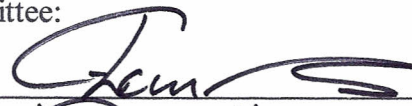


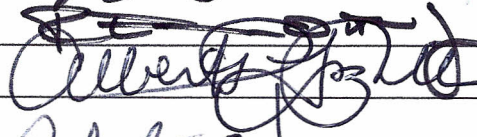


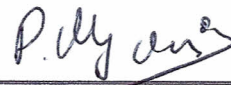
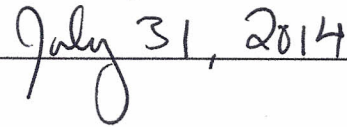


MITOCHONDRIAL CONTROL REGION DIVERSITY AND PHYLOGEOGRAPHIC PATTERNS OF THE ATLANTIC WHITE-SIDED DOLPHIN (LAGENORHYNCHUS ACUTUS) ALONG THE EAST COAST OF THE UNITED STATES

by

Heather Anne Abrahams  
A Thesis  
Submitted to the  
Graduate Faculty  
of  
George Mason University  
in Partial Fulfillment of  
The Requirements for the Degree  
of  
Master of Science  
Environmental Science and Policy

Committee:

	Dr. ECM Parsons, Thesis Director
	Dr. Patrick Gillevet, Committee Member
	Dr. R. Edward Otto, Committee Member
	Dr. Albert P. Torzilli, Graduate Program Director
	Dr. Robert B. Jonas, Department Chairperson
	Dr. Donna Fox, Associate Dean, Student Affairs & Special Programs, College of Science
	Dr. Peggy Agouris, Dean, College of Science
Date: 	Summer Semester 2014 George Mason University Fairfax, VA

Mitochondrial Control Region Diversity and Phylogeographic Patterns of the Atlantic  
White-sided Dolphin (*Lagenorhynchus acutus*) Along the East Coast of the United States

A Thesis submitted in partial fulfillment of the requirements for the degree of Master of  
Science at George Mason University

by

Heather Anne Abrahams  
Bachelor of Arts  
Virginia Polytechnic Institute and State University, 2009

Director: ECM Parsons, Professor  
Department of Environmental Science and Policy

Summer Semester 2014  
George Mason University  
Fairfax, VA



This work is licensed under a [creative commons attribution-noncommercial 3.0 unported license](https://creativecommons.org/licenses/by-nc/3.0/).

## **DEDICATION**

This is dedicated to my family and friends – without all of your support over the years I would not have been able to pursue my education and passions while keeping track of what is really important. I love you all.

## ACKNOWLEDGEMENTS

I would like to first thank my advisors, Drs. Parsons, Gillevet, and Otto, for accepting me as a student, guiding me through the ups and downs of grad school, and all their wonderful instruction both in and out of the classroom. I would also like to thank my “unofficial committee” at the Smithsonian: Charley Potter and Dr. Jesus Maldonado for their unwavering support, knowledge, and guidance from the conception through completion of this project. A huge thank you to Dr. Nicole Vollmer for all of her help and patience while teaching and refining my lab techniques, as well as her insight into the greater field of marine mammal genetics. Without her knowledge and persistence this project would not have been possible. I would also like to thank Lillian Parker and Mirian Tsuchiya, for without their help and guidance during analysis, the completion of this project would not have been possible on time. Thank you to the Smithsonian Institution for not only providing the funding for this project, but also for the access to their resources and collections, and the supplementation of samples. Likewise, I would like to thank Frederick Wenzel at NOAA in Woods Hole, MA for donating the majority of the samples and helping with the collection of the background metadata. Finally, many thanks are due to my colleagues and friends in the ESP department and at the L.A.B., who contributed invaluable intellectual and moral support throughout the creation of this work.

## TABLE OF CONTENTS

	Page
List of Tables.....	vii
List of Figures .....	viii
List of Abbreviations .....	ix
Abstract.....	x
Introduction.....	1
Bycatch: A Conservation Management Issue.....	2
Mitochondrial DNA .....	5
Phylogeography .....	6
<i>Lagenorhynchus acutus</i> .....	9
Distribution.....	9
Phylogeography .....	10
Population Structure.....	12
Population Size .....	14
Main threats .....	15
Behavior .....	15
Study Objectives and Hypotheses .....	17
Materials and Methods .....	20
Sample Collection.....	20
DNA Extraction .....	20
DNA Amplification.....	21
Optimizing PCR Reaction .....	23
DNA Sequencing .....	23
Data Analysis.....	24
Sequence Editing .....	24
Measures of Genetic Diversity .....	24
Genetic Structure .....	25

Mismatch Distribution Analysis and Neutrality tests .....	25
Haplotype network.....	27
Spatial Temporal Analysis .....	27
Results.....	28
Genetic Variation at the mtDNA Control Region .....	28
Measures of Genetic Diversity .....	30
Genetic Structure .....	36
Mismatch Distribution Analysis and Neutrality Tests .....	36
Haplotype Network.....	38
Comparison to Published Diversity .....	42
Spatial Temporal Analysis .....	43
Discussion .....	45
Appendix.....	50
Complete Alignment .....	52
References.....	73

## LIST OF TABLES

Table	Page
Table 1. Sequence variation in the mitochondrial control region .....	32
Table 2. Percent divergence between haplotypes.....	34
Table 3. Base pair differences between haplotypes.....	35
Table 4. Dates and locations of “South” samples .....	43



## LIST OF FIGURES

Figure	Page
Figure 1 Distribution of <i>Lagenorhynchus acutus</i> .....	10
Figure 2 Map of Gulf of Maine.....	14
Figure 3 North and South sampling location sites.....	29
Figure 4 Haplotypes by count with locality.....	31
Figure 5 Mismatch distribution in the South.....	37
Figure 6 Mismatch distribution in the North.....	37
Figure 7 Median-joining haplotype network.....	39
Figure 8 Maximum likelihood tree depicting evolutionary relationships among haplotypes.....	40
Figure 9 Maximum parsimony tree depicting evolutionary relationships among haplotypes.....	41
Figure 10 Month of sample collection.....	44
Figure 11 Sequence Quality.....	50
Figure 12 Clustal W Alignment.....	51

## LIST OF ABBREVIATIONS

Analysis of Molecular Variance.....	AMOVA
Base Pairs .....	bp
Bovine Serum Albumin .....	BSA
Control Region .....	CR
Marine Mammal Protection Act.....	MMPA
Maximum likelihood .....	ML
Maximum parsimony.....	MP
Median-joining .....	MJ
Mitochondrial DNA.....	mtDNA
National Oceanic and Atmospheric Administration.....	NOAA
Polymerase Chain Reaction .....	PCR

## ABSTRACT

### MITOCHONDRIAL CONTROL REGION DIVERSITY AND PHYLOGEOGRAPHIC PATTERNS OF THE ATLANTIC WHITE-SIDED DOLPHIN (*LAGENORHYNCHUS ACUTUS*) ALONG THE EAST COAST OF THE UNITED STATES

Heather Anne Abrahams, M.S.

George Mason University, 2014

Thesis Director: Dr. ECM Parsons

*Lagenorhynchus acutus*, the Atlantic white-sided dolphin, is a highly mobile marine species occupying temperate and sub-polar pelagic waters across the entire North Atlantic Ocean. Currently managed as a single population, three stocks have been proposed in the western North Atlantic waters off of New England and Canada. However, over the past few years their distribution seems to be changing in this region with increasing numbers of the species found in waters as far south as North Carolina in the United States. This species greatest threats are derived from anthropogenic sources and it is important to know if any division is forming in the newly expanded region for proper management. This study had two main objectives: to assess genetic diversity of Atlantic white-sided dolphins found along the east coast of the United States in the western North Atlantic, and to identify geographic patterns of haplotype frequency to serve as a basis of comparison by which to identify the origin of individual dolphins

found in the southern part of the range. This was in order to see if this species, which is adapted to the pelagic habitat, will show panmixia across a broad geographic range or display finer scale north/south geographic isolations.

The evolutionary history and population structure of *L. acutus* was assessed using a fragment of the control region of the mitochondrial DNA (d-loop). This marker is hypervariable and was selected due to its relatively fast mutation rate, the availability of primers, and for easy comparison to previous published sequences for this species in other parts of their range. This region was successfully amplified and sequenced from 110 total samples for *L. acutus* in two geographic areas along the east coast (North, N = 89; South, N = 21). The species displayed moderate haplotypic diversity (0.896) but very low nucleotide diversity (0.00706). These findings suggest that this species was affected by historical bottleneck events that reduced their population size in the past and that the population is currently in expansion. The star-like shape of the haplotype phylogeny, which may be indicative of recent population expansion, provided further support for the bottleneck hypothesis. When addressing the population division, the  $F_{ST}$  value (-0.00697) suggests the existence of one continuous population of *L. acutus* along the east coast of the United States. These results correspond with other studies on the species throughout its entire geographic range.

Future studies should utilize higher resolution molecular markers such as microsatellites or a panel of highly polymorphic SNPs to elucidate fine spatial genetic structure and make possible determining whether or not this species is separating into stocks or can be managed as one panmictic population. Research should also focus on the

spatial temporal relationship in order to determine if a portion of the population is migrating south during a specific time frame, or if there is more year round presence indicating an expansion into the range due to climatic or other explanations.

## INTRODUCTION

Early in the 1980s, a study by Stephen O'Brien and his colleagues found cheetahs (*Acinonyx jubatus*) to be considerably lacking genetic variation, a result that surprised many scientists and wildlife conservationists (O'Brien 1983, Cohn 1990). This one study in particular has led to similar studies on an exponentially increasing number of species worldwide. In today's world the degradation of species' habitats and the consequent loss of diversity in natural populations, due to both anthropogenic and natural causes, are almost unavoidable. In effort to combat these issues and conserve species for future generations, wildlife biologists such as O'Brien have increasingly turned to molecular methods using studies of mitochondrial and nuclear DNA. The use of molecular studies allows better understanding of biological diversity and helps provide a basis for the effective management and conservation of natural populations. Mitochondrial and nuclear microsatellite markers have been extensively used in the study of cetacean populations in order to establish patterns of gene flow and evaluate the causes of loss of diversity; the use of mitochondrial markers further allowed the use of coalescent theory (Kingman 1982) to analyze the distribution of haplotypes. This leads to increased understanding how past demographic events have influenced the current distribution of species and populations (Roger and Harpending 1992; Austerlitz et al. 1997; Wakeley and Hey 1997).

Directly related to the evolutionary radiation of species, is the pattern of diversity within species and the forces that generate those patterns. Relatively few boundaries that can lead to differentiation by drift exist in the marine environment, unlike the terrestrial environment which has barriers such as mountains and rivers. Due to this lack of restricted movement, one would expect to find in species with strong dispersal potential such as highly mobile marine vertebrates, either isolation of natural populations by distance or panmixia across large geographic regions (Natoli et al. 2003). However, there is evidence that marine mammals, which have great capacity for dispersal, often show fine-scale population structure within species, although the extent varies among species (Hoelzel 2009). Hoelzel (1998a) has argued that this could be due to a combination of behavioral specializations for resources, social structure, and historical environmental change. This has in fact been observed for a number of marine taxa, and is referred to as the “marine speciation paradox” (Palumbi 1994, Bierne et al. 2003) and has many different management implications.

### **Bycatch: A Conservation Management Issue**

In the United States, the Marine Mammal Protection Act (MMPA) of 1972 mandates that ‘population stocks’ be maintained to the level that they remain a ‘significant functioning element in the ecosystem of which they are a part’ with ‘population stock’ defined as: ‘a group of marine mammals of the same species or smaller taxa in a common spatial arrangement, that interbreed when mature’ [Section 3(11)]. It is very difficult to determine directly whether individuals in a group of marine

mammals are interbreeding and as previously mentioned, we have a limited understanding of what barriers to movement and gene flow may be encountered by highly mobile creatures such as marine mammals. Thus, it is difficult to determine where one population boundary ends and the next one begins in order to define separate management stocks.

The MMPA also recognizes that ‘certain species and population stocks of marine mammals are, or may be, in danger of extinction or depletion as a result of man’s activities’. In the past, conservation of cetacean populations has been focused on the effects that direct takes, pollution, habitat destruction and competition for prey resources have had on the sustainability of species. However, bycatch –incidental capture while fishing– is now being recognized as one of the key threats to cetacean species, and as being the major cause of human induced mortality amongst aquatic organisms. The high levels of induced mortality have threatened many populations that could represent different evolutionary units or emerging species (Bickham et al. 1996; Secchi et al. 1998; Rosel et al. 1999a; Pichler and Baker 2000). These studies have shown that bottlenecks (a reduction in population size within a short time period) in species affected by commercial hunting or accidental takes can result in serious effects on the long-term viability of the population, and has the potential to influence the density, behavior, demographics and long-term survival of species (Rosel et al. 1999a; Pichler and Baker 2000). This is particularly noticeable in cetacean populations because their longevity and relatively low reproductive rates make them more vulnerable to the increasing influences of humans.



With the added complication of defining a particular stock, bycatch is additionally hard to manage, especially in cases of continuous distributions. Take the example of the harbor porpoise (*P. phocoena*) which in the Northwest Atlantic ranges roughly from the Northeast United States to Canada in all coastal waters with no clear gaps in its distribution. In the US, it is currently managed as one stock—the Gulf of Maine/Bay of Fundy population—which suffers from high incidents of bycatch in gillnets (Rosel et al. 1999a). Satellite data indicates home ranges that are small relative to their large range within the North Atlantic Ocean (Read and Westgate 1997) so a hypothesis of panmixia is biologically highly implausible. Nevertheless, it is likely that the stock boundaries drawn within the range will have individuals that regularly cross back and forth. This is further complicated with the possibility of migrations. It is known that they leave summer breeding areas during the late winter and early spring months, but it is not known where they go. Increased strandings and incidental gillnet takes along in the mid-Atlantic region indicate a southern migration for some animals, but it is not known from which stock (Canadian or Gulf of Maine/Bay of Fundy) they originated. It is imperative to determine from which summer breeding stock these animals originated in order to establish accurate estimates of incidental mortality effects on the populations (Rosel et al. 1999a). If stocks experience a large reduction in their effective population sizes, not only is there a reduction in genetic diversity, but there is also an increased rate of inbreeding, which increases the risk of extinction (Frankham 1995, Bijlsma et al. 2000). Consequently, the identification of loss of genetic variability in populations and the identification of stocks and other management units have become important goals for conservation biologists.

## **Mitochondrial DNA**

Nucleic acid sequencing is a commonly used method to address genetic questions at the population or taxonomic level (Parker et al. 1998). In population genetics, it is important to choose a genetic marker characterized by high levels of intraspecific polymorphism (e.g. mitochondrial genes or variable regions of the nuclear genome such as introns or ribosomal RNA genes; Sunnucks 2000). Mitochondrial DNA (mtDNA) markers are commonly used to address population level questions (including population structure and patterns of intraspecific geographic variation) and to elucidate phylogenetic relationships between closely related animal taxa. This marker is inherited in a clonal fashion through the maternal lineage and evolves at a rate five to ten times faster than nuclear genes (Wilson et al. 1985) making it appropriate for such studies due to its relatively high rate of mutation resulting in high levels of polymorphism. Also, mtDNA is one of the most well understood regions of the animal genome and its structure is fairly well conserved across taxa. The control region (CR) is a particularly useful molecular marker because it constitutes the most rapidly evolving portion of mtDNA of mammals (e.g., see Saccone et al. 1991) thus containing hypervariable regions that may evolve four to five times faster than the entire mtDNA molecule (Brown et al. 1979; Greenberg et al., 1983). Commonly called the D-loop, the CR contains a highly variable left domain, a conserved central region, and a variable right domain in vertebrates (Awise 2004).

There have been multiple studies where mitochondrial DNA markers, and specifically the CR, have been used to answer population-level genetic questions in marine mammals. For example, a study conducted by Caballero et al. (2012) revealed that the common bottlenose dolphin (*Tursiops truncatus*) in the Caribbean included two

groups—the ‘inshore’ ecotype and ‘worldwide distributed form’ of bottlenose dolphins in Wider Caribbean waters. At the mitochondrial level, genetic differentiation between these two groups was significant and analyses of mitochondrial DNA sequences at a wider geographic level revealed three genetically differentiated population units: Puerto Rico, Cuba/Colombia/Bahamas/Mexico, and Honduras with evidence of low female-mediated gene flow among these population units.

Variation in the CR has also been correlated with geographic isolation. For example, Bickham et al. (1996) found that the Steller sea lion (*Eumetopias jubatus*) has high levels of variation in the CR illuminating patterns of macrogeographic variation. This indicated the presence of two genetically differentiated populations of Steller sea lions—a western population including rookeries from the Commander Islands in Russia and the Aleutian Islands and Gulf of Alaska in Alaska and an eastern population including rookeries from southeastern Alaska and Oregon. Phenetic analysis of the mtDNA haplotypes indicated that certain haplotype lineages were specific to either one or the other population meaning that these populations have been separated for a sufficient amount of time to allow diversification of lineages. However, the authors found the two populations are paraphyletic with respect to mtDNA, indicating that they do not trace their ancestries back to a single maternal ancestor in either case and that the populations likely diverged as a result of separation in different glacial refugia.

### **Phylogeography**

By linking together molecular data, biogeographical patterns and historical events, the study of evolutionary processes has been advanced (e.g., Avise 1994; Avise

2000; Emerson and Hewitt 2005; Knowles and Richards 2005). Statistical approaches and mathematical models allow the signature of historical and demographic processes to be determined from the analysis of DNA (Avice 1994; Avice 2000). For example, the application of the coalescence theory to sequence data makes it possible to trace the shared history of genes back into the past, to the time that they coalesce and reach a common ancestor. This theory predicts that the growth or decline in a population and the temporal scales in which they take place (i.e. ancient or recent) is recognizable in the pattern of DNA substitution amongst sequences drawn from a population (Emerson et al. 2001). Thus, it is possible to estimate population parameters within species or amongst closely related species such as migration rates, recombination, effective population sizes, etc. from gene sequences and to build a gene genealogy or tree. The shape of the tree will depend on the demographic history of the populations under study (Austerlitz et al. 1997; Wakeley and Hey 1997; Posada and Crandall 2001).

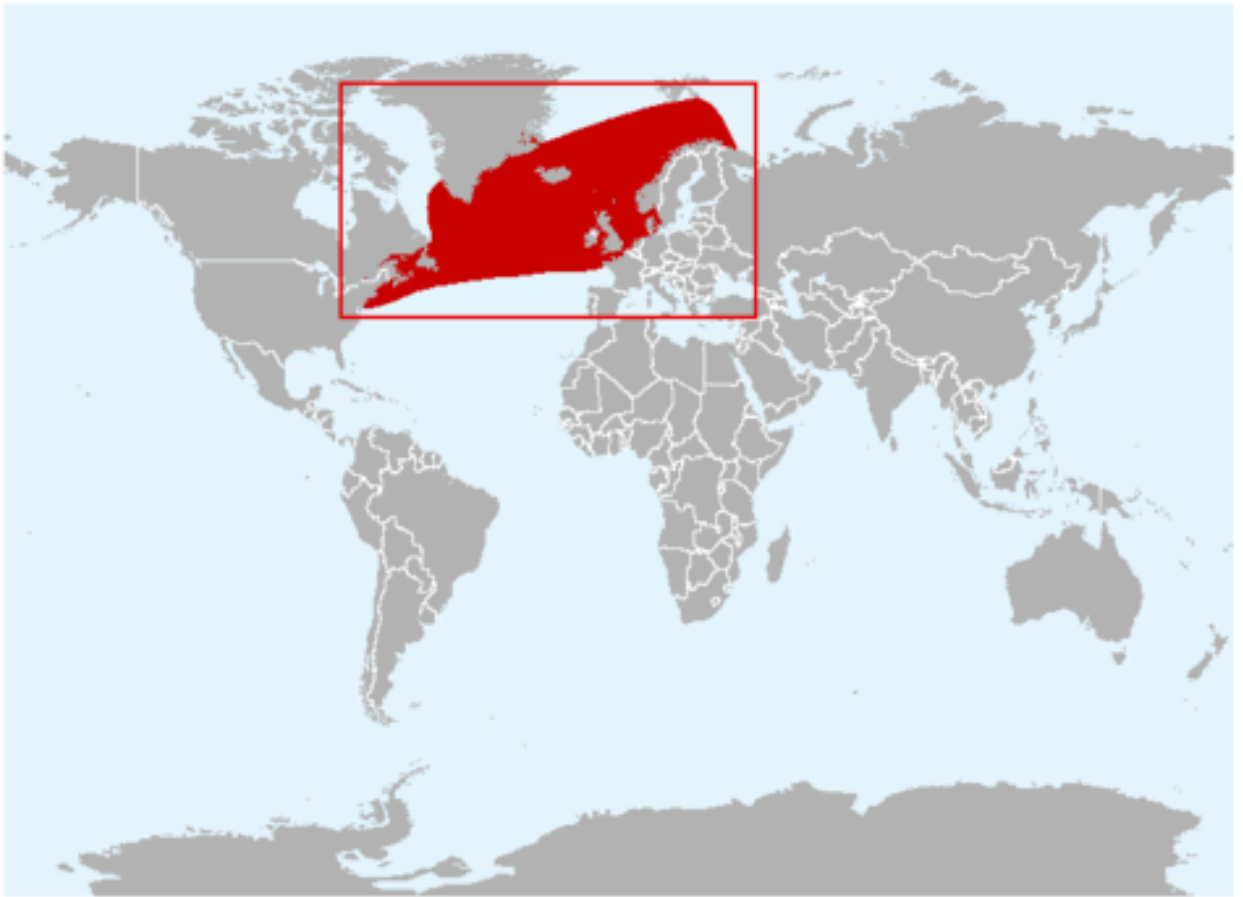
The interpretation of phylogeographic patterns within the context of evolutionary and biogeographic models is important, not only for recognizing the relationships between population structure and demographic structure and understanding the effect of past events in the actual distribution of species, but also for identifying accurate scales of management and conservation in natural populations (Avice 1994; Hoelzel 1998; Avice 2000; Arbogast and Kenagy 2001). For example, Pichler et al. (2001), combined data on demographic history and historical processes with the analysis of the mtDNA control region. They hypothesized that the radiation of the genus *Cephalorhynchus* into the Southern Hemisphere was possibly constrained by the sub-Antarctic current system,

which may have acted as a barrier to more northerly dispersal. These authors also suggest that the split of *Cephalorhynchus* into two South American species (*Cephalorhynchus eutropia* and *Cephalorhynchus commersoni*) was the result of glaciations in Tierra del Fuego isolating a population in the northern point of their range. A similar pattern of dispersion and speciation has been also suggested for the species of the genus *Lagenorhynchus* distributed in the southern hemisphere (Cassens et al. 2003; Harlin-Cognato et al. 2007).

## *LAGENORHYNCHUS ACUTUS*

### **Distribution**

The Atlantic white-sided dolphin (*Lagenorhynchus acutus*, Gray 1828) is a pelagic species, endemic to the North Atlantic, with a preference for temperate and sub-polar waters (Mikkelsen and Lund 1994; Weinrich et al. 2001). Its geographic range extends across the North Atlantic, from Cape Cod, Massachusetts to southern Greenland in the western North Atlantic, across to Svalbard and from there as far south as Brittany (France) in the eastern Atlantic Ocean (Gaskin 1992, Reeves et al. 1999; Cipriano 2009) (Figure 1). The species rarely enters the Baltic Sea (Kinze et al. 1997) and it has been seen as far south as Strait of Gibraltar (Hammond et al. 2008). In the eastern North Atlantic it is commonly distributed from Iceland and the western Barents Sea, south to the Bay of Biscay, being more abundant at 56°N than south of this latitude (Evans 1992). In the British Isles, its distribution is concentrated around the Hebrides, northern Isles and northern North Sea in waters 100-500 m deep. It also occurs regularly off western Ireland, but has not been reported frequently in the Irish Sea and is considered very rare in the southern North Sea (Evans 1992; Gaskin 1992; Reeves et al. 1999). In the western North Atlantic the species commonly inhabits waters from central West Greenland to Massachusetts and is more commonly being found as far south as North Carolina (Evans 1987; Hamazaki 2002).



**Figure 1.** Distribution of *Lagenohynchus acutus* in the North Atlantic Ocean. Map via <http://kimsmithdesigns.wordpress.com/2011/04/20/first-responders-for-stranded-marine-animals/>

### **Phylogeography**

Although the general distribution of *L. acutus* has been well studied, few studies have been published about their seasonal migration and spatial and temporal distribution in specific areas (e.g., Sergeant et al. 1980; Northridge et al. 1997; Weir et al. 2001; Hammond et al. 2002; Waring et al. 2006, 2007; MacLeod et al. 2007; Weir et al. 2007). In the western North Atlantic it has been categorized as a near-shore species commonly

reported in waters between 10-15°C and depths from 400-500 m (Reeves et al. 1999; Hamazaki 2002).

Studies on terrestrial and fresh water organisms have shown that populations distributed in the highest latitudes frequently have a lower degree of genetic diversity than species distributed in lower latitudes; i.e. the tropics (Hewitt 2001). This pattern has been attributed to climatic and environmental changes in the northern hemisphere during the ice ages, which generate the isolation of populations in refugias and their subsequent and rapid increase in population sizes due to the colonization of new, unoccupied habitats after the retreat of the ice (Stanley et al. 1996; Hewitt 1996, 1999, 2000). The effects of these processes -reduction of population sizes, colonization and expansion- in the DNA of the organisms have been well documented (Rogers and Harpending 1992; Harpending 1994; Harpending et al. 1998; Schneider and Excoffier 1999; Excoffier 2004), and the statistical theories associated with demographic expansion are now common ways to address hypotheses about the time of expansion and the effective sizes of populations before and after expansion (e.g., Hare et al. 2002; Palo 2003; Pastene et al. 2007). As reported for other species of marine mammals (e.g., Palo 2003; Palo et al. 2003; Palo and Vainola 2006; Pastene et al. 2007), it is possible that the spatial distribution of lineages, demography history and genetic diversity of *L. acutus* populations were affected by the glacial cycles in the North Atlantic. If this is so, a loss of allelic diversity will be expected in this species due to genetic drift in bottlenecked refugia, and a clear unimodal shape in the distribution of pairwise differences resulting from range expansions in warmer periods.



## **Population Structure**

Due to the lack of phenotypic differences amongst the skulls of 228 specimens of *L. acutus* from the eastern and western North Atlantic, Mikkelsen and Lund (1994) proposed the existence of a single population across its geographic range. They did not find evidence to subdivide populations into a northern and southern stock in either of the two areas studied or into the western and eastern North Atlantic. More detailed knowledge about population structure of *L. acutus* is limited (e.g., Northridge et al. 1997; Weir et al. 2001; Hammond et al. 2002; MacLeod et al. 2007; Waring et al. 2007; Weir et al. 2007). In the eastern North Atlantic population structure is poorly understood; studies about the species have been based mostly on opportunistic surveys and only a few long-term surveys (e.g., Hammond et al. 2002; Evans and Hammond 2004). In the western North Atlantic studies based mainly on sightings; strandings and incidental takes have suggested the existence of three population stocks: Gulf of Maine, Gulf of St. Lawrence and Labrador Sea (Palka et al. 1997). Evidence for a separation between the population in the southern Gulf of Maine and the Gulf of St. Lawrence population comes from a virtual absence of summer sightings along the Atlantic side of Nova Scotia. White-sided dolphins were seen frequently in Gulf of Maine waters and in waters at the mouth of the Gulf of St. Lawrence, but only a few sightings were recorded between these two regions (Waring et al. 2013).

The Gulf of Maine (Figure 2) population of white-sided dolphins is most common in continental shelf waters from Hudson Canyon (approximately 39°N) on to Georges Bank, and in the Gulf of Maine and lower Bay of Fundy. Sightings data indicate seasonal shifts in distribution (Northridge et al. 1997). During January to May, low numbers of

white-sided dolphins are found from Georges Bank to Jeffrey's Ledge (off New Hampshire), with even lower numbers south of Georges Bank, as documented by a few strandings collected on beaches of Virginia and North Carolina. From June through September, large numbers of white-sided dolphins are found from Georges Bank to the lower Bay of Fundy. From October to December, white-sided dolphins occur at intermediate densities from southern Georges Bank to southern Gulf of Maine (Payne and Heinemann 1990). Sightings south of Georges Bank, particularly around Hudson Canyon, occur year round but at low densities. The Virginia and North Carolina observations appear to represent the southern extent of the species' range during the winter months. The seasonal spatial distribution of this species appears to have been changing during the last few years (Waring et al. 2013). No published genetic studies to date have looked at the growing number of *L. acutus* found further south to determine their stock of origin.

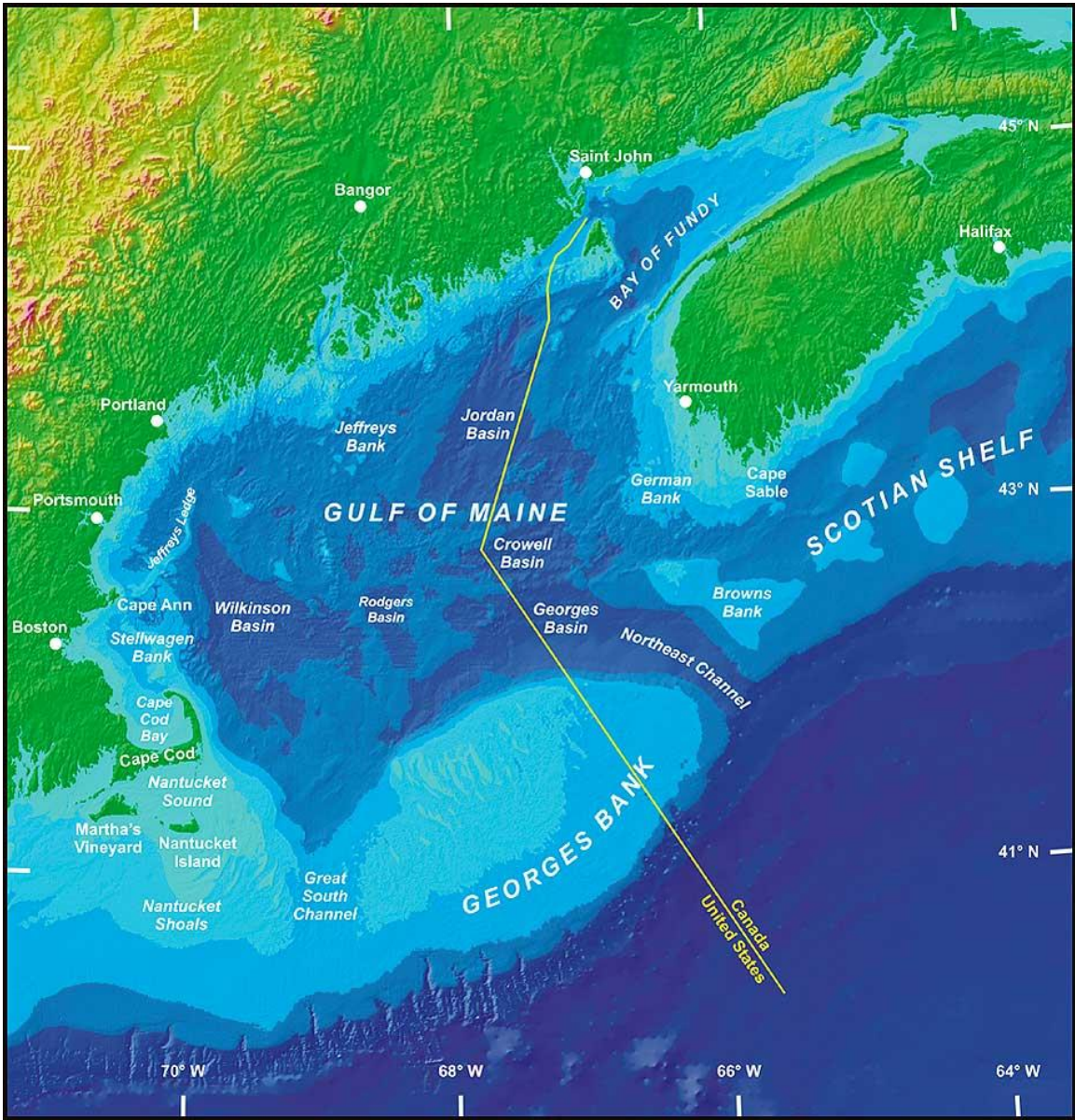


Figure 2. Map of the Gulf of Maine via [http://www.necwa.org/images/maps/map\\_gulf-maine-L.jpg](http://www.necwa.org/images/maps/map_gulf-maine-L.jpg)

### Population Size

The best abundance estimate for this species in the western North Atlantic is the result of the 2011 survey [48,819 (CV=0.61) with a minimum population estimate of 30,401] reported by Waring et al. (2013). However, because of the apparent changes in

the seasonal distribution of this species, the best available abundance estimate may come from one of the non-summer abundance surveys that will be conducted in 2011-2015. No population estimate exists for the species in the eastern North Atlantic.

### **Main threats**

On both sides of the Atlantic, *L. acutus* inhabits some of the most intensively fished waters in the world, especially over the continental shelf (Morizur et al. 1999). Mass strandings (possibly caused by interaction with pelagic trawling), high bycatch rate in fishing nets, and commercial hunting have been reported as the major threats affecting these populations (Alling and Whitehead 1987; Reeves and Leatherwood 1994; Reeves et al. 1999; Waring et al. 2006; Bogomolni et al. 2010). In addition, it is known that this species has been subjected to direct exploitation in Southwest Greenland, where the catch has been estimated as approximately 50 individuals per year (Reeves and Leatherwood 1994; Reeves et al. 1999) and in the Faeroe Islands, where annual takes can number more than 500 dolphins in the traditional drive fisheries (Bloch and Mikkelsen 2009). These historical harvests may be a threat to the population; however no accurate population size estimates are available for most of the North Atlantic as mentioned above. In addition little is known about their conservation status including effective population size, life history and stock boundaries; all of which are essential for effective management.

### **Behavior**

*L. acutus* is a gregarious species and may be found in groups of up to 1,000 individuals. However, groups of only 6 to 8 individuals are more common off of Canada and in other places along the western Atlantic. Inshore herds are also small, ranging from

about 10 to 60 animals. It seems that immature animals and newly mature males are absent from larger breeding groups, which may indicate some form of segregation among the herds (Jefferson et al. 1993; Reeves et al. 1999). *L. acutus* typically dives for less than five minutes (Cipriano, 2009). These animals are sometimes seen riding the bow waves of larger species. Mass strandings of *L. acutus* are common on northern Atlantic shores. The strandings sometimes occur in groups of 3 to 15 or more animals, although they usually occur in pairs (Jefferson et al. 1993; Carwardine, 1995). The species appears to be very nomadic but there are no data showing a set of seasonal migrations. The distribution patterns may correspond to abundance of important prey species (Klinowska, 1991).

## STUDY OBJECTIVES AND HYPOTHESES

Given this species' high mobility and pelagic distribution, it may be expected that it would show little evidence of population structure across the species range. However, various studies on other small cetacean species have suggested an influence of recent climatic cycles on the structure of re-expanding populations in the North Atlantic and North Sea (e.g. Tolley et al. 2001; Banguera-Hinestroza et al. 2010). The identification of population boundaries in *L. acutus* is complicated by the difficulties in carrying out long-term studies and the restrictions imposed by the habitat and behavior of marine species. Thus the availability of samples from stranded animal and biopsies of free living animals are an important resource of genetic material for assessing population parameters in this species using molecular markers. One of the major contributions of molecular ecology to conservation has been the evaluation of the viability of populations by detecting the partitioning of genetic diversity within and among populations (Haig 1998). An assessment of population structure with molecular markers in *L. acutus* is the best way to evaluate and provide a more comprehensive picture of its population biology, detect fragmented and vulnerable populations, and therefore allocate resources for its conservation (e.g., Caballero et al. 2012; Haig 1998).

The goals of this study are (1) to assess genetic diversity of Atlantic white-sided dolphins found along the east coast of the United States in the western North Atlantic, and (2) to identify

geographic patterns of haplotype frequency to serve as a basis of comparison by which to identify the origin of individual dolphins found in the southern part of the range. This is in order to see if this species, which is adapted to the pelagic habitat, will show panmixia across a broad geographic range or display finer scale north/south geographic isolations.

The objectives of this study are as follows:

1. Sequence the highly variable D-loop of the mtDNA control region for *L. acutus* from several geographic locations along the east coast of the United States ranging from Maine to North Carolina. Analyze sequences to test for genetic variation for this region.

Hypothesis 1: The control region in this species will be highly variable due to the large number of individuals for this species.

2. Use consensus sequences to determine if there is differentiation among populations along the east coast.

Hypothesis 2: Individuals from the northern geographic location (Maine to Connecticut) and from the southern locations (New York to North Carolina) will have the same or similar haplotypes. However, due to a recent expansion, the same or similar haplotypes in will present in the south – with the different haplotypes differing by a few base pairs only.

The null hypotheses to be tested are as follows:

Despite the large number of individuals there is little genetic variation in the species. Haplotypes are shared across population sites, and there is no evidence of a correlation between geographic distance and genetic distance between sequences. The southern individuals have either not been separated long enough for the mtDNA marker

to resolve population structure at this fine level of detail, or the groups are acting as a single interbreeding population.



## **MATERIALS AND METHODS**

### **Sample Collection**

Tissue samples for the Atlantic white-sided dolphin were collected along the east coast of the United States in the western North Atlantic range for the species (N=119). Samples from Connecticut to Maine represent the northern range (N=95) and samples from New York to North Carolina represent the expanded southern part of the range (N=24). All samples are from recent collections; mostly from the 1990s or 2000s. Tissue samples were acquired from stranded beachcast animals, bycatch associated with fisheries or through the use of remote skin biopsy sampling. Samples were obtained through the Smithsonian Institution's specimen collection and donated by The National Oceanic and Atmospheric Administration (NOAA). All samples were either stored frozen or in a 20% DMSO/saturated NaCl solution.

### **DNA Extraction**

DNA extraction was performed in the pre-PCR room at the Smithsonian Institution's Laboratory for Analytical Biology (L.A.B.) using the DNeasy Blood and Tissue extraction kit (Qiagen) according to manufacturer protocols with an additional 1 minute spin at 6000rpm before the removal of supernatant due to the presence of undigested tissue. For each set of extractions a blank sample was tested to verify that no contamination occurred thus ensuring the quality of the extracted products. Extracted DNA was qualified via electrophoresis on a 1.5% SeaKem LE agarose gel (Lonza) stained with GelRed (Biotium). This process allows one to confirm the

presence of high molecular weight DNA; if the DNA were highly degraded, smaller fragments would migrate farther through the gel than intact genomic DNA. It is important to note that one cannot discern between *L. acutus* DNA or other DNA using this process, so it is not useful for comparing samples yield or specificity. Additionally, DNA was quantified using an Epoch microplate spectrophotometer (BioTek). Most extractions were successful the first time (as determined by visualization by gel electrophoresis, measurements from spectrophotometer and successful PCRs), but a small subset of samples were re-extracted with the above mentioned method in attempt to improve yield, verify initial results or eliminate contamination. Using results from the Epoch microplate spectrophotometer, all applicable samples were diluted with DEPC water to a concentration of 25 ng/ $\mu$ L in a 25 $\mu$ L solution. Samples which tested at levels of 50ng/mL or less were not diluted. The stock extraction DNA was then stored at -80 °C and subsamples stored in the refrigerator at 0°C until use.

### **DNA Amplification**

For this research, a portion of the mtDNA genome known as the control region (CR), or D-loop was selected. This marker was selected due to its rapid rate of mutation relative to nuclear DNA. Studies of the mtDNA control region have been useful in tracking female gene flow and identifying population substructure (Lamont et al. 1996, Stanley et al. 1996, Burg et al. 1999, O'Corry-Crowe et al. 2003). The CR of mtDNA is a non-protein coding region that is highly variable, making it a good marker for detecting differences below the species level such as for populations and subpopulations (Brown et al.1978). Universal primers developed for the 5' end of the highly variable CR (a region of about 485 base pairs) by Rosel et al. (1999b, 1994 respectively) were utilized. These primers are commercially available and are named L15824 (forward primer, sequence 5'-CCTCACTCCTCCCTAAGACT-3') and H16498 (reverse primer, sequence 5'-CCTGAAGTAAGAACCAGATG-3').

Polymerase chain reaction (PCR) was performed in the post-PCR room at L.A.B. PCR products were again qualified using gel electrophoresis on a 1.5% SeaKem LE agarose gel (Lonza) stained with GelRed (Biotium); quality products were cleaned up with the Sephadex protocol and sequenced in house using ABI sequencers. If the sex of the animal was unknown from field examination, it was genetically determined in the lab using ZFXY and SRY-specific primers (Rosel 2003).

Before attempting a mass PCR, a test PCR was conducted using standard protocols and the L15824 and H16498 primers. No attempt was made to optimize the reaction, but the success of this reaction (indicated by the presence/absence of PCR product) verified that the initial protocol worked in a new laboratory environment. Next, PCR conditions were optimized to maximize product in a large PCR. Optimal PCR conditions varied depending on the sample; however, the PCR conditions that were successful for most samples were as follows: (1) PCRs were performed in a total volume of 25 $\mu$ L; (2) mixes contained 18.67 $\mu$ L DEPC water, 2.50 $\mu$ L 10X buffer solution, 0.75 $\mu$ L MgCl<sub>2</sub> solution, 0.38 $\mu$ L dNTPs, 0.75 $\mu$ L forward primer (10 $\mu$ M), 0.75 $\mu$ L reverse primer (10 $\mu$ M), 0.20 $\mu$ L Taq polymerase (Bioline), and 1 $\mu$ L (25ng/  $\mu$ L) DNA; (3) cycling conditions were: 1 cycle at 95°C for 30s; 30 cycles at 95°C for 30s, 55°C for 30s, and 72°C for 30s, followed by 1 cycle at 72°C for 7 min. PCR products were visualized via agarose gel electrophoresis using a 1.5% SeaKem LE agarose gel (Lonza) stained with GelRed (Biotium).

## **Optimizing PCR Reaction**

For the samples that failed to amplify under standard conditions, I increased the amount of DNA added to the reaction and/or added or increased the proportion of Bovine Serum Albumin (BSA) used. BSA has been shown to relieve PCR inhibition for some known inhibitors (Kreader 1996). Adding and increasing the amount of BSA (New England BioLabs) used resulted in amplification of one of the problem samples. Four samples failed to produce any product. It is assumed that these samples either contained PCR inhibitors that prevented successful amplification, or the DNA extracted from the tissue samples was highly degraded.

Partway through the PCRs, pipettes were calibrated and a new bulb was installed on the transilluminator within a week. Although it is unsure if these events were related, all subsequent PCR products using the standard protocol appeared to be over amplified or showed non-specific amplification when visualized via gel electrophoresis. The PCR was then optimized by diluting the 25 ng/ $\mu$ L working stocks with 1:10 serial dilution increments, increasing the annealing temperature, and switching to new type of Taq polymerase (GoTaq HotStart Colorless Master Mix). The PCR conditions that were successful after optimization were as follows: (1) PCRs were performed in a total volume of 25 $\mu$ L; (2) mixes contained 13.00 $\mu$ L DEPC water, 10.00 $\mu$ L GoTaq, 0.50 $\mu$ L forward primer (10 $\mu$ M), 0.50 $\mu$ L reverse primer (10 $\mu$ M), and 1 $\mu$ L DNA (of varying concentration depending on previous PCR reactions visual result); (3) cycling conditions were: 1 cycle at 95°C for 30s; 30 cycles at 95°C for 30s, 58°C for 30s, and 72°C for 30s, followed by 1 cycle at 72°C for 7:00min. PCR products were again visualized via agarose gel electrophoresis to ensure quality. These changes successfully amplified all twenty problem samples.

## **DNA Sequencing**

All successful products were purified using ExoSAP-IT (Affymetrix USB). The standard protocol was altered by using 1 $\mu$ L of a 1:1 dilution of the Exo-SAP-IT with 5 $\mu$ L PCR product. The mixture was incubated at 37°C for 30:00min followed by 30:00min at 80°C. Once purification

was completed, PCR products were sequenced in both forward and reverse directions to provide double coverage and to confirm the accuracy of the sequence data. Cycle sequencing was performed under the following conditions: (1) PCRs were performed in a total volume of 10 $\mu$ L; (2) mixes contained 4.68 $\mu$ L DEPC water, 2.00 $\mu$ L Buffer (ABI, 5x), 0.32 $\mu$ L forward or reverse primer (10 $\mu$ M), 1.00 $\mu$ L BigDye 3.1 (ABI), and 2 $\mu$ L DNA; (3) cycling conditions were: 1 cycle at 96°C for 1:00min; 25 cycles at 96°C for 10s, 50°C for 5s, and 60°C for 4:00min. After cycle sequencing, DNA was then cleaned with GE Healthcare G-50 Fine Sephadex using the standard protocol and submitted for in house sequencing on either the ABI 3730 or ABI 3130 machines.

Once the sequences were made available online, I downloaded and edited fragments using Sequencher® (Gene Codes Corporation, Version 5.1). Using this program, I checked the quality of sequences, and corrected possible mistakes made during base calling. Forward and reverse sequences were aligned to create a consensus sequence. The edited data were then compared to the sequences in NCBI's sequence database via an online BLASTn search (Altschul *et al.* 1999).

## **Data Analysis**

### **Sequence Editing**

Consensus sequences were exported and aligned using the Clustal W algorithm in Mega v6.06 (Kumar *et al.* 2001).

### **Measures of Genetic Diversity**

The extent of genetic variation in the control region was assessed by examining the number of haplotypes (h), haplotype (gene) diversity (Hd) (Nei 1987), nucleotide diversity ( $\pi$ ) (Nei 1987), and estimating the number of polymorphic sites (S) using DnaSP v5.10.01 (Librado and Rozas 2009). Genetic diversity, also called haplotypic diversity, is defined as the probability that two randomly chosen haplotypes are different

in the sample. Nucleotide diversity is defined as the probability that two randomly chosen homologous nucleotide sites are different. DnaSP was also used to define unique haplotypes which were imported into Mega v6.06 (Kumar *et al.* 2001). This software was used to create a matrix of the number of pairwise differences among haplotypes. These metrics were calculated for each sampling location separately and compared to metrics reported in Banguera-Hintroza *et al.* (2014).

### **Genetic Structure**

The distribution of nucleotide diversity was measured using an Analysis of Molecular Variance (AMOVA) as implemented in Arlequin v 3.5.1.2 (Excoffier and Lischer 2010). This analysis is based on analyses of variance of gene frequencies, and it takes into account the number of mutations among molecular haplotypes (Excoffier *et al.* 2007). Sequences were grouped by location to test for population structure (testing for significant sequence diversity between regions). Significant differences in haplotype frequencies between the two regions were quantified by using the  $F_{ST}$  index (Wright 1951, Excoffier *et al.* 1992, Goudet *et al.* 1996).

### **Mismatch Distribution Analysis and Neutrality tests**

Mismatch distribution and neutrality were tested using DnaSP v5.10.01 (Librado and Rozas 2009). The distribution of the number of observed differences between pairs of DNA sequences (mismatch distribution; Roger and Harpending 1992) was used as an assessment of demographic history of the population. Sudden demographic expansion usually leads to unimodal shapes in the distributions of pairwise differences, while

multimodal shapes are frequently associated with populations that have been stable over long periods of time (Rogers and Harpending 1992).

Population growth frequently has an effect on the distribution of several test statistics of neutrality (Sano and Tachida 2005). In this study, Fu's test (Fu 1997) and Tajima's D (Tajima 1989) were used to evaluate the demographic history of *L. acutus* populations. Fu's test (Fu 1997), which is based on the infinite-site model without recombination, is especially useful to test for an excess of rare alleles in short DNA sequences. This statistic is very sensitive to population demographic expansion, which leads to large negative F values. In this test a P value of 0.02 is considered significant. Tajima's D-statistic (Tajima 1989) also assumes an infinite-site mutation model (each mutation will occur in a new position), and it compares two measures of divergence based on the number of segregating sites ( $\theta$ ) and the average number of nucleotide differences ( $\pi$ ) to test whether the region is neutral or under selection and whether or not the population is in equilibrium. Positive values of Tajima's D ( $\theta < \pi$ ) are indicative of either balancing selection or admixture of two genetically different populations (Pichler 2002); whereas negative values suggest a selective sweep or sudden expansion. Significant D values are often related to factors other than selection such as population bottlenecks and subsequent expansion or heterogeneity of mutation rates (Excoffier et al. 2007). The significance of Tajima's D was determined by generating 1,000 random samples under the assumption of selective neutrality with a coalescent simulation algorithm (Hudson 1990). Mismatch distributions were run with 1,000 replicates for the parametric bootstrap.

**Haplotype network**

The genealogical relationships among haplotypes were visualized in a parsimony based network using a median-joining algorithm in Network version 4.6.1.2 (Bandelt et al. 1999). Including unknown individuals in the network allowed us to visualize where haplotypes are most likely to have originated. Maximum likelihood and maximum parsimony trees using the Tamura and Nei substitution model (Tamura and Nei 1993) were constructed to estimate phylogenetic relationships among haplotypes using MEGA v6.06.

**Spatial Temporal Analysis**

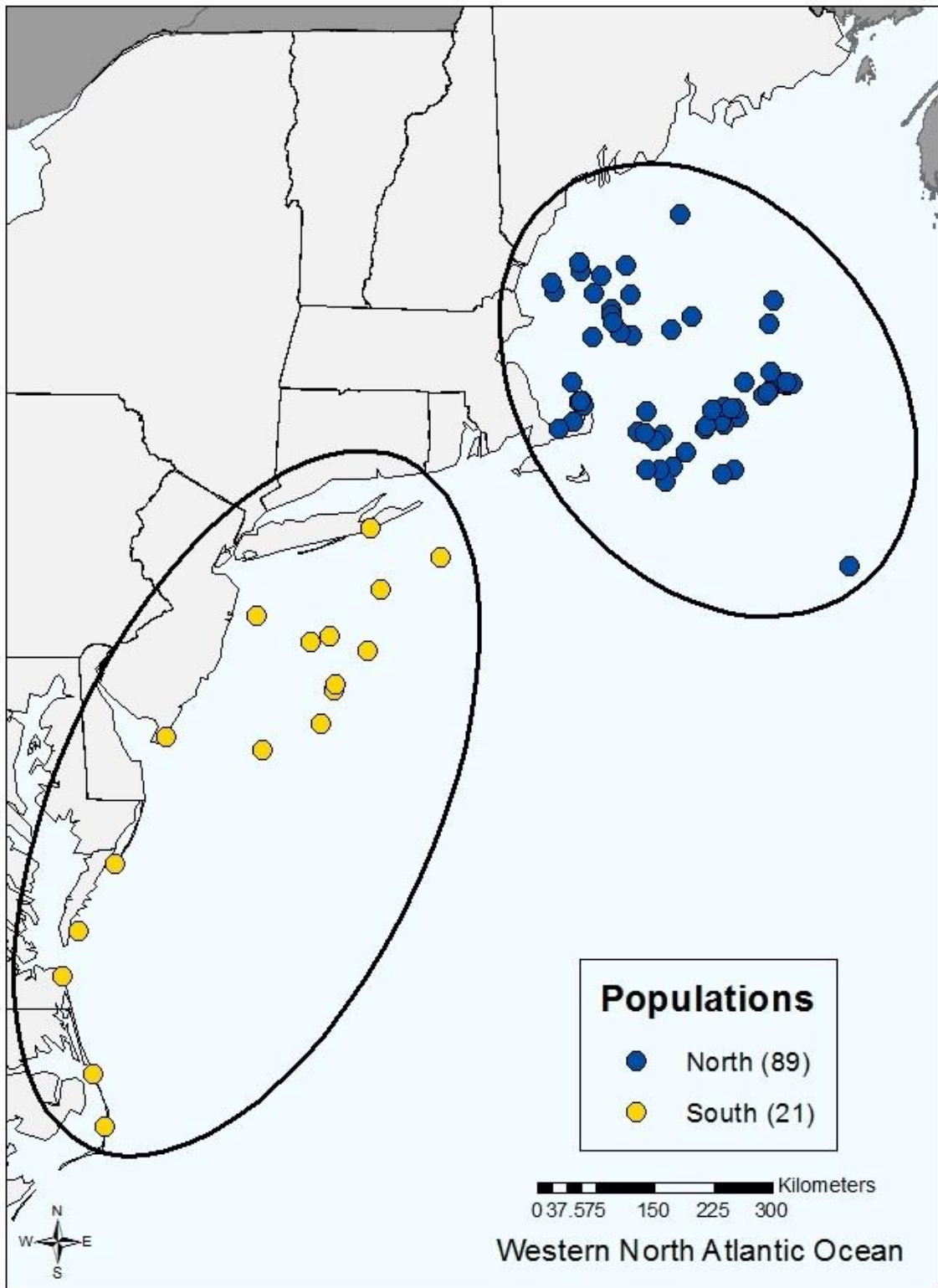
The relationships between time of year and location collected were visualized using ArcMap 10.2 (ESRI). By combining a sample's geographic location with the time of year the sample was collected, any patterns and possible correlation in the movements of the population could be investigated.



## RESULTS

### **Genetic Variation at the mtDNA Control Region**

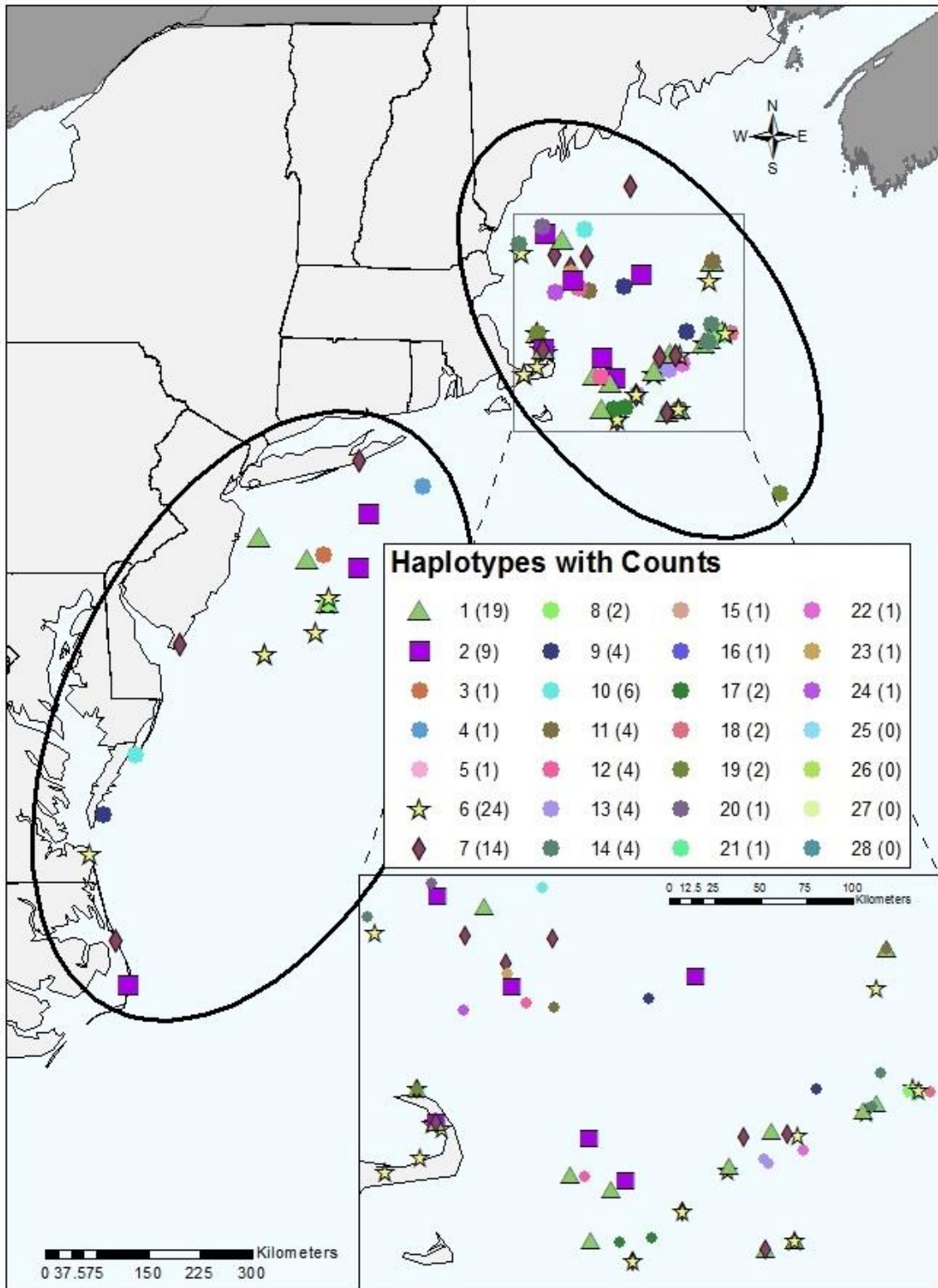
A total of 115 out of 119 collected tissue samples were successfully amplified and sequenced, i.e., a success rate of 96.64%. Three samples did not amplify successfully and one sample produced a short, low-quality sequence. All sequences were compared with NCBI's database using an online BLASTn search (Altschul et al. 1990). Three sequences were not included in subsequent analyses because the results of the BLASTn search suggested that the samples were likely misidentified or substantially contaminated, and were in fact a different species (*Phocoena phocoena*, *Lagenorhynchus albirostris*, and *Tursiops truncatus* respectively). All other sequences aligned with previously published sequences from *L. acutus*, eliminating the possibility of contamination. Two of these sequences were omitted from subsequent analysis; one due to heteroplasmy and the other to lack of confirmed location data. The final alignment contained 110 sequences of 485 base pairs (bp) in length. Samples were initially divided into two geographic zones in the Western North Atlantic: North (N=89) and South (N=21). Population locations are illustrated in Figure 3.



**Figure 3.** North and South sampling location sites. Dots indicate individuals/sampling locations.

### **Measures of Genetic Diversity**

A total of 24 total haplotypes (h) were found among the 110 samples sequenced. Of the 485 total base pairs, 25 sites were polymorphic (S) representing 25 mutations, and 18 were parsimony informative. The average number of nucleotide differences between haplotypes (k) was 2.958. Three unique haplotypes were found in the South and 14 unique haplotypes were found in the North (see Figure 4 and Table 1 below; illustration in the network tree shown in Figure 7). The remaining seven haplotypes were found in both the North and the South.



**Figure 4.** Haplotypes with counts by locality. Symbols indicate individuals/sampling locations.

Haplotypes	Nucleotide Position																				Location, # of samples with each haplotype							
	1	1	1	1	1	1	1	1	2	2	3	3	3	3	3	3	3	3	3	4	4	4	N	South	North			
	2	2	4	5	6	7	8	9	9	2	6	0	0	2	2	4	4	4	5	6	6	7				1	3	5
Hap 01	T	T	T	T	C	A	G	T	C	C	T	C	T	A	C	T	T	T	C	T	G	A	C	T	A	19	3	16
Hap 02	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	9	3	6	
Hap 03	.	C	.	.	.	.	.	.	.	T	C	.	.	T	.	.	.	.	.	.	.	.	.	.	1	1	0	
Hap 04	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	1	1	0	
Hap 05	.	.	.	.	G	.	C	.	T	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	1	1	0	
Hap 06	.	.	.	.	.	.	.	T	T	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	24	6	18	
Hap 07	.	.	C	.	G	.	.	T	.	.	.	.	T	.	C	.	.	.	.	.	.	.	.	.	14	3	11	
Hap 08	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	2	1	1	
Hap 09	.	.	.	.	G	.	.	T	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	4	1	3	
Hap 10	.	.	C	.	G	A	.	T	.	.	.	.	T	.	C	.	.	.	.	.	.	.	.	.	6	1	5	
Hap 11	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	G	.	4	0	4	
Hap 12	.	C	.	.	.	.	.	T	C	.	.	.	T	.	.	.	.	.	.	.	.	C	.	.	4	0	4	
Hap 13	.	.	.	.	G	.	C	T	.	.	.	.	T	.	.	.	.	.	G	.	.	.	.	.	4	0	4	
Hap 14	C	.	.	.	G	.	.	T	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	4	0	4	
Hap 15	.	.	.	T	G	.	.	T	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	1	0	1	
Hap 16	.	.	.	.	G	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	0	1	
Hap 17	C	.	.	.	G	.	.	T	.	.	.	.	T	.	.	.	.	A	.	.	.	.	.	.	2	0	2	
Hap 18	.	.	.	.	G	.	.	T	.	.	.	.	T	.	.	T	.	.	.	.	G	.	.	.	2	0	2	
Hap 19	.	.	.	.	G	.	.	T	.	.	.	.	T	.	C	.	.	.	.	.	.	.	.	.	2	0	2	
Hap 20	.	.	.	.	G	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	0	1	
Hap 21	.	.	.	.	G	.	.	T	.	.	.	.	T	.	.	C	.	T	.	.	.	.	.	.	1	0	1	
Hap 22	.	C	.	.	.	.	.	T	C	.	.	.	T	C	.	.	.	.	.	.	.	.	.	.	1	0	1	
Hap 23	.	.	.	.	G	.	.	T	.	G	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	0	1	
Hap 24	.	.	.	.	.	.	.	T	T	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	1	0	1	
																						# haps at each location						
N = The total number of samples with each haplotype																						110	21	89				

**Table 1.** Sequence variation in the mitochondrial control region.

Overall haplotypic (gene) diversity ( $H_d$ ), which is a measure of the number and frequency of different haplotypes, was  $0.896 \pm 0.015$ . Overall nucleotide diversity ( $\pi$ ), which is the average number of nucleotide differences per site between sequences, was  $0.00706 \pm 0.00346$ .

Pairwise distances were calculated between haplotypes in percent of sequence divergence, with the Kimura 2-parameter correction (allowing for different substitution rates for transitions and transversions (Kimura 1980). Percent variation between

haplotype sequences ranged from 0% to 1.46% (Table 2). Pairwise distances were also calculated in the form of the number of nucleotide differences between sequences.

Haplotypes differed by 1 to 7 base pairs (Table 3).

	Hap_1	Hap_2	Hap_3	Hap_4	Hap_5	Hap_6	Hap_7	Hap_8	Hap_9	Hap_10	Hap_11	Hap_12	Hap_13	Hap_14	Hap_15	Hap_16	Hap_17	Hap_18	Hap_19	Hap_20	Hap_21	Hap_22	Hap_23	Hap_24	
Hap_1																									
Hap_2	0.41%																								
Hap_3	0.83%	1.25%																							
Hap_4	0.21%	0.21%	1.04%																						
Hap_5	0.83%	1.25%	0.83%	1.04%																					
Hap_6	0.62%	1.04%	0.62%	0.83%	0.62%																				
Hap_7	1.04%	1.04%	1.04%	0.83%	0.62%	0.83%																			
Hap_8	0.41%	0.83%	0.83%	0.62%	0.83%	0.62%	1.04%																		
Hap_9	0.62%	1.04%	0.62%	0.83%	0.21%	0.41%	0.41%	0.62%																	
Hap_10	1.25%	1.25%	1.25%	1.04%	0.83%	1.04%	0.21%	1.25%	0.62%																
Hap_11	0.41%	0.41%	1.25%	0.21%	1.25%	1.04%	1.04%	0.83%	1.04%	1.25%															
Hap_12	1.04%	1.46%	0.21%	1.25%	1.04%	0.83%	1.25%	1.04%	0.83%	1.46%	1.46%														
Hap_13	1.04%	1.46%	1.04%	1.25%	0.21%	0.83%	0.83%	1.04%	0.41%	1.04%	1.46%	1.25%													
Hap_14	0.83%	1.25%	0.83%	1.04%	0.41%	0.62%	0.62%	0.83%	0.21%	0.83%	1.25%	1.04%	0.62%												
Hap_15	0.83%	1.25%	0.83%	1.04%	0.41%	0.62%	0.62%	0.83%	0.21%	0.83%	1.25%	1.04%	0.62%	0.41%											
Hap_16	0.62%	1.04%	1.04%	0.83%	0.62%	0.83%	0.83%	0.62%	0.41%	1.04%	1.04%	1.25%	0.83%	0.62%	0.62%										
Hap_17	1.04%	1.46%	1.04%	1.25%	0.62%	0.83%	0.83%	0.62%	0.41%	1.04%	1.46%	1.25%	0.83%	0.21%	0.62%	0.83%									
Hap_18	1.04%	1.46%	1.04%	1.25%	0.62%	0.83%	0.83%	1.04%	0.41%	1.04%	1.04%	1.25%	0.83%	0.62%	0.83%	0.83%									
Hap_19	0.83%	1.25%	0.83%	1.04%	0.41%	0.62%	0.62%	0.83%	0.21%	0.83%	1.25%	1.04%	0.62%	0.41%	0.62%	0.62%	0.62%								
Hap_20	0.41%	0.83%	0.83%	0.62%	0.41%	0.62%	0.62%	0.41%	0.21%	0.83%	1.04%	0.62%	0.41%	0.41%	0.21%	0.62%	0.62%	0.41%							
Hap_21	1.04%	1.46%	1.04%	1.25%	0.62%	0.83%	0.83%	1.04%	0.41%	1.04%	1.46%	1.25%	0.83%	0.62%	0.83%	0.83%	0.62%	0.62%	0.62%						
Hap_22	1.04%	1.46%	0.21%	1.25%	1.04%	0.83%	1.25%	1.04%	0.83%	1.46%	1.46%	1.25%	0.41%	1.25%	1.04%	1.25%	1.25%	1.04%	1.04%	1.25%					
Hap_23	0.62%	1.04%	1.04%	0.83%	0.62%	0.83%	0.83%	0.62%	0.41%	1.04%	1.04%	1.25%	0.83%	0.62%	0.41%	0.83%	0.83%	0.62%	0.21%	0.83%	1.25%				
Hap_24	0.62%	1.04%	0.62%	0.83%	0.62%	0.41%	0.83%	0.62%	0.41%	1.04%	1.04%	0.83%	0.62%	0.62%	0.83%	0.83%	0.62%	0.62%	0.83%	0.62%	0.83%	0.83%	0.83%	0.83%	0.83%

**Table 1.** Pairwise distance estimates of evolutionary divergence between 24 identified haplotypes, using the Tamura-Nei model of evolution. Estimates are in the form of % of sequence divergence. All positions containing gaps were eliminated from calculations.

	Hap_1	Hap_2	Hap_3	Hap_4	Hap_5	Hap_6	Hap_7	Hap_8	Hap_9	Hap_10	Hap_11	Hap_12	Hap_13	Hap_14	Hap_15	Hap_16	Hap_17	Hap_18	Hap_19	Hap_20	Hap_21	Hap_22	Hap_23	Hap_24
Hap_1	0.00																							
Hap_2	2.00	0.00																						
Hap_3	4.00	6.00	0.00																					
Hap_4	1.00	1.00	5.00	0.00																				
Hap_5	4.00	6.00	4.00	5.00	0.00																			
Hap_6	3.00	5.00	3.00	4.00	3.00	0.00																		
Hap_7	5.00	5.00	5.00	4.00	3.00	4.00	0.00																	
Hap_8	2.00	4.00	4.00	3.00	4.00	3.00	5.00	0.00																
Hap_9	3.00	5.00	3.00	4.00	1.00	2.00	2.00	3.00	0.00															
Hap_10	6.00	6.00	6.00	5.00	4.00	5.00	1.00	6.00	3.00	0.00														
Hap_11	2.00	2.00	6.00	1.00	6.00	5.00	5.00	4.00	5.00	6.00	0.00													
Hap_12	5.00	7.00	1.00	6.00	5.00	4.00	6.00	5.00	4.00	7.00	7.00	0.00												
Hap_13	5.00	7.00	5.00	6.00	1.00	4.00	4.00	5.00	2.00	5.00	7.00	6.00	0.00											
Hap_14	4.00	6.00	4.00	5.00	2.00	3.00	3.00	4.00	1.00	4.00	6.00	5.00	3.00	0.00										
Hap_15	4.00	6.00	4.00	5.00	2.00	3.00	3.00	4.00	1.00	4.00	6.00	5.00	3.00	2.00	0.00									
Hap_16	3.00	5.00	5.00	4.00	3.00	4.00	3.00	2.00	5.00	5.00	6.00	4.00	3.00	3.00	3.00	0.00								
Hap_17	5.00	7.00	5.00	6.00	3.00	4.00	4.00	3.00	2.00	5.00	7.00	6.00	4.00	1.00	3.00	4.00	0.00							
Hap_18	5.00	7.00	5.00	6.00	3.00	4.00	4.00	5.00	2.00	5.00	5.00	6.00	4.00	3.00	3.00	4.00	0.00							
Hap_19	4.00	6.00	4.00	5.00	2.00	3.00	3.00	4.00	1.00	4.00	6.00	5.00	3.00	2.00	2.00	3.00	3.00	0.00						
Hap_20	2.00	4.00	4.00	3.00	2.00	3.00	3.00	2.00	1.00	4.00	4.00	5.00	3.00	2.00	2.00	1.00	3.00	2.00	0.00					
Hap_21	5.00	7.00	5.00	6.00	3.00	4.00	4.00	5.00	2.00	5.00	7.00	6.00	4.00	3.00	3.00	4.00	4.00	3.00	0.00					
Hap_22	5.00	7.00	1.00	6.00	5.00	4.00	6.00	5.00	4.00	7.00	7.00	2.00	6.00	5.00	5.00	6.00	4.00	3.00	5.00	0.00				
Hap_23	3.00	5.00	5.00	4.00	3.00	4.00	4.00	3.00	2.00	5.00	5.00	6.00	4.00	3.00	3.00	2.00	4.00	4.00	3.00	1.00	4.00	6.00	0.00	
Hap_24	3.00	5.00	3.00	4.00	3.00	2.00	4.00	3.00	2.00	5.00	5.00	4.00	4.00	3.00	3.00	4.00	4.00	3.00	3.00	3.00	4.00	4.00	4.00	0.00

**Table 2.** Estimates of evolutionary divergence between sequences. The number of base pair differences are shown. All positions containing gaps were eliminated from the analysis.

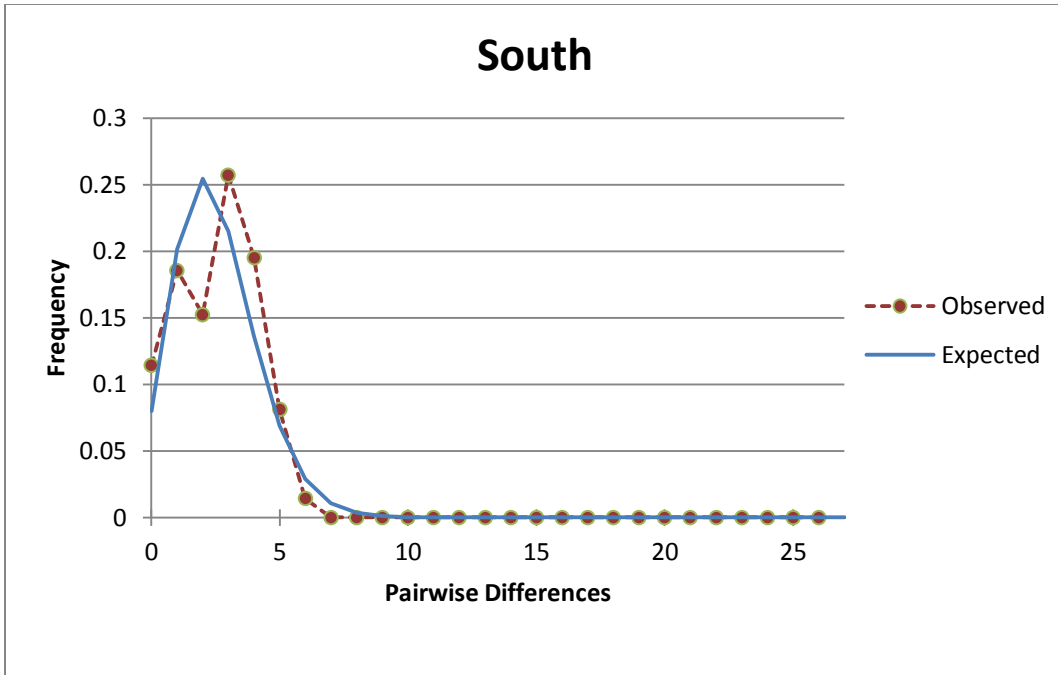


### **Genetic Structure**

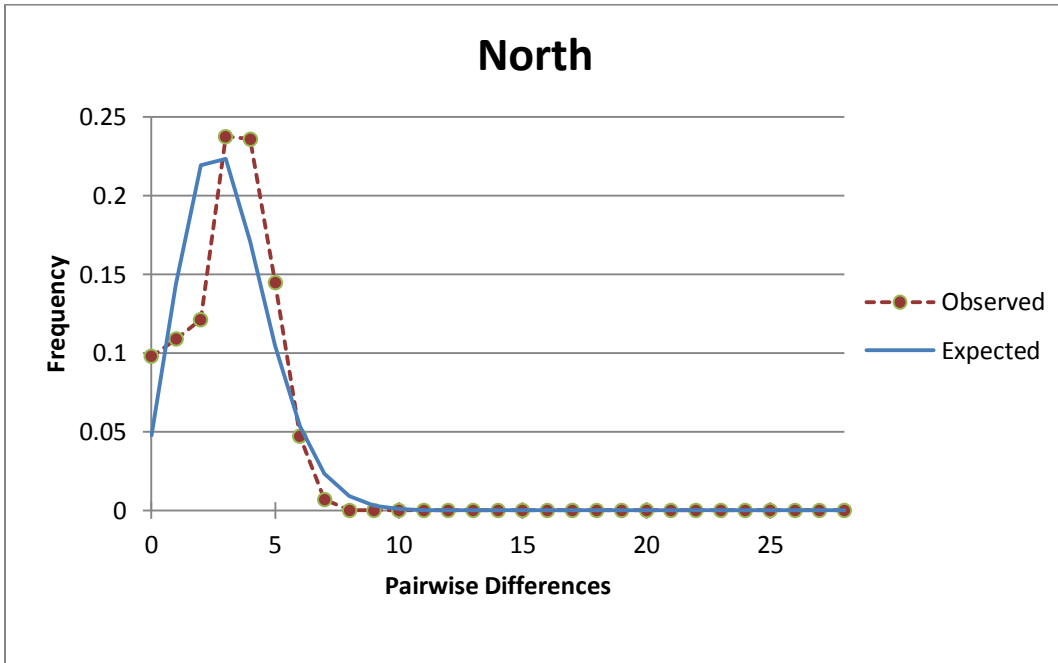
Population structure was assessed assuming *a priori* populations (region = population). An Analysis of Molecular Variance (AMOVA) - conducted in Arlequin, using conventional F-statistics from haplotype frequencies - estimated that 100% of the genetic variation could be explained as a result of the differences within populations:  $F_{ST} = -0.00697$  ( $P = 0.55034 \pm 0.01716$ ). *P* values were calculated based on a null distribution created from 1,023 permutations (random shuffling of individuals across locations). This  $F_{ST}$  value shows that there is little genetic differentiation between the North and the South.

### **Mismatch Distribution Analysis and Neutrality Tests**

The mismatch distributions show a clear unimodal shape in both populations (Figures 5 and 6). The variance (mean SSD =  $0.00080 \pm 0.24042$ ) and the small, non-significant values of the raggedness index (mean  $r = 0.00401 \pm 0.20506$ ) suggested that the curves did not differ significantly from that expected under a model of sudden expansion.



**Figure 5.** Mismatch distribution in the South.

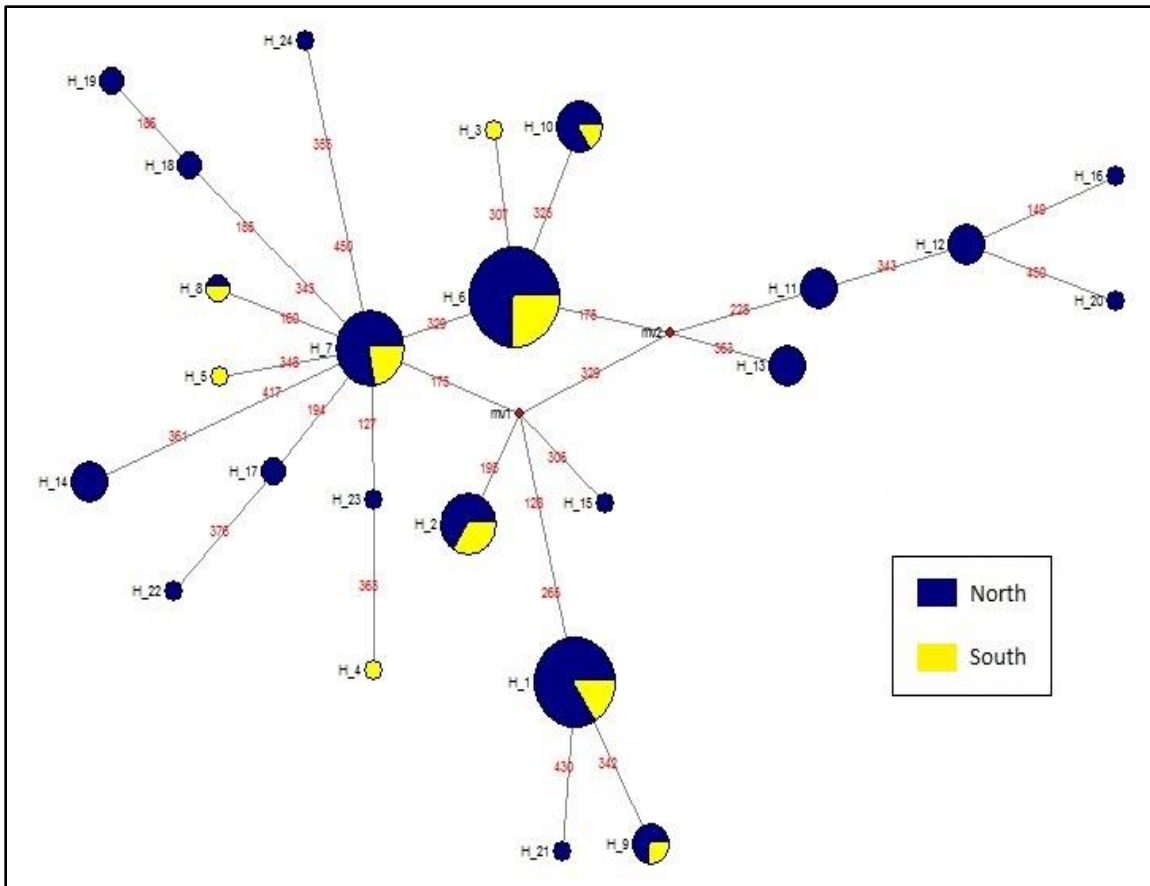


**Figure 6.** Mismatch distribution in the North.

This sudden expansion was also corroborated by the negative and significant values of Tajima's D for the South (-0.85247,  $P > 0.22800$ ) and the North (-1.12246,  $P > 0.11100$ ). A negative value of Tajima's D indicates an excess of low-frequency polymorphisms relative to the expectation under the neutral theory model (equilibrium between mutation and genetic drift). Fu's statistics showed large negative and highly significant values in both populations; -26.66145,  $P > 0.00000$  for the South and -26.39417,  $P > 0.00000$  for the North. When the two regions were combined into one large population, the results were the same.

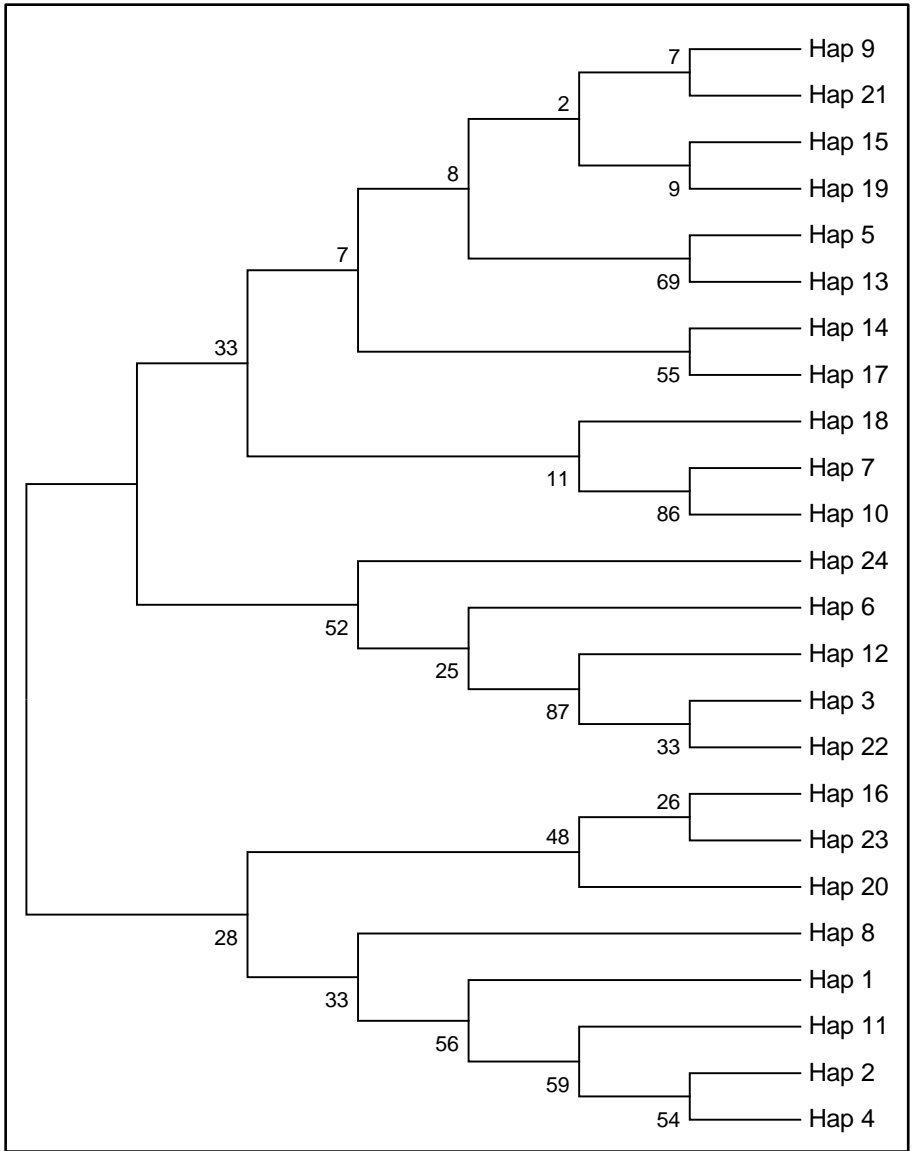
### **Haplotype Network**

The median-joining (MJ) haplotype network revealed three main haplotypes: Haplotype 1 (n = 19), Haplotype 6 (n = 24), and Haplotype 7 (n = 14). There are 21 additional satellite haplotypes of low frequency (Figure 7). The trunk of this network is made up of four haplotypes: two of which are missing from this study (mv1 and mv2) as well as Haplotypes 6 and 7; remaining haplotypes radiate out from these core four. The star-like shape of the MJ network may be indicative of one or more sudden recent population expansions (Lorenzo-Carballa et al. 2012), further supporting the above results.

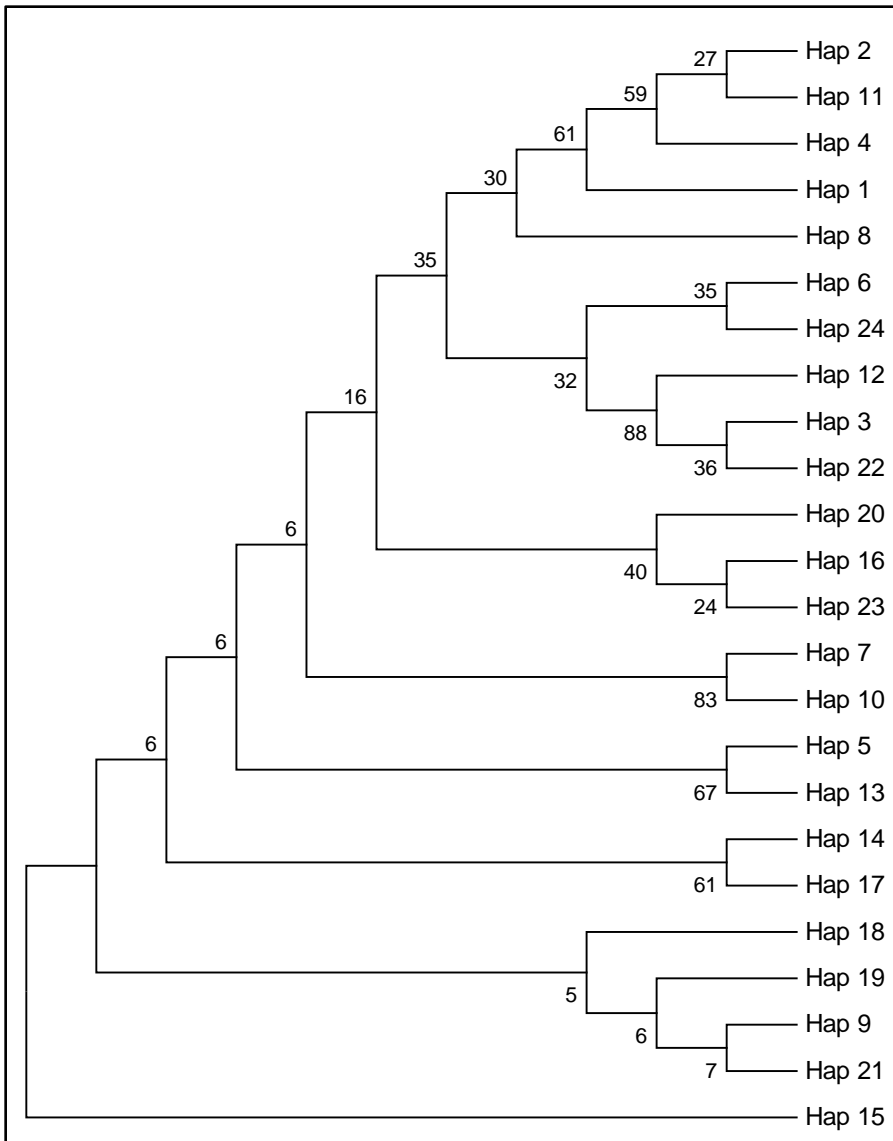


**Figure 7.** Median-joining haplotype network. Circle sizes are proportional to the frequency of each haplotype. The nucleotide position of each mutation between haplotypes is shown in red.

Genealogical relationships between haplotypes were estimated using maximum likelihood (ML) assuming the General Time Reversal model of molecular evolution with a uniform mutation rate at all sites. The nearest neighbor interchange heuristic algorithm was used (Figure 8). The relationships between haplotypes were also estimated using maximum parsimony (MP), using a subtree-pruning-regrafting (SPR) search method (Figure 9). For both trees, 500 bootstrap replicates were run.



**Figure 8.** Maximum likelihood tree depicting genealogical relationships among the 24 haplotypes of *Lagenorhynchus acutus* samples. Bootstrap values are shown above and below nodes.



**Figure 9.** Maximum parsimony tree depicting evolutionary relationships of the 24 haplotypes of *Lagenorhynchus acutus* samples. Bootstrap values are shown above and below nodes.

The two trees varied greatly in their topologies, and were highly unresolved.

Almost all nodes lacked significant bootstrap support. This result is not surprising, given the low level of divergence among sequences. The relationships among haplotypes are better represented by the MJ network which allows for the coexistence of ancestral and

extant sequences and multifurcations (Posada and Crandall 2001). The most notable difference in the topologies of the ML and MP trees is the absence/presence of a most basal member of the tree. In the ML tree, there is no one particular basal member, but in the MP tree a basal member is represented by Haplotype 15 (Figure. 9). In the ML tree, this sequence forms a sister clade with Haplotype 19 (Figure. 8).

### **Comparison to Published Diversity**

A total of 110 mtDNA control region sequences were obtained from *L. acutus* from our two sampling localities. mtDNA haplotype diversity was found to be overall  $Hd = 0.896 \pm 0.015$  and nucleotide diversity to be  $\pi = 0.00706 \pm 0.00346$ . These values are extremely similar to the values found in an analogous geographic location by Banguera-Hintroza et al. (2014) ( $N= 62$ ,  $Hd = 0.9159 \pm 0.0199$ ,  $\pi = 0.0093 \pm 0.0055$ ). Similar values of high haplotype diversity and low nucleotide diversity have been reported for multiple cetacean populations worldwide (Pichler and Baker 2000, Cassens et al. 2003, Harlin et al. 2003, Natoli et al. 2006). According to Rogers and Harpending (1992) this pattern of high haplotypic diversity and low nucleotide diversity is generally consistent with population expansion. As the populations expand, an excess of haplotypes differing by one or a few mutations are created. Various authors have noted an association between signals for expansion and past climatic events (e.g. Pleistocene glaciations) that suggest bottlenecked populations in glacial refugia (see Hewitt 2000; Wares 2002; Hewitt 2004; Banguera-Hintroza et al. 2010). The possibility of a population expansion was also supported in our study by the Tajima's D statistics, the Fu's statistics, and the mismatch distribution analysis. Furthermore, the fact that much of the diversity shown in the

haplotype network analysis (Figure 7) is derived from a few dominant haplotypes is also indicative of a recent expansion signal.

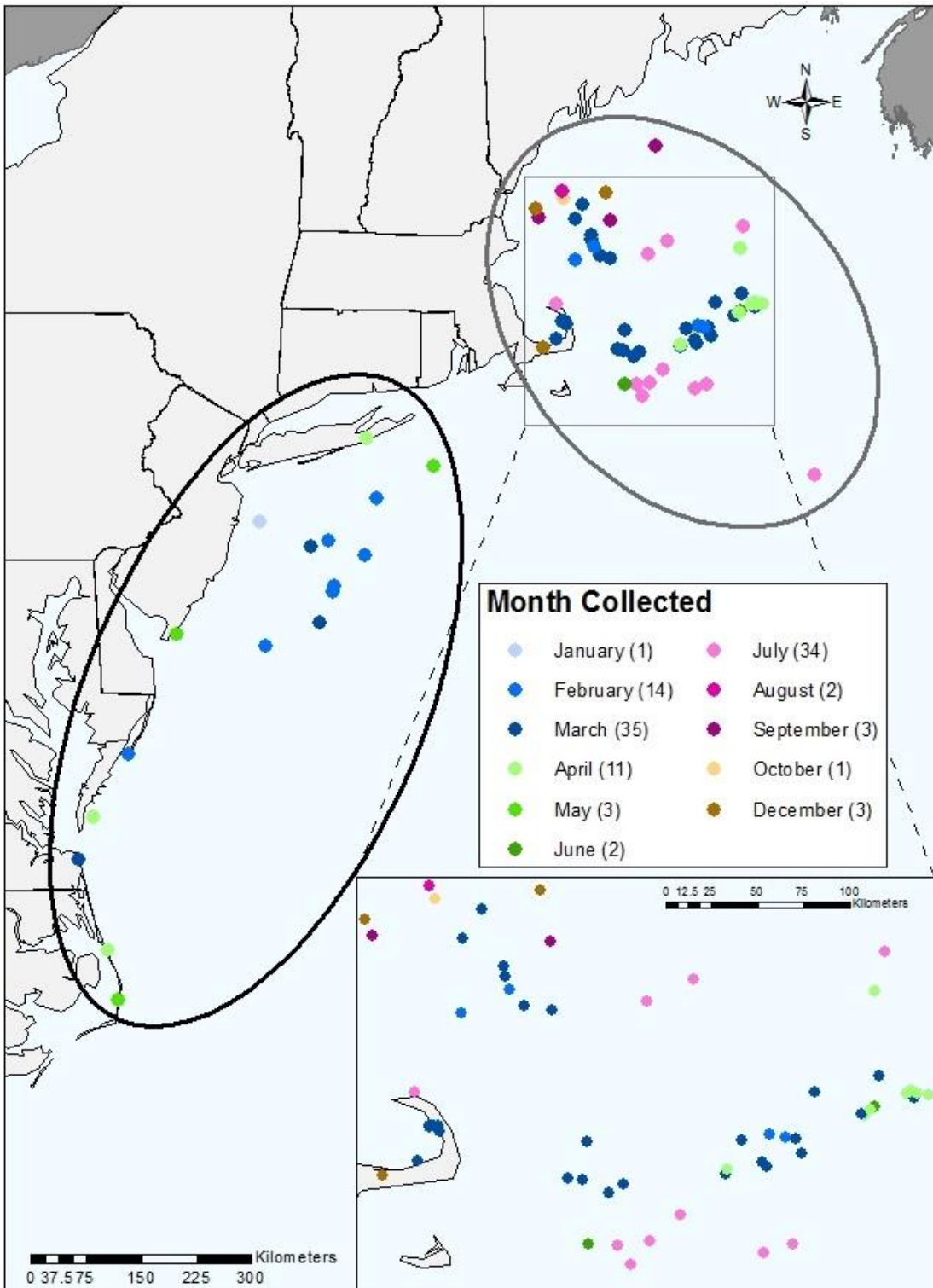
### **Spatial Temporal Analysis**

March was the most common month of sample collection with 37 individuals, closely followed by July with 34 individuals (Figure 10). Of all the 21 samples in the South, they were exclusively collected from January to May (February being the most common with N = 11), corresponding with the winter and early spring months (Table 4).

**Table 4.** Dates and haplotypes of “South” samples.

<b>Sample</b>	<b>Haplotype</b>	<b>Latitude</b>	<b>Logitude</b>	<b>Collection Date</b>
Lacu053	1	40.0833	-73.7583	Jan 22 1997
Lacu075	2	39.7683	-72.4783	Feb 27 2004
Lacu082	1	39.8517	-73.1283	Mar 3 2009
Lacu083	3	39.9050	-72.9183	Feb 5 2006
Lacu084	4	40.5903	-71.6428	May 11 2006
Lacu086	2	40.3033	-72.3367	Feb 11 2006
Lacu090	1	39.42	-72.87	Feb 22 1989
Lacu095	5	39.42	-72.87	Feb 18 2004
Lacu102	6	39.42	-72.87	Feb 02 1989
Lacu103	7	40.8478	-72.4528	Apr 16 2004
Lacu104	7	35.95129	-75.61941	Apr 5 1999
Lacu105	7	39.0122	-74.7842	May 30 1999
Lacu106	8	39.42	-72.87	Feb 02 1989
Lacu108	9	37.25845	-75.79891	Apr 7 1999
Lacu109	6	39.48	-72.85	Feb 21 1989
Lacu110	10	37.875	-75.3733	Feb 24 1990
Lacu111	6	38.9	-73.68	Feb-89
Lacu112	6	38.9	-73.68	Feb-89
Lacu113	6	39.13	-73.02	Mar 14 1989
Lacu116	6	36.8506	-75.9779	Mar 16 1997
Lacu117	2	35.46004	-75.48267	May 11 1999





**Figure 10.** Month of sample collection. Dots indicate individuals/sampling locations. Strandings are located along the coast line, bycatch and biopsy samples occur further from shore.

## DISCUSSION

This study provides the first data concerning the genetic diversity of the Atlantic white-sided dolphin living in the southern part of their range along the east coast of the United States. Our data provides evidence that *L. acutus* in this area of the Western North Atlantic may have relatively high haplotype diversity but low nucleotide diversity. As suggested by Banguera-Hintroza et al. (2014), this possible lack of nucleotide diversity might be the result of historic bottleneck events. The sequence data also suggest that this population has recently expanded. This may be due to the population rebounding after one or more previous bottlenecks, or expanding from the original founding population. The implications for conservation are that populations of *L. acutus* have reduced mtDNA nucleotide diversity throughout its range, suggesting possible vulnerability to exploitation (e.g. in bycatch, direct takes and habitat degradation).

These data should serve as a baseline for ongoing monitoring of genetic diversity over time, as well as a standard for comparison to *L. acutus* throughout the Atlantic. Monitoring genetic diversity is important because the loss of diversity can significantly reduce a population's fitness. Two mechanisms can result in decreased fitness. Firstly, increased homozygosity can lead to an increase in deleterious recessive alleles. Secondly, decreased heterozygosity can lead to a decrease in heterozygous alleles that may provide a selective advantage in the face of changing environmental conditions (e.g. the presence

of a novel pathogen; O'Brien and Evermann 1988). Having a baseline for comparison will allow managers to assess the impact of their decisions over time with regard to maintaining the genetic viability of the population.

The total of 110 mitochondrial DNA control region sequences obtained from *L. acutus* were evaluated in order to address questions about the processes that have influenced the evolution, differentiation and genetic diversity of this species along the east coast of the United States. The mtDNA genetic diversity found in this species ( $Hd = 0.896 \pm 0.015$ ) contrasts with its low nucleotide diversity ( $\pi = 0.00706 \pm 0.00346$ ); this nucleotide diversity range is lower than has been found in other dolphin populations, which sometimes show values higher than 0.1 (see Pichler and Baker 2000). The pattern of high haplotype diversity and low nucleotide diversity as found in *L. acutus* is normally attributed to population expansion, which creates an excess of haplotypes differing by one or a few mutations (Rogers and Harpending 1992). To establish whether or not the pattern of genetic diversity found in this species is due to population expansion, the mismatch distribution was analyzed and is discussed below.

The results from this study show a clear pattern of unimodal shape in the mismatch distribution in all regional populations of this species that were studied. This can be explained either by a rapid increase in population size followed by a period of large and constant population size, or due to a "selective sweep". Selective sweep is where natural selection acting in favor of one mitochondrial genotype results in a rapid increase in the number of individuals carrying the preferred mitochondrial type (see Roger and Harpending 1992). Although mtDNA can be affected by natural selection, the

consistency of the expansion signal among populations of *L. acutus* supports the idea of a general effect explaining the patterns found in this species rather than selection which is less likely to affect all populations the same manner.

On average, haplotype sequences differed by 4.05 bp. Both the most common haplotype, Haplotype 6, and the second most common, Haplotype 1, were found in both localities sampled and together were made up 39% of sequenced individuals. Both the South and the North had some unique haplotypes (N= 3 and N= 14 respectively) (Figure 5). It is possible that these unique individuals may represent expansion; however, it is not possible to dismiss the possibility this finding is simply due to small sample size and all haplotypes are found in both localities.

The nearly ubiquitous distributions of Haplotypes 1 and 6, along with the results from the haplotype network, suggest that *L. acutus* has historically acted as a single, panmictic population in the Western North Atlantic Ocean. The AMOVA results indicate that all of the variation in CR sequences was due to intra-group variation, suggesting high rates of historic gene flow. To address the question about genetic differentiation among populations of *L. acutus* across its geographic range, the Fixation Index was evaluated. Pairwise  $F_{ST}$  values suggest that there is no significant differentiation among sampling localities ( $F_{ST} = -0.00697$ ), but this finding may be largely due to the small sample sizes within the southern locality and the possibility that some individuals may have been re-sampled.

These results partially agree with the results reported by Mikkelsen and Lund (1994) and Banguera-Hintroza et al. (2014) who looked at this species on a larger scale:

across the entire North Atlantic. Mikkelsen and Lund (1994) did not find any craniometrical differences among samples from *L. acutus* on either side of the North Atlantic, and Banguera-Hintroza et al. (2014) did not find any genetic evidence of differentiation. Since evidence of separation was not found in a smaller region of the range, this supports the evidence found on the larger scale.

Three population stocks have been proposed in the Northern area of this region: Gulf of Maine, Gulf of St. Lawrence and Labrador Sea, based mainly on sightings; strandings and incidental takes (Palka et al. 1997); however, divergent stock statuses have not been suggested for the recent expansion of numbers of this species in the South. The existence of any of these stocks has not been evaluated yet with molecular approaches. Although there was not any significant evidence to support a North/South division, the three currently proposed stocks were not investigated at a finer scale. In the future, higher-resolution markers such as microsatellites or a panel of highly polymorphic SNPs should be used to elucidate population differentiation at a fine spatial scale across the entire region. This information would allow the National Oceanic and Atmospheric Administration (NOAA) to determine whether or not this species is separated into stocks or can be managed as one panmictic population.

Another aspect of the data that can contribute to future monitoring is the spatial/temporal relationship. While the month of all sample collections varies across the seasons, the fall months are almost excluded. The majority of our samples are from bycatch and biopsy, which may include some sampling bias based on when ships are working. However, there are similar results for the stranding samples, which are most

common in the winter and spring. Some strandings occur during the summer months, but again there are none during the fall.

As the species is being more commonly found as far south as North Carolina, it has been suggested that the spatial distribution change over the last few years is due to seasonal patterns. Virginia and North Carolina observations appear to represent the southern extent of the species' range during the winter months (Waring et al. 2013). Our data corroborates these observations. Unfortunately due to our small sampling size, no conclusions can be drawn from this relationship. In the future, research (including average surface temperatures and patterns in the North Atlantic Current) must be completed in order to determine if a portion of the population is migrating south over this time frame, or if there is a more year-round presence indicating an expansion into the range due to climatic or other explanations.

# APPENDIX

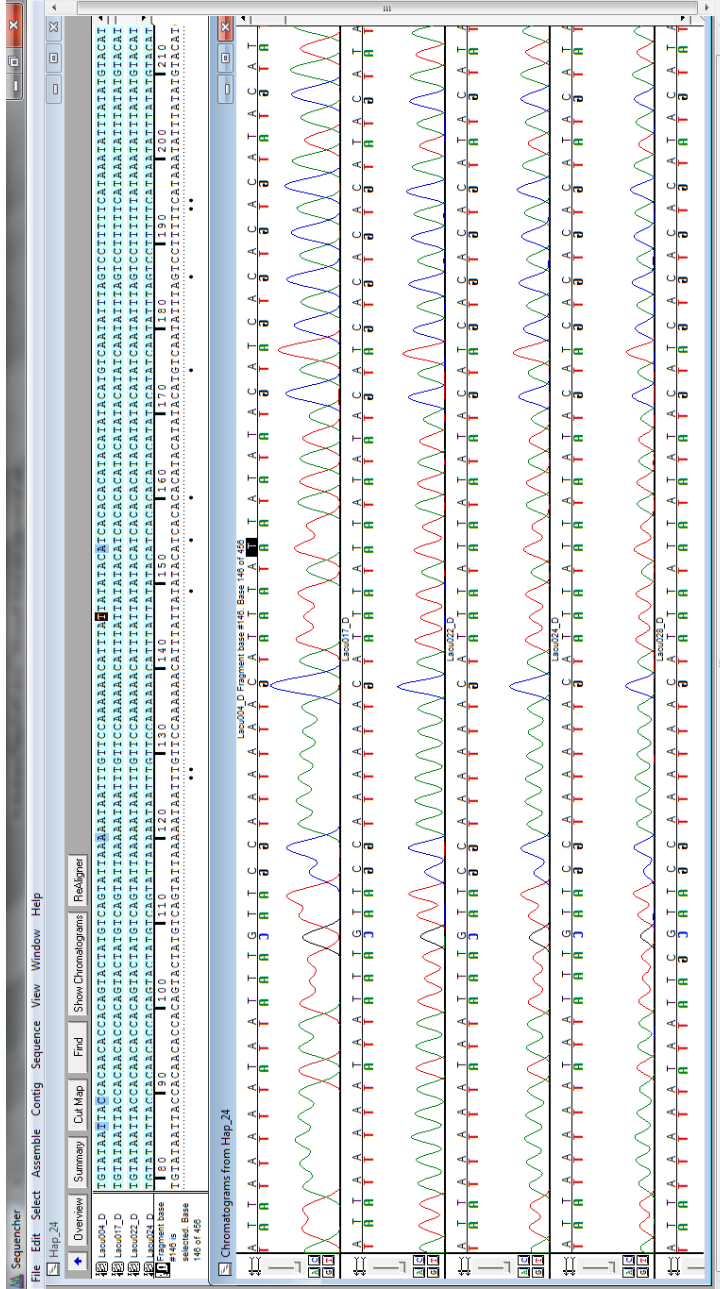
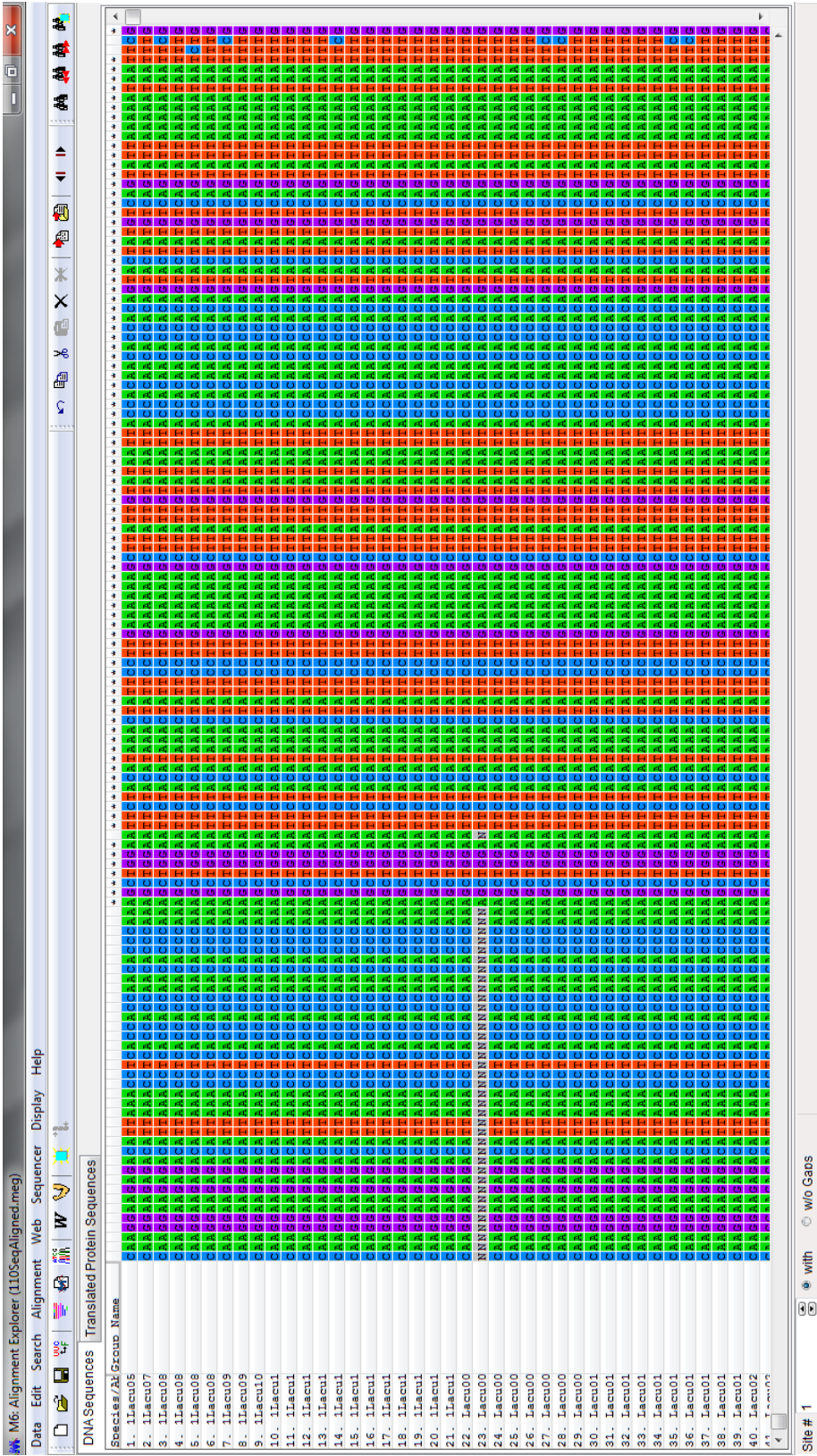


Figure 11. Screenshot of sequence quality captured in Sequencher.



**Figure 12.** Clustal W alignment created in MEGA 6.06



## Complete Alignment

>1Lacu053

```
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTCGT
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA
AAGCCCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA
TCCTCTAACAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--
```

>1Lacu075

```
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTT
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA
TCCTCTAACAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--
```

>1Lacu082b

```
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTCGT
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA
AAGCCCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA
TCCTCTAACAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--
```

>1Lacu083b

```
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCACGCTCTTACATATTATATA
TCCCCTAACAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--
```

>1Lacu084b

```
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATCTGT
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA
TCCTCTAACAATTTTATTTCCATTATATCCTATGGTCACTCCATTAGATCACGAGCTTAATCACC
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--
```

>1Lacu086b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTT  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>1Lacu090

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTCGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTT  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>1Lacu095

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTT  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAATTTTATTTCCACTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>1Lacu102

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTT  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>1Lacu103

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTT  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>1Lacu104

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTT  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA

AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>1Lacu105

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>1Lacu106

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACATACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>1Lacu108

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTCGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCCTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTACTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>1Lacu109

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>1Lacu110

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATG  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

```

>1Lacu111
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--
>1Lacu112
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--
>1Lacu113
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--
>1Lacu116
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--
>1Lacu117
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTT
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA
TCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--
>Lacu001
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC

```

ATAAATATTTATATGTACATGCTATGTATTATCGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNATCTTTATAAGA--

>Lacu002

NNAGCTGGANTTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATCGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATCTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNATCTTTATAAGA--

>Lacu004

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>Lacu005

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCACTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>Lacu006

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGCCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTTGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>Lacu007

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATAATTCGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTACTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC

ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTNNNNNNATCTTTATAAGA--

>Lacu008

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCTCTAACAAATTTTACTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTNNNNNNATCTTTATAAGA--

>Lacu009

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATG  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>Lacu010

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGTATGCTCTTACATATTATATA  
TCCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>Lacu011

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>Lacu012

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATG  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>Lacu013

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATCGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATCTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAATCTTTATAAGA--

>Lacu014

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAÖÖ-----

>Lacu015

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTCGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATNNNNNNNNNN,,,"-----

>Lacu016

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTCGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAÖÖ-----

>Lacu017

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATCGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAÖÖ-----

>Lacu018

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA

AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu019

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATCGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATCTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAÖÖ-----

>Lacu020

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTCC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAÿÿ-----

>Lacu021

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAsasswordChar0\X

>Lacu022

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTT  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu023

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----



>Lacu024

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCACTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu025

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACACCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATCTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu026

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTCGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu027

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATG  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu028

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTCGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu029

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC

ATAAATATTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu030

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu031

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTTATTATATACACCACACACATACATATACATGTCAATATTTAATCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATCTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu034

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGAY-----

>Lacu035

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTCGT  
TCCAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA\_δX-----

>Lacu036

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTCGT  
TCCAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC

ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu037

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATCGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu038

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTCGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu039

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu040

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu041

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu042

CACGAAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATG  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu043

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATCGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu044

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTCC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu045

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu046

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATCGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATCTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu047

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA

AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu048

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu049

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTCGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu050

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu051

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATG  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu052

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACACCACACACATACATATACATGTCAATATTTAATCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATCTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu054

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu055

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATCGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATCTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATGACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu056b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTCGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu057b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu058b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu059b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC

ATAAATATTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCGCGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu060b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCACTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu061b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTT  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu062b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu063b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATCTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu064b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACACCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATCTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC

ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu065b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACATACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu066

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu067

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTCGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCCTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu068

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTCGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCCTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu069

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGCCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTTGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu070



CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu071

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTCGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu072

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCACTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu073

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTCGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu074

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu076

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTCGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA

AAGCCCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu077

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTCGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTACTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu078b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu079b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu080b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu081b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTTCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTCGT  
TCCAAAAAACATTTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu085b

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCCCCTGATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu087

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAATTTTATTTCCATTATATCCTATGGCCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTTGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu088

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAATTTTATTTCCATTATATCCTATGGCCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTTGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu089

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATCGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAATTTTATCTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu091

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu092

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAAAAATAATTTGT  
TCCAAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC

ATAAATATTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu093

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATGACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu094

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTT  
ATAAATATTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu096

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTT  
ATAAATATTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu098

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC  
ATAAATATTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCCCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC  
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG  
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----

>Lacu099

CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT  
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATTTGT  
TCCAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTT  
ATAAATATTTATATGTACATGCTATGTATTATTGTGCATTTCATTTATTTTCCATACGATAAGTTA  
AAGCTCGTATTAATTATCATTAAATTTTACATATTACATAAATTTGCATGCTCTTACATATTATATA  
TCCTCTAACAAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC

```
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----
>Lacu100
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATAATTCGT
TCCAAAAACATTTATTATATACATCACACACATACATATACATATCAATATTTAGTCCTTTTTTC
ATAAATATTTATATGTACATGCTATGTATTATTGTGCATTCATTTATTTTCCATACGATAAGTTA
AAGCCCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA
TCCTCTAACAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----
>Lacu101
CAAGGAAGAGACATTAAACCTCACCACCAACACCCAAAGCTGGAATTCTACATAAACTATTCCCTT
GAAAAAAGCTTATTGTATAATTACCACAACACCACAGTACTATGTCAGTATTAATAAATAATTTGT
TCCAAAAACATTTATTATATACATCACACACATACATATACATGTCAATATTTAGTCCTTTTTTC
ATAAATATTTATATGTACATGCTATGTATTATTGTGCATTCATTTATTTTCCATACGATAAGTTA
AAGCTCGTATTAATTATCATTAATTTTACATATTACATAATTTGCATGCTCTTACATATTATATA
TCCTCTAACAATTTTATTTCCATTATATCCTATGGTCGCTCCATTAGATCACGAGCTTAATCACC
ATGCCGCGTGAAACCAGCAACCCGCTCGGCAGGGATCCCTCTTCTCGCACCCGGGCCATAACTCG
TGGGGGTAGCTAACAGTGATCTTTATAAGA-----
```

## REFERENCES

- Alling, A.K. and Whitehead, H.P. 1987. A preliminary study of the status of whitebeaked dolphins, *Lagenorhynchus albirostris*, and other small cetaceans off the coast of Labrador. *Canadian Field Naturalist* 1012: 131-135.
- Altschul, S.F., Gish, W., Miller, W., Myers, E.W., Lipman, D.J. 1990. Basic local alignment search tool. *Journal of Molecular Biology* 215: 403–410.
- Arbogast, B.S. and Kenagy, G.J. 2001. Comparative phylogeography as an integrative approach to historical biogeography. *Journal of Biogeography* 28: 819-825.
- Austerlitz, F., JungMuller, B., Godelle, B., and Gouyon, P.H. 1997. Evolution of coalescence times, genetic diversity and structure during colonization. *Theoretical Population Biology* 51: 148-164.
- Avise, J.C., Walker, D., and Johns, G.C. 1998. Speciation durations and Pleistocene effects on vertebrate phylogeography. *Proceeding of the Royal Society of London* 265: 1707-1712.
- Avise, J.C. 1994. *Molecular Markers, Natural History and Evolution*. Chapman and Hall, New York, NY.
- Avise, J.C. 2000. *Phylogeography. The History and Formation of Species*. Harvard University Press, Cambridge, MA.
- Bandelt, H.J., Forster, P., Röhl, A. 1999. Median-joining networks for inferring intraspecific phylogenies. *Molecular Biology and Evolution* 16: 37-48
- Banguera-Hinestroza, E., Bjørge, A., Reid, R.J., Jepson, P., Hoelzel, A.R. 2010. The influence of glacial epochs and habitat dependence on the diversity and phylogeography of a coastal dolphin species: *Lagenorhynchus albirostris*. *Conservation Genetics* 11: 1823–1836.
- Banguera-Hinestroza, E., Evans, P.G.H., Mirimin, L., Reid, R.J., Mikkelsen, B., Couperus, A.S., Deaville, R., Rogan, E., Hoelzel, A.R. 2014. Phylogeography and population dynamics of the white-sided dolphin (*Lagenorhynchus acutus*) in the North Atlantic. *Conservation Genetics*. DOI 10.1007/s10592-014-0578-z.

- Bierne, N. Bonhomme, F., David, P. 2003. Habitat preference and the marine-speciation paradox. *Proceedings of the Royal Society of London Series B-Biological Sciences* 270: 1399-1406.
- Bijlsma, R. Bundgaard, J., Boerema, A.C. 2000. Does inbreeding affect the extinction risk of small populations? Predictions from *Drosophila*. *Journal of Evolutionary Biology* 13:502-514.
- Bloch D, Mikkelsen B (2009) Catch history and distribution of whitesided dolphin (*Lagenorhynchus acutus*) of the Faroe Islands. *Fro´dskaparrit* 57: 190–198.
- Bickham, J.W., Patton J.C., Loughlin, T.R. 1996. High variability for control-region sequences in a marine mammal: implications for conservation and biogeography of Steller sea lions (*Eumetopias jubatus*). *Journal of Mammalogy* 77: 95-108.
- Brown, W.M., George, M., Wilson, C. 1979. Rapid evolution of animal mitochondrial DNA. *Proceedings of the National Academy of Sciences of the United States of America* 76: 1967–1971.
- Burg, T.M., Trites, A.W., Smith, M.J. 1999. Mitochondrial and microsatellite DNA analyses of harbor seal population structure in the Northeast Pacific Ocean. *Canadian Journal of Zoology* 77: 930-943.
- Caballero, S., Islas-Villanueva, V., Tezanos-Pinto, G., Duchene, S., Delgado-Estrella, A., Sanchez-Okrucky, R., Mignucci-Giannoni, A.A. 2012. Phylogeography, genetic diversity and population structure of common bottlenose dolphins in the Wider Caribbean inferred from analyses of mitochondrial DNA control region sequences and microsatellite loci: conservation and management implications. *Animal Conservation* 15: 95–112.
- Carwardine, M. 1995. Whales, dolphins and porpoises. Dorling Kindersley, London, UK, pp 257.
- Cassens, I., Van Waerebeek, K., Best, P.B., Crespo, E.A., Reyes, J., Milinkovitch, M.C. 2003. The phylogeography of dusky dolphins (*Lagenorhynchus obscurus*): a critical examination of network methods and rooting procedures. *Molecular Ecology* 12: 1781-1792.
- Cipriano, F. 1997. Antitropical distribution and speciation in dolphins of the genus *Lagenorhynchus*: a preliminary analysis. In: *Molecular genetics of marine mammals* (Dizon, A.E., Chivers, S.J., and Perrin, W.F., eds.). Society for Marine Mammalogy, Lawrence, KS, pp 305-316.

- Cipriano, F. 2009. Atlantic white-sided dolphin *Lagenorhynchus acutus*. In: Encyclopedia of marine mammals 2nd Ed. (Perrin, W.F., Würsig, B., Thewissen, J.G.M., eds.). Academic Press, Amsterdam, pp 56-58.
- Clement, M., Posada, D., Crandall, K.A. 2000. TCS: a computer program to estimate genealogies. *Molecular Ecology* 9 (10): 1657-1660.
- Cohn, J.P. 1990. Genetics for wildlife conservation. *BioScience* 40(3): 167-171.
- Emerson, B.C. and Hewitt G.M. 2005. Phylogeography. *Current Biology* 15: R367-R371.
- Emerson, B.C., Paradis, E. and Christophe, T. 2001. Revealing the demographic histories of species using DNA sequences. *Trends in Ecology and Evolution* 16: 707-716.
- Evans, P.G.H. 1987. *The Natural History of Whales and Dolphins*, Christopher Helm, London. pp 343.
- Evans, P.G.H. 1992. Status Review of Cetaceans in British and Irish Waters. UK Department of the Environment. London.
- Evans, P.G.H., Hammond, P.S. 2004. Monitoring cetaceans in European waters. *Mammal Review* 34: 131-156.
- Excoffier, L. 2004. Patterns of DNA sequence diversity and genetic structure after a range expansion: lessons from the infinite-island model. *Molecular Ecology* 13: 853-864.
- Excoffier, L., Smouse, P.E., Quattro, J.M. 1992. Analysis of molecular variance inferred from metric distances among DNA haplotypes: application to human mitochondrial DNA restriction data. *Genetics* 131: 479-491.
- Excoffier, L., Lischer, H. 2010. Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows. *Molecular Ecology Resources* 10: 564-567.
- Frankham, R. 1995. Inbreeding and extinction: a threshold effect. *Conservation Biology* 9: 792-799.
- Fu, X.Y. 1997. Statistical neutrality of mutations against population growth, hitchhiking and background selection. *Genetics* 147: 915-925.
- Gaskin, D.E. 1992. Status of the Atlantic white-sided dolphin, *Lagenorhynchus acutus*, in Canada. *Canadian Field-Naturalist* 106: 64-72.



- Goudet, J., Raymond, M., de Meeus, T., Rousset, F. 1996. Testing differentiation in diploid populations. *Genetics* 144: 1933–1940.
- Greenberg, D., Newbold, J.E., Sugino, A. 1983. Intraspecific nucleotide sequence variability surrounding the origin of replication in human mitochondrial DNA. *Genetics* 21: 33-49.
- Haig, S.M. 1998. Molecular contributions to conservation. *Ecology* 79: 413-425.
- Hamazaki, T. 2002. Spatiotemporal prediction models of cetacean habitats in the midwestern North Atlantic Ocean (from Cape Hatteras, North Carolina, USA to Nova Scotia, Canada). *Marine Mammal Science* 18: 920-939.
- Hammond, P.S., Berggren, P., Benke, H., Borchers, D.L., Collet, A., Heide-Jorgensen, M.P., Heimlich, S., Hiby, A.R., Leopold, M.F., Oiens, N. 2002. Abundance of harbour porpoise and other cetaceans in the North Sea and adjacent water. *Journal of Applied Ecology* 39: 361-376.
- Hammond, P.S., Bearzi, G., Bjørge, A., Forney, K., Karczmarski, L., Kasuya, T., Perrin, W.F., Scott, M.D., Wang, J.Y., Wells, R.S., Wilson, B. 2008. *Lagenorhynchus acutus*. In: IUCN 2009. IUCN Red List of Threatened Species. Version 2009.2. <[www.iucnredlist.org](http://www.iucnredlist.org)>.
- Hare, M.P., Cipriano, F., Palumbi, S.R. 2002. Genetic evidence on the demography of speciation in allopatric dolphin species. *Evolution* 56: 804-816.
- Harlin-Cognato, A.D., Markowitz, T., Würsig, B., Honeycut, R.L. 2007. Multilocus phylogeography of the dusky dolphin (*Lagenorhynchus obscurus*): passive dispersal via the west-wind drift or response to prey species and climate change? *BMC Evolutionary Biology* 7: 1-17.
- Harpending, R.C. 1994. Signature of ancient population growth in a low-resolution mitochondrial DNA mismatch distribution. *Human Biology* 66: 591-600.
- Harpending, R.C., Batzer, M.A., Gurven, M., Jorde, L.B., Rogers, A.R. 1998. Genetic traces of ancient demography. *Proceeding of the National Academic of Sciences, USA* 95: 1961-1967.
- Hewitt, G.M. 1996. Some genetic consequences of ice ages, and their role in divergence and speciation *Biological Journal of the Linnean Society* 58: 247-276.
- Hewitt, G.M. 1999. Post-glacial re-colonization of European biota. *Biological Journal of the Linnean Society* 68: 87-112.

- Hewitt, G.M. 2000. The genetic legacy of the Quaternary ice ages. *Nature* 405: 907-913.
- Hewitt, G.M. 2001. Speciation, hybrid zones and phylogeography - or seeing genes in space and time. *Molecular Ecology* 10: 537-549.
- Hoelzel, A.R. 2009. Evolution of population structure in marine mammals. In: *Population genetics for animal conservation*. (Bertorelle, G., Bruford, M.W., Hauffe, H.C., eds). Cambridge University Press, Cambridge.
- Hoelzel, A.R., 1998. Genetic structure of cetacean population in sympatry, parapatry and mixed assemblages: implications for conservation policy. *Journal of Heredity* 89: 451-458.
- Hoelzel, A.R., Potter, C.W. and Best, P.B. 1998a. Genetic differentiation between parapatric 'nearshore' and 'offshore' populations of the bottlenose dolphin. *Proceedings of the Royal Society of London Series B-Biological Sciences* 265: 1177-1183.
- Jefferson, T.A., Leatherwood, S., Webber, M.A. 1993. *FAO Species identification guide. Marine mammals of the world*. UNEP/FAO, Rome. pp 320.
- Kimura, M. 1980. A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* 16: 111-120.
- Kingman, J.F.C. 1982. On the genealogy of large populations. *Journal of Applied Probability* 19: 27-43.
- Kinze, C.C., Addink, M., Smeenk, C., Garda Hartmann, M., Richards, H.W., Sonntag, R.P. and Benke, H. 1997. The white-beaked dolphin (*Lagenorhynchus albirostris*) and the white-sided dolphin (*Lagenorhynchus acutus*) in the North and Baltic seas: review of available information. *Reports of the International Whaling Commission* 47: 675-683.
- Klinowska, M. 1991. *Dolphins, Porpoises and Whales of the World*. Gland, Switzerland and Cambridge, U. K.: IUCN.
- Kreader, C.A. 1996. Relief of Amplification Inhibition in PCR with Bovine Serum Albumin or T4 Gene 32 Protein. *Applied and Environmental Microbiology* 62: 1102-1106.
- Knowles, L.L., Richards, C.L. 2005. Importance of genetic drift during Pleistocene divergence as revealed by analyses of genomic variation. *Molecular Ecology* 14: 4023-4032.

- Lamont, M.M., Vida, J.T., Harvey, J.T., Jeffries, S., Brown, R., Huber, H.H., DeLong, R., and Thomas, W.K. 1996. Genetic substructure of the Pacific harbor seal (*Phoca vitulina richardsi*) off Washington, Oregon, and California. *Marine Mammal Science* 12: 402-413.
- MacLeod, C. D., Weir, C.R., Pierpoint, C., Harland, E.J. 2007. The habitat preferences of marine mammals in the west of Scotland (UK). *Journal of the Marine Biological Association of the United Kingdom* 87: 157-164.
- Mikkelsen, A.M.H. and Lund, A. 1994. Intraspecific variation in the dolphins *Lagenorhynchus albirostris* and *L. acutus* (Mammalia, cetacean) in metrical and nonmetrical skull characters, with remarks on occurrence. *Journal of Zoology London* 234: 289-299.
- Morizur Y, Berrow S.D., Tregenza, N.J., Couperus, AS., Pouvreau, S. 1999. Incidental catches of marine mammals in pelagic trawl fisheries of the Northeast Atlantic. *Fisheries Research* 41: 297-307.
- Natoli, A., Peddemors, V.M., Hoelzel, A.R. 2003. Population structure and speciation in the genus *Tursiops* based on microsatellite and mitochondrial DNA analyses. *Journal of Evolutionary Biology* 17: 363-375.
- Northridge, S.P., Tasker, M.L., Webb, A., Camphuysen, K., Leopold, M. 1997. White-beaked *Lagenorhynchus albirostris* and Atlantic white-sided dolphin *L. acutus* distributions in Northwest European and U.S. North Atlantic waters. *Reports of the International Whaling Commission* 47: 797-805.
- O'Brien, S.J., Wildt, D.E., Goldman, D., Merrill, C.R., Bush, M. 1983. The cheetah is depauperate in genetic variation. *Science* 221: 459-462.
- O'Brien, S.J. and Evermann, J.F. 1988. Interactive influence of infectious disease and genetic diversity in natural populations. *Trends in Ecology and Evolution* 3: 254-259.
- O'Corry-Crowe, G.M., Martien, K.K., Taylor, B.L. 2003. The analysis of population genetic structure in Alaskan harbor seals, *Phoca vitulina*, as a framework for the identification of management stocks. *Administrative Report LJ-03-08*. pp 64.
- Palka, D., Read, A., Potter, C. 1997. Summary of knowledge of white-sided dolphins (*Lagenorhynchus acutus*) from the U.S. and Canadian North Atlantic waters. *Reports of the International Whaling Commission* 47: 729-34.

- Palo, J.U. 2003. Genetic diversity and phylogeography of landlocked seals. Academic dissertation, Department of Ecology and Systematics. Division of Population Biology. University of Helsinki, Finland. pp 29.
- Palo, J.U., Hyvarinen, H., Helle E, Makinen, H.S. and Vainola, R. 2003. Postglacial loss of microsatellite variation in the landlocked Lake Saimaa ringed seal. *Conservation Genetics* 4: 117-128.
- Palo, J.U., Vainola, R. 2006. The enigma of the landlocked Baikal and Caspian seals addressed through phylogeny of phocine mitochondrial sequences. *Biological Journal of the Linnean Society* 88: 61-72.
- Palumbi, S.R. 1994. Genetic-divergence, reproductive isolation, and marine speciation. *Annual Review of Ecology and Systematics* 25: 547-572.
- Pastene, L.A., Goto, M., Kanda, N., Zerbini, O.K., Watanabe, K., Bessho, Y., Hasegawa, M., Nielsen, R., Larsen, F., Palsbøll, P. 2007. Radiation and speciation of pelagic organism during periods of global warming: the case of the common minke whale, *Balaenoptera acutorostrata*. *Molecular Ecology* 16: 1481-1495.
- Payne, M., Heinemann, D.W. 1990. A distributional assessment of cetaceans in the shelf and shelf edge waters of the northeastern United States based on aerial and shipboard surveys, 1978-1988. Report to NMFS. [Available from National Marine Fisheries Science Center, 166 Water St., Woods Hole, MA 02543], pp 108.
- Pichler, F.B., Baker, C.S. 2000. Loss of genetic diversity in the endemic Hector's dolphin due to fisheries-related mortality. *Proceedings of the Royal Society of London Series B-Biological Sciences* 267: 97-102.
- Pichler, F.B., Robineau, D., Goodall, R.N., Meyer, M.A., Olivania, C., Baker, C.S. 2001. Origin and radiation of Southern Hemisphere coastal dolphins (genus *Cephalorhynchus*) *Molecular Ecology* 10: 2215-2223.
- Posada, D., Crandall, K.A. 2001. Intraspecific gene genealogies: trees grafting into networks. *Trends in Ecology and Evolution* 16: 37-45.
- Read, A.J., Westgate, A.J. 1997. Monitoring the movements of harbour porpoises (*Phocoena phocoena*) with satellite telemetry. *Marine Biology* 130: 315-322.
- Reeves, R.R. and Leatherwood, S. 1994. Dolphins, porpoises, and whales. 1994-1998 Action Plan for the conservation of cetaceans. pp 89.

- Reeves, R.R., Smeenk, C., Brownell, L. and Kinze, C.C. 1999. Atlantic white-sided dolphin *Lagenorhynchus acutus* (Gray, 1828). In: Handbook of Marine Mammals Vol. 6: The second book of dolphins and porpoises. (Ridgway, S.H., Harrison, S.R., Eds.) Academic Press, San Diego. pp 31-56.
- Rogers, A.R., Harpending, H. 1992. Population growth makes waves in the distribution of pairwise genetic differences. *Molecular Biology and Evolution* 9: 552-569.
- Rosel, P.E. 2003. PCR-based sex determination in Odontocete cetaceans. *Conservation Genetics* 4: 647-649.
- Rosel, P.E., France, S.C., Wang, J.Y., Kocher, T.D. 1999a. Genetic structure of harbour porpoise *Phocoena phocoena* populations in the northwest Atlantic based on mitochondrial and nuclear markers. *Molecular Ecology* 8: S41-S51.
- Rosel, P.E., Tiedemann, R., Walton, M. 1999b. Genetic evidence for limited trans-Atlantic movements of the harbor porpoise *Phocoena phocoena*. *Marine Biology* 133: 583-591.
- Rosel, P.E., Dizon, A.E., Heyning, J.E. 1994. Genetic analysis of sympatric morphotypes of common dolphins (genus *Delphinus*). *Marine Biology* 119: 159-167.
- Rozas, J., Rozas, R. 1999. DnaSP version 3: an integrated program for molecular population genetics and molecular evolution analysis. *Bioinformatics* 15: 174-175.
- Saccone, C., Grazianno, P., Sbisà, E. 1991. The main regulatory region of mammalian mitochondrial DNA: structure-function model and evolutionary pattern. *Journal of Molecular Evolution* 33: 83-91.
- Schneider, S., Excoffier, L. 1999. Estimation of past demographic parameters from the distribution of pairwise differences when the mutation rates vary among sites: application to human mitochondrial DNA. *Genetics* 152: 1079-1089.
- Secchi, E.R., Wang, J.Y., Murray, B.W., Rocha-Campos, C.C., White, B.N. 1998. Population differentiation in the franciscana (*Pontoporia blainvillei*) from two geographic locations in Brazil as determined from mitochondrial DNA control region sequences. *Canadian Journal of Zoology* 76: 1622-1627.
- Sergeant, D.E., Aubin, D.J., Geraci, J.R. 1980. Life history and Northwest Atlantic status of the Atlantic white-sided dolphin, *Lagenorhynchus acutus*. *Cetology* 37: 1-12.

- Stanley, H.F., Casey, S., Carnahan, J.M., Goodman, S., Harwood, J., Wayne, R.K. 1996. Worldwide patterns of mitochondrial DNA differentiation in the harbor seal (*Phoca vitulina*). *Molecular Biology and Evolution* 13: 368-382.
- Sunnucks, P. 2000. Efficient genetic markers for population biology. *Trends in Ecology and Evolution* 15: 199-203.
- Tajima, F. 1997. Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. *Genetics* 123: 585-595.
- Tolley, K.A., Vikingsson, G.A., Rosel, P.E. 2001. Mitochondrial DNA sequence variation and phylogeographic patterns in harbor porpoises (*Phocoena phocoena*) from the North Atlantic. *Conservation Genetics* 2: 349-361.
- Wakeley, J., Hey, J. 1997. Estimating ancestral population parameters. *Genetics* 145: 847-855.
- Waring, G.T., Josephson, E., Fairfield, C.P., Maze-Foley, K. 2006. U.S. Atlantic and Gulf of Mexico Marine Mammal Stock Assessments -2005. NOAA Tech Memo NMFS NE 201 pp 29-77. <http://nefsc.noaa.gov/publications/tm/tm201/pdfs/69-77.pdf>
- Waring, G.T., Josephson, E., Fairfield, C.P., Maze-Foley, K. 2007. U.S. Atlantic and Gulf of Mexico Marine Mammal Stock Assessments -2006. NOAA Tech Memo NMFS NE 205 pp 120-128. <http://nefsc.noaa.gov/publications/tm/tm205/pdfs/120WhiteSideD.pdf>
- Waring, G.T., Josephson, E., Fairfield, C.P., Maze-Foley, K. Editors. 2013. Draft U.S. Atlantic and Gulf of Mexico Marine Mammal Stock Assessments -2013. 78 Federal Register 66681. pp 190-201. [http://www.nmfs.noaa.gov/pr/sars/pdf/ao2013\\_draft.pdf](http://www.nmfs.noaa.gov/pr/sars/pdf/ao2013_draft.pdf)
- Weinrich, M.T., Belt, C.R., Morin, D. 2001. Behavior and Ecology of Atlantic White-sided dolphin (*Lagenorhynchus acutus*) in coastal New England waters. *Marine Mammal Science* 17: 231-248.
- Weir, C.R., Pollock, C., Cronin, C., Taylor, S. 2001. Cetacean of the Atlantic Frontier, North and West of Scotland. *Continental Shelf Research* 21: 1047-1071.
- Weir, C.R., Stockin, K.A., Pierce, G.J. 2007. Spatial and temporal trends in the distribution of harbour porpoises, white-beaked dolphins and minke whales off Aberdeenshire (UK), north-western North Sea. *Journal of Marine Biology* 87: 327-338.

Wilson A.C., Cann, R.L., Carr, S.M., George, M., Gyllensten, U.B., Helm-Bychowski, K.M., Higuchi, R.F., Palumbi, S.R., Prager, E.M., Sage, R.D., and Stoneking, M. 1985. Mitochondrial DNA and two perspectives on evolutionary genetics. *Biological Journal of the Linnaean Society* 26: 375-400.

Wright, S. 1951. The genetic structure of populations. *Annals of Eugenics* 15: 323–354

## **BIOGRAPHY**

Heather Anne Abrahams graduated from Lake Braddock Secondary School, Burke, Virginia, in 2005. She received her Bachelor of Arts from Virginia Polytechnic Institute and State University in 2009.