Island records show stocking from Missouri and Oklahoma, as well as, "Midwest," "Western States," and unknown sources. Furthermore, Johnston (1972) describes the possible introduction to the region during this time of five subspecies, *S. floridanus mallurus*, S.f. *alacer*, S.f. *mearnsi*, S.f. *similis*, S.f. *llanesis*, as well as, *S. auduboni*.

While Fenderson et al. (2011) recently focused on New England cottontail genetic diversity, a comparative genetic analysis between the two sympatric species has not been conducted since the one by Litvaitis et al. (1997). The Litvaitis et al. (1997) study had a limited sample numbers and almost no haplotype replicates for eastern cottontail samples (46 specimens collected and 45 haplotypes identified). Considering the extent of eastern cottontail introductions and the dramatic decline of New England cottontails in the region, an extensive comparative phylogenetic study may give insight into the New England cottontail's decline and the concurrent eastern cottontail's expansion. Many invasive species fit a model of expansion where the species in question is not *a priori* better adapted to a habitat but, through multiple introductions and hybridization among populations with different origins, evolutionary changes that increase invasive characteristics may take place (Ellstrand and Schierenbeck 2000). Here, we used mitochondrial (mtDNA) haplotypes to: 1) Estimate the number of haplotypes for the three lagomorph species found in northeastern United States; and 2) Determine if there are any phylogenetic patterns in the geographic distribution of haplotypes.

Methods

Sampling, DNA extraction, PCR amplification, sequencing, species identification, and haplotype identification

We sampled for Lagomorphs in five northeastern states, Connecticut, Massachusetts, New Hampshire, New York, and Rhode Island. We processed fecal, tissue, or blood samples depending upon the mode of sampling used, trapping vs. non-invasive sampling. Non-invasive sampling was conducted after snowfall when it was possible to maximize the freshness of pellets and the pellet color contrast with the substrate, therefore increasing the collector's ability to observe pellets. Sampling areas in four of these states, Connecticut, Massachusetts, New Hampshire, and New York, were decided upon by the appropriate state and federal agencies, depending on their surveying needs to determine were New England cottontails persist in their respective state. Sampling in Rhode Island focused on determining where New England cottontails existed with five sample site categories: 1) sites identified using a Habitat Suitability Index (HSI) model developed by Dr. Steven Fuller; 2) sites identified using an Early Successional Habitat (ESH) Geographic Information System (GIS) model by

Dr. William Buffum; 3) Historical Sites (HS) where New England cottontails were reported between 1970 and 2005; 4) haphazard sites; and 5) RI Department of Environmental Management and U.S. Fish and Wildlife Service sites. Therefore, sampling in these five states are biased towards New England cottontail collection. Historic Sites, ESH, and HS sites were surveyed using 50- x 50-m plots split into quadrants and sampled thoroughly for Lagomorph activity signs and fecal pellets on three separate occasions throughout the winter months. Haphazard samples were collected from areas that fell outside of HSI, ESH, or HS sites. State agency samples were collected according to their sampling needs. While active sampling took place between 2010 and 2012, we also processed tissue samples from Connecticut and Rhode Island that were collected prior to 2010. Sample storage, extraction, amplification, sequencing, species identification, and haplotype identification are described in Sullivan et al. (in preparation).

Phylogeographic analyses

We used partial sequences from the mtDNA control region gene for phylogenetic analysis because this region has been used in previous phylogenetic work for New England and eastern cottontails (Litvaitis et al. 1997). Sequence length ranged from 565 to 480 base pairs depending on the primer used (Sullivan et al. in preperation). For each species, New England cottontails, eastern cottontails, and snowshoe hares, we aligned all haplotypes using ClustalW 2.011 (Larkin et al. 2007) cost matrix in Geneious (Biomatters, New Zealand) and included an outgroup for each species. We used an eastern cottontail haplotype, Sth099 (accession number will be here), as the outgroup for New England cottontails, a New England cottontail haplotype (Sth005 accession number will be here) as the outgroup for eastern cottontails, and an eastern cottontail haplotype (Sth095 accession number will be here) as the outgroup for snowshoe hares. We used MrModelTest 2.3 (Nylander 2004) to identify the best model for Bayesian tree construction based on Akaike Information Criterion (AIC) (Akaike 1973) and MrBayes 2.3 (Huelsenbeck and Ronquist 2001; Ronquist and Huelsenbeck 2003) for tree construction. For the MrBayes phylogenetic analyses, we increased the number of generations until the average standard deviation of split frequency was below 0.01 for three independent runs. Phylogenetic trees were visualized using FigTree 1.4 (Rambaut 2012).

To further investigate the relationships among haplotypes, we used TCS version 1.21 (Clement et al. 2000) to create haplotype networks for all three species. We treated gaps as missing data and used a 95% connection limit. Because a majority of samples were fecal, not tissue samples from tagged animals, and mtDNA was used, we could not identify samples to the individual. Thus, we did not incorporate haplotype frequency into the network analysis because we were not able to accurately represent the number of individuals with specific haplotypes. We also calculated nucleotide diversity within each species using Arlequin v3.11 (Excoffier 2005) without incorporating the frequency of each haplotype among samples.

Results

We sequenced 1,773 samples from five northeastern states, 165 from Connecticut, 286 from Massachusetts, 34 from New Hampshire, 50 from New York, and 1,238 from Rhode Island (Fig. 2.1). Although sampling efforts were biased towards collecting New England cottontail samples, we identified the majority of samples as eastern cottontails. For Connecticut, we identified 122 eastern cottontails, 43 New England cottontails, and no snowshoe hares. For Massachusetts, we identified 160 eastern cottontails, 122 New England cottontails, and four snowshoe hares. For New Hampshire, we identified 10 eastern cottontails, 10 New England cottontails, and 14 snowshoe hares. For New York, we identified 49 eastern cottontails, one New England cottontail, and no snowshoe hares. For Rhode Island, we identified 1,236 eastern cottontails, two New England cottontails, and four snowshoe hares. For all northeastern states combined, we identified 101 eastern cottontail haplotypes, 12 New England haplotypes, and 8 snowshoe hare haplotypes. We based haplotype distribution in each state by the county in which it was collected (Tables 2.1-2.5).

For eastern cottontails, MrModelTest 2.3 identified HKY+I+G as the optimal model and the next best model had a delta AIC value of 4.49. For New England cottontails, MrModelTest 2.3 identified HKY+G as the appropriate model with the lowest AIC value (2068.57), the next two models, HKY+I and HKY+I+G, with the lowest AIC value had a delta of 0.07 and 1.31 respectively. For snowshoe hares, MrModelTest 2.3 identified HKY+I as the appropriate model with the lowest AIC value (2068.57), the next two models, HKY+I+G and GTR+I, with the lowest AIC value had a delta of 0.69 and 1.04 respectively. For both New England cottontails and snowshoe hares, phylogenetic trees produced with the next appropriate model did not drastically change relationships among haplotypes. A notable difference for New England cottontail haplotypes was that Sth003 and Sth0013 did not group with Sth001 and Sth002. Snowshoe hare haplotypes, Lah001 grouped with Lah007 and Lah003 but with low support. Eastern cottontails exhibit five major clades, which we labeled

A through E, although these clades did not group geographically (Fig. 2.2 through Fig. 2.6). New England cottontail and snowshoe hare showed very little phylogenetic structure and haplotypes did not structure geographically (Fig. 2.7 and Fig 2.8).

The network analysis shows similar grouping to the Bayesian tree for eastern cottontails with clade C broken into three separate networks. One haplotype from clade D separated out completely and clades A and B are connected (Fig. 2.9). The network analysis for New England cottontail and snowshoe hare haplotypes reflected the low phylogenetic structure found in the Bayesian tree, however, there were many unsampled haplotypes found on the snowshoe hare network (Fig. 2.10 and Fig. 2.11). Nucleotide diversity for New England cottontail haplotypes was calculated to be 0.006 with a standard deviation of ± 0.004. For eastern cottontail haplotypes the nucleotide diversity was 0.037 with a standard deviation of ± 0.018. Nucleotide diversity for snowshoe hare haplotypes was calculated to be 0.01 with a standard deviation of ± 0.006.

Discussion

While there were many eastern cottontail haplotypes that were collected in only one state, there was little geographic relationship to the phylogenetic trees produced from these haplotypes (Fig. 2.2 through Fig. 2.6). Furthermore, the network analysis revealed high genetic variability among haplotypes that grouped together in a similar pattern to the phylogenetic tree, but did not correspond geographically. For instance, the network analysis found that Sfh043 in clade C was found to be an interior haplotype, a haplotype from which others mutated, but was sampled in Connecticut, Massachusetts, and Rhode Island. Furthermore, haplotypes that grouped with Sfh043 on the Bayesian tree and network analysis were found in all five states (Fig. 2.5 and Fig. 2.9). Although areas of introduction may be distinguished by haplotype hotspots, where areas with high haplotype diversity indicate introduction centers (Lacoursiere-Roussel et al. 2012), this pattern did not suggest that Sfh043 was established in one area and subsequently spread. Alternatively, the Sfh043 could have been established in multiple areas during anthropogenic movement of the species. Similar lack of geographic pattern for different haplotypes was found by Litviatis et. al (1997).

Low genetic variability was found for New England cottontails with little phylogeographic pattern. It is possible that New England cottontails were moved from one northeastern state to another during eastern cottontails stocking events, which could offer an explanation for the lack of mtDNA geographic structure. The network analysis and low nucleotide diversity revealed that among the 12 haplotypes there was low genetic variability (Fig. 10). However, because of the dramatic reduction in New England cottontail populations (Litvaitis et al. 2006), we cannot be completely confident that all existing haplotypes were sampled. Similarly, Fenderson et al. (2011) described low genetic variation in New England cottontail using nuclear microsatellite markers, but they did find structure between populations. Litvaitis et al. (1997) do not find separation between Appalachian and New England cottontails despite the prediction made by Chapman et al. (1992) that the separation of these species occurred over the last 18,000 to 10,000 years. This indicates that enough time may not have elapsed since populations of New England cottontails have become separated to show haplotype structure.

The snowshoe hare Bayesian tree did not indicate much structure, however, the network analysis did reveal variation among sampled haplotypes. Because of the high number of haplotypes to number of snowshoe hares sampled (8 haplotypes from 18 samples), it is likely that the snowshoe hare was under sampled in our study. Furthermore, this species has a wide range, from Alaska to Newfoundland, extending south through the Appalachian Mountains to Tennessee (Godin 1977). It is very unlikely that we were able to capture a representative number of snowshoe hares from this region.

Eastern cottontails provide an interesting case of non-native species invasion. Unlike many other invasive species, eastern cottontails were purposely introduced by hunting clubs and state agencies as a game species (Johnston 1972; Dice 1927) from many states. A lag period is often a characteristic of an invasive species' spread, and is expected if evolutionary changes are taking place (Sakai et al. 2001). Determining if there was a lag time for eastern cottontail's invasion is difficult due to incomplete records and biases in data collection. Work done by Johnston et al. (1972), however, indicates that eastern cottontail distribution may have increased dramatically from 1950 to 1970. Considering that most introductions were recorded to have occurred from 1920 to 1940 (Dice 1927; Johnston 1972), this may constitute a lag time from introductions to population expansion, however, it is important to note that introductions continued beyond 1940.

The variety of source populations used for eastern cottontail stocking has most probably lead to the large number of haplotypes seen in the Northeast today. Increased genetic variation, rather than the typical decrease in genetic variation due to bottlenecking, has been recorded for invasive species that have undergone multiple introduction events (Kolbe et al. 2004). We discovered 101 haplotypes for the eastern cottontail, which offers a striking contrast to the 12 New England cottontail haplotypes. The possibility of hybrid vigor due to mixing of populations after stocking has been suggested for eastern cottontail populations in Maryland,where Chapman and Morgan (1973) documented the introduction of non-endemic populations of eastern cottontails and subsequent hybridization with endemic populations of the same species. They describe eastern cottontails as being able to "utilize its newfound genetic variability to pioneer into habitats previously undesirable" (Chapman and Morgan 1973). They also note that these "previously undesirable" habitats include those occupied by Appalachian cottontails (then considered *S. transitionalis*). Hybridization of populations of the same species that would normally be geographically constrained may allow considerable swift adaptive transitions to occur (Perez 2012). While we cannot prove that eastern cottontails have adaptive advantage over eastern cottontails due to hybrid vigor eastern cottontails exhibit greater nucleotide diversity (0.037) in the gene sampled than New England cottontails (0.006). It is likely that eastern cottontails may have acquired adaptive advantage over New England cottontails due to hybrid vigor, which may have resulted in the species' ability to use a greater range of habitat types, but this requires further research.

With the addition of nuclear DNA analysis, the story of eastern cottontail introduction may be made clearer. Microsatellite markers would allow for identification of sampled individuals and the incorporation of haplotype abundance for counties entered into the network analysis, which would allow the incorporation of haplotype prevalence into the study. Microsatellite markers also may provide insight into more recent movements of eastern cottontails throughout the landscape and provide information on this species' spread. Dr. Tim King is currently developing species-specific markers in collaboration with the University of Rhode Island's Regional Conservation Genetics Labaratory and the University of New Hampshire. Hybridization between eastern and New England cottontails also may be a factor in the New England cottontail's decline. While hybridization between eastern and Appalachian cottontails has been recorded (Chapman and Morgan 1973), New England and eastern cottontail hybridization has not been documented. If species-specific alleles are found for New England and eastern cottontail markers, a wide-range microsatellite study of both species may determine if hybridization is taking place between these two species.

Table 2. 1. Haplotypes from Connecticut listed by the county in which they were collected from 2010 to 2012 with some samples collected earlier in century

Sylvilalgus floridanus

County	Haplotypes	Frequency*	Unique haplotypes
Hartford	Sfh051, Sfh067, Sfh070	0.03	Sfh070
Litchfield	Sfh065, Sfh067	0.02	
Middlesex	Sfh020, Sfh034, Sfh037, Sfh038, Sfh043, Sfh065, Sfh067	0.07	Sfh020, Sfh037, Sfh038
New Haven	Sfh067	0.01	
New London	Sfh016, Sfh034, Sfh050, Sfh057, Sfh063, Sfh067, Sfh068	0.07	Sfh050, Sfh068
Tolland	Sfh031, Sfh063	0.02	Sfh031
Windham	Sfh051, Sfh063, Sfh067, Sfh069, Sfh099	0.05	Sfh099

Sylvilagus transitionalis

County	Haplotypes	Frequency	Unique haplotypes
New Haven	Sth002, Sth007	0.17	Sth007
New London	Sth001, Sth002	0.17	Sth001
Tolland	Sth010	0.08	
Windham	Sth014, Sth002	0.17	Sth014

*Frequency = number of haplotypes/total number of haplotypes in the study. For the state as a whole: *S. floridanus* - Total haplotypes = 17, Total unique haplotypes = 8, Total haplotype frequency = 0.17; *S. transitionalis* - Total haplotypes = 6, Total unique haplotypes = 3, Total haplotype frequency = 0.5 (Sth003 is present in Connecticut but county location is unknown)

Sylvilagus floridanus

County	Haplotypes	Frequency	Unique haplotypes
Barnstable	Sfh006, Sfh017, Sfh018, Sfh021, Sfh044, Sfh045, Sfh047, Sfh048, Sfh054, Sfh056, Sfh079, Sfh080, Sfh081, Sfh085, Sfh086, Sfh087	0.16	Sfh017, Sfh018, Sfh021, Sfh080, Sfh085, Sfh086, Sfh087
Berkshire	Sfh019, Sfh027, Sfh065, Sfh066, Sfh069, Sfh072, Sfh090	0.07	Sfh027, Sfh090
Bristol	Sfh079		
Hampden	Sfh035, Sfh057	0.02	Sfh035
Hampshire	Sfh057, Sfh069, Sfh079	0.03	
Franklin	Sfh069, Sfh098	0.02	
Martha's Vineyard	Sfh072	0.01	
Middlesex	Sfh018, Sfh043, Sfh054, Sfh057, Sfh069, Sfh084	0.06	
Nantucket	Sfh044, Sfh056, Sfh072, Sfh075, Sfh079, Sfh083	0.06	Sfh044, Sfh075, Sfh083
Worcester	Sfh024, Sfh048, Sfh056, Sfh065, Sfh069, Sfh082	0.06	Sfh082

Table 2. 2. Haplotypes collected in Massachusetts listed by the county in which they were collected from 2010 to 2012

Table 2.2 continued

Sylvilagus transitionalis

County	Haplotypes	Frequency	Unique haplotypes
Barnstable	Sth003, Sth004, Sth010, Sth013	0.3	Sth013
Berkshire	Sth004, Sth010	0.17	Sth004
Hampden	Sth004	0.08	
Nantucket	Sth003, Sth012	0.17	Sth012

Lepus americanus

County	Haplotypes	Frequency	Unique haplotypes
Plymouth	Lah001	0.13	
Middlesex	Lah001, Lah002	0.25	Lah002

Frequency = number of haplotypes/total number of haplotypes in the study. For the state as a whole: *S. floridanus* - Total haplotypes = 34, Total unique haplotypes = 20, Total haplotype frequency = 0.34; *S. transitionalis* - Total haplotypes = 5, Total unique haplotypes = 3, Total haplotype frequency = 0.42 (Sth089 is present in Connecticut but county location is unknown)

Table 2. 3. Haplotypes collected in New Hampshire listed by the county in which they were collected from 2010 to 2012

Sylvilagus floridanus

County	Haplotypes	Frequency	Unique haplotypes
Hillsborough	Sfh084	0.01	
Merrimack	Sfh084	0.01	
Rockingham	Sfh033	0.01	
Strafford	Sfh033, Sfh049, Sfh088	0.03	Sfh088

Sylvilagus transitionalis

County	Haplotypes	Frequency	Unique haplotypes
Rockingham	Sth002, Sth005, Sth006	0.25	Sth006
Strafford	Sth005	0.8	

Lepus americanus

County	Haplotypes	Frequency	Unique haplotypes
Hillsborough	Lah008	0.13	
Merrimack	Lah006, Lah008	0.25	Lah006
Rockingham	Lah001, Lah003	0.25	Lah003
Strafford	Lah001, Lah005, Lah007	0.38	Lah005, Lah007

Frequency = number of haplotypes/total number of haplotypes in the study. For the state as a whole: *S. floridanus* - Total haplotypes = 4, Total unique haplotypes = 2, Total haplotype frequency = 0.04; *S. transitionalis* - Total haplotypes = 3, Total unique haplotypes = 2, Total haplotype frequency = 0.25

Table 2. 4. Haplotypes collected in New York listed by the county in which they were collected from 2010 to 2012

Sylvilagus floridanus

County	Haplotypes	Frequency	Unique haplotypes
Columbia	Sfh065, Sfh067, Sfh069, Sfh069, Sfh072	0.05	
Dutchess	Sfh019, Sfh056, Sfh065, Sfh066, Sfh069, Sfh092, Sfh092, Sfh094, Sfh100, Sfh101	0.1	Sfh092, Sfh094, Sfh100, Sfh101

Sylvilagus transitionalis

County	Haplotypes	Frequency	Unique haplotypes
Putnam	Sth010	0.07	

Frequency = number of haplotypes/total number of haplotypes in the study. For the state as a whole: *S. floridanus* – Total haplotypes = 11, Total unique haplotypes = 4, Total haplotype frequency = 0.11; *S. transitionalis* – Total haplotypes = 1, Total unique haplotypes = 0, Total haplotype frequency = 0.08

Table 2. 5. Haplotypes from Rhode Island listed by the county in which they were collected from 2010 to 2012 with some samples collected earlier in century

Sylvilalgus floridanus

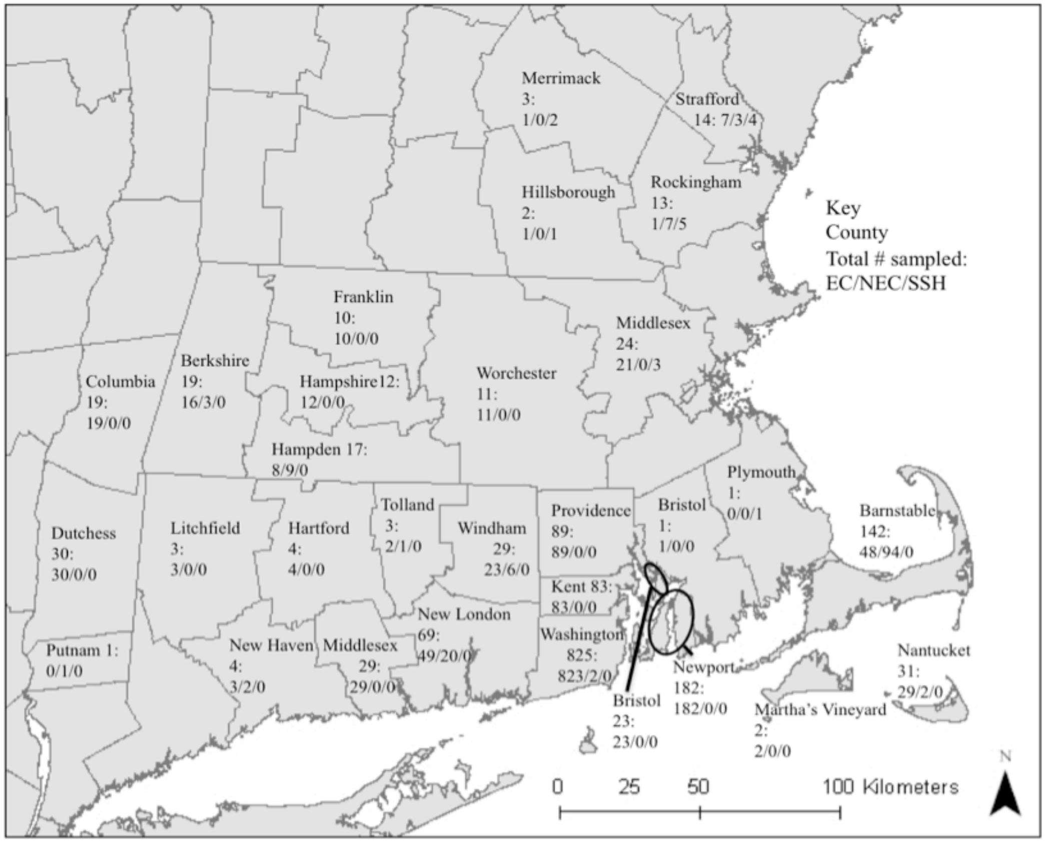
County	Haplotypes	Frequency	Unique haplotypes
Bristol	Sfh034, Sfh041, Sfh042, Sfh043, Sfh049, Sfh057, Sfh062, Sfh073	0.08	
Kent	Sfh008, Sfh011, Sfh013, Sfh019, Sfh032, Sfh034, Sfh040, Sfh045, Sfh063, Sfh067, Sfh095	0.11	Sfh008, Sfh011, Sfh013, Sfh095
Newport	Sfh001, Sfh006, Sfh009, Sfh016, Sfh019, Sfh029, Sfh030, Sfh034, Sfh040, Sfh041, Sfh042, Sfh045, Sfh047, Sfh049, Sfh051, Sfh052, Sfh057, Sfh060, Sfh061, Sfh097, Sfh098	0.21	Sfh009, Sfh029, Sfh030, Sfh052, Sfh061, Sfh097
Providence	Sfh003, Sfh004, Sfh012, Sfh013, Sfh014, Sfh024, Sfh025, Sfh036, Sfh039, Sfh043, Sfh053, Sfh054, Sfh060, Sfh063, Sfh067, Sfh071, Sfh073, Sfh074, Sfh076, Sfh091, Sfh096	0.21	Sfh003, Sfh012, Sfh013, Sfh014, Sfh025, Sfh036, Sfh039, Sfh053, Sfh071, Sfh074, Sfh091, Sfh096
Washington	Sfh001, Sfh002, Sfh004, Sfh005, Sfh006, Sfh007, Sfh008, Sfh015, Sfh016, Sfh019, Sfh022, Sfh023, Sfh024, Sfh026, Sfh030, Sfh032, Sfh040, Sfh040, Sfh043, Sfh045, Sfh046, Sfh047, Sfh049, Sfh054, Sfh055, Sfh057, Sfh058, Sfh059, Sfh060, Sfh062, Sfh063, Sfh064, Sfh066, Sfh067, Sfh073, Sfh077, Sfh093	0.37	Sfh002, Sfh005, Sfh007, Sfh008, Sfh015, Sfh022, Sfh023, Sfh026, Sfh030, Sfh032, Sfh046, Sfh055, Sfh058, Sfh059, Sfh062, Sfh064, Sfh077, Sfh093

Sylvilagus transitionalis

County	Haplotypes	Frequency	Unique haplotypes
Washington	Sth011	0.08	Sth011

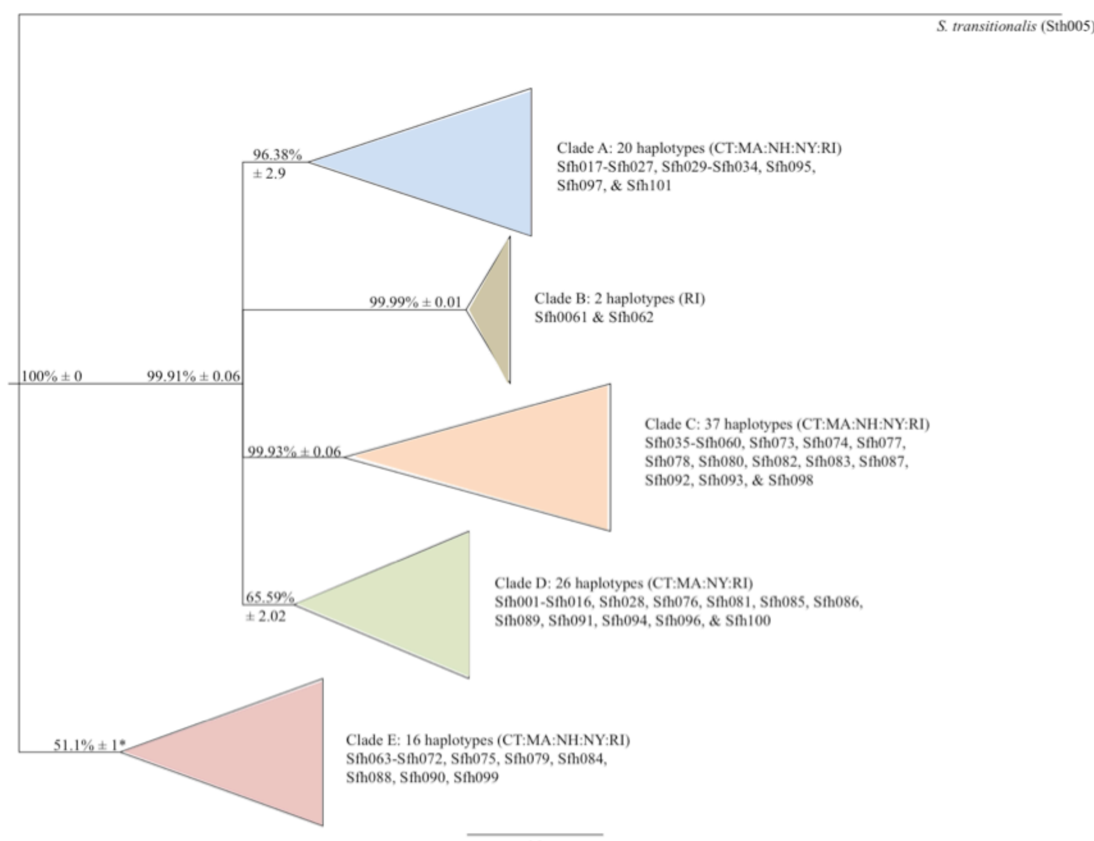
Frequency = number of haplotypes/total number of haplotypes in the study. For the state as a whole: *S. floridanus* - Total haplotypes = 64, Total unique haplotypes = 48, Total haplotype frequency = 0.63; *S. transitionalis* - Total haplotypes = 1, Total unique haplotypes = 1, Total haplotype frequency = 0.08

Figure 2. 1. Samples collected in Connecticut, Massachusetts, New Hampshire, New York, and Rhode Island from 2010 through 2012 with some samples collected earlier in the century summarized by county



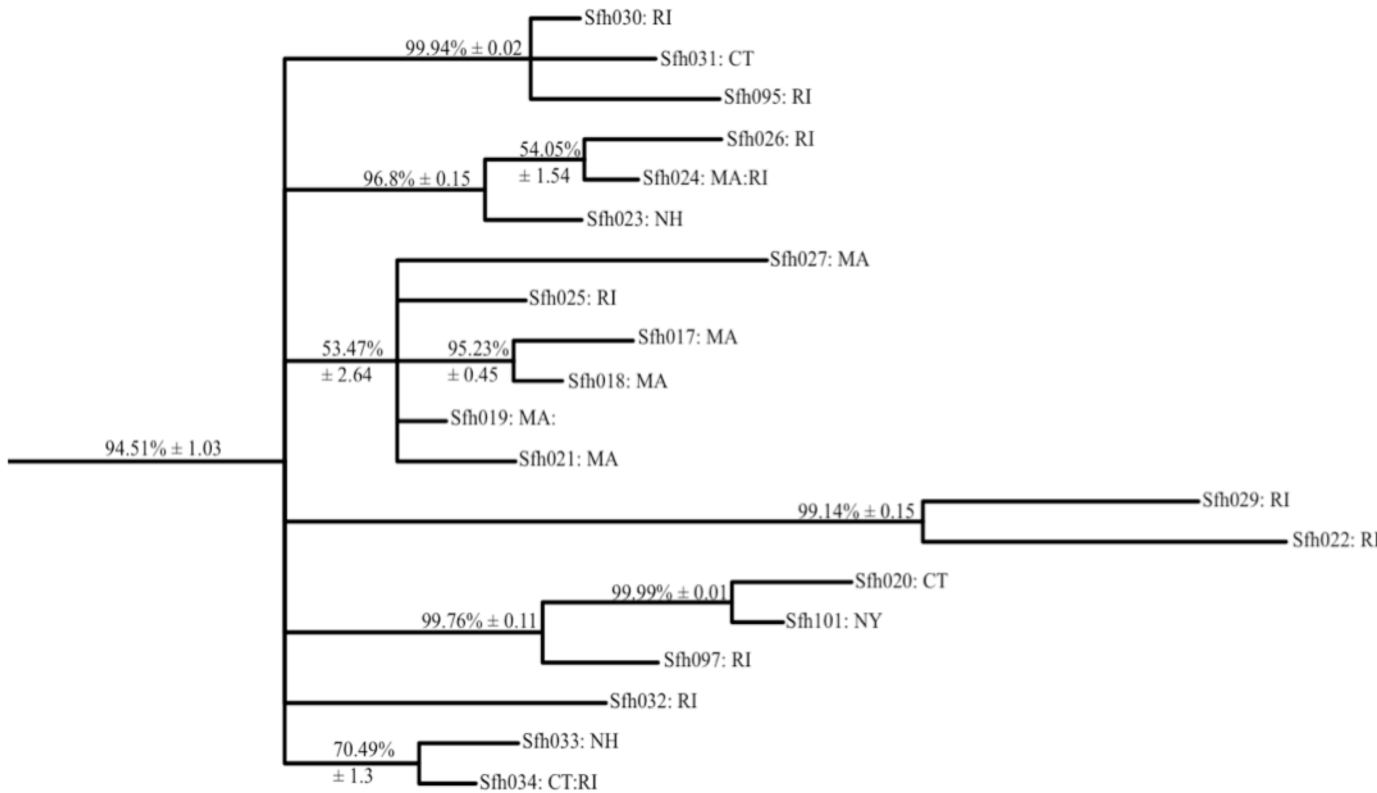
Some samples were collected before 2010 but not analyzed until this study. Samples with unknown county locations are not included above, as described in the key above where EC is eastern cottontails, NEC is New England cottontails, and SSH is snowshoe hares. Samples with unknown county locations are as follows: 9/14/0 for Connecticut, 2/14/0 for Massachusetts, 0/0/2 for New Hampshire, and 36/0/0 for Rhode Island.

Figure 2. 2. Bayesian phylogenetic tree and haplotype distribution of eastern cottontail (*Sylvilagus floridanus*) collected in Connecticut (CT), Massachusetts (MA), New Hampshire (NH), New York (NY), and Rhode Island (RI) between 2010 and 2012, with some samples collected earlier in the century. *S. transitionalis* as the outgroup.



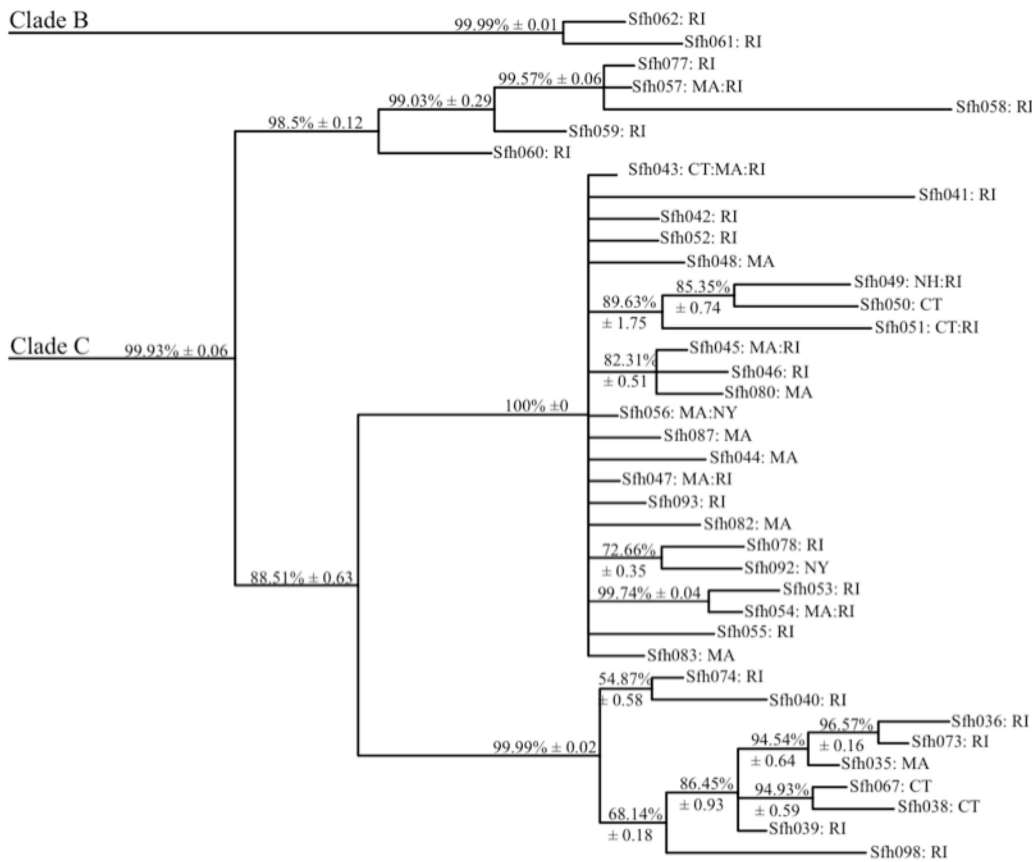
Analysis was repeated three times, average clade credibility values shown with ± standard deviation, * indicates that the standard deviation was calculated from two values because the third tree did not support this clade. Clades are collapsed.

Figure 2. 3. Clade A from the Fig. 2 Bayesian phylogenetic tree and haplotype distribution of eastern cottontail (*Sylvilagus floridanus*) collected in Connecticut (CT), Massachusetts (MA), New Hampshire (NH), New York (NY), and Rhode Island (RI) between 2010 and 2012, with some samples collected earlier in the century



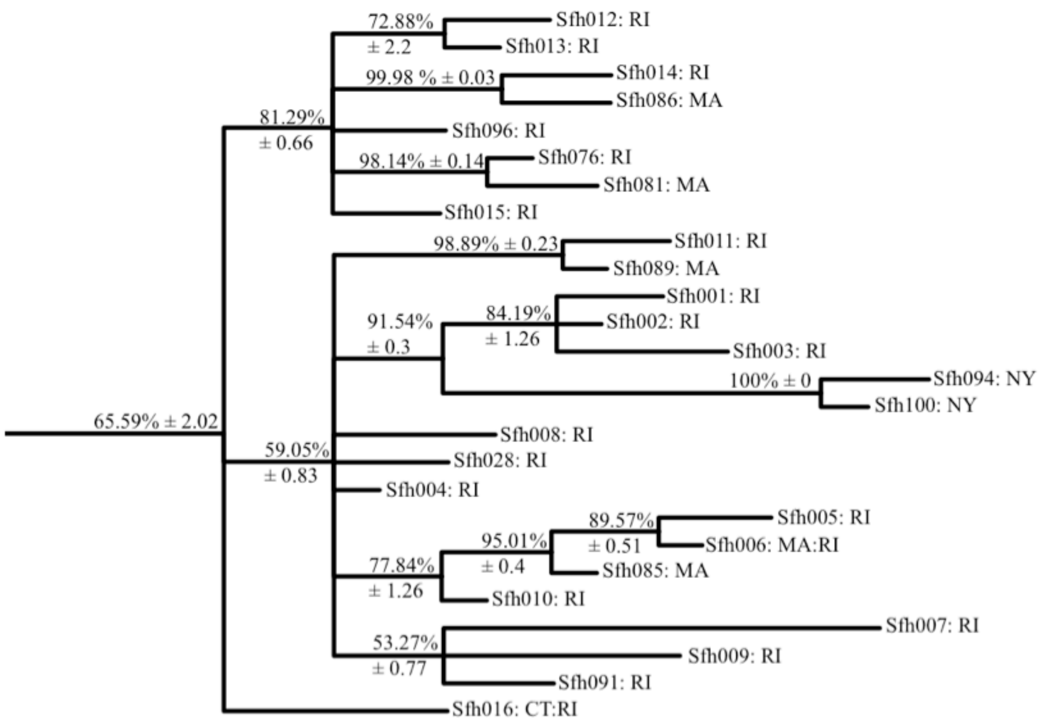
Analysis was repeated three times, average clade credibility values shown with ± standard deviation.

Figure 2. 4. Clades B and C from the Fig. 2 Bayesian phylogenetic tree and haplotype distribution of eastern cottontail (*Sylvilagus floridanus*) collected in Connecticut (CT), Massachusetts (MA), New Hampshire (NH), New York (NY), and Rhode Island (RI) between 2010 and 2012, with some samples collected earlier in the century



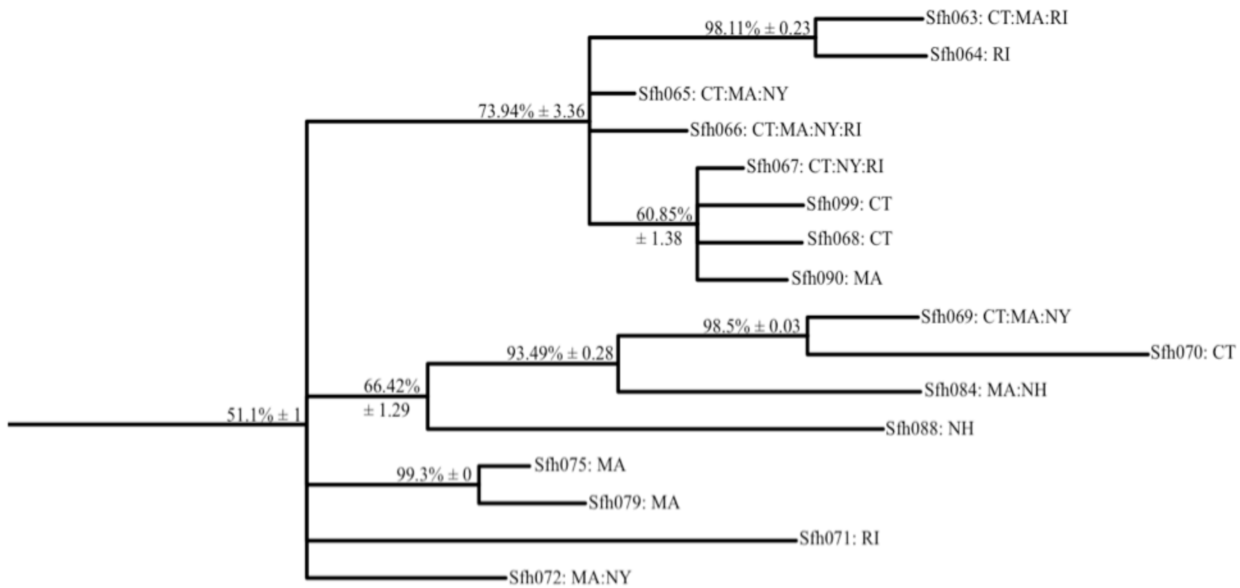
Analysis was repeated three times, average clade credibility values shown with ± standard deviation.

Figure 2. 5. Clade D from the Fig. 2 Bayesian phylogenetic tree and haplotype distribution of eastern cottontail (*Sylvilagus floridanus*) collected in Connecticut (CT), Massachusetts (MA), New York (NY), and Rhode Island (RI) between 2010 and 2012, with some samples collected earlier in the century



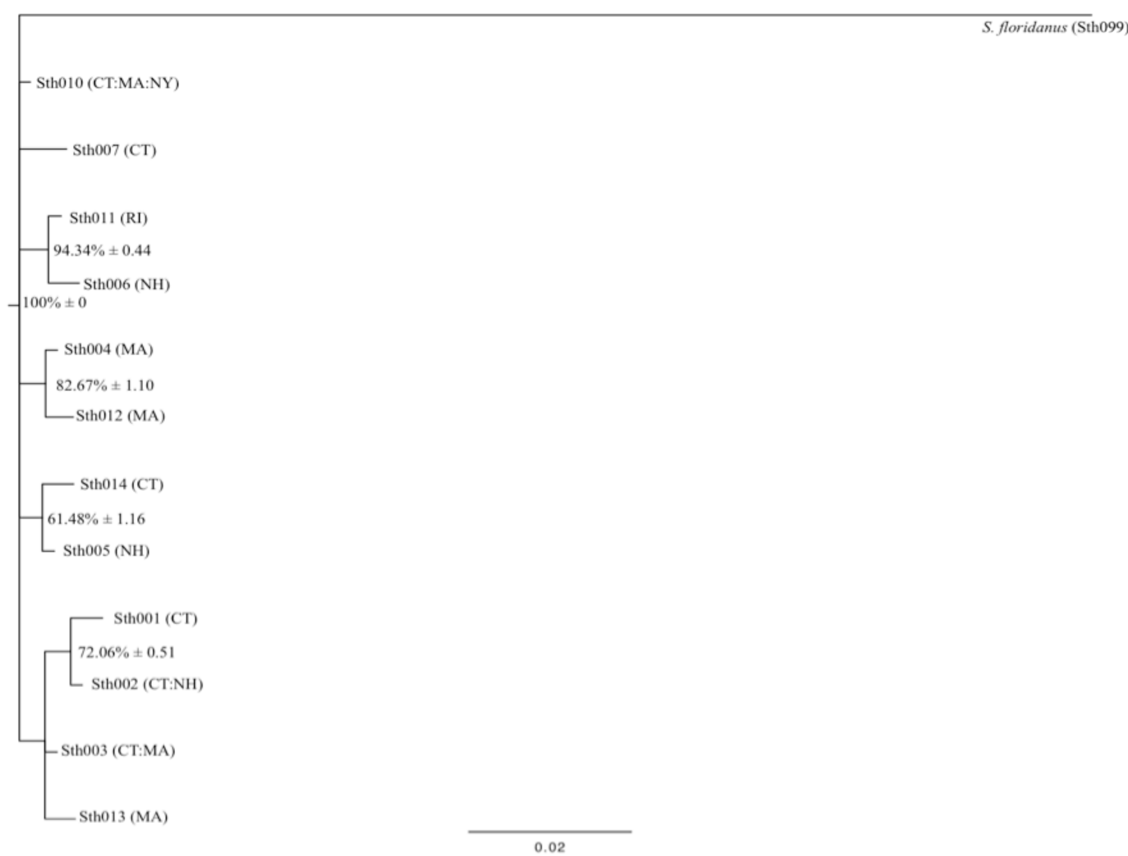
Analysis was repeated three times, average clade credibility values shown with ± standard deviation.

Figure 2. 6. Clade E from the Fig. 2 Bayesian phylogenetic tree and haplotype distribution of eastern cottontail (*Sylvilagus floridanus*) collected in Connecticut (CT), Massachusetts (MA), New Hampshire (NH), New York (NY), and Rhode Island (RI) between 2010 and 2012, with some samples collected earlier in the century



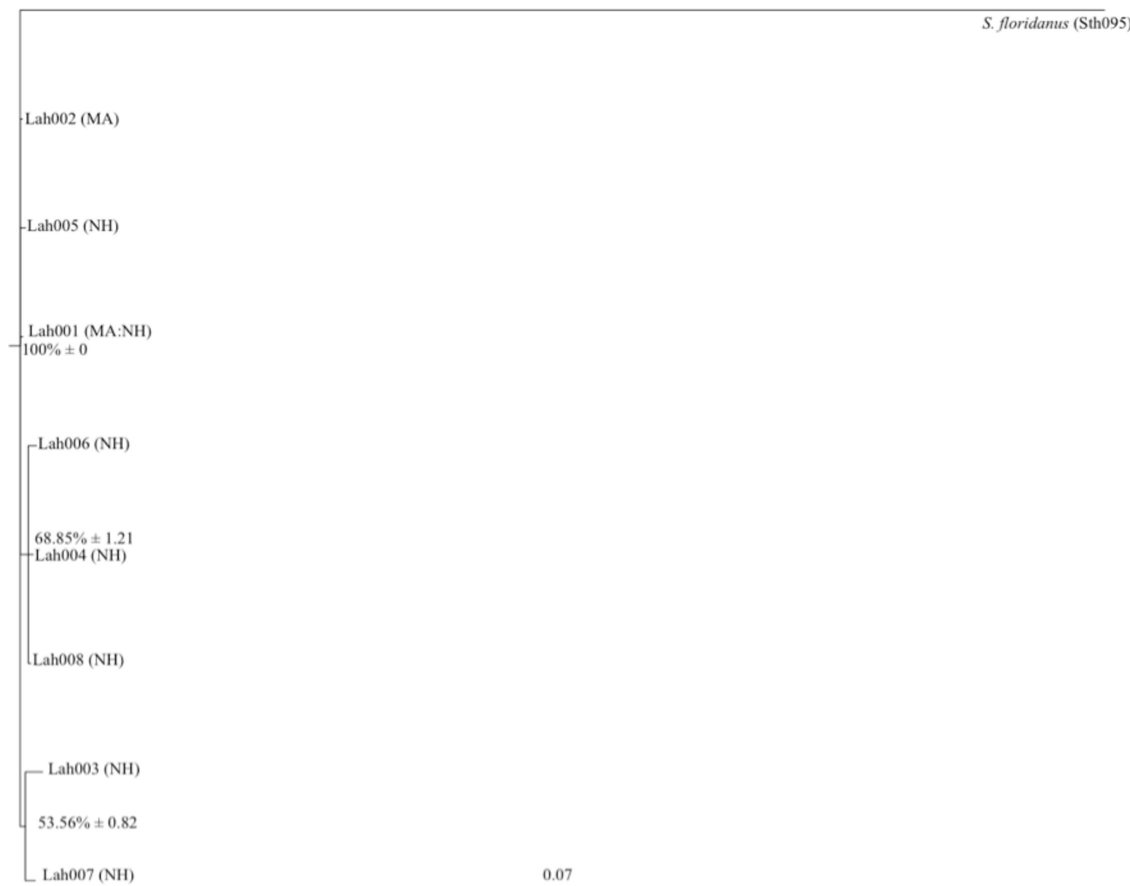
Analysis was repeated three times, average clade credibility values for two runs that supported this clade are shown with ± standard deviation.

Figure 2. 7. Bayesian phylogenetic tree and haplotype distribution of New England cottontails (*Sylvilagus transitionalis*) collected in C onnecticut (CT), Massachusetts (MA), New Hampshire (NH), New York (NY), and Rhode Island (RI) between 2010 and 2012. *S. floridanus* as the outgroup



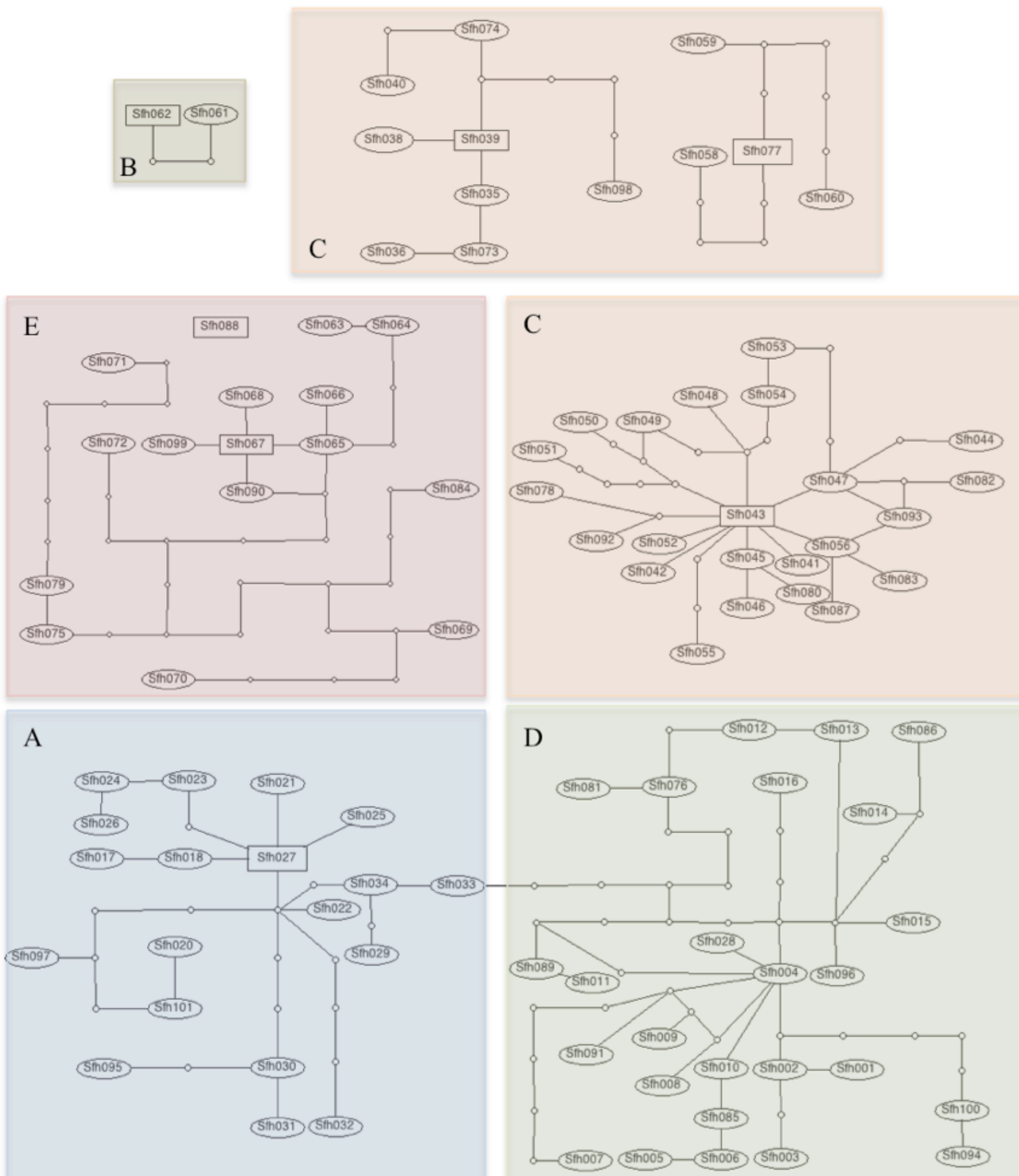
Analysis was repeated three times, average clade credibility values shown with ± standard deviation.

Figure 2. 8. Bayesian phylogenetic tree and haplotype distribution of snowshoe hare (Lepus *americanus*) collected in Massachusetts (MA) and New Hampshire (NH) between 2010 and 2012. *S. floridanus* as the outgroup



Analysis was repeated three times, average clade credibility values shown with standard deviation.

Figure 2. 9. Network analysis of eastern cottontail (*Sylvilagus floridanus*) haplotypes collected in Connecticut (CT), Massachusetts (MA), New Hampshire (NH), New York (NY), and Rhode Island (RI) between 2010 and 2012, with some samples collected earlier in the century using TCS version 1.21 (Clement et al. 2000)



Colors and letters correspond to clades found in the Bayesian phylogenetic analysis

Figure 2. 10. Network analysis of New England cottontail (*Sylvilagus transitionalis*) haplotypes collected in Connecticut (CT), Massachusetts (MA), New Hampshire (NH), New York (NY), and Rhode Island (RI) between 2010 and 2012

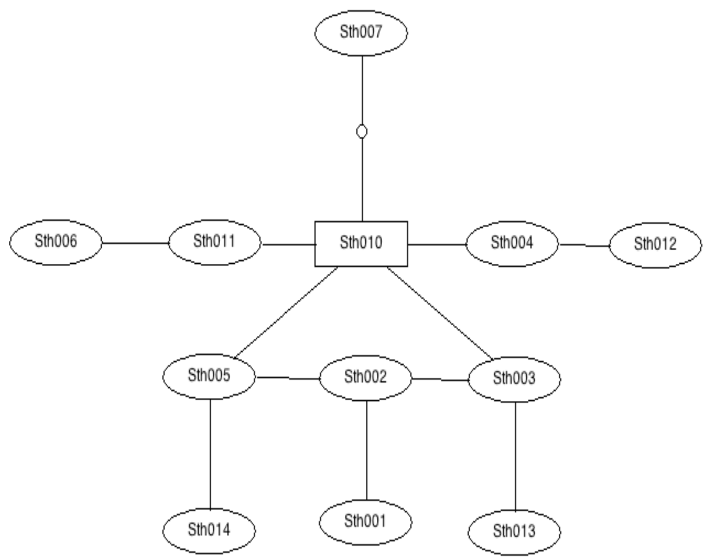
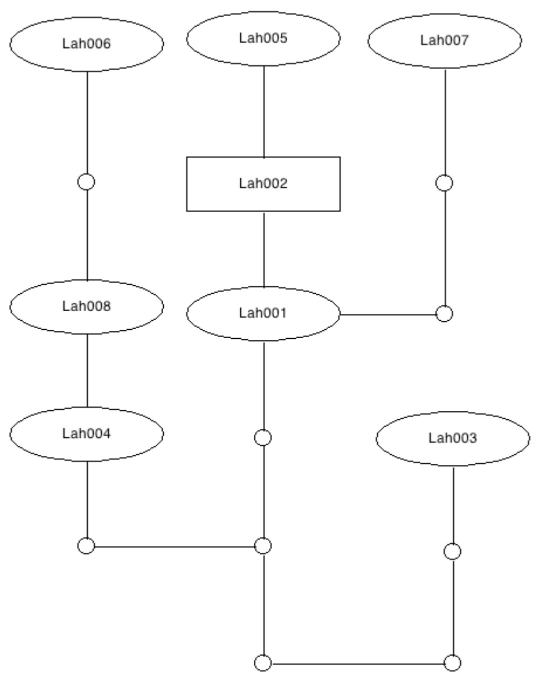


Figure 2. 11. Network analysis of snowshoe hare (*Lepus americanus*) haplotypes collected in Massachusetts (MA) and New Hampshire (NH) between 2010 and 2012



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Appendix 1: Samples received from Connecticut with sample type, county that the sample was collected in, haplotype of sample, and species identification

Sample ID	Sample Type	County	Haplotype	Species ID
CT-11-001	Fecal	New London	Sfh067	EC
CT-11-002	Fecal	New London	Sfh067	EC
CT-11-003	Fecal	New London	Sfh067	EC
CT-11-004	Fecal	New London	Sfh067	EC
CT-11-005	Fecal	New London	Sfh067	EC
CT-11-006	Fecal	New London	Sfh067	EC
CT-11-007	Fecal	New London	Sfh067	EC
CT-11-008	Fecal	New London	Sfh067	EC
CT-11-009	Fecal	New London	Sfh067	EC
CT-11-010	Fecal	New London	Sfh067	EC
CT-11-011	Fecal	New London	Sfh067	EC
CT-11-012	Fecal	New London	Sfh034	EC
CT-11-013	Fecal	New London	Sfh067	EC
CT-11-014	Fecal	New London	Sfh067	EC
CT-11-015	Fecal	New London	Sfh034	EC
CT-11-016	Fecal	New London	Sfh067	EC
CT-11-017	Fecal	New London	Sfh034	EC
CT-11-018	Fecal	New London	Sfh067	EC
CT-11-019	Fecal	New London	Sfh034	EC
CT-11-020	Fecal	New London	Sfh034	EC
CT-11-021	Fecal	New London	Sfh067	EC
CT-11-022	Fecal	New London	Sfh067	EC
CT-11-023	Fecal	New London	Sfh067	EC
CT-11-024	Fecal	New London	Sfh067	EC
CT-11-025	Fecal	New London	Sfh067	EC
CT-11-026	Fecal	New London	Sth002	NEC
CT-11-027	Fecal	New London	Sth002	NEC
CT-11-028	Fecal	New London	Sth002	NEC
CT-11-029	Fecal	New London	Sth002	NEC
CT-11-030	Fecal	New London	Sth002	NEC
CT-11-031	Fecal	New London	Sth002	NEC
CT-11-032	Fecal	New London	Sth008	NEC
CT-11-033	Fecal	New London	Sth002	NEC
CT-11-034	Fecal	New London	Sth001	NEC
CT-11-035	Fecal	New London	Sth001	NEC
CT-11-036	Fecal	New London	Sth002	NEC
CT-11-037	Fecal	New London	Sth002	NEC
CT-11-038	Fecal	New London	Sth001	NEC
CT-11-039	Fecal	New London	Sth001	NEC
CT-11-040	Fecal	New London	Sth002	NEC
CT-11-041	Fecal	New London	Sth002	NEC
CT-11-042	Fecal	New London	Sth001	NEC
CT-11-043	Fecal	New Haven	Sfh067	EC

Appendix 1: continued

Sample ID	Sample Type	County	Haplotype	Species ID
CT-11-044	Fecal	New Haven	Sth002	NEC
CT-11-045	Fecal/Tissue	New Haven	Sth007	NEC
CT-11-046	Fecal	New Haven	Sfh067	EC
CT-11-047	Fecal	New Haven	Sfh067	EC
CT-12-001	Tissue	Hartford	Sfh051	EC
CT-12-002	Tissue	Tolland	Sth010	NEC
CT-12-003	Tissue	Windham	Sfh067	EC
CT-12-004	Tissue	New London	Sfh034	EC
CT-12-005	Tissue	New London	Sfh034	EC
CT-12-006	Tissue	Windham	Sth014	NEC
CT-12-007	Tissue	Windham	Sfh067	EC
CT-12-008	Tissue	Windham	Sfh063	EC
CT-12-009	Tissue	Windham	Sfh067	EC
CT-12-010	Tissue	Tolland	Sfh063	EC
CT-12-011	Tissue	Windham	Sfh051	EC
CT-12-013	Tissue	Windham	Sfh099	EC
CT-12-014	Tissue	Windham	Sfh063	EC
CT-12-015	Tissue	Windham	Sfh067	EC
CT-12-016	Tissue	Windham	Sfh067	EC
CT-12-017	Tissue	Windham	Sfh051	EC
CT-12-018	Tissue	Windham	Sfh067	EC
CT-12-019	Tissue	Windham	Sfh063	EC
CT-12-020	Tissue	Windham	Sfh067	EC
CT-12-021	Tissue	Windham	Sfh063	EC
CT-12-022	Tissue	Windham	Sfh067	EC
CT-12-023	Tissue	Windham	Sfh063	EC
CT-12-024	Tissue	Windham	Sfh069	EC
CT-12-025	Tissue	Windham	Sfh069	EC
CT-12-026	Tissue	Windham	Sth014	NEC
CT-12-027	Tissue	Windham	Sfh067	EC
CT-12-028	Tissue	Unknown	Sth002	NEC
CT-12-029	Tissue	Unknown	Sth002	NEC
CT-12-030	Tissue	Unknown	Sfh063	EC
CT-12-031	Tissue	Unknown	Sfh063	EC
CT-12-032	Tissue	Unknown	Sfh063	EC
CT-12-033	Tissue	Unknown	Sfh067	EC
CT-12-034	Tissue	Unknown	Sfh034	EC
CT-12-035	Tissue	Unknown	Sfh034	EC
CT-12-036	Tissue	Unknown	Sfh034	EC
CT-12-037	Tissue	Unknown	Sth003	EC
CT-12-038	Tissue	Unknown	Sfh067	EC
CT-12-039	Tissue	Windham	Sfh067	EC
CT-12-040	Tissue	Windham	Sfh067	EC
CT-12-041	Tissue	Windham	Sfh063	EC

Appendix 1: continued

Sample ID	Sample Type	County	Haplotype	Species ID
CT-12-042	Tissue	Windham	Sfh063	EC
CT-EX-001	Tissue	Hartford	Sfh070	EC
CT-EX-002	Tissue	Hartford	Sfh067	EC
CT-EX-004	Tissue	Hartford	Sfh067	EC
CT-EX-005	Tissue	Middlesex	Sfh38	EC
CT-EX-006	Tissue	Middlesex	Sfh020	EC
CT-EX-007	Tissue	Middlesex	Sfh038	EC
CT-EX-008	Tissue	Middlesex	Sfh020	EC
CT-EX-009	Tissue	Middlesex	Sfh067	EC
CT-EX-010	Tissue	Middlesex	Sfh037	EC
CT-EX-011	Tissue	Middlesex	Sfh038	EC
CT-EX-013	Tissue	Middlesex	Sfh037	EC
CT-EX-014	Tissue	Middlesex	Sfh037	EC
CT-EX-015	Tissue	Middlesex	Sfh067	EC
CT-EX-016	Tissue	Middlesex	Sfh067	EC
CT-EX-017	Tissue	Middlesex	Sfh037	EC
CT-EX-018	Tissue	Middlesex	Sfh043	EC
CT-EX-019	Tissue	Middlesex	Sfh034	EC
CT-EX-020	Tissue	Middlesex	Sfh043	EC
CT-EX-022	Tissue	Middlesex	Sfh043	EC
CT-EX-023	Tissue	Middlesex	Sfh034	EC
CT-EX-024	Tissue	Middlesex	Sfh067	EC
CT-EX-025	Tissue	Middlesex	Sfh067	EC
CT-EX-026	Tissue	Middlesex	Sfh034	EC
CT-EX-028	Tissue	Middlesex	Sfh043	EC
CT-EX-029	Tissue	Middlesex	Sfh043	EC
CT-EX-030	Tissue	Middlesex	Sfh067	EC
CT-EX-031	Tissue	Middlesex	Sfh065	EC
CT-EX-032	Tissue	Middlesex	Sfh067	EC
CT-EX-033	Tissue	Middlesex	Sfh043	EC
CT-EX-034	Tissue	Middlesex	Sfh043	EC
CT-EX-035	Tissue	Middlesex	Sfh043	EC
CT-EX-036	Tissue	Middlesex	Sfh067	EC
CT-EX-037	Tissue	New London	Sfh063	EC
CT-EX-038	Tissue	New London	Sfh063	EC
CT-EX-039	Tissue	New London	Sfh067	EC
CT-EX-040	Tissue	New London	Sfh057	EC
CT-EX-041	Tissue	New London	Sfh067	EC
CT-EX-042	Tissue	New London	Sfh067	EC
CT-EX-043	Tissue	Litchfield	Sfh065	EC
CT-EX-045	Tissue	Litchfield	Sfh067	EC
CT-EX-047	Tissue	New London	Sfh034	EC

Appendix 1: continued

Sample ID	Sample Type	County	Haplotype	Species ID
CT-EX-048	Tissue	New London	Sfh063	EC
CT-EX-049	Tissue	New London	Sfh067	EC
CT-EX-050	Tissue	New London	Sfh068	EC
CT-EX-051	Tissue	New London	Sfh067	EC
CT-EX-052	Tissue	New London	Sfh034	EC
CT-EX-053	Tissue	New London	Sfh034	EC
CT-EX-054	Tissue	New London	Sfh068	EC
CT-EX-055	Tissue	New London	Sfh016	EC
CT-EX-056	Tissue	New London	Sfh067	EC
CT-EX-057	Tissue	New London	Sfh068	EC
CT-EX-058	Tissue	New London	Sfh067	EC
CT-EX-059	Tissue	New London	Sfh034	EC
CT-EX-060	Tissue	New London	Sfh067	EC
CT-EX-061	Tissue	New London	Sfh050	EC
CT-EX-062	Tissue	New London	Sfh067	EC
CT-EX-063	Tissue	Litchfield	Sfh065	EC
CT-EX-064	Tissue	Tolland	Sfh031	EC
RWPZ-008	Tissue/Fecal	Unknown	Sth002	NEC
RWPZ-009	Tissue/Fecal	Unknown	Sth002	NEC
RWPZ-010	Tissue/Fecal	Unknown	Sth002	NEC
RWPZ-011	Tissue/Fecal	Unknown	Sth002	NEC
RWPZ-024	Tissue/Fecal	Unknown	Sth002	NEC
RWPZ-025	Tissue/Fecal	Unknown	Sth002	NEC
RWPZ-028	Tissue/Fecal	Unknown	Sth002	NEC
RWPZ-029	Tissue/Fecal	Unknown	Sth006	NEC
RWPZ-030	Tissue/Fecal	Unknown	Sth002	NEC
RWPZ-031	Tissue/Fecal	Unknown	Sth002	NEC
RWPZ-032	Tissue/Fecal	Unknown	Sth008/ Sth002	NEC
RWPZ-033	Tissue/Fecal	Unknown	Sth002	NEC
RWPZ-10-001	Tissue/Fecal/Blood	Windham	Sth009/ Sth014	NEC
RWPZ-10-002	Tissue/Fecal/Blood	Windham	Sth009/ Sth014	NEC
RWPZ-10-003	Tissue/Fecal/Blood	Windham	Sth002	NEC
RWPZ-10-004	Tissue/Fecal/Blood	Windham	Sth002	NEC
RWPZ-10-005	Tissue/Fecal/Blood	New London	Sth002	NEC
RWPZ-10-006	Tissue/Fecal/Blood	New London	Sth002	NEC
RWPZ-10-007	Tissue/Fecal/Blood	New London	Sth002	NEC

Appendix 2: Samples received from Massachusetts with sample type, county that the sample was collected in, haplotype of sample, and species identification

Sample ID	Sample Type	County	Haplotype	Species ID
MA-10-001	Tissue	Barnstable	Sfh079	EC
MA-10-002	Tissue/Blood	Barnstable	Sfh044	EC
MA-10-003	Tissue/Blood	Barnstable	Sfh044	EC
MA-10-004	Tissue/Blood	Barnstable	Sfh044	EC
MA-10-005	Tissue/Blood	Barnstable	Sfh044	EC
MA-10-006	Tissue	Barnstable	Sfh044	EC
MA-10-007	Tissue	Unknown	Sfh079	EC
MA-10-008	Fecal/Blood	Barnstable	Sth003	NEC
MA-10-009	Fecal/Tissue/Blood	Barnstable	Sth003	NEC
MA-10-010	Tissue/Blood	Barnstable	Sth003	NEC
MA-11-011	Tissue/Blood	Barnstable	Sth003	NEC
MA-11-012	Tissue/Blood	Barnstable	Sth003	NEC
MA-11-013	Tissue/Blood	Barnstable	Sfh044	EC
MA-11-014	Tissue/Blood	Barnstable	Sth003	NEC
MA-11-015	Fecal	Hampden	Sth004	NEC
MA-11-016	Fecal	Hampden	Sth004	NEC
MA-11-017	Fecal	Hampden	Sth004	NEC
MA-11-018	Fecal	Hampden	Sth004	NEC
MA-11-019	Fecal	Hampden	Sth004	NEC
MA-11-020	Fecal	Hampden	Sth004	NEC
MA-11-021	Fecal	Hampden	Sth004	NEC
MA-11-022	Fecal	Hampden	Sth004	NEC
MA-11-023	Fecal	Hampden	Sth004	NEC
MA-11-024	Fecal	Hampden	Sfh035	EC
MA-11-025	Fecal	Berkshire	Sfh066	EC
MA-11-026	Fecal	Berkshire	Sth004	NEC
MA-11-027	Fecal	Berkshire	Sth004	NEC
MA-11-028	Fecal	Berkshire	Sfh072	EC
MA-11-029	Fecal	Berkshire	Sfh072	EC
MA-11-030	Fecal	Berkshire	Sfh065	EC
MA-11-031	Fecal	Berkshire	Sfh065	EC
MA-11-032	Fecal	Berkshire	Sfh069	EC
MA-11-033	Fecal	Berkshire	Sfh066	EC
MA-11-034	Fecal	Berkshire	Sth010	NEC
MA-11-035	Fecal	Berkshire	Sfh066	EC
MA-11-036	Fecal	Barnstable	Sfh018	EC
MA-11-037	Fecal	Barnstable	Sth003	NEC
MA-11-038	Fecal	Barnstable	Sth003	NEC
MA-11-039	Fecal	Barnstable	Sth003	NEC
MA-11-040	Fecal	Barnstable	Sth003	NEC
MA-11-041	Fecal	Barnstable	Sth003	NEC
MA-11-042	Fecal	Barnstable	Sth003	NEC
MA-11-043	Fecal	Barnstable	Sth003	NEC

Appendix 2: continued

Sample ID	Sample Type	County	Haplotype	Species ID
MA-11-044	Tissue/Blood	Barnstable	Sfh021	EC
MA-11-045	Tissue/Blood	Barnstable	Sfh021	EC
MA-11-046	Tissue/Blood	Barnstable	Sth003	NEC
MA-11-049	Fecal/Tissue/Blood	Barnstable	Sth010	NEC
MA-11-050	Tissue/Blood	Barnstable	Sth003	NEC
MA-11-051	Tissue/Blood	Barnstable	Sth003	NEC
MA-11-052	Tissue/Blood	Barnstable	Sth003	NEC
MA-11-054	Tissue/Blood	Barnstable	Sth003	NEC
MA-11-055	Tissue/Blood	Barnstable	Sfh048	EC
MA-11-056	Tissue/Blood	Barnstable	Sfh018	EC
MA-11-058	Tissue/Blood	Barnstable	Sfh044	EC
MA-11-060	Fecal/Tissue/Blood	Barnstable	Sth003	NEC
MA-11-061	Fecal/Tissue/Blood	Barnstable	Sth010	NEC
MA-11-062	Fecal/Tissue/Blood	Barnstable	Sth003	NEC
MA-11-063	Tissue	Barnstable	Sth003	NEC
MA-11-065	Tissue	Barnstable	Sfh017	EC
MA-11-066	Tissue	Barnstable	Sth003	NEC
MA-11-069	Fecal	Barnstable	Sfh048	EC
MA-11-071	Fecal	Berkshire	Sfh069	EC
MA-11-072	Fecal	Berkshire	Sfh027	EC
MA-11-073	Fecal	Hampden	Sfh057	EC
MA-11-074	Fecal	Berkshire	Sfh019	EC
MA-11-075	Fecal	Berkshire	Sfh065	EC
MA-11-076	Fecal	Berkshire	Sfh069	EC
Ma-11-077	Fecal	Berkshire	Sfh069	EC
MA-11-078	Fecal	Hampden	Sfh057	EC
MA-11-079	Fecal	Hampden	Sfh057	EC
MA-11-080	Fecal	Hampden	Sfh057	EC
MA-11-081	Fecal	Hampden	Sfh035	EC
MA-11-083	Blood	Barnstable	Sth003	NEC
MA-11-084	Blood	Barnstable	Sth003	NEC
MA-11-085	Blood	Barnstable	Sth003	NEC
MA-11-087	Tissue/Blood	Barnstable	Sth003	NEC
MA-11-088	Fecal/Tissue/Blood	Barnstable	Sth003	NEC
MA-11-089	Tissue/Blood	Martha's Vineyard	Sfh072	EC
MA-11-090	Tissue/Blood	Martha’s Vineyard	Sfh072	EC
MA-11-091	Fecal	Nantucket	Sfh079	EC
MA-11-092	Fecal	Nantucket	Sfh079	EC
MA-11-093	Fecal	Nantucket	Sfh079	EC
MA-11-094	Fecal	Nantucket	Sth003	NEC
MA-11-095	Tissue	Barnstable	Sfh044	EC
MA-11-096	Tissue	Barnstable	Sth003	NEC
MA-11-097	Tissue	Middlesex	Sfh043	EC

Appendix 2: continued

Sample ID	Sample Type	County	Haplotype	Species ID
MA-11-099	Tissue	Middlesex	Sfh043	EC
MA-11-100	Tissue	Nantucket	Sfh056	EC
MA-11-101	Tissue	Nantucket	Sfh075	EC
MA-11-102	Tissue	Nantucket	Sfh056	EC
MA-11-103	Tissue	Nantucket	Sfh079	EC
MA-11-104	Tissue/Blood	Nantucket	Sfh079	EC
MA-11-105	Tissue/Blood	Nantucket	Sfh079	EC
MA-11-106	Tissue/Blood	Nantucket	Sfh075	EC
MA-11-107	Tissue/Blood	Nantucket	Sfh056	EC
MA-11-108	Tissue/Blood	Nantucket	Sfh072	EC
MA-11-109	Tissue/Blood	Nantucket	Sfh056	EC
MA-11-110	Tissue/Blood	Nantucket	Sfh056	EC
MA-11-111	Tissue/Blood	Nantucket	Sth012	EC
MA-11-112	Tissue	Nantucket	Sfh072	EC
MA-11-113	Tissue	Nantucket	Sfh079	EC
MA-11-114	Tissue	Nantucket	Sfh072	EC
MA-12-001	Fecal/Tissue/Blood	Barnstable	Sfh044	EC
MA-12-002	Fecal/Tissue/Blood	Barnstable	Sfh021	EC
MA-12-003	Fecal/Tissue/Blood	Barnstable	Sfh044	EC
MA-12-004	Fecal/Tissue/Blood	Barnstable	Sfh017	EC
MA-12-005	Fecal/Tissue/Blood	Barnstable	Sth003	NEC
MA-12-006	Fecal/Tissue/Blood	Barnstable	Sth003	NEC
MA-12-007	Tissue/Blood	Barnstable	Sfh080	EC
MA-12-008	Tissue/Blood	Barnstable	Sth003	NEC
MA-12-009	Tissue/Blood	Barnstable	Sfh081	EC
MA-12-010	Tissue/Blood	Barnstable	Sfh080	EC
MA-12-011	Tissue	Barnstable	Sfh080	EC
MA-12-012	Fecal	Worcester	Sfh082	EC
MA-12-013	Fecal	Franklin	Sfh098	EC
MA-12-014	Fecal	Franklin	Sfh069	EC
MA-12-015	Fecal	Franklin	Sfh069	EC
MA-12-016	Fecal	Franklin	Sfh098	EC
MA-12-017	Fecal	Franklin	Sfh098	EC
MA-12-018	Fecal	Franklin	Sfh069	EC
MA-12-019	Fecal	Franklin	Sfh069	EC
MA-12-020	Fecal	Franklin	Sfh069	EC
MA-12-021	Fecal	Franklin	Sfh069	EC
MA-12-022	Fecal	Franklin	Sfh069	EC
MA-12-023	Tissue/Blood	Worcester	Sfh048	EC
MA-12-024	Tissue	Worcester	Sfh048	EC
MA-12-025	Tissue/Blood	Worcester	Sfh048	EC
MA-12-026	Tissue/Blood	Worcester	Sfh048	EC
MA-12-027	Fecal	Worcester	Sfh048	EC
MA-12-028	Fecal	Worcester	Sfh082	EC

Appendix 2: continued

Sample ID	Sample Type	County	Haplotype	Species ID
MA-12-030	Fecal	Berkshire	Sfh066	EC
MA-12-031	Fecal	Hampshire	Sfh079	EC
MA-12-032	Fecal	Hampshire	Sfh069	EC
MA-12-033	Fecal	Hampshire	Sfh069	EC
MA-12-034	Fecal	Hampshire	Sfh069	EC
MA-12-035	Fecal	Hampshire	Sfh069	EC
MA-12-036	Fecal	Middlesex	Lah002	SSH
MA-12-037	Fecal	Middlesex	Lah001	SSH
MA-12-038	Fecal	Middlesex	Lah001	SSH
MA-12-039	Fecal	Middlesex	Sfh057	EC
MA-12-040	Fecal	Middlesex	Sfh069	EC
MA-12-041	Fecal	Middlesex	Sfh043	EC
MA-12-042	Fecal	Middlesex	Sfh018	EC
MA-12-043	Fecal	Middlesex	Sfh057	EC
MA-12-044	Tissue/Blood	Nantucket	Sfh079	EC
MA-12-045	Tissue/Blood	Nantucket	Sfh083	EC
MA-12-046	Tissue/Blood	Nantucket	Sfh083	EC
MA-12-047	Tissue/Blood	Nantucket	Sfh083	EC
MA-12-048	Fecal	Nantucket	Sfh072	EC
MA-12-049	Fecal	Nantucket	Sfh079	EC
MA-12-050	Fecal	Nantucket	Sfh079	EC
MA-12-051	Fecal	Nantucket	Sfh079	EC
MA-12-052	Fecal	Nantucket	Sfh079	EC
MA-12-053	Fecal	Nantucket	Sfh079	EC
MA-12-054	Fecal	Nantucket	Sfh044	EC
MA-12-055	Fecal	Middlesex	Sfh057	EC
MA-12-056	Fecal	Middlesex	Sfh043	EC
MA-12-057	Fecal	Middlesex	Sfh084	EC
MA-12-058	Fecal	Middlesex	Sfh084	EC
MA-12-059	Fecal	Middlesex	Sfh084	EC
MA-12-060	Fecal	Middlesex	Sfh069	EC
MA-12-061	Fecal	Middlesex	Sfh069	EC
MA-12-062	Tissue	Middlesex	Sfh018	EC
MA-12-063	Tissue/Blood	Middlesex	Sfh043	EC
MA-12-064	Tissue	Middlesex	Sfh057	EC
MA-12-065	Tissue	Middlesex	Sfh043	EC
MA-12-066	Tissue	Middlesex	Sfh043	EC
MA-12-067	Tissue	Barnstable	Sfh017	EC
MA-12-068	Tissue	Middlesex	Sfh054	EC
MA-12-069	Tissue/Blood	Barnstable	Sth003	NEC
MA-12-070	Tissue/Blood	Barnstable	Sth003	NEC
MA-12-071	Fecal/Tissue/Blood	Barnstable	Sth003	NEC
MA-12-072	Tissue/Blood	Barnstable	Sth003	NEC
MA-12-073	Tissue/Blood	Barnstable	Sfh079	EC

Appendix 2: continued

Sample ID	Sample Type	County	Haplotype	Species ID
MA-12-074	Tissue/Blood	Barnstable	Sfh079	EC
MA-12-075	Tissue/Blood	Barnstable	Sth003	NEC
MA-12-076	Tissue/Blood	Barnstable	Sth003	NEC
MA-12-077	Tissue/Blood	Barnstable	Sth003	NEC
MA-12-078	Tissue/Blood	Barnstable	Sfh079	EC
MA-12-079	Tissue/Blood	Barnstable	Sfh079	EC
MA-12-080	Blood	Worchester	Sfh024	EC
MA-EX-12-001	Tissue	Barnstable	Sth003	NEC
MA-EX-12-002	Tissue	Barnstable	Sth003	NEC
MA-EX-12-003	Tissue	Barnstable	Sth013	NEC
MA-EX-12-004	Tissue	Barnstable	Sth004	NEC
MA-EX-12-005	Tissue	Barnstable	Sth003	NEC
MA-EX-12-006	Tissue	Barnstable	Sth003	NEC
MA-EX-12-007	Tissue	Barnstable	Sth003	NEC
MA-EX-12-008	Tissue	Barnstable	Sth003	NEC
MA-EX-12-009	Tissue	Barnstable	Sth003	NEC
MA-EX-12-010	Tissue	Barnstable	Sfh085	EC
MA-EX-12-011	Tissue	Barnstable	Sth003	NEC
MA-EX-12-012	Tissue	Barnstable	Sfh021	EC
MA-EX-12-013	Tissue	Barnstable	Sth003	NEC
MA-EX-12-014	Tissue	Barnstable	Sth003	NEC
MA-EX-12-015	Tissue	Barnstable	Sth003	NEC
MA-EX-12-016	Tissue	Barnstable	Sth003	NEC
MA-EX-12-017	Tissue	Barnstable	Sth003	NEC
MA-EX-12-018	Tissue	Barnstable	Sth003	NEC
MA-EX-12-019	Tissue	Barnstable	Sth003	NEC
MA-EX-12-020	Tissue	Barnstable	Sth003	NEC
MA-EX-12-021	Tissue	Barnstable	Sth003	NEC
MA-EX-12-022	Tissue	Barnstable	Sth003	NEC
MA-EX-12-023	Tissue	Barnstable	Sth003	NEC
MA-EX-12-024	Tissue	Barnstable	Sfh021	EC
MA-EX-12-025	Tissue	Barnstable	Sfh006	EC
MA-EX-12-026	Tissue	Barnstable	Sth003	NEC
MA-EX-12-027	Tissue	Barnstable	Sth003	NEC
MA-EX-12-028	Tissue	Hampshire	Sfh069	EC
MA-EX-12-029	Tissue	Barnstable	Sfh006	EC
MA-EX-12-030	Tissue	Barnstable	Sth003	NEC
MA-EX-12-031	Tissue	Barnstable	Sth003	NEC
MA-EX-12-032	Tissue	Barnstable	Sfh086	EC
MA-EX-12-033	Tissue	Barnstable	Sfh085	EC
MA-EX-12-034	Tissue	Barnstable	Sfh006	EC
MA-EX-12-035	Tissue	Barnstable	Sth003	NEC
MA-EX-12-036	Tissue	Berkshire	Sfh090	EC
MA-EX-12-037	Tissue	Worcester	Sfh069	EC

Appendix 2: continued

Sample ID	Sample Type	County	Haplotype	Species ID
MA-EX-12-038	Tissue	Hampshire	Sfh057	EC
MA-EX-12-039	Tissue	Barnstable	Sth003	NEC
MA-EX-12-040	Tissue	Barnstable	Sth003	NEC
MA-EX-12-041	Tissue	Barnstable	Sth003	NEC
MA-EX-12-042	Tissue	Barnstable	Sth003	NEC
MA-EX-12-043	Tissue	Barnstable	Sfh087	EC
MA-EX-12-044	Tissue	Barnstable	Sth003	NEC
MA-EX-12-045	Tissue	Barnstable	Sth003	NEC
MA-EX-12-046	Tissue	Barnstable	Sfh056	EC
MA-EX-12-047	Tissue	Barnstable	Sfh044	EC
MA-EX-12-048	Tissue	Barnstable	Sfh079	EC
MA-EX-12-049	Tissue	Barnstable	Sth003	NEC
MA-EX-12-050	Tissue	Barnstable	Sth003	NEC
MA-EX-12-051	Tissue	Barnstable	Sfh047	EC
MA-EX-12-052	Tissue	Worcester	Sfh056	EC
MA-EX-12-053	Tissue	Barnstable	Sth003	NEC
MA-EX-12-054	Tissue	Barnstable	Sth003	NEC
MA-EX-12-055	Tissue	Barnstable	Sth003	NEC
MA-EX-12-056	Tissue	Barnstable	Sth003	NEC
MA-EX-12-057	Tissue	Barnstable	Sth003	NEC
MA-EX-12-058	Tissue	Barnstable	Sth003	NEC
MA-EX-12-059	Tissue	Hampshire	Sfh069	EC
MA-EX-12-060	Tissue	Hampshire	Sfh069	EC
MA-EX-12-061	Tissue	Hampshire	Sfh069	EC
MA-EX-12-062	Tissue	Barnstable	Sth003	NEC
MA-EX-12-063	Tissue	Barnstable	Sfh054	EC
MA-EX-12-064	Tissue	Barnstable	Sfh045	EC
MA-EX-12-065	Tissue	Barnstable	Sfh056	EC
MA-EX-12-066	Tissue	Plymouth	Lah001	SSH
MA-EX-12-067	Tissue	Hampshire	Sfh069	EC
MA-EX-12-068	Tissue	Barnstable	Sth003	NEC
MA-EX-12-069	Tissue	Unknown	Sth003	NEC
MA-EX-12-070	Tissue	Unknown	Sth003	NEC
MA-EX-12-071	Tissue	Unknown	Sth003	NEC
MA-EX-12-072	Tissue	Unknown	Sth003	NEC
MA-EX-12-073	Tissue	Unknown	Sth003	NEC
MA-EX-12-074	Tissue	Unknown	Sth003	NEC
MA-EX-12-075	Tissue	Unknown	Sth003	NEC
MA-EX-12-076	Tissue	Unknown	Sth003	NEC
MA-EX-12-077	Tissue	Unknown	Sth003	NEC
MA-EX-12-078	Tissue	Unknown	Sth003	NEC
MA-EX-12-079	Tissue	Unknown	Sth003	NEC
MA-EX-12-080	Tissue	Unknown	Sth003	NEC
MA-EX-12-081	Tissue	Unknown	Sfh089	EC

Appendix 2: continued

Sample ID	Sample Type	County	Haplotype	Species ID
MA-EX-12-082	Tissue	Unknown	Sth003	NEC
MA-EX-12-083	Tissue	Unknown	Sth003	NEC
MA-EX-12-084	Tissue	Barnstable	Sth003	NEC
MA-EX-12-085	Tissue	Barnstable	Sth003	NEC
MA-EX-12-086	Tissue	Barnstable	Sth003	NEC
MA-EX-12-088	Tissue	Barnstable	Sth003	NEC
MA-EX-12-089	Tissue	Barnstable	Sth003	NEC
MA-EX-12-090	Tissue	Barnstable	Sth003	NEC
MA-EX-12-091	Tissue	Barnstable	Sth003	NEC
MA-EX-12-092	Tissue	Barnstable	Sth010	NEC
MA-EX-12-093	Tissue	Hampden	Sfh057	EC
MA-EX-12-094	Tissue	Hampden	Sfh057	EC
MA-EX-12-095	Tissue	Barnstable	Sfh044	EC
MA-EX-12-097	Tissue	Nantucket	Sfh072	EC
MA-EX-12-098	Tissue	Barnstable	Sth003	NEC
MA-EX-12-099	Tissue	Barnstable	Sth003	NEC
MA-EX-12-100	Tissue	Bristol	Sfh079	EC
MA-EX-12-101	Tissue	Worchester	Sfh065	EC
MA-EX-12-102	Tissue	Barnstable	Sfh079	EC
MA-EX-12-104	Tissue	Hampshire	Sfh057	EC
MA-EX-12-105	Tissue	Barnstable	Sfh006	EC
MA-EX-12-107	Tissue	Barnstable	Sth003	NEC
MA-EX-12-109	Tissue	Barnstable	Sth003	NEC

Appendix 3: Samples received from New Hampshire with sample type, county that the sample was collected in, haplotype of sample, and species identification

Sample ID	Sample Type	County	Haplotype	Species ID
NH-11-001	Fecal	Rockingham	Lah001	SSH
NH-11-002	Fecal	Rockingham	Sth005	NEC
NH-11-003	Fecal	Rockingham	Sth006	NEC
NH-11-004	Fecal	Rockingham	Sfh033	EC
NH-11-005	Fecal	Rockingham	Sth005	NEC
NH-11-006	Fecal	Rockingham	Sth005	NEC
NH-11-007	Fecal	Rockingham	Sth005	NEC
NH-11-008	Fecal	Rockingham	Sth002	NEC
NH-11-009	Fecal	Rockingham	Sth002	NEC
NH-11-010	Fecal	Strafford	Sth005	NEC
NH-11-011	Fecal	Strafford	Sth005	NEC
NH-11-012	Fecal	Strafford	Sfh049	EC
NH-12-001	Fecal	Merrimack	Lah006	SSH
NH-12-002	Fecal	Rockingham	Lah007	SSH
NH-12-003	Fecal	Strafford	Sfh049	EC
NH-12-004	Fecal	Strafford	Sfh049	EC
NH-12-005	Fecal	Strafford	Sfh049	EC
NH-12-006	Fecal	Strafford	Sfh049	EC
NH-12-007	Fecal	Strafford	Sfh033	EC
NH-12-008	Fecal	Strafford	Sth005	NEC
NH-12-009	Fecal	Strafford	Lah001	SSH
NH-12-010	Fecal	Strafford	Lah007	SSH
NH-12-011	Fecal	Strafford	Sfh088	EC
NH-12-012	Fecal	Rockingham	Lah003	SSH
NH-12-013	Fecal	Rockingham	Lah003	SSH
NH-12-014	Fecal	Rockingham	Lah004	SSH
NH-12-015	Fecal	Strafford	Lah007	SSH
NH-12-016	Fecal	Strafford	Lah005	SSH
NH-12-017	Fecal	Merrimack	Lah008	SSH
NH-12-019	Fecal	Merrimack	Sfh084	EC
NH-12-020	Fecal	Hillsborough	Sfh084	EC
NH-12-021	Fecal	Hillsborough	Lah008	SSH
NH-12-022	Fecal	Unknown	Lah008	SSH
NH-12-023	Fecal	Unknown	Lah007	SSH

Appendix 4: Samples received from New York with sample type, county that the sample was collected, haplotype of sample, and Species identification

Sample ID	Sample Type	County	Haplotype	Species ID
NY-12-001	Fecal	Dutchess	Sfh092	EC
NY-12-002	Fecal	Dutchess	Sfh101	EC
NY-12-003	Fecal	Dutchess	Sfh092	EC
NY-12-004	Fecal	Columbia	Sfh067	EC
NY-12-005	Fecal	Columbia	Sfh072	EC
NY-12-006	Fecal	Columbia	Sfh072	EC
NY-12-007	Fecal	Columbia	Sfh065	EC
NY-12-008	Fecal	Columbia	Sfh065	EC
NY-12-009	Fecal	Columbia	Sfh069	EC
NY-12-010	Fecal	Columbia	Sfh069	EC
NY-12-011	Fecal	Columbia	Sfh069	EC
NY-12-012	Fecal	Columbia	Sfh069	EC
NY-12-013	Fecal	Dutchess	Sfh066	EC
NY-12-014	Fecal	Dutchess	Sfh066	EC
NY-12-015	Fecal	Dutchess	Sfh069	EC
NY-12-016	Fecal	Dutchess	Sfh069	EC
NY-12-017	Fecal	Dutchess	Sfh069	EC
NY-12-018	Fecal	Dutchess	Sfh066	EC
NY-12-019	Fecal	Dutchess	Sfh066	EC
NY-12-020	Fecal	Dutchess	Sfh065	EC
NY-12-021	Fecal	Dutchess	Sfh092	EC
NY-12-022	Fecal	Dutchess	Sfh065	EC
NY-12-023	Fecal	Dutchess	Sfh065	EC
NY-12-024	Fecal	Dutchess	Sfh065	EC
NY-12-025	Fecal	Dutchess	Sfh065	EC
NY-12-026	Fecal	Dutchess	Sfh065	EC
NY-12-027	Fecal	Dutchess	Sfh065	EC
NY-12-028	Fecal	Dutchess	Sfh065	EC
NY-12-029	Fecal	Dutchess	Sfh100	EC
NY-12-030	Fecal	Dutchess	Sfh065	EC
NY-12-031	Fecal	Dutchess	Sfh065	EC
NY-12-032	Fecal	Dutchess	Sfh069	EC
NY-12-033	Fecal	Dutchess	Sfh065	EC
NY-12-034	Fecal	Putnam	Sth010	NEC
NY-12-035	Fecal	Dutchess	Sfh056	EC
NY-12-036	Fecal	Dutchess	Sfh019	EC
NY-12-037	Fecal	Dutchess	Sfh069	EC
NY-12-038	Fecal	Dutchess	Sfh066	EC
NY-12-039	Fecal	Dutchess	Sfh094	EC
NY-12-040	Fecal	Dutchess	Sfh069	EC
NY-12-041	Fecal	Columbia	Sfh069	EC
NY-12-042	Fecal	Columbia	Sfh065	EC
NY-12-043	Fecal	Columbia	Sfh072	EC

Appendix 4: continued

Sample ID	Sample Type	County	Haplotype	Species ID
NY-12-044	Fecal	Columbia	Sfh065	EC
NY-12-045	Fecal	Columbia	Sfh065	EC
NY-12-046	Fecal	Columbia	Sfh065	EC
NY-12-047	Fecal	Columbia	Sfh069	EC
NY-12-048	Fecal	Columbia	Sfh065	EC
NY-12-049	Fecal	Columbia	Sfh065	EC
NY-12-050	Fecal	Columbia	Sfh067	EC

Appendix 5: Samples received from Rhode Island with sample type, county that the sample was collected in, haplotype of sample, and species identification

Sample ID	County	Sample Type	Haplotype	Species ID
CL18	Unknown	Fecal	Sfh045	EC
CL22	Unknown	Fecal	Sfh040	EC
CL30	Unknown	Fecal	Sfh019	EC
CL31	Unknown	Fecal	Sfh019	EC
RI-03-010	Unknown	Tissue	Sfh028	EC
RI-03-011	Unknown	Tissue	Sfh043	EC
RI-03-012	Unknown	Tissue	Sfh049	EC
RI-03-014	Unknown	Tissue	Sfh019	EC
RI-03-017	Unknown	Tissue	Sfh067	EC
RI-03-018	Unknown	Tissue	Sfh052	EC
RI-03-019	Unknown	Tissue	Sfh040	EC
RI-03-020	Unknown	Tissue	Sfh054	EC
RI-03-023	Unknown	Tissue	Sfh009	EC
RI-03-025	Unknown	Tissue	Sfh010	EC
RI-03-026	Unknown	Tissue	Sfh010	EC
RI-03-027	Unknown	Tissue	Sfh010	EC
RI-03-028	Unknown	Tissue	Sfh010	EC
RI-03-030	Unknown	Tissue	Sfh034	EC
RI-03-031	Unknown	Tissue	Sfh034	EC
RI-03-CB-027	Unknown	Tissue	Sfh062	EC
RI-06-001	Kent	Tissue	Sfh019	EC
RI-08-001	Unknown	Tissue	Sfh043	EC
RI-09-001	Washington	Fecal	Sfh057	EC
RI-09-002	Washington	Fecal	Sfh057	EC
RI-09-003	Washington	Fecal	Sfh077	EC
RI-10-002	Washington	Fecal	Sfh076	EC
RI-10-005	Washington	Fecal	Sfh076	EC
RI-10-006	Washington	Fecal	Sfh076	EC
RI-10-007	Washington	Fecal	Sfh076	EC
RI-10-008	Washington	Fecal	Sfh076	EC
RI-10-009	Washington	Fecal	Sfh076	EC
RI-10-010	Washington	Fecal	Sfh043	EC
RI-10-011	Kent	Fecal	Sfh019	EC
RI-10-012	Washington	Fecal	Sfh008	EC
RI-10-014	Washington	Fecal	Sfh019	EC
RI-10-016	Washington	Fecal	Sfh024	EC
RI-10-017	Washington	Fecal	Sfh024	EC
RI-10-018	Washington	Fecal	Sfh043	EC
RI-10-019	Washington	Fecal	Sfh043	EC
RI-10-020	Washington	Fecal	Sfh043	EC
RI-10-021	Washington	Fecal	Sfh043	EC
RI-10-022	Washington	Fecal	Sfh043	EC
RI-10-023	Washington	Fecal	Sfh043	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-10-024	Washington	Fecal	Sfh043	EC
RI-10-025	Washington	Fecal	Sfh043	EC
RI-10-026	Washington	Fecal	Sfh043	EC
RI-10-027	Washington	Fecal	Sfh043	EC
RI-10-028	Washington	Fecal	Sfh076	EC
RI-10-029	Washington	Fecal	Sfh076	EC
RI-10-030	Washington	Fecal	Sfh076	EC
RI-10-031	Washington	Fecal	Sfh076	EC
RI-10-032	Washington	Fecal	Sfh043	EC
RI-10-033	Washington	Fecal	Sfh043	EC
RI-10-034	Washington	Fecal	Sfh043	EC
RI-10-035	Washington	Fecal	Sfh043	EC
RI-10-036	Washington	Fecal	Sfh043	EC
RI-10-037	Washington	Fecal	Sfh043	EC
RI-10-038	Washington	Fecal	Sfh043	EC
RI-10-039	Washington	Fecal	Sfh062	EC
RI-10-041	Washington	Fecal	Sfh073	EC
RI-10-042	Washington	Fecal	Sfh073	EC
RI-10-043	Washington	Fecal	Sfh046	EC
RI-10-046	Washington	Fecal	Sfh073	EC
RI-10-047	Washington	Fecal	Sfh046	EC
RI-10-048	Washington	Fecal	Sfh046	EC
RI-10-049	Washington	Fecal	Sfh046	EC
RI-10-050	Washington	Fecal	Sfh046	EC
RI-10-051	Washington	Fecal	Sfh046	EC
RI-10-052	Washington	Fecal	Sfh062	EC
RI-10-053	Washington	Fecal	Sfh062	EC
RI-10-054	Washington	Fecal	Sfh062	EC
RI-10-055	Providence	Fecal	Sfh071	EC
RI-10-056	Providence	Fecal	Sfh036	EC
RI-10-057	Washington	Fecal	Sfh004	EC
RI-10-058	Washington	Fecal	Sfh043	EC
RI-10-059	Washington	Fecal	Sfh004	EC
RI-10-060	Washington	Fecal	Sfh004	EC
RI-10-061	Washington	Fecal	Sfh004	EC
RI-10-062	Bristol	Fecal	Sfh073	EC
RI-10-063	Bristol	Fecal	Sfh073	EC
RI-10-064	Bristol	Fecal	Sfh073	EC
RI-10-065	Bristol	Fecal	Sfh073	EC
RI-10-066	Providence	Fecal	Sfh013	EC
RI-10-067	Washington	Fecal	Sfh043	EC
RI-10-068	Unknown	Fecal	Sfh073	EC
RI-10-069	Unknown	Fecal	Sfh073	EC
RI-10-070	Unknown	Fecal	Sfh073	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-10-071	Washington	Fecal	Sfh057	EC
RI-10-073	Washington	Fecal	Sfh057	EC
RI-10-074	Washington	Tissue/Fecal	Sfh057	EC
RI-10-075	Washington	Fecal	Sfh057	EC
RI-10-077	Washington	Fecal	Sfh057	EC
RI-10-078	Washington	Fecal	Sfh001	EC
RI-10-079	Washington	Fecal	Sfh057	EC
RI-10-080	Washington	Fecal	Sfh057	EC
RI-10-081	Washington	Fecal	Sfh055	EC
RI-10-083	Washington	Tissue	Sfh057	EC
RI-10-084	Washington	Tissue	Sfh057	EC
RI-10-085	Washington	Tissue	Sfh057	EC
RI-10-086	Washington	Tissue	Sfh057	EC
RI-10-087	Washington	Tissue	Sfh057	EC
RI-10-088	Washington	Tissue	Sfh057	EC
RI-10-089	Washington	Tissue	Sfh057	EC
RI-10-090	Washington	Tissue	Sfh057	EC
RI-10-091	Newport	Tissue	Sfh057	EC
RI-10-092	Newport	Tissue	Sfh049	EC
RI-10-093	Newport	Tissue	Sfh040	EC
RI-10-094	Newport	Tissue	Sfh040	EC
RI-10-095	Newport	Tissue	Sfh040	EC
RI-10-096	Newport	Tissue	Sfh062	EC
RI-10-097	Newport	Tissue	Sfh040	EC
RI-10-098	Newport	Tissue	Sfh040	EC
RI-10-099	Newport	Tissue	Sfh001	EC
RI-10-100	Washington	Tissue/Fecal/Blood	Sfh057	EC
RI-10-101	Washington	Tissue/Fecal/Blood	Sfh060	EC
RI-10-102	Bristol	Fecal	Sfh057	EC
RI-10-103	Bristol	Fecal	Sfh062	EC
RI-10-104	Bristol	Fecal	Sfh062	EC
RI-10-105	Washington	Fecal	Sfh055	EC
RI-10-107	Washington	Tissue	Sfh057	EC
RI-10-108	Washington	Tissue/Fecal/Blood	Sfh057	EC
RI-10-109	Providence	Fecal	Sfh012	EC
RI-10-110	Bristol	Fecal	Sfh043	EC
RI-10-111	Washington	Tissue/Blood	Sfh057	EC
RI-10-112	Washington	Tissue/Fecal/Blood	Sfh057	EC
RI-10-113	Washington	Tissue/Blood	Sfh057	EC
RI-10-114	Washington	Tissue/Fecal/Blood	Sfh049	EC
RI-10-115	Washington	Fecal	Sfh057	EC
RI-11-100	Washington	Tissue/Blood	Sfh057	EC
RI-11-101	Washington	Tissue/Blood	Sfh060	EC
RI-11-102	Washington	Fecal	Sfh073	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-103	Washington	Fecal	Sfh062	EC
RI-11-104	Washington	Fecal	Sfh062	EC
RI-11-116	Washington	Tissue/Fecal/Blood	Sfh058	EC
RI-11-117	Washington	Tissue	Sfh057	EC
RI-11-118	Washington	Tissue	Sfh057	EC
RI-11-119	Washington	Tissue/Blood	Sfh057	EC
RI-11-120	Washington	Tissue/Blood	Sfh058	EC
RI-11-121	Washington	Tissue/Fecal	Sfh057	EC
RI-11-122	Washington	Fecal	Sfh049	EC
RI-11-123	Washington	Tissue/Fecal/Blood	Sfh057	EC
RI-11-124	Washington	Tissue/Fecal/Blood	Sfh057	EC
RI-11-125	Washington	Tissue/Fecal/Blood	Sfh057	EC
RI-11-126	Washington	Fecal	Sfh057	EC
RI-11-127	Washington	Fecal	Sfh057	EC
RI-11-128	Washington	Fecal	Sfh057	EC
RI-11-129	Washington	Fecal	Sfh049	EC
RI-11-130	Washington	Fecal	Sfh057	EC
RI-11-131	Washington	Fecal	Sfh057	EC
RI-11-132	Washington	Fecal	Sfh057	EC
RI-11-133	Washington	Fecal	Sfh054	EC
RI-11-134	Washington	Fecal	Sfh054	EC
RI-11-135	Washington	Fecal	Sfh043	EC
RI-11-136	Washington	Fecal	Sfh043	EC
RI-11-137	Washington	Fecal	Sfh043	EC
RI-11-138	Washington	Fecal	Sfh043	EC
RI-11-139	Washington	Fecal	Sfh043	EC
RI-11-140	Washington	Fecal	Sfh054	EC
RI-11-141	Washington	Fecal	Sfh043	EC
RI-11-142	Washington	Fecal	Sfh043	EC
RI-11-143	Washington	Fecal	Sfh022	EC
RI-11-144	Washington	Fecal	Sfh022	EC
RI-11-145	Washington	Fecal	Sfh008	EC
RI-11-146	Washington	Fecal	Sfh049	EC
RI-11-147	Washington	Fecal	Sfh049	EC
RI-11-149	Kent	Fecal	Sfh011	EC
RI-11-150	Kent	Fecal	Sfh011	EC
RI-11-151	Newport	Fecal	Sfh040	EC
RI-11-152	Washington	Fecal	Sfh057	EC
RI-11-153	Washington	Fecal	Sfh057	EC
RI-11-154	Washington	Fecal	Sfh057	EC
RI-11-155	Washington	Fecal	Sfh057	EC
RI-11-156	Washington	Fecal	Sfh057	EC
RI-11-157	Washington	Fecal	Sfh057	EC
RI-11-158	Washington	Fecal	Sfh016	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-159	Washington	Fecal	Sfh016	EC
RI-11-160	Washington	Fecal	Sfh016	EC
RI-11-161	Washington	Fecal	Sfh016	EC
RI-11-163	Washington	Fecal	Sfh016	EC
RI-11-164	Washington	Fecal	Sfh016	EC
RI-11-165	Washington	Fecal	Sfh016	EC
RI-11-166	Washington	Fecal	Sfh022	EC
RI-11-167	Washington	Fecal	Sfh022	EC
RI-11-168	Washington	Fecal	Sfh022	EC
RI-11-169	Washington	Fecal	Sfh022	EC
RI-11-170	Washington	Fecal	Sfh022	EC
RI-11-171	Washington	Fecal	Sfh022	EC
RI-11-172	Washington	Fecal	Sfh022	EC
RI-11-173	Washington	Fecal	Sfh022	EC
RI-11-174	Washington	Fecal	Sfh022	EC
RI-11-175	Washington	Fecal	Sfh057	EC
RI-11-176	Washington	Fecal	Sfh057	EC
RI-11-177	Washington	Fecal	Sfh057	EC
RI-11-178	Washington	Fecal	Sfh057	EC
RI-11-179	Washington	Fecal	Sfh057	EC
RI-11-180	Washington	Fecal	Sfh057	EC
RI-11-181	Washington	Fecal	Sfh022	EC
RI-11-182	Washington	Fecal	Sfh022	EC
RI-11-183	Washington	Fecal	Sfh022	EC
RI-11-184	Washington	Fecal	Sfh046	EC
RI-11-185	Washington	Fecal	Sfh002	EC
RI-11-186	Washington	Fecal	Sfh002	EC
RI-11-187	Washington	Fecal	Sfh002	EC
RI-11-188	Washington	Fecal	Sfh022	EC
RI-11-190	Washington	Fecal	Sfh007	EC
RI-11-191	Washington	Fecal	Sfh002	EC
RI-11-192	Washington	Fecal	Sfh002	EC
RI-11-193	Washington	Fecal	Sfh002	EC
RI-11-194	Kent	Fecal	Sfh011	EC
RI-11-195	Kent	Fecal	Sfh011	EC
RI-11-196	Kent	Fecal	Sfh011	EC
RI-11-197	Washington	Fecal	Sfh024	EC
RI-11-198	Washington	Fecal	Sfh007	EC
RI-11-199	Washington	Fecal	Sfh007	EC
RI-11-200	Washington	Fecal	Sfh007	EC
RI-11-201	Washington	Fecal	Sfh007	EC
RI-11-202	Washington	Fecal	Sfh002	EC
RI-11-203	Washington	Fecal	Sfh002	EC
RI-11-205	Washington	Fecal	Sfh002	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-206	Washington	Fecal	Sfh002	EC
RI-11-207	Washington	Fecal	Sfh002	EC
RI-11-208	Washington	Fecal	Sfh002	EC
RI-11-209	Washington	Fecal	Sfh005	EC
RI-11-210	Washington	Fecal	Sfh002	EC
RI-11-211	Washington	Fecal	Sfh002	EC
RI-11-212	Washington	Fecal	Sfh002	EC
RI-11-213	Washington	Fecal	Sfh005	EC
RI-11-214	Washington	Fecal	Sfh005	EC
RI-11-215	Washington	Fecal	Sfh002	EC
RI-11-216	Washington	Fecal	Sfh005	EC
RI-11-217	Washington	Fecal	Sfh024	EC
RI-11-218	Washington	Fecal	Sfh024	EC
RI-11-219	Washington	Fecal	Sfh024	EC
RI-11-221	Washington	Fecal	Sfh024	EC
RI-11-223	Washington	Fecal	Sfh024	EC
RI-11-224	Washington	Fecal	Sfh024	EC
RI-11-227	Washington	Fecal	Sfh046	EC
RI-11-228	Washington	Fecal	Sfh046	EC
RI-11-229	Washington	Fecal	Sfh046	EC
RI-11-230	Washington	Fecal	Sfh057	EC
RI-11-231	Washington	Fecal	Sfh030	EC
RI-11-232	Washington	Fecal	Sfh030	EC
RI-11-233	Washington	Fecal	Sfh030	EC
RI-11-235	Washington	Fecal	Sfh046	EC
RI-11-236	Washington	Fecal	Sfh030	EC
RI-11-237	Washington	Fecal	Sfh046	EC
RI-11-238	Washington	Fecal	Sfh030	EC
RI-11-239	Washington	Fecal	Sfh057	EC
RI-11-240	Washington	Fecal	Sfh057	EC
RI-11-241	Washington	Fecal	Sfh057	EC
RI-11-242	Washington	Fecal	Sfh057	EC
RI-11-243	Washington	Fecal	Sfh057	EC
RI-11-244	Washington	Fecal	Sfh057	EC
RI-11-245	Washington	Fecal	Sfh057	EC
RI-11-246	Washington	Fecal	Sfh057	EC
RI-11-247	Washington	Fecal	Sfh057	EC
RI-11-248	Washington	Fecal	Sfh057	EC
RI-11-249	Washington	Fecal	Sfh057	EC
RI-11-250	Washington	Fecal	Sfh057	EC
RI-11-251	Washington	Fecal	Sfh057	EC
RI-11-252	Washington	Fecal	Sfh057	EC
RI-11-253	Washington	Fecal	Sfh057	EC
RI-11-254	Washington	Fecal	Sfh057	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-255	Washington	Fecal	Sfh057	EC
RI-11-256	Washington	Fecal	Sfh057	EC
RI-11-257	Washington	Fecal	Sfh057	EC
RI-11-258	Washington	Fecal	Sfh057	EC
RI-11-259	Washington	Fecal	Sfh057	EC
RI-11-260	Washington	Fecal	Sfh057	EC
RI-11-261	Washington	Fecal	Sfh022	EC
RI-11-262	Washington	Fecal	Sfh046	EC
RI-11-263	Washington	Fecal	Sfh073	EC
RI-11-264	Washington	Fecal	Sfh073	EC
RI-11-265	Washington	Fecal	Sfh073	EC
RI-11-266	Washington	Fecal	Sfh030	EC
RI-11-267	Washington	Fecal	Sfh030	EC
RI-11-268	Washington	Fecal	Sfh073	EC
RI-11-269	Washington	Fecal	Sfh073	EC
RI-11-270	Washington	Fecal	Sfh073	EC
RI-11-271	Washington	Fecal	Sfh073	EC
RI-11-272	Washington	Fecal	Sfh046	EC
RI-11-273	Providence	Fecal	Sfh060	EC
RI-11-274	Washington	Fecal	Sfh046	EC
RI-11-275	Washington	Fecal	Sfh022	EC
RI-11-276	Washington	Fecal	Sfh046	EC
RI-11-277	Washington	Fecal	Sfh022	EC
RI-11-278	Washington	Fecal	Sfh046	EC
RI-11-279	Washington	Fecal	Sfh022	EC
RI-11-280	Washington	Fecal	Sfh022	EC
RI-11-281	Washington	Fecal	Sfh022	EC
RI-11-282	Washington	Fecal	Sfh002	EC
RI-11-283	Washington	Fecal	Sfh002	EC
RI-11-284	Washington	Fecal	Sfh002	EC
RI-11-285	Washington	Fecal	Sfh002	EC
RI-11-286	Washington	Fecal	Sfh002	EC
RI-11-287	Washington	Fecal	Sfh002	EC
RI-11-288	Washington	Fecal	Sfh002	EC
RI-11-289	Washington	Fecal	Sfh007	EC
RI-11-290	Washington	Fecal	Sfh007	EC
RI-11-291	Washington	Fecal	Sfh007	EC
RI-11-292	Washington	Fecal	Sfh046	EC
RI-11-293	Washington	Fecal	Sfh046	EC
RI-11-294	Washington	Fecal	Sfh030	EC
RI-11-295	Washington	Fecal	Sfh046	EC
RI-11-296	Washington	Fecal	Sfh046	EC
RI-11-297	Washington	Fecal	Sfh046	EC
RI-11-298	Washington	Fecal	Sfh046	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-299	Washington	Fecal	Sfh046	EC
RI-11-300	Washington	Fecal	Sfh046	EC
RI-11-301	Washington	Fecal	Sfh046	EC
RI-11-302	Washington	Fecal	Sfh046	EC
RI-11-303	Washington	Fecal	Sfh057	EC
RI-11-304	Washington	Fecal	Sfh046	EC
RI-11-305	Washington	Fecal	Sfh057	EC
RI-11-306	Washington	Fecal	Sfh057	EC
RI-11-307	Washington	Fecal	Sfh057	EC
RI-11-308	Washington	Fecal	Sfh057	EC
RI-11-309	Washington	Fecal	Sfh057	EC
RI-11-310	Washington	Fecal	Sfh076	EC
RI-11-311	Washington	Fecal	Sfh076	EC
RI-11-312	Washington	Fecal	Sfh076	EC
RI-11-313	Providence	Fecal	Sfh071	EC
RI-11-314	Providence	Fecal	Sfh036	EC
RI-11-315	Providence	Fecal	Sfh036	EC
RI-11-316	Providence	Fecal	Sfh036	EC
RI-11-317	Providence	Fecal	Sfh036	EC
RI-11-318	Providence	Fecal	Sfh036	EC
RI-11-319	Providence	Fecal	Sfh060	EC
RI-11-320	Providence	Fecal	Sfh060	EC
RI-11-321	Kent	Fecal	Sfh011	EC
RI-11-322	Kent	Fecal	Sfh011	EC
RI-11-323	Kent	Fecal	Sfh011	EC
RI-11-324	Kent	Fecal	Sfh011	EC
RI-11-325	Kent	Fecal	Sfh011	EC
RI-11-326	Kent	Fecal	Sfh011	EC
RI-11-327	Kent	Fecal	Sfh011	EC
RI-11-328	Kent	Fecal	Sfh011	EC
RI-11-329	Kent	Fecal	Sfh011	EC
RI-11-330	Washington	Fecal	Sfh046	EC
RI-11-331	Washington	Fecal	Sfh046	EC
RI-11-332	Washington	Fecal	Sfh046	EC
RI-11-333	Washington	Fecal	Sfh030	EC
RI-11-334	Washington	Fecal	Sfh046	EC
RI-11-335	Washington	Fecal	Sfh030	EC
RI-11-336	Washington	Fecal	Sfh030	EC
RI-11-337	Washington	Fecal	Sfh046	EC
RI-11-338	Washington	Fecal	Sfh046	EC
RI-11-339	Washington	Fecal	Sfh046	EC
RI-11-340	Washington	Fecal	Sfh073	EC
RI-11-341	Washington	Fecal	Sfh046	EC
RI-11-342	Washington	Fecal	Sfh073	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-343	Washington	Fecal	Sfh030	EC
RI-11-344	Washington	Fecal	Sfh046	EC
RI-11-345	Washington	Fecal	Sfh073	EC
RI-11-346	Washington	Fecal	Sfh046	EC
RI-11-347	Washington	Fecal	Sfh046	EC
RI-11-348	Washington	Fecal	Sfh046	EC
RI-11-349	Washington	Fecal	Sfh046	EC
RI-11-350	Washington	Fecal	Sfh073	EC
RI-11-351	Washington	Fecal	Sfh046	EC
RI-11-352	Washington	Fecal	Sfh073	EC
RI-11-353	Washington	Fecal	Sfh002	EC
RI-11-354	Washington	Fecal	Sfh005	EC
RI-11-355	Washington	Fecal	Sfh002	EC
RI-11-356	Washington	Fecal	Sfh002	EC
RI-11-357	Washington	Fecal	Sfh002	EC
RI-11-358	Washington	Fecal	Sfh005	EC
RI-11-359	Washington	Fecal	Sfh002	EC
RI-11-360	Washington	Fecal	Sfh005	EC
RI-11-361	Washington	Fecal	Sfh002	EC
RI-11-362	Washington	Fecal	Sfh005	EC
RI-11-363	Washington	Fecal	Sfh002	EC
RI-11-364	Washington	Fecal	Sfh002	EC
RI-11-365	Washington	Fecal	Sfh007	EC
RI-11-366	Washington	Fecal	Sfh007	EC
RI-11-367	Washington	Fecal	Sfh007	EC
RI-11-368	Washington	Fecal	Sfh002	EC
RI-11-369	Washington	Fecal	Sfh007	EC
RI-11-370	Washington	Fecal	Sfh005	EC
RI-11-371	Washington	Fecal	Sfh005	EC
RI-11-372	Washington	Fecal	Sfh005	EC
RI-11-373	Washington	Fecal	Sfh016	EC
RI-11-375	Washington	Fecal	Sfh022	EC
RI-11-376	Washington	Fecal	Sfh076	EC
RI-11-377	Washington	Fecal	Sfh057	EC
RI-11-378	Washington	Fecal	Sfh057	EC
RI-11-379	Washington	Fecal	Sfh049	EC
RI-11-380	Washington	Fecal	Sfh049	EC
RI-11-381	Washington	Fecal	Sfh057	EC
RI-11-382	Washington	Fecal	Sfh057	EC
RI-11-383	Washington	Fecal	Sfh057	EC
RI-11-384	Bristol	Fecal	Sfh034	EC
RI-11-385	Bristol	Fecal	Sfh034	EC
RI-11-386	Bristol	Fecal	Sfh034	EC
RI-11-387	Bristol	Fecal	Sfh034	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-388	Bristol	Fecal	Sfh034	EC
RI-11-389	Bristol	Fecal	Sfh034	EC
RI-11-390	Washington	Fecal	Sfh024	EC
RI-11-391	Washington	Fecal	Sfh046	EC
RI-11-392	Washington	Fecal	Sfh015	EC
RI-11-393	Newport	Fecal	Sfh040	EC
RI-11-394	Newport	Fecal	Sfh040	EC
RI-11-395	Newport	Fecal	Sfh040	EC
RI-11-396	Newport	Fecal	Sfh040	EC
RI-11-397	Newport	Fecal	Sfh040	EC
RI-11-398	Newport	Fecal	Sfh040	EC
RI-11-399	Newport	Fecal	Sfh034	EC
RI-11-400	Newport	Fecal	Sfh040	EC
RI-11-401	Newport	Fecal	Sfh040	EC
RI-11-402	Newport	Fecal	Sfh040	EC
RI-11-403	Newport	Fecal	Sfh040	EC
RI-11-404	Newport	Fecal	Sfh040	EC
RI-11-405	Newport	Fecal	Sfh040	EC
RI-11-406	Newport	Fecal	Sfh040	EC
RI-11-407	Newport	Fecal	Sfh040	EC
RI-11-408	Newport	Fecal	Sfh040	EC
RI-11-409	Newport	Fecal	Sfh062	EC
RI-11-410	Newport	Fecal	Sfh040	EC
RI-11-411	Newport	Fecal	Sfh040	EC
RI-11-412	Washington	Fecal	Sfh016	EC
RI-11-413	Kent	Fecal	Sfh034	EC
RI-11-414	Kent	Fecal	Sfh034	EC
RI-11-415	Kent	Fecal	Sfh034	EC
RI-11-416	Kent	Fecal	Sfh034	EC
RI-11-417	Kent	Fecal	Sfh034	EC
RI-11-419	Kent	Fecal	Sfh063	EC
RI-11-420	Washington	Fecal	Sfh016	EC
RI-11-421	Kent	Fecal	Sfh011	EC
RI-11-422	Kent	Fecal	Sfh011	EC
RI-11-423	Kent	Fecal	Sfh011	EC
RI-11-424	Kent	Fecal	Sfh011	EC
RI-11-425	Kent	Fecal	Sfh011	EC
RI-11-426	Kent	Fecal	Sfh011	EC
RI-11-427	Kent	Fecal	Sfh011	EC
RI-11-428	Kent	Fecal	Sfh011	EC
RI-11-429	Kent	Fecal	Sfh011	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-430	Kent	Fecal	Sfh011	EC
RI-11-431	Kent	Fecal	Sfh011	EC
RI-11-432	Kent	Fecal	Sfh011	EC
RI-11-433	Kent	Fecal	Sfh011	EC
RI-11-434	Kent	Fecal	Sfh011	EC
RI-11-435	Kent	Fecal	Sfh011	EC
RI-11-436	Kent	Fecal	Sfh011	EC
RI-11-437	Bristol	Fecal	Sfh062	EC
RI-11-438	Bristol	Fecal	Sfh043	EC
RI-11-439	Washington	Fecal	Sfh002	EC
RI-11-440	Washington	Fecal	Sfh002	EC
RI-11-441	Washington	Fecal	Sfh002	EC
RI-11-442	Washington	Fecal	Sfh002	EC
RI-11-443	Washington	Fecal	Sfh002	EC
RI-11-444	Washington	Fecal	Sfh002	EC
RI-11-445	Washington	Fecal	Sfh002	EC
RI-11-446	Washington	Fecal	Sfh057	EC
RI-11-447	Washington	Fecal	Sfh022	EC
RI-11-448	Washington	Fecal	Sfh022	EC
RI-11-449	Washington	Fecal	Sfh022	EC
RI-11-450	Washington	Fecal	Sfh022	EC
RI-11-451	Washington	Fecal	Sfh019	EC
RI-11-452	Washington	Fecal	Sfh019	EC
RI-11-453	Washington	Fecal	Sfh019	EC
RI-11-454	Washington	Fecal	Sfh019	EC
RI-11-455	Washington	Fecal	Sfh024	EC
RI-11-456	Washington	Fecal	Sfh024	EC
RI-11-457	Washington	Fecal	Sfh024	EC
RI-11-458	Washington	Fecal	Sfh024	EC
RI-11-459	Washington	Fecal	Sfh024	EC
RI-11-460	Washington	Fecal	Sfh002	EC
RI-11-461	Washington	Fecal	Sfh002	EC
RI-11-462	Washington	Fecal	Sfh007	EC
RI-11-463	Washington	Fecal	Sfh002	EC
RI-11-464	Washington	Fecal	Sfh002	EC
RI-11-465	Washington	Fecal	Sfh002	EC
RI-11-466	Washington	Fecal	Sfh002	EC
RI-11-467	Washington	Fecal	Sfh002	EC
RI-11-468	Washington	Fecal	Sfh002	EC
RI-11-469	Washington	Fecal	Sfh002	EC
RI-11-470	Washington	Fecal	Sfh002	EC
RI-11-471	Washington	Fecal	Sfh007	EC
RI-11-472	Washington	Fecal	Sfh002	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-474	Washington	Fecal	Sfh002	EC
RI-11-475	Washington	Fecal	Sfh002	EC
RI-11-476	Washington	Fecal	Sfh007	EC
RI-11-477	Washington	Fecal	Sfh005	EC
RI-11-478	Washington	Fecal	Sfh005	EC
RI-11-479	Washington	Fecal	Sfh005	EC
RI-11-480	Washington	Fecal	Sfh005	EC
RI-11-481	Washington	Fecal	Sfh005	EC
RI-11-482	Washington	Fecal	Sfh002	EC
RI-11-483	Washington	Fecal	Sfh043	EC
RI-11-485	Washington	Fecal	Sfh007	EC
RI-11-486	Washington	Fecal	Sfh007	EC
RI-11-487	Washington	Fecal	Sfh007	EC
RI-11-488	Washington	Fecal	Sfh007	EC
RI-11-489	Washington	Fecal	Sfh007	EC
RI-11-490	Washington	Fecal	Sfh007	EC
RI-11-491	Washington	Fecal	Sfh007	EC
RI-11-492	Washington	Fecal	Sfh067	EC
RI-11-493	Washington	Fecal	Sfh067	EC
RI-11-494	Washington	Fecal	Sfh067	EC
RI-11-495	Washington	Fecal	Sfh067	EC
RI-11-496	Washington	Fecal	Sfh002	EC
RI-11-497	Washington	Fecal	Sfh002	EC
RI-11-498	Washington	Fecal	Sfh002	EC
RI-11-499	Washington	Fecal	Sfh002	EC
RI-11-500	Washington	Fecal	Sfh002	EC
RI-11-501	Washington	Fecal	Sfh002	EC
RI-11-502	Washington	Fecal	Sfh024	EC
RI-11-503	Washington	Fecal	Sfh024	EC
RI-11-504	Washington	Fecal	Sfh024	EC
RI-11-505	Washington	Fecal	Sfh024	EC
RI-11-506	Washington	Fecal	Sfh024	EC
RI-11-507	Washington	Fecal	Sfh024	EC
RI-11-508	Washington	Fecal	Sfh024	EC
RI-11-509	Washington	Fecal	Sfh024	EC
RI-11-510	Washington	Fecal	Sfh007	EC
RI-11-511	Washington	Fecal	Sfh002	EC
RI-11-512	Washington	Fecal	Sfh002	EC
RI-11-513	Washington	Fecal	Sfh002	EC
RI-11-514	Washington	Fecal	Sfh007	EC
RI-11-515	Washington	Fecal	Sfh002	EC
RI-11-516	Washington	Fecal	Sfh002	EC
RI-11-517	Washington	Fecal	Sfh002	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-518	Washington	Fecal	Sfh002	EC
RI-11-519	Washington	Fecal	Sfh022	EC
RI-11-520	Washington	Fecal	Sfh016	EC
RI-11-521	Washington	Fecal	Sfh016	EC
RI-11-523	Washington	Fecal	Sfh022	EC
RI-11-524	Washington	Fecal	Sfh022	EC
RI-11-525	Providence	Fecal	Sfh013	EC
RI-11-526	Washington	Fecal	Sfh067	EC
RI-11-527	Washington	Fecal	Sfh067	EC
RI-11-528	Washington	Fecal	Sfh067	EC
RI-11-529	Washington	Fecal	Sfh067	EC
RI-11-530	Washington	Fecal	Sfh067	EC
RI-11-531	Washington	Fecal	Sfh067	EC
RI-11-532	Washington	Fecal	Sfh067	EC
RI-11-533	Bristol	Fecal	Sfh049	EC
RI-11-534	Bristol	Fecal	Sfh049	EC
RI-11-535	Washington	Fecal	Sfh016	EC
RI-11-536	Washington	Fecal	Sfh016	EC
RI-11-537	Kent	Fecal	Sfh034	EC
RI-11-538	Kent	Fecal	Sfh034	EC
RI-11-539	Kent	Fecal	Sfh034	EC
RI-11-540	Kent	Fecal	Sfh034	EC
RI-11-541	Kent	Fecal	Sfh063	EC
RI-11-542	Newport	Fecal	Sfh040	EC
RI-11-543	Newport	Fecal	Sfh040	EC
RI-11-544	Newport	Fecal	Sfh001	EC
RI-11-545	Newport	Fecal	Sfh001	EC
RI-11-546	Newport	Fecal	Sfh040	EC
RI-11-547	Newport	Fecal	Sfh030	EC
RI-11-548	Newport	Fecal	Sfh040	EC
RI-11-549	Newport	Fecal	Sfh040	EC
RI-11-550	Newport	Fecal	Sfh040	EC
RI-11-551	Newport	Fecal	Sfh040	EC
RI-11-552	Newport	Fecal	Sfh041	EC
RI-11-553	Newport	Fecal	Sfh040	EC
RI-11-554	Newport	Fecal	Sfh041	EC
RI-11-555	Newport	Fecal	Sfh001	EC
RI-11-556	Washington	Fecal	Sfh076	EC
RI-11-557	Washington	Fecal	Sfh076	EC
RI-11-558	Washington	Fecal	Sfh043	EC
RI-11-559	Washington	Fecal	Sfh043	EC
RI-11-560	Washington	Fecal	Sfh043	EC
RI-11-561	Washington	Fecal	Sfh043	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-562	Washington	Fecal	Sfh016	EC
RI-11-563	Washington	Fecal	Sfh004	EC
RI-11-564	Washington	Fecal	Sfh004	EC
RI-11-565	Washington	Fecal	Sfh006	EC
RI-11-566	Washington	Fecal	Sfh024	EC
RI-11-567	Washington	Fecal	Sfh024	EC
RI-11-568	Washington	Fecal	Sfh024	EC
RI-11-569	Washington	Fecal	Sfh024	EC
RI-11-570	Washington	Fecal	Sfh024	EC
RI-11-571	Washington	Fecal	Sfh024	EC
RI-11-572	Washington	Fecal	Sfh024	EC
RI-11-573	Washington	Fecal	Sfh024	EC
RI-11-574	Washington	Fecal	Sfh024	EC
RI-11-575	Washington	Fecal	Sfh024	EC
RI-11-576	Washington	Fecal	Sfh024	EC
RI-11-577	Washington	Fecal	Sfh024	EC
RI-11-578	Washington	Fecal	Sfh043	EC
RI-11-579	Washington	Fecal	Sfh043	EC
RI-11-580	Washington	Fecal	Sfh004	EC
RI-11-581	Washington	Fecal	Sfh043	EC
RI-11-582	Washington	Fecal	Sfh004	EC
RI-11-583	Washington	Fecal	Sfh043	EC
RI-11-584	Washington	Fecal	Sfh004	EC
RI-11-585	Washington	Fecal	Sfh043	EC
RI-11-586	Washington	Fecal	Sfh043	EC
RI-11-587	Washington	Fecal	Sfh004	EC
RI-11-588	Washington	Fecal	Sfh043	EC
RI-11-589	Newport	Fecal	Sfh006	EC
RI-11-590	Newport	Fecal	Sfh006	EC
RI-11-591	Newport	Fecal	Sfh006	EC
RI-11-592	Newport	Fecal	Sfh006	EC
RI-11-593	Newport	Fecal	Sfh006	EC
RI-11-594	Newport	Fecal	Sfh006	EC
RI-11-595	Newport	Fecal	Sfh006	EC
RI-11-596	Newport	Fecal	Sfh006	EC
RI-11-597	Newport	Fecal	Sfh006	EC
RI-11-598	Newport	Fecal	Sfh006	EC
RI-11-599	Newport	Fecal	Sfh006	EC
RI-11-600	Newport	Fecal	Sfh006	EC
RI-11-601	Newport	Fecal	Sfh006	EC
RI-11-602	Newport	Fecal	Sfh006	EC
RI-11-603	Newport	Fecal	Sfh006	EC
RI-11-604	Newport	Fecal	Sfh006	EC
RI-11-605	Newport	Fecal	Sfh006	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-606	Newport	Fecal	Sfh006	EC
RI-11-607	Newport	Fecal	Sfh006	EC
RI-11-608	Newport	Fecal	Sfh006	EC
RI-11-609	Newport	Fecal	Sfh006	EC
RI-11-610	Newport	Fecal	Sfh006	EC
RI-11-611	Newport	Fecal	Sfh006	EC
RI-11-612	Newport	Fecal	Sfh006	EC
RI-11-613	Newport	Fecal	Sfh006	EC
RI-11-614	Newport	Fecal	Sfh006	EC
RI-11-615	Newport	Fecal	Sfh006	EC
RI-11-616	Newport	Fecal	Sfh006	EC
RI-11-617	Newport	Fecal	Sfh006	EC
RI-11-618	Newport	Fecal	Sfh006	EC
RI-11-619	Newport	Fecal	Sfh006	EC
RI-11-620	Newport	Fecal	Sfh006	EC
RI-11-621	Washington	Fecal	Sfh055	EC
RI-11-622	Washington	Fecal	Sfh007	EC
RI-11-623	Washington	Fecal	Sfh007	EC
RI-11-624	Washington	Fecal	Sfh007	EC
RI-11-625	Washington	Fecal	Sfh007	EC
RI-11-626	Washington	Fecal	Sfh007	EC
RI-11-627	Washington	Fecal	Sfh007	EC
RI-11-628	Washington	Fecal	Sfh007	EC
RI-11-629	Washington	Fecal	Sfh002	EC
RI-11-630	Washington	Fecal	Sfh002	EC
RI-11-631	Washington	Fecal	Sfh002	EC
RI-11-632	Washington	Fecal	Sfh002	EC
RI-11-633	Washington	Fecal	Sfh002	EC
RI-11-634	Washington	Fecal	Sfh002	EC
RI-11-635	Washington	Fecal	Sfh002	EC
RI-11-636	Washington	Fecal	Sfh002	EC
RI-11-637	Washington	Fecal	Sfh002	EC
RI-11-638	Washington	Fecal	Sfh002	EC
RI-11-639	Washington	Fecal	Sfh024	EC
RI-11-640	Washington	Fecal	Sfh023	EC
RI-11-641	Washington	Fecal	Sfh023	EC
RI-11-642	Washington	Fecal	Sfh023	EC
RI-11-643	Washington	Fecal	Sfh023	EC
RI-11-644	Washington	Fecal	Sfh026	EC
RI-11-645	Washington	Fecal	Sfh024	EC
RI-11-646	Washington	Fecal	Sfh024	EC
RI-11-647	Washington	Fecal	Sfh024	EC
RI-11-648	Washington	Fecal	Sfh024	EC
RI-11-649	Washington	Fecal	Sfh026	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-650	Washington	Fecal	Sfh024	EC
RI-11-651	Washington	Fecal	Sfh022	EC
RI-11-652	Washington	Fecal	Sfh022	EC
RI-11-653	Washington	Fecal	Sfh022	EC
RI-11-654	Washington	Fecal	Sfh024	EC
RI-11-655	Washington	Fecal	Sfh024	EC
RI-11-656	Washington	Fecal	Sfh024	EC
RI-11-657	Washington	Fecal	Sfh024	EC
RI-11-658	Washington	Fecal	Sfh024	EC
RI-11-659	Washington	Fecal	Sfh024	EC
RI-11-660	Washington	Fecal	Sfh024	EC
RI-11-661	Washington	Fecal	Sfh024	EC
RI-11-662	Bristol	Fecal	Sfh049	EC
RI-11-663	Bristol	Fecal	Sfh049	EC
RI-11-664	Bristol	Fecal	Sfh042	EC
RI-11-665	Bristol	Fecal	Sfh049	EC
RI-11-666	Washington	Fecal	Sth011	NEC
RI-11-667	Washington	Fecal	Sfh019	EC
RI-11-668	Washington	Fecal	Sfh019	EC
RI-11-669	Washington	Fecal	Sfh049	EC
RI-11-670	Providence	Fecal	Sfh067	EC
RI-11-671	Providence	Fecal	Sfh014	EC
RI-11-672	Providence	Fecal	Sfh014	EC
RI-11-673	Providence	Fecal	Sfh043	EC
RI-11-674	Providence	Fecal	Sfh039	EC
RI-11-675	Providence	Fecal	Sfh024	EC
RI-11-676	Providence	Fecal	Sfh024	EC
RI-11-677	Washington	Fecal	Sfh002	EC
RI-11-678	Washington	Fecal	Sfh002	EC
RI-11-679	Washington	Fecal	Sfh002	EC
RI-11-680	Washington	Fecal	Sfh002	EC
RI-11-681	Washington	Fecal	Sfh002	EC
RI-11-682	Washington	Fecal	Sfh002	EC
RI-11-683	Washington	Fecal	Sfh002	EC
RI-11-684	Washington	Fecal	Sfh002	EC
RI-11-685	Providence	Fecal	Sfh004	EC
RI-11-686	Providence	Fecal	Sfh025	EC
RI-11-687	Providence	Fecal	Sfh025	EC
RI-11-688	Providence	Fecal	Sfh004	EC
RI-11-689	Providence	Fecal	Sfh004	EC
RI-11-690	Washington	Fecal	Sfh024	EC
RI-11-691	Washington	Fecal	Sfh024	EC
RI-11-693	Washington	Fecal	Sfh024	EC
RI-11-694	Washington	Fecal	Sfh024	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-695	Washington	Fecal	Sfh024	EC
RI-11-696	Washington	Fecal	Sfh024	EC
RI-11-697	Washington	Fecal	Sfh024	EC
RI-11-698	Washington	Fecal	Sfh024	EC
RI-11-699	Washington	Fecal	Sfh024	EC
RI-11-700	Washington	Fecal	Sfh024	EC
RI-11-701	Washington	Fecal	Sfh024	EC
RI-11-702	Washington	Fecal	Sfh024	EC
RI-11-703	Newport	Fecal	Sfh057	EC
RI-11-705	Newport	Fecal	Sfh029	EC
RI-11-706	Newport	Fecal	Sfh029	EC
RI-11-707	Newport	Fecal	Sfh019	EC
RI-11-708	Newport	Fecal	Sfh045	EC
RI-11-709	Newport	Fecal	Sfh045	EC
RI-11-710	Newport	Fecal	Sfh057	EC
RI-11-711	Newport	Fecal	Sfh019	EC
RI-11-712	Washington	Fecal	Sfh043	EC
RI-11-713	Washington	Fecal	Sfh043	EC
RI-11-714	Washington	Fecal	Sfh043	EC
RI-11-715	Washington	Fecal	Sfh043	EC
RI-11-716	Washington	Fecal	Sfh043	EC
RI-11-717	Washington	Fecal	Sfh043	EC
RI-11-718	Washington	Fecal	Sfh043	EC
RI-11-719	Washington	Fecal	Sfh043	EC
RI-11-720	Newport	Fecal	Sfh019	EC
RI-11-721	Newport	Fecal	Sfh019	EC
RI-11-722	Newport	Fecal	Sfh019	EC
RI-11-723	Newport	Fecal	Sfh019	EC
RI-11-724	Newport	Fecal	Sfh019	EC
RI-11-726	Newport	Fecal	Sfh019	EC
RI-11-727	Newport	Fecal	Sfh034	EC
RI-11-729	Newport	Fecal	Sfh029	EC
RI-11-730	Newport	Fecal	Sfh029	EC
RI-11-731	Newport	Fecal	Sfh029	EC
RI-11-732	Newport	Fecal	Sfh029	EC
RI-11-733	Newport	Fecal	Sfh029	EC
RI-11-734	Newport	Fecal	Sfh034	EC
RI-11-735	Newport	Fecal	Sfh034	EC
RI-11-736	Newport	Fecal	Sfh034	EC
RI-11-738	Kent	Fecal	Sfh032	EC
RI-11-739	Kent	Fecal	Sfh032	EC
RI-11-740	Kent	Fecal	Sfh032	EC
RI-11-741	Kent	Fecal	Sfh032	EC
RI-11-742	Kent	Fecal	Sfh032	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-743	Kent	Fecal	Sfh032	EC
RI-11-744	Providence	Fecal	Sfh024	EC
RI-11-745	Providence	Fecal	Sfh024	EC
RI-11-746	Providence	Fecal	Sfh074	EC
RI-11-747	Providence	Fecal	Sfh074	EC
RI-11-748	Providence	Fecal	Sfh074	EC
RI-11-749	Providence	Fecal	Sfh074	EC
RI-11-750	Providence	Fecal	Sfh074	EC
RI-11-751	Providence	Fecal	Sfh074	EC
RI-11-752	Providence	Fecal	Sfh053	EC
RI-11-753	Providence	Fecal	Sfh053	EC
RI-11-754	Providence	Fecal	Sfh053	EC
RI-11-755	Providence	Fecal	Sfh053	EC
RI-11-756	Providence	Fecal	Sfh053	EC
RI-11-757	Providence	Fecal	Sfh060	EC
RI-11-758	Providence	Fecal	Sfh060	EC
RI-11-759	Providence	Fecal	Sfh060	EC
RI-11-760	Providence	Fecal	Sfh060	EC
RI-11-761	Providence	Fecal	Sfh060	EC
RI-11-762	Providence	Fecal	Sfh060	EC
RI-11-763	Providence	Fecal	Sfh060	EC
RI-11-764	Newport	Fecal	Sfh009	EC
RI-11-765	Newport	Fecal	Sfh009	EC
RI-11-766	Newport	Fecal	Sfh009	EC
RI-11-767	Newport	Fecal	Sfh009	EC
RI-11-768	Newport	Fecal	Sfh049	EC
RI-11-769	Newport	Fecal	Sfh049	EC
RI-11-770	Newport	Fecal	Sfh009	EC
RI-11-771	Providence	Fecal	Sfh003	EC
RI-11-772	Providence	Fecal	Sfh003	EC
RI-11-773	Providence	Fecal	Sfh003	EC
RI-11-774	Providence	Fecal	Sfh003	EC
RI-11-775	Providence	Fecal	Sfh003	EC
RI-11-776	Providence	Fecal	Sfh043	EC
RI-11-777	Providence	Fecal	Sfh043	EC
RI-11-778	Providence	Fecal	Sfh043	EC
RI-11-779	Providence	Fecal	Sfh043	EC
RI-11-780	Providence	Fecal	Sfh043	EC
RI-11-781	Providence	Fecal	Sfh043	EC
RI-11-782	Providence	Fecal	Sfh043	EC
RI-11-783	Providence	Fecal	Sfh063	EC
RI-11-784	Providence	Fecal	Sfh076	EC
RI-11-785	Providence	Fecal	Sfh003	EC
RI-11-786	Providence	Fecal	Sfh063	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-788	Providence	Fecal	Sfh036	EC
RI-11-789	Providence	Fecal	Sfh036	EC
RI-11-790	Providence	Fecal	Sfh036	EC
RI-11-791	Providence	Fecal	Sfh036	EC
RI-11-792	Providence	Fecal	Sfh036	EC
RI-11-793	Providence	Fecal	Sfh036	EC
RI-11-794	Washington	Fecal	Sfh016	EC
RI-11-795	Washington	Fecal	Sfh016	EC
RI-11-796	Washington	Fecal	Sfh016	EC
RI-11-797	Washington	Fecal	Sfh064	EC
RI-11-798	Washington	Fecal	Sfh016	EC
RI-11-800	Washington	Fecal	Sfh016	EC
RI-11-801	Washington	Fecal	Sfh016	EC
RI-11-802	Washington	Fecal	Sfh016	EC
RI-11-803	Washington	Fecal	Sfh016	EC
RI-11-804	Washington	Fecal	Sfh067	EC
RI-11-805	Washington	Fecal	Sfh067	EC
RI-11-806	Washington	Fecal	Sfh067	EC
RI-11-807	Washington	Fecal	Sfh024	EC
RI-11-808	Washington	Fecal	Sfh024	EC
RI-11-809	Washington	Fecal	Sfh024	EC
RI-11-810	Washington	Fecal	Sfh024	EC
RI-11-811	Washington	Fecal	Sfh024	EC
RI-11-812	Washington	Fecal	Sfh024	EC
RI-11-813	Washington	Fecal	Sfh024	EC
RI-11-814	Washington	Fecal	Sfh024	EC
RI-11-815	Washington	Fecal	Sfh060	EC
RI-11-816	Washington	Fecal	Sfh060	EC
RI-11-817	Washington	Fecal	Sfh024	EC
RI-11-818	Washington	Fecal	Sfh024	EC
RI-11-819	Washington	Fecal	Sfh024	EC
RI-11-820	Washington	Fecal	Sfh024	EC
RI-11-821	Washington	Fecal	Sfh024	EC
RI-11-822	Washington	Fecal	Sfh024	EC
RI-11-823	Washington	Fecal	Sfh024	EC
RI-11-824	Washington	Fecal	Sfh024	EC
RI-11-825	Washington	Fecal	Sfh024	EC
RI-11-826	Providence	Fecal	Sfh004	EC
RI-11-827	Washington	Fecal	Sfh073	EC
RI-11-828	Washington	Fecal	Sfh073	EC
RI-11-829	Washington	Fecal	Sfh046	EC
RI-11-830	Washington	Fecal	Sfh046	EC
RI-11-831	Washington	Fecal	Sfh046	EC
RI-11-832	Washington	Fecal	Sfh046	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-833	Washington	Fecal	Sfh046	EC
RI-11-834	Washington	Fecal	Sfh046	EC
RI-11-835	Washington	Fecal	Sfh022	EC
RI-11-836	Washington	Fecal	Sfh046	EC
RI-11-837	Washington	Fecal	Sfh046	EC
RI-11-838	Washington	Fecal	Sfh022	EC
RI-11-839	Washington	Fecal	Sfh022	EC
RI-11-840	Washington	Fecal	Sfh030	EC
RI-11-841	Washington	Fecal	Sfh030	EC
RI-11-842	Washington	Fecal	Sfh030	EC
RI-11-843	Washington	Fecal	Sfh030	EC
RI-11-844	Washington	Fecal	Sfh046	EC
RI-11-846	Washington	Fecal	Sfh046	EC
RI-11-847	Washington	Fecal	Sfh030	EC
RI-11-848	Washington	Fecal	Sfh057	EC
RI-11-849	Washington	Fecal	Sfh030	EC
RI-11-850	Washington	Fecal	Sfh007	EC
RI-11-851	Washington	Fecal	Sfh002	EC
RI-11-852	Washington	Fecal	Sfh002	EC
RI-11-854	Washington	Fecal	Sfh059	EC
RI-11-855	Washington	Fecal	Sfh002	EC
RI-11-856	Washington	Fecal	Sfh002	EC
RI-11-857	Washington	Fecal	Sfh002	EC
RI-11-858	Washington	Fecal	Sfh002	EC
RI-11-859	Washington	Fecal	Sfh002	EC
RI-11-860	Washington	Fecal	Sfh016	EC
RI-11-861	Washington	Fecal	Sfh016	EC
RI-11-862	Washington	Fecal	Sfh016	EC
RI-11-863	Washington	Fecal	Sfh016	EC
RI-11-864	Washington	Fecal	Sfh016	EC
RI-11-865	Kent	Fecal	Sfh011	EC
RI-11-866	Kent	Fecal	Sfh011	EC
RI-11-867	Kent	Fecal	Sfh011	EC
RI-11-868	Kent	Fecal	Sfh011	EC
RI-11-870	Kent	Fecal	Sfh067	EC
RI-11-871	Kent	Fecal	Sfh067	EC
RI-11-872	Washington	Fecal	Sfh002	EC
RI-11-873	Washington	Fecal	Sfh002	EC
RI-11-874	Washington	Fecal	Sfh002	EC
RI-11-876	Washington	Fecal	Sfh002	EC
RI-11-877	Washington	Fecal	Sfh002	EC
RI-11-878	Washington	Fecal	Sfh002	EC
RI-11-879	Washington	Fecal	Sfh005	EC
RI-11-881	Washington	Fecal	Sfh007	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-883	Washington	Fecal	Sfh005	EC
RI-11-884	Washington	Fecal	Sfh005	EC
RI-11-885	Washington	Fecal	Sfh005	EC
RI-11-886	Washington	Fecal	Sfh005	EC
RI-11-887	Washington	Fecal	Sfh005	EC
RI-11-888	Washington	Fecal	Sfh005	EC
RI-11-889	Washington	Fecal	Sfh005	EC
RI-11-890	Providence	Fecal	Sfh073	EC
RI-11-892	Providence	Fecal	Sfh073	EC
RI-11-893	Washington	Tissue	Sfh057	EC
RI-11-894	Newport	Tissue	Sfh040	EC
RI-11-895	Newport	Tissue	Sfh040	EC
RI-11-896	Newport	Tissue	Sfh040	EC
RI-11-897	Newport	Tissue	Sfh040	EC
RI-11-898	Newport	Tissue	Sfh034	EC
RI-11-899	Newport	Tissue	Sfh040	EC
RI-11-900	Newport	Tissue	Sfh051	EC
RI-11-902	Bristol	Tissue/Blood	Sfh041	EC
RI-11-903	Newport	Tissue/Blood	Sfh040	EC
RI-11-905	Newport	Tissue	Sfh040	EC
RI-11-906	Newport	Tissue	Sfh061	EC
RI-11-907	Newport	Tissue	Sfh040	EC
RI-11-908	Newport	Tissue	Sfh047	EC
RI-11-909	Newport	Tissue/Fecal	Sfh040	EC
RI-11-910	Newport	Tissue	Sfh040	EC
RI-11-911	Newport	Tissue	Sfh052	EC
RI-11-912	Newport	Tissue	Sfh040	EC
RI-11-913	Newport	Tissue	Sfh040	EC
RI-11-914	Newport	Tissue	Sfh040	EC
RI-11-915	Newport	Tissue	Sfh040	EC
RI-11-916	Newport	Tissue	Sfh047	EC
RI-11-917	Newport	Tissue/Blood	Sfh061	EC
RI-11-918	Newport	Tissue/Blood	Sfh040	EC
RI-11-919	Newport	Tissue	Sfh041	EC
RI-11-920	Washington	Fecal	Sfh002	EC
RI-11-921	Washington	Fecal	Sfh002	EC
RI-11-922	Washington	Fecal	Sfh002	EC
RI-11-923	Washington	Fecal	Sfh002	EC
RI-11-924	Washington	Fecal	Sfh002	EC
RI-11-925	Washington	Fecal	Sfh002	EC
RI-11-926	Washington	Fecal	Sfh002	EC
RI-11-927	Washington	Fecal	Sfh002	EC
RI-11-928	Washington	Fecal	Sfh002	EC
RI-11-929	Washington	Fecal	Sfh002	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-930	Washington	Tissue	Sfh043	EC
RI-11-931	Providence	Tissue	Sfh054	EC
RI-11-932	Washington	Tissue	Sfh016	EC
RI-11-933	Unknown	Tissue	Sfh057	EC
RI-11-934	Washington	Fecal	Sfh024	EC
RI-11-935	Washington	Fecal	Sfh023	EC
RI-11-936	Washington	Fecal	Sfh024	EC
RI-11-937	Washington	Fecal	Sfh023	EC
RI-11-938	Washington	Fecal	Sfh024	EC
RI-11-939	Washington	Fecal	Sfh023	EC
RI-11-940	Washington	Fecal	Sfh024	EC
RI-11-942	Washington	Fecal	Sfh024	EC
RI-11-943	Washington	Fecal	Sfh024	EC
RI-11-944	Washington	Fecal	Sfh024	EC
RI-11-945	Washington	Fecal	Sfh024	EC
RI-11-946	Washington	Fecal	Sfh022	EC
RI-11-947	Washington	Fecal	Sfh016	EC
RI-11-948	Washington	Fecal	Sfh016	EC
RI-11-949	Washington	Fecal	Sfh022	EC
RI-11-950	Washington	Fecal	Sfh016	EC
RI-11-951	Washington	Fecal	Sfh024	EC
RI-11-952	Washington	Fecal	Sfh024	EC
RI-11-953	Washington	Fecal	Sfh024	EC
RI-11-954	Washington	Fecal	Sfh040	EC
RI-11-955	Washington	Fecal	Sfh040	EC
RI-11-956	Washington	Fecal	Sfh040	EC
RI-11-958	Washington	Fecal	Sfh024	EC
RI-11-959	Washington	Fecal	Sfh024	EC
RI-11-960	Washington	Fecal	Sfh024	EC
RI-11-961	Washington	Fecal	Sfh024	EC
RI-11-962	Washington	Fecal	Sfh024	EC
RI-11-963	Washington	Fecal	Sfh024	EC
RI-11-964	Washington	Fecal	Sfh024	EC
RI-11-965	Washington	Fecal	Sfh024	EC
RI-11-966	Washington	Fecal	Sfh024	EC
RI-11-967	Washington	Fecal	Sfh024	EC
RI-11-968	Washington	Fecal	Sfh024	EC
RI-11-969	Washington	Fecal	Sfh030	EC
RI-11-970	Washington	Fecal	Sfh073	EC
RI-11-973	Washington	Fecal	Sfh073	EC
RI-11-975	Washington	Fecal	Sfh055	EC
RI-11-977	Washington	Fecal	Sfh030	EC
RI-11-978	Washington	Fecal	Sfh073	EC
RI-11-979	Washington	Fecal	Sfh030	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-11-980	Washington	Fecal	Sfh046	EC
RI-11-981	Washington	Fecal	Sfh046	EC
RI-11-982	Washington	Fecal	Sfh046	EC
RI-11-983	Washington	Fecal	Sfh046	EC
RI-11-984	Washington	Fecal	Sfh046	EC
RI-11-985	Washington	Fecal	Sfh046	EC
RI-11-986	Washington	Fecal	Sfh073	EC
RI-11-987	Washington	Fecal	Sfh046	EC
RI-11-988	Washington	Fecal	Sfh073	EC
RI-11-989	Washington	Fecal	Sfh046	EC
RI-11-990	Washington	Fecal	Sfh073	EC
RI-12-001	Washington	Fecal	Sfh001	EC
RI-12-002	Washington	Tissue/Fecal/Blood	Sfh016	EC
RI-12-003	Washington	Tissue/Fecal/Blood	Sfh016	EC
RI-12-004	Washington	Fecal	Sfh063	EC
RI-12-005	Washington	Fecal	Sfh016	EC
RI-12-006	Washington	Fecal	Sfh016	EC
RI-12-007	Washington	Fecal	Sfh063	EC
RI-12-008	Washington	Fecal	Sfh016	EC
RI-12-009	Washington	Fecal	Sfh016	EC
RI-12-010	Washington	Fecal	Sfh016	EC
RI-12-011	Washington	Fecal	Sfh016	EC
RI-12-012	Washington	Fecal	Sfh063	EC
RI-12-013	Washington	Fecal	Sfh063	EC
RI-12-014	Washington	Fecal	Sfh016	EC
RI-12-015	Washington	Fecal	Sfh016	EC
RI-12-016	Washington	Fecal	Sfh063	EC
RI-12-017	Washington	Fecal	Sfh016	EC
RI-12-018	Washington	Fecal	Sfh016	EC
RI-12-019	Washington	Fecal	Sfh016	EC
RI-12-020	Washington	Fecal	Sfh063	EC
RI-12-021	Washington	Fecal	Sfh063	EC
RI-12-022	Washington	Fecal	Sfh063	EC
RI-12-023	Washington	Fecal	Sfh063	EC
RI-12-024	Washington	Fecal	Sfh019	EC
RI-12-025	Washington	Fecal	Sfh019	EC
RI-12-026	Washington	Fecal	Sfh019	EC
RI-12-027	Washington	Fecal	Sfh019	EC
RI-12-028	Washington	Fecal	Sfh019	EC
RI-12-029	Washington	Fecal	Sfh019	EC
RI-12-030	Washington	Tissue/Fecal/Blood	Sfh016	EC
RI-12-031	Washington	Fecal	Sfh016	EC
RI-12-032	Kent	Fecal	Sfh067	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-12-033	Kent	Fecal	Sfh067	EC
RI-12-034	Kent	Fecal	Sfh067	EC
RI-12-035	Kent	Fecal	Sfh067	EC
RI-12-036	Kent	Fecal	Sfh067	EC
RI-12-037	Kent	Fecal	Sfh067	EC
RI-12-038	Washington	Fecal	Sfh076	EC
RI-12-040	Washington	Fecal	Sfh076	EC
RI-12-041	Washington	Fecal	Sfh076	EC
RI-12-042	Washington	Fecal	Sfh016	EC
RI-12-043	Washington	Fecal	Sfh076	EC
RI-12-044	Washington	Fecal	Sfh076	EC
RI-12-045	Washington	Fecal	Sfh076	EC
RI-12-046	Washington	Fecal	Sfh076	EC
RI-12-047	Washington	Fecal	Sfh076	EC
RI-12-048	Washington	Fecal	Sfh076	EC
RI-12-049	Washington	Fecal	Sfh076	EC
RI-12-050	Washington	Fecal	Sfh016	EC
RI-12-051	Washington	Fecal	Sfh076	EC
RI-12-052	Washington	Fecal	Sfh016	EC
RI-12-053	Washington	Fecal	Sfh024	EC
RI-12-054	Washington	Fecal	Sfh043	EC
RI-12-055	Washington	Fecal	Sfh043	EC
RI-12-056	Washington	Fecal	Sfh043	EC
RI-12-057	Washington	Fecal	Sfh043	EC
RI-12-058	Washington	Fecal	Sfh019	EC
RI-12-059	Washington	Fecal	Sfh019	EC
RI-12-060	Washington	Fecal	Sfh045	EC
RI-12-061	Washington	Fecal	Sfh019	EC
RI-12-062	Washington	Fecal	Sth011	NEC
RI-12-063	Washington	Fecal	Sfh019	EC
RI-12-064	Washington	Fecal	Sfh019	EC
RI-12-065	Washington	Fecal	Sfh019	EC
RI-12-066	Washington	Fecal	Sfh019	EC
RI-12-067	Washington	Fecal	Sfh019	EC
RI-12-068	Washington	Fecal	Sfh093	EC
RI-12-069	Washington	Fecal	Sfh093	EC
RI-12-070	Washington	Fecal	Sfh093	EC
RI-12-071	Washington	Fecal	Sfh019	EC
RI-12-072	Washington	Fecal	Sfh019	EC
RI-12-073	Washington	Fecal	Sfh019	EC
RI-12-074	Washington	Fecal	Sfh016	EC
RI-12-075	Washington	Fecal	Sfh019	EC
RI-12-076	Washington	Fecal	Sfh019	EC
RI-12-077	Washington	Fecal	Sfh019	EC

Appendix 5: continued

Sample ID	County	Sample Type	Haplotype	Species ID
RI-12-078	Washington	Fecal	Sfh019	EC
RI-12-079	Washington	Fecal	Sfh019	EC
RI-12-080	Washington	Fecal	Sfh019	EC
RI-12-081	Washington	Fecal	Sfh019	EC
RI-12-082	Washington	Fecal	Sfh032	EC
RI-12-083	Washington	Fecal	Sfh016	EC
RI-12-085	Washington	Fecal	Sfh032	EC
RI-12-086	Washington	Fecal	Sfh016	EC
RI-12-087	Washington	Fecal	Sfh016	EC
RI-12-088	Washington	Fecal	Sfh016	EC
RI-12-089	Washington	Fecal	Sfh016	EC
RI-12-090	Washington	Fecal	Sfh016	EC
RI-12-091	Washington	Fecal	Sfh016	EC
RI-12-092	Washington	Fecal	Sfh032	EC
RI-12-093	Washington	Fecal	Sfh032	EC
RI-12-094	Washington	Fecal	Sfh024	EC
RI-12-095	Washington	Fecal	Sfh016	EC
RI-12-097	Washington	Fecal	Sfh067	EC
RI-12-098	Washington	Fecal	Sfh043	EC
RI-12-099	Washington	Fecal	Sfh049	EC
RI-12-100	Washington	Fecal	Sfh019	EC
RI-12-101	Washington	Fecal	Sfh024	EC
RI-12-102	Washington	Fecal	Sfh024	EC
RI-12-103	Washington	Fecal	Sfh024	EC
RI-12-104	Washington	Fecal	Sfh024	EC
RI-12-105	Newport	Fecal	Sfh042	EC
RI-12-106	Newport	Fecal	Sfh051	EC
RI-12-107	Newport	Fecal	Sfh042	EC
RI-12-108	Newport	Fecal	Sfh042	EC
RI-12-109	Washington	Fecal	Sfh024	EC
RI-12-110	Washington	Fecal	Sfh024	EC
RI-12-111	Washington	Fecal	Sfh024	EC
RI-12-112	Washington	Fecal	Sfh060	EC
RI-12-113	Washington	Fecal	Sfh063	EC
RI-12-114	Washington	Fecal	Sfh019	EC
RI-12-115	Washington	Fecal	Sfh019	EC
RI-12-116	Kent	Fecal	Sfh095	EC
RI-12-117	Kent	Fecal	Sfh095	EC
RI-12-119	Providence	Fecal	Sfh091	EC
RI-12-121	Providence	Fecal	Sfh067	EC
RI-12-122	Providence	Fecal	Sfh067	EC
RI-12-123	Providence	Fecal	Sfh067	EC
RI-12-124	Providence	Fecal	Sfh091	EC

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Sample ID	County	Sample Type	Haplotype	Species ID
RI-12-125	Kent	Fecal	Sfh032	EC
RI-12-126	Kent	Fecal	Sfh032	EC
RI-12-127	Kent	Fecal	Sfh032	EC
RI-12-128	Washington	Fecal	Sfh076	EC
RI-12-130	Washington	Fecal	Sfh076	EC
RI-12-131	Washington	Fecal	Sfh076	EC
RI-12-132	Washington	Fecal	Sfh043	EC
RI-12-133	Washington	Fecal	Sfh043	EC
RI-12-134	Washington	Fecal	Sfh043	EC
RI-12-135	Washington	Fecal	Sfh043	EC
RI-12-136	Washington	Fecal	Sfh043	EC
RI-12-137	Washington	Fecal	Sfh067	EC
RI-12-138	Washington	Tissue	Sfh043	EC
RI-12-139	Kent	Tissue/Fecal	Sfh008	EC
RI-12-140	Washington	Fecal	Sfh043	EC
RI-12-141	Washington	Fecal	Sfh049	EC
RI-12-142	Washington	Fecal	Sfh057	EC
RI-12-143	Washington	Fecal	Sfh057	EC
RI-12-144	Washington	Fecal	Sfh057	EC
RI-12-145	Washington	Fecal	Sfh057	EC
RI-12-146	Washington	Fecal	Sfh067	EC
RI-12-147	Providence	Fecal	Sfh096	EC
RI-12-148	Providence	Fecal	Sfh096	EC
RI-12-149	Providence	Fecal	Sfh096	EC
RI-12-150	Newport	Fecal	Sfh049	EC
RI-12-151	Newport	Fecal	Sfh042	EC
RI-12-152	Newport	Fecal	Sfh042	EC
RI-12-153	Newport	Fecal	Sfh049	EC
RI-12-154	Washington	Fecal	Sfh076	EC
RI-12-155	Newport	Fecal	Sfh019	EC
RI-12-156	Newport	Fecal	Sfh019	EC
RI-12-157	Newport	Fecal	Sfh052	EC
RI-12-158	Newport	Fecal	Sfh097	EC
RI-12-159	Newport	Fecal	Sfh051	EC
RI-12-160	Newport	Fecal	Sfh042	EC
RI-12-162	Washington	Fecal	Sfh024	EC
RI-12-164	Kent	Fecal	Sfh045	EC
RI-12-165	Kent	Fecal	Sfh045	EC
RI-12-166	Kent	Fecal	Sfh045	EC
RI-12-167	Kent	Fecal	Sfh045	EC
RI-12-168	Kent	Fecal	Sfh040	EC
RI-12-169	Kent	Fecal	Sfh013	EC
RI-12-170	Kent	Fecal	Sfh045	EC
RI-12-171	Kent	Fecal	Sfh045	EC

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Sample ID	County	Sample Type	Haplotype	Species ID
RI-12-172	Kent	Fecal	Sfh045	EC
RI-12-174	Newport	Fecal	Sfh030	EC
RI-12-175	Newport	Fecal	Sfh040	EC
RI-12-176	Newport	Fecal	Sfh040	EC
RI-12-177	Newport	Fecal	Sfh040	EC
RI-12-178	Newport	Fecal	Sfh030	EC
RI-12-179	Newport	Fecal	Sfh030	EC
RI-12-180	Newport	Fecal	Sfh030	EC
RI-12-181	Newport	Fecal	Sfh030	EC
RI-12-182	Newport	Fecal	Sfh040	EC
RI-12-183	Newport	Fecal	Sfh040	EC
RI-12-184	Washington	Fecal	Sfh076	EC
RI-12-185	Washington	Fecal	Sfh067	EC
RI-12-186	Washington	Fecal	Sfh016	EC
RI-12-189	Washington	Fecal	Sfh067	EC
RI-12-190	Washington	Fecal	Sfh063	EC
RI-12-191	Washington	Fecal	Sfh063	EC
RI-12-192	Washington	Fecal	Sfh067	EC
RI-12-193	Kent	Fecal	Sfh045	EC
RI-12-195	Washington	Fecal	Sfh019	EC
RI-12-196	Washington	Fecal	Sfh024	EC
RI-12-197	Washington	Fecal	Sfh024	EC
RI-12-198	Washington	Fecal	Sfh024	EC
RI-12-199	Washington	Fecal	Sfh024	EC
RI-12-200	Washington	Fecal	Sfh063	EC
RI-12-201	Washington	Fecal	Sfh067	EC
RI-12-202	Washington	Fecal	Sfh067	EC
RI-12-203	Washington	Fecal	Sfh067	EC
RI-12-204	Providence	Fecal	Sfh096	EC
RI-12-205	Providence	Fecal	Sfh096	EC
RI-12-206	Providence	Fecal	Sfh096	EC
RI-12-207	Providence	Fecal	Sfh060	EC
RI-12-208	Providence	Fecal	Sfh060	EC
RI-12-209	Washington	Fecal	Sfh024	EC
RI-12-211	Providence	Fecal	Sfh074	EC
RI-12-212	Providence	Fecal	Sfh074	EC
RI-12-213	Providence	Fecal	Sfh074	EC
RI-12-214	Washington	Fecal	Sfh016	EC
RI-12-215	Washington	Fecal	Sfh067	EC
RI-12-216	Washington	Fecal	Sfh016	EC
RI-12-217	Washington	Fecal	Sfh067	EC
RI-12-218	Newport	Fecal	Sfh042	EC
RI-12-219	Newport	Fecal	Sfh049	EC
RI-12-220	Newport	Fecal	Sfh042	EC

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Sample ID	County	Sample Type	Haplotype	Species ID
RI-12-221	Newport	Fecal	Sfh042	EC
RI-12-222	Providence	Fecal	Sfh074	EC
RI-12-223	Washington	Fecal	Sfh002	EC
RI-12-224	Washington	Fecal	Sfh066	EC
RI-12-225	Kent	Fecal	Sfh045	EC
RI-12-226	Kent	Fecal	Sfh045	EC
RI-12-227	Kent	Fecal	Sfh045	EC
RI-12-228	Kent	Fecal	Sfh045	EC
RI-12-229	Kent	Fecal	Sfh045	EC
RI-12-230	Kent	Fecal	Sfh013	EC
RI-12-231	Washington	Fecal	Sfh067	EC
RI-12-232	Washington	Fecal	Sfh076	EC
RI-12-233	Washington	Fecal	Sfh067	EC
RI-12-234	Washington	Fecal	Sfh067	EC
RI-12-235	Washington	Tissue	Sfh002	EC
RI-12-236	Washington	Tissue	Sfh043	EC
RI-12-237	Newport	Tissue	Sfh098	EC
RI-12-238	Newport	Fecal	Sfh001	EC
RI-12-239	Newport	Fecal	Sfh001	EC
RI-12-240	Newport	Fecal	Sfh098	EC
RI-12-241	Newport	Fecal	Sfh098	EC
RI-12-242	Newport	Fecal	Sfh001	EC
RI-12-243	Newport	Fecal	Sfh001	EC
RI-12-244	Newport	Fecal	Sfh098	EC
RI-12-245	Newport	Fecal	Sfh098	EC
RI-12-246	Newport	Fecal	Sfh098	EC
RI-12-247	Newport	Fecal	Sfh098	EC
RI-12-249	Newport	Fecal	Sfh016	EC
RI-12-250	Newport	Fecal	Sfh098	EC
RI-12-251	Newport	Fecal	Sfh098	EC
RI-12-252	Newport	Fecal	Sfh041	EC
RI-12-253	Newport	Fecal	Sfh062	EC
RI-12-254	Newport	Fecal	Sfh098	EC
RI-12-255	Newport	Fecal	Sfh062	EC
RI-12-256	Newport	Fecal	Sfh062	EC
RI-12-257	Newport	Fecal	Sfh098	EC
RI-12-258	Newport	Fecal	Sfh016	EC
RI-12-259	Newport	Fecal	Sfh001	EC
RI-12-260	Newport	Fecal	Sfh060	EC
RI-12-261	Newport	Fecal	Sfh001	EC
RI-12-262	Newport	Fecal	Sfh001	EC
RI-12-266	Washington	Fecal	Sfh067	EC
RI-12-267	Washington	Fecal	Sfh067	EC
RI-12-268	Washington	Fecal	Sfh063	EC

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Sample ID	County	Sample Type	Haplotype	Species ID
RI-12-269	Washington	Fecal	Sfh067	EC
RI-12-270	Washington	Fecal	Sfh043	EC
RI-12-271	Unknown	Fecal	Sfh016	EC
RI-12-272	Unknown	Fecal	Sfh016	EC
RI-12-273	Unknown	Fecal	Sfh016	EC
RI-MS-003	Unknown	Tissue	Sfh049	EC
RI-MS-005	Unknown	Tissue	Sfh019	EC
RI-MS-006	Unknown	Tissue	Sfh019	EC
RI-MS-007	Unknown	Tissue	Sfh043	EC
RI-MS-008	Unknown	Tissue	Sfh043	EC
RI-MS-009	Unknown	Tissue	Sfh043	EC
RI-MS-010	Unknown	Tissue	Sfh055	EC
RI-MS-011	Unknown	Tissue	Sfh078	EC
URI-10-01	Washington	Tissue	Sfh047	EC
WC-10-01	Newport	Tissue	Sfh047	EC

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