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The Genetics of Conservation Translocations: A Comparison of North American Golden Eagles (Aquila chrysaetos canadensis) and Bald Eagles (Haliaeetus leucocephalus)

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THE GENETICS OF CONSERVATION TRANSLOCATIONS: A COMPARISON OF NORTH AMERICAN GOLDEN EAGLES (*Aquila chrysaetos canadensis*) AND BALD EAGLES (*Haliaeetus leucocephalus*)

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By

Maria Wheeler

August 2014

THE GENETICS OF CONSERVATION TRANSLOCATIONS: A COMPARISON OF NORTH AMERICAN GOLDEN EAGLES (*Aquila chrysaetos canadensis*) AND BALD EAGLES (*Haliaeetus leucocephalus*)

By

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ABSTRACT

THE GENETICS OF CONSERVATION TRANSLOCATIONS: A COMPARISON OF NORTH AMERICAN GOLDEN EAGLES (*Aquila chrysaetos canadensis*) AND BALD EAGLES (*Haliaeetus leucocephalus*)

By

Maria Wheeler

August 2014

Dissertation supervised by Dr. Brady Porter

In the past half-century, two raptors with similar life histories, bald eagles (*Haliaeetus leucocephalus*) and golden eagles (*Aquila chrysaetos canadensis*) were the subjects of either broad-scale reintroduction or translocation projects in North America. These two different conservation approaches provided the framework for a retrospective natural experiment. The goal of my research was to determine the effects of these two conservation management approaches on the genetic population structure of each species. Methods included sequencing *cyt b* mtDNA and genotyping 10 microsatellite loci for contemporary and historic golden eagles and bald eagles. Contemporary samples were collected from captive and wild birds, and historic samples were collected from museum specimens preserved before 1980. We inferred pre- and post-translocation population structure based on genotypic data using Bayesian analysis, multiple indices of genetic diversity, and principal coordinated analysis. Results indicate that both contemporary (n=146 individuals) and historic (n=55 individuals) golden eagle populations across North America lack phylogeographic structure. This suggests the translocations did not have a significant impact on the genetic population structure of golden eagles. However, bald eagle microsatellite data suggested the presence of slight genetic cline in historic populations (n=23 individuals) from the northwest to the southeast—a pattern that is not currently observed in contemporary populations (n=82 individuals). The contemporary bald eagle population's genetic structure reflects the mixed genetic origins of extant birds given their reintroduction history. Comparing the results of these two species demonstrates different potential outcomes of conservation translocations and suggests the value of genetic analyses in conservation management plans.

DEDICATION

I would like to dedicate my dissertation to the memory of Marion “Bo” Wells. He wasn’t famous, he wasn’t someone that history will remember, and he wasn’t even technically family to me. Yet it was impossible to meet him without realizing that he was someone unique—independent in spite of his disabilities, gentle yet strong, a snappy wit, and a stranger to no one. He had the kind of quiet spirit and resilience that characterizes legendary unlikely heroes, but also the love and warmth of a grandfather who tells those heroes’ stories. Few people like him have ever walked this earth, and I was lucky enough to have known him for the last fifteen of his seventy-plus years. I didn’t purposely choose my research project because of him, but he loved bald eagles more than anyone I have ever known. He would have been so excited and proud of my research, and if he hasn’t been watching, I’ll tell him all about it someday.

Love you always, Bo. Am I still not talking too much? ☺

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Prologue

Wildlife Reintroductions and Translocations

Reintroductions and translocations are forms of *in situ* conservation that have captured popular attention as a wildlife management tool. Often romanticized through conservation success stories of charismatic megafauna such as the Arabian oryx (*Oryx, leucoryx*, Mesochina et al 2003) and the peregrine falcon (*Falco peregrinus*, Tordoff and Redig 2001), reintroductions are defined by the International Union for the Conservation of Nature (IUCN) as "an attempt to establish a species in an area which was once part of its historical range, but from which it has been extirpated or become extinct" (IUCN 1995). Reintroductions most frequently involve captive bred or captive rehabilitated animals. Associatively, translocations are often defined synonymously with reintroductions, (Griffith et al 1989) but more typically involve moving a member, or members, of a population to a part of the species' historical range where the population has either declined or been extirpated.

North American species alone account for numerous success stories of reintroductions and translocations. Canada geese are a prominent example. Driven nearly to extinction due to overhunting, and added to the Endangered Species list in 1966, Canada geese (*Branta canadensis*) were early subjects of translocations to the US midwest and northeast in the 1940's (Cooper and Keefe 1997, National Audubon Society). Today, few would question the recovery success of these birds, now often considered pests due to their over-abundance. Similarly, white-tailed deer (*Odocoileus virginianus*) were nearly extirpated from much the Eastern US due to overhunting and habitat loss after European colonization. Reintroductions began around 1890 and continued through the 1970’s (Leberg et al. 1994). Like the Canada goose, the white-tailed deer has now recovered to the point of overpopulation in many regions (Rawinski 2008).

Alternatively, species can also be unintentionally introduced into regions to which they are not native. Given favorable conditions (such as little to no predation, abundant resources, and a familiar climate), an introduced species can quickly become invasive and pose distinct threats to both native wildlife and human economies. For example, the emerald ash borer is invasive species of insect that has devastated some North American populations of ash trees (Muirhead et al. 2006). Indigenous to Southeast Asia, these beetles first appeared in the US in 2002 and have threatened both horticultural and forest ash trees throughout the Northeastern US. It has been estimated that they have the potential to cause over $300 billion worth of forestry damage if they are not curbed. Another Asian species that has wreaked havoc in the US is kudzu (*Pueraria lobata*). Introduced to American horticulture because of its aesthetic appeal and to American civil engineering because of its ability to slow erosion, kudzu is a semi-woody creeping plant that has escaped human control (Sun et al 2004). Images of spreading kudzu slowly covering houses and hillsides have become the vine’s infamous trademark, and its damage to property, forest, and crop land costs the US millions of dollars per year.

However, carefully planned introductions do not typically result in nuisances. A more positive example from both a genetic and a conservation standpoint is the Florida panther (*Puma concolor coryi*). Florida panthers’ numbers were down to as low as 19 by the 1980’s, and the remaining individuals all carried a few negative traits (such as kinked tails and low quality of male) that had accumulated into a genetic load due to small population size. To augment the Florida panther's numbers and attempt to introduce diversity into their genetic population structure, eight individuals from Texas were trapped and relocated to Florida. The translocations of these pumas led to 13% annual growth rate in the population, and by 2008, there were at least 108 Florida panthers in the wild, the vast majority of which were free of the negative physical traits (Hedrick and Fredrickson 2009).

In spite of the publicized success stories, many costly reintroduction and translocation attempts have failed—often numerous times. However, the exact numbers of failed reintroductions are unavailable. This is partially due to the fact that unsuccessful studies often go unpublished and partially due to the fact that until recent decades, little to no follow-up monitoring of reintroduced populations was ever carried out (Seddon et al. 2007). This is especially true for vertebrate species whose establishment is more costly and presents more challenges than required for plants or invertebrate animals. One such example of a failed reintroduction was the pygmy rabbit (*Brachylagus idahoensis*) of northwestern US. This lagopmorph has been the focus of emergency reintroduction efforts (WA FWS 2003); however it was still declared extirpated from Washington state in 2007 (Zeoli et al. 2008). In this case, it is thought that the combination of a short life-span, high adult mortality, small litter sizes and severely fragmented habitat have been the key factors in failed reintroductions. For other species, population declines have been the result of both anthropogenic habitat fragmentation and introduced predators. In these situations reintroductions are futile without the removal of the introduced predator. Another bird now extinct from the wild is the Ala'la (Corvus hawaiiensis), or Hawaiian crow. Although many reintroduction attempts were made, US Fish and Wildlife declared the bird was extinct from the wild in 2002 (FWS 2003). Approximately fifty still remain in captivity, keeping future reintroduction attempts a possibility. However, the captive birds are all inbred to some degree (in particular, many individuals are the progeny of a mother-son cross), giving the remaining Ala'la individuals low genetic diversity and the species a formidable hurdle (CLS 1992).

The causes behind the success or failure of reintroductions can be difficult to determine. As already mentioned, early failed reintroductions were poorly documented, and even today, resources for follow-up monitoring are often very limited. Another issue is the fact that there is no consensus as to what defines a reintroduction "success." Some conservation biologists define success as when the birth rate of a newly integrated population exceeds the death rate, others define it as three to five years of stability, and still others say a minimum viable population of 500 is required (Sarrazin and Barboult 1996). However, none of these definitions take into account the life histories of more than one or two species, which makes them useless as general definitions. For example, the introduction of a long-lived animal, such as a raptor will require several years of follow-up monitoring since they have long generation times. Alternately, shorter-lived animals, such as song birds, have much shorter generation times. Thus, it could take significantly less time for a song bird's population to become stable when compared to a raptor. This suggests that simply outlining a few years of monitoring without thought to generation time may not ultimately be useful.

Another serious constraint on measuring the success or failure of reintroduction events is the lack of genetic planning that goes into project development and follow-up monitoring. Though reintroduction may consider pedigrees and lineages, little consideration is given to the animals' origins—which jeopardizes locally adapted traits or losing overall genetic variation and adaption potential. In fact, between 1979 and 2005, as few as 68 genetic studies were carried out on populations arisen from reintroduced individuals. In contrast, hundreds of studies have been conducted on behavior, ecosystems effects, general management, and population dynamics (Seddon et al 2007). This shows a clear need for genetic analyses of modern populations that are the product of reintroductions to ensure we are not setting up a population to become homogenized and vulnerable.

The bearded vulture (*Gypaetus barbatus*) provides one clear example of a situation of where the exclusion of genetics could negatively impact a reintroduction program. In the 20th century, bearded vultures were slowly extirpated from much of their historical western European range. Reintroduction efforts began in the Alps in 1986 (Schaub et al. 2009) by releasing captive-born juveniles of Asian origin. Since then, reintroductions have occurred in several countries throughout Europe, and the reintroduced birds have survived to establish breeding territories. In recent years, however, studies have emerged to determine whether captive breeding needs to continue or what regions need the releases to continue. One such study used computer modeling to assess demographic trends in Alpine bearded vultures. Results of population modeling suggested that the wild populations were well enough re-established to discontinue reintroductions in that region and focus on other parts of Europe instead (Schaub et al. 2009). In opposition to these findings, however, bearded vulture genetics offer quite a different story. A comparison of mitochondrial haplotypes of modern bearded vultures and museum specimens of historical bearded vultures indicated that the genetic variation of modern populations when compared to former populations had dramatically decreased (Godoy et al 2004). Modern local populations had begun undergoing genetic drift in their respective environments. The overall conclusion of this work was that stopping the reintroductions and translocations of bearded vultures could have a negative effect on the population (Godoy et al 2004).

Genetic Management of Small Populations and Populations of Conservation Concern

With such examples as the bearded vulture in mind, it can be inferred that newly reintroduced populations need genetic monitoring. Fitness (the ability to pass on one's genes) is directly correlated with genetic diversity (Reed and Frankham 2003)—in other words, more diverse populations demonstrate greater viability long term (Reed 2010). Though all populations could be subject to some degree of intra-population homogeneity simply because of local allelic frequencies and genetic response to the environment, populations already in danger of extirpation may not be able to handle the added burden of low diversity/low fitness. Another danger in low genetic diversity is the build up of deleterious alleles and, thus, maladaptive phenotypes, as occurred in Florida panther populations. When the genetic variation was increased through gene flow by the addition of the cats from Texas, the phenotypic frequency of these inbred traits decreased (Hedrick and Fredrickson 2010).

A distinct danger of low genetic diversity, especially to a small and vulnerable population, is low resistance to the spread of disease. In one recent study, two colonies of honey bees were raised nearly identically but for one factor: the queen of one colony was only ever inseminated by a single related male while the other colony's queen was inseminated by multiple males of various degrees of relatedness. Both colonies were then exposed to the fungal pathogen *Ascosphaera apis*. After inoculation, the number of viable broods in the colonies was significantly lower for the colony with low genetic diversity than the colony with high genetic diversity (Tarpy 2003). Similarly, it has been theorized that vertebrates often face lower population disease resistance in situations with low genetic diversity (Lamont 1998, Lyles and Dobson 1993, Spielman et al. 2004).

Low genetic diversity can arise from inbreeding and can contribute to local extirpation. For examples, a study on the fritillary butterfly (*Melitaea cinxia*) determined that local extinctions were a direct result of high inbreeding and high homozygosity (Saccheri et al 1998). It was found that the within a small population of these insects, egg hatching, larval mortality, and adult life spans were all negatively impacted by the aforementioned genetic factors. Since these traits all have a direct effect on population sustainability, it can be safely surmised that genetic diversity is key to the viability of populations (both natural and reintroduced) in the wild.

Long term population viability can depend a great deal on genetic diversity. A loss in heterozygosity can lead to allelic fixation or allelic extinction, both of which can be considered responsible for an increased genetic load. Low diversity also increases vulnerability to environmental disruptions given that high genetic diversity directly correlates with a population’s ability to adapt (Frankham et al 2002). Therefore, when a population is already at risk and requires reintroductions, management programs not taking genetics into account may homogenize the population and set them up for failure.

However, in the quest for genetic diversity, those overseeing the management of small or reintroduced populations must be wary of outbreeding depression. Outbreeding depression is the loss of fitness due to the disruption of co-adapted gene complexes. In cases of reintroductions, there is a distinct possibly that the addition of members of one population into another could disrupt genes co-adapted to the local environment (Fenster and Galloway 2000). This has been seen in reintroduced slimy sculpins with multiple source populations. The hybrid F2 generations demonstrated lower fitness and smaller size than their parental generations (Huff et al. 2010).

Bald Eagles and Golden Eagles in North America

In spite of the role genetics plays in population persistence—particularly small or vulnerable populations—the subject has received relatively little consideration in reintroduction or translocation management planning (Seddon et al. 2007). It should be noted that most reintroduction plans today do at least account for the lineage of breeding stock before captive breeding takes place to avoid mixing relatives. Still, there has been a rising interest in the use of various forms of conservation translocations. They have been suggested as managerial response to conservation issues ranging from climate change to genetic loads in small populations. Therefore, understanding the impact of genetics is crucial.

With this in mind, conservation biology would greatly benefit from the evaluation of previous translocation and reintroduction efforts. I had the unique opportunity to perform a retrospective evaluation of two such management efforts carried out at roughly the same time. The two species at the center of the efforts were the bald eagle (*Haliaeetus leucocephalus*) and the North American golden eagle (*Aquila chrysaetos canadensis*).

Bald Eagles

Bald eagles are on the return from a severe population decline. In the early twentieth century, illegal hunting and habitat fragmentation had caused a strong enough decline to prompt the National Bald Eagle Protection Act of 1940 to stop the hunting and curb habitat loss. However, the introduction of the pesticide DDT reversed any positive demographic trends engendered by this legislation. DDT, an organochlorine endocrine disruptor, was a pesticide that made its way into riverine systems through run-off. The DDT biomagnified through trophic levels and ultimately became acted as endocrine disruptor in fish-eating raptors, including bald eagles. Ultimately, the presence of DDT caused severe eggshell thinning and, thus, halted reproduction. DDT was not banned until 1972, and the Endangered Species Act didn't arise until 1973. By that time, bald eagles were extirpated from most of their historical range in the eastern US, and only 487 nesting pairs remained in the Lower 48 states by 1963 (USFWS).

Reintroduction of bald eagles to their native range took several forms. The most successful form of management was "hacking," translocating bald eagle chicks from either captivity or healthy populations into regions that had been depleted. Hacking, a method derived from recreational falconer practices, most commonly involves removing chicks between the ages of six and eight weeks old from their home nests, and raising them in a human-made nest in a new region. The nests are generally built on a high platform with a small shelter behind it, from which handlers can unobtrusively observe the chicks and feed them without acclimating them to human presence. The chicks are purposely removed at a young age in the hopes that the chicks will return to the hacking site as adults, as opposed to their original birth sites.

Hacking was the primary method for releasing at least 1200 bald eagles into historic habitat between 1976 and 1985 (Nye 1988, Alan Jenkins—Sutton Center, pers. comm). Of this count, it is known that 275 of these birds were moved as nestlings from

Florida to Oklahoma in the 1980's (Alan Jenkins—Sutton Center, pers. comm). Of the remaining 390 birds, approximately 18% came from captive breeding facilities or were at least partially raised in captivity, the remaining 82% were wild-born. The majority of the hacked juveniles were from Alaska (41%) and Canada (31%). Another 24% of the birds came from a combination of the Pacific Northwest and Great Lakes states, and the origins of 4% are unknown. The hacking locations (release sites) of the juveniles ranged all throughout the southern US, New England, and included the Midwestern states of Indiana, Ohio, Missouri, and Oklahoma (Nye 1988).

Essentially, bald eagles from healthy populations were used to restart or bolster other populations wherever was needed. Birds from Florida were hacked in Oklahoma (Sutton Center) and Canadian birds were released to the Tennessee Valley (USFWS James Grier, pers. comm).—there was little time to plan for an organized pattern of reintroductions when the species was down to 412 pairs in the continental US in the 1960's (FWS). Through the twenty-first century, captive facilities around the US have continued to breed bald eagles and are releasing them into the wild to this day, thus there is no real way of knowing how many birds have been reintroduced or translocated.

Golden Eagles

Many golden eagles were hacked into the eastern USA in the 1980's and 1990's (Touchstone 1997). Though it is not known whether or not the eastern US has ever been home to a strong breeding population of golden eagles, in 1971, one moderately successful nesting pair was recorded in the US east of the Mississippi (Spofford 1971). Beginning in 1982, 111 nestlings from Wyoming, Zoo America in Hershey, Pennsylvania, and the Raptor Propagation Center in St. Louis, Missouri were hacked to new locations in Georgia (Touchstone 1997). In another effort from 1980 – 1986, multiple agencies including Tennessee Valley Authority, the US Fish and Wildlife Service (US FWS), and the North Carolina Wildlife Resources Commission, twenty-six western golden eagle nestlings were released into North Carolina (C. McGrath, pers. comm). Also, forty-seven captive nestlings were hacked into Tennessee by private organizations from 1995-2006; at least some of these birds were later observed to attempt to breed in central Tennessee (S. Somershoe, pers. comm).. In addition, at least six birds were released into Pennsylvania from 1983 – 1990 via private efforts. The birds' origins are unclear, but it is assumed they were from western US (T. Becker, pers. comm). Finally, news of various releases have led to a conservative estimate of at least another five goldens being translocated in the eastern US. In total, it is unclear whether any of these introductions have led to a significant increase in breeding populations. Eastern birds still primarily breed in northern Quebec, Labrador, and a small region of Ontario. These birds seem to appear in the US only as winter migrants (Kochert and Steenhoff 2002).

In spite of reintroduction efforts, recent studies of golden eagles indicate potential declines in the lower 48 states (Kochert and Steenhoff 2002) and an overall lack of knowledge on species status. For instance, nesting success data has indicated a decline in the species' status (Kochert and Steenhoff 2002); however, informal hawk watch data has indicated potentially increased usage of various migratory corridors in eastern birds.

One aspect of golden eagle biology that is especially not well understood is the relatedness between birds in the eastern US and the western US. The geographic ranges of these two populations seem to be allopatric, but are they truly reproductively isolated?

Historically, the two populations may have been genetically distinct, but would there even be any difference today in the two because of the recent reintroductions? Because the eastern population is small, complete genetic isolation could make them vulnerable, especially due to impacts of increasing human activity such as the growing predominance of wind turbines which could disrupt migratory flyways to summer and wintering grounds.

Project Objectives

The objective of my research is to determine how their respective translocation and reintroduction strategies has affected their modern populations. Both species' current North American populations have been influenced to some degree by past reintroductions of captive or translocated birds, creating the basis for a natural experiment in genetic trajectories.

When the plight of bald eagles was made public, the status of being a national symbol and charismatic megafauna gave these birds a distinct advantage in public attention when compared to less "popular" wildlife. Reintroductions were well funded and relied on hacked eagles from a wide variety of locations, with birds originating thousands of miles apart being released in the same locations. These reintroductions continued for years, and, to a much lesser extent, continue today from captive birds born to various institutions (Peter Nye, NY DEC 2010 pers. comm.; Bob Hatcher, AEF 2010 pers. comm.; Jeremy Carpenter, Columbus Zoo and Aquarium 2010 pers. comm.; Jody Millar, FWS 2010 pers. comm.; Michael Jenkins and Maurice Patten, Sutton Center 2010 pers. comm.; James Grier, NDSU 2010 pers. comm)..

Golden eagle reintroductions, on the other hand, garnered little public notice. These projects also involved birds from multiple origins; however, the number and geographic diversity of birds used was minute compared to bald eagle releases. Also, reintroductions efforts for goldens were short-lived compared to that of the bald eagle, and the actual extent to which hacked birds entered the breeding population is not known.

It is unknown which strategy has ultimately been more beneficial to these species. Golden eagles and bald eagles have similar life histories (see Table 1) and both of their distribution ranges cover the majority of North America. Therefore, this situation presents an ideal opportunity to compare which reintroduction styles have been more beneficial to which species. Eastern golden eagles were managed by a quick population augmentation while bald eagles experienced continuous, long term reintroductions. I hypothesize that bald eagles should have the greater diversity within their population, but for the sake of posterity and other threatened species, this must be conclusively determined.

My goal was to determine the extent to which the different reintroduction histories of eastern North American golden and bald eagles have influenced the current genetic structure of their modern populations. Specifically, I used DNA sequencing and microsatellite amplification/analysis as methods of evaluation. I sequenced the mitochondrial *cytochrome b* gene (Farias et al. 2001) as a method of species analysis to create phylogenetic trees, indicated the relatedness between my sample birds and reveal large-scale population structure. I also amplified genomic microsatellites to set the stage for a fine-scale evaluation of both the historic and contemporary population structure of each species.

Table P.1. Comparison of the demographics, life histories, distribution, and reintroduction histories of bald and golden eagles in North America.

	Bald Eagles	**Golden Eagles**
Annual Reproduction	~2 eggs per clutch ~50% first year mortality (AEF)	~2 eggs per clutch
Habitat type	Forested land near a body of water (i.e. river, lake, ocean)	Mountainous forest, grasslands
Distribution (Breeding and Migration)	Both permanent and migratory populations exist across most of the US. Highest density in Florida, Washington, and Wisconsin. Lowest density in New Mexico, Utah, and Nevada.	Winter and breed across western US (California, Oregon, Washington, Idaho, Nevada, Utah, Arizona, New Mexico, Colorado, Texas, Montana, and the Dakotas). Winter in the eastern US.
Source of Reintroduced Birds	Canada, Alaska, Minnesota, Wisconsin, Washington, California, Michigan, Maryland, Virginia, Florida, Missouri, and captive facilities	Wyoming and captive facilities
Total Number of Reintroduced Birds*	1360+	195+
Lowest US Population Estimate	487 pairs in 1963 (FWS)	unknown
Current US Breeding Population Estimate	19,578 individuals in 2007 (FWS)	27,392 individuals in 2004 (FWS)

*These figures are the tallies from the original reintroduction/translocation efforts for each species. However, reintroductions continue through today, but the total number of reintroduced individuals is not known because a lack of a unified approach.

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CHAPTER ONE

Impact of Translocations on the Genetic Population Structure of Golden Eagles in North America

Allopatric speciation can arise from genetic structure within populations—which in turn is dependent on a variety of factors, such as animal movement, seasonal migration, behavior, genetic drift, selection, and even human activity. Humans can impact wildlife genetic population structure through conservation efforts such as reintroduction and translocation. To better understand the interaction between within-population structure and processes that drive speciation in a human-altered environment, we evaluated genetic structuring within populations of North American golden eagles (*Aquila chrysaetos canadensis)*. Eastern and western populations of golden eagles in North America appear to be geographically isolated, but a series of unrelated efforts relocated ~200 western birds into the east from 1981-2006. We evaluated the impact of this by determining the genetic structure of pre- and post-translocation populations of golden eagles using analysis of ten different microsatellite loci and mitochondrial cytochrome *b* gene sequencing. Analyses revealed minimal evidence of east-west genetic population structuring in either past or present populations. To verify these results were not an artifact of low diversity in selected molecular markers, I also compared North American *A. c. canadensis* to representatives of *A. c. chrysaetos* and determined that the chosen loci were polymorphic enough to detect structuring between completely isolated populations of golden eagles.

Introduction

Speciation can arise from genetic structure within populations—which in turn is dependent on a variety of factors, such as animal movement, seasonal migration, behavior, genetic drift, selection, and even human activity. Understanding the interaction between these various factors and intra-population genetic diversity can lead to insight to the mechanisms that underlie speciation. It is more important than ever that these processes are understood given the current situation of global climate change, given that wildlife management responses have included translocations—such as assisted migration/colonization. Thus, now is a critical time in conservation biology to understand how genetic population structure arises naturally and how humans can impact it.

Population Structure

Physical landscape barriers or even sheer distance can reduce or halt gene flow between populations and subpopulations and create genetic distinction on either continental or island scales (Graham and Burg 2012; Tammeleht et al. 2010; Hoglund et al. 2011). In contrast to the more familiar geographical or landscape-influenced examples, foraging and prey acquisition have been noted as an allopatric driver of population differentiation (Foote et al. 2011; Foote et al. 2013) as well as social behavior, mating systems, and migratory movement (DeWoody 2005; Koopman et al. 2007; Ficetola et al. 2009). Conversely, though the processes that affect population structuring are prevalent in nature, genetic differentiation between putative populations may be weak or absent altogether due to gene flow working around a presumed barrier. Marine species have also demonstrated homogeneity across oceans and globally (Ahrens 2013; Winklemann et al. 2013). Also, various avian species populations show high degrees of homogeny in spite of such barriers as natal philopatry and separation across continents, (Ando et al. 2011; Koopman et al. 2007; Krauss et al. 2012).

Human Impacts on Population Structure

Humans can also impact wildlife genetic population structure is through such conservation efforts as reintroduction and translocation. Numerous examples of reintroduction have been highly publicized (Beck et al. 1991, Parsons 1998, Tordoff and Redig 2001) and genetic rescue efforts of a wide variety of taxa have been successful (Pimm et al. 2006, Hedrick and Fredrickson 2009; Miller et al 2012; Laws and Jamieson 2010). However, there are potential downsides to reintroduction as a management tool, in particular when the role of genetics is not considered in the planning stages. The species under consideration could be subject to negative repercussions in subsequent generations. For example, inbreeding and loss of genetic diversity have been noted in the generations after reintroductions due to founder effect since the number of reintroduced individuals is often small (Jamieson 2011). At the opposite end of the spectrum, outbreeding depression has also emerged as a concern after being documented in the progeny of mixed-source reintroductions (Huff et al. 2011; McClelland and Naish 2007). It has even been shown that even when reintroduced populations have high genetic diversity, the degree of diversity may be lower than the original remnant population and there can be a loss of rare alleles (Brekke et al. 2011). These human-driven processes, in theory, could act either synergistically with natural processes or could subvert natural processes that are involved in local adaptation or speciation.

Genetic Population Structure of North American Golden Eagles

To better understand the interaction between within-population structure and processes that drive speciation in a human-altered environment, we evaluated genetic structuring within populations of golden eagles that were potentially heavily impacted by human actions. Golden eagles (*Aquila chrysaetos canadensis*) in North America are a species of particular interest because their genetic population structure is largely unknown. There is continuous migratory and breeding habitat in the western half of the continent that supports approximately ~30,000 individuals (Good et al. 2007). East of the Mississippi, there exists another population—presumed to be orders of magnitude smaller—that breeds in Canada and migrates into eastern US states for winter (Katzner et al. 2012). The degree of reproductive isolation between these two putative populations is unknown, but many of the processes that affect genetic structure may have been disrupted in the eastern population due to a series of unrelated translocation projects. From 1981 until at least 2006, these translocations released approximately 200 birds (most of them from Wyoming) into various eastern states via hacking (Touchstone 1997, C. McGrath, pers. comm., S. Somershoe, pers. comm). The size of the eastern population is unknown, but it has been estimated to be as low as 2000 individuals (Katzner et al. 2012). Thus, the genetic consequence of these translocations is unknown but is potentially substantial with translocations given the small total estimated size of the population.

These translocations, however, present a unique opportunity. Golden eagles are a long-lived, highly vagile species; and many of the speciation processes discussed earlier (including human interference) may be a part of their ecology. To better understand the interplay between some of these processes, we asked 1). Are there two genetically distinct populations of golden eagles in the east and the west, 2). Would there have been two genetically distinct populations of goldens without the translocations, and 3). Are the contemporary populations of eastern and western birds genetically similar to their respective historic counterparts? In this study, we answer these three questions using cytochrome *b* gene sequencing and microsatellite analysis of extant and historic populations of golden eagles from across North America. As verification of our findings, we also confirmed our molecular markers' ability to detect differences between golden eagles from decidedly distinct populations by comparing North American *A. c. canadensis* to European *A. c. chrysaetos* individuals from Sweden.

Methods

Study System

Golden eagles are found across most of the Northern Hemisphere. In western North America (roughly defined as west of 100° longitude), the species range extends from Mexico to Alaska, where individuals occur as both migrants and non-migrants. In eastern North America (roughly defined as east of the Mississippi River), golden eagles nest on cliff sides in Quebec, Ontario, Labrador, and possibly Newfoundland, but spend their winters in eastern US states (Kochert and Steenhoff 2002). Throughout the year, both populations feed on a wide variety of terrestrial prey, including carrion; and both face threats from human activity in the form of lead poisoning, incidental trapping, and wind energy (Katzner et al. 2012).

Sample Collection

To compare structure of contemporary and historical eagle populations, we used blood, tissue, or feather samples collected by twenty-seven different wildlife centers, state agencies, and eagle biologists from across the US and Canada (see Figure

1). To represent historic populations, toe pad tissue was collected from golden eagle study skins at eighteen museums in the US and Canada (see Appendix for complete list). Only study skins prepared prior to 1980 (before the first translocation) were considered representative of historic populations. In addition, blood samples from Swedish birds were collected by biologists at Sveriges lantbruksuniversitet (the Swedish University of Agricultural Sciences) working in northern Sweden and tissue samples from recent birds were collected at the Naturhistorika riksmuseet (Natural History Museum) in Stockholm.

Sample Collection, Storage, and DNA Extractions

Samples were stored at room temperature in a lysis buffer (Rudnick et al. 2005). From there, DNA from both sample types was extracted using standard phenol:chloroform protocols (Maniatis et al. 1982). Feather samples were kept in paper envelopes store at room temperature. Extractions from feathers followed the protocol found in Rudnick et al. (2005), but with the modification of adding both dithiothreitol (DTT) and ProteinaseK just before digestion to reduce degradation of DTT in the buffer during long term buffer storage. (For more detail, see Appendix A).

Cytochrome b Gene Amplification and Sequencing

The *cyt b* gene was chosen because it has been used in raptor studies in the past (Lerner and Mitchell 2005) and because of its genetic variability, making it ideal for demonstrating genetic divergence (Farias et al. 2001). I amplified the gene using avian primers H16964 and L14996 (Sorenson et al. 1999). PCR was performed in a 50 μL reaction using Fisher buffer B, 2.5 mM $MgCl_2$, 0.8 mM dNTPs, 1.5 units of Taq, 400-700 ng of DNA, and 0.6 mM avian primers H16964 and L14996. For PCR details, see Appendix A.

The PCR product was purified by Sephadex column-cleaning and amplified via ABI Big Dye reaction using nested avian primers H15646 and L15560 (Sorenson et al. 1999). After another round of Sephadex purification, the DNA was dried, reconstituted with DI formamide, and analyzed on an Avant 3130 Genetic Analyzer.

Microsatellites

I optimized amplification techniques for ten different loci originally developed in other species: Aa11, Aa15, Aa27, Aa36 (developed for *Aquila aldaberti;* Martinez-Cruz et al. 2002), Hal-10, Hal-13 (developed for *Haliaeetus albicilla*; Hailer et al. 2005), IEAAAG-04, IE-13, and IEAAAG-14 (Busch et al. 2005). Amplifications were carried out in a 20 μL reaction that included Fisher buffer B, 2.5 mM $MgCl_2$, 1 mM dNTPs, 1 unit of Taq, 50-100 ng of DNA, and 0.6 mM of each primer. Primers were labeled with either 6-FAM, VIC, NED, or PET. Genotypes were scored using Peak Scanner v 1.0, and loci were tested for allelic drop-out and null alleles using Micro-Checker.

Method Modification for Historic Samples

Extractions from historic tissue were carried out in a dedicated UV hood in a certified forensics teaching lab. To minimize the risk of contamination, neither amplicon nor contemporary golden eagle samples were permitted in the lab. During the extraction process, the phenol:chloroform step was repeated to ensure the removal of as many PCR inhibitors as possible. PCR reactions for historic samples included the addition of 24 mM BSA.

Comparison of Population Structure

To detect differences in population structure, we conducted three sets of analyses. First, we analyzed the genetic population structure for historic birds from eastern and western North America—birds who lived prior to 1980. Second, we looked for differences between contemporary birds from eastern and western North America. Finally, to verify efficacy of microsatellite selection, we compared North American golden eagles to Swedish golden eagles—with the rationale that if we were unable to detect structure between populations separated an ocean, we would be unlikely to find differences within North American birds.

We used multiple population genetics statistics methods based on genotypic data in our analyses. First, we tested six indices of diversity: F_{IS}, F_{ST}, G_{ST}, G'_{ST}, G''_{ST}, and Jost's D. Each index ranges from 0 to 1 (see Table 6) but is corrected slightly to account for the context of our data. First, F_{IS} is an inbreeding coefficient that indicates the relatedness of mating individuals. F_{ST} (Nei and Chesser 1983 is a standard indicator of genetic diversity that measures the amount of genetic variation between potential subpopulations relative to the amount of variation across the entire population (Nei and Chesser 1983). We also calculated G_{ST} (Nei 1987) —the multiallelic corrected version of Fst that allows for a more accurate assessment with more than two alleles per locus (Nei 1987). However, even with absolute differentiation between populations, as a matter of calculation, G_{ST} can never reach 1. To correct for this, we also use G´st, which takes into account a potential for high levels diversity among individuals (Hedrick 2005). However, even with absolute differentiation between populations, as a matter of calculation, Gst can never reach 1. Finally, there is still a potential for bias when the potential number of populations is small (such as in our case, k=1 or k=2); thus, we also used G´´st (Meirmans and Hedrick 2011). Aside from G-statistics, we also used Jost's D, which is based on effective number of alleles rather than primarily on heterozygosity (Jost 2008). All indices were calculated using the program GenAlEx 6.5 (Peakall and Smouse 2006).

To visualize population structure, we used two different methods: principal coordinated analysis (PCoA) and the Bayesian analysis of STRUCTURE along with an accompanying ΔK analysis (Evanno et al. 2005). PCoA relies on multi-dimensional scaling of data and assigning clustering of data points based on Eigen vectors (PCoA) , which in our case were derived from genetic distance. This was performed using GenAlEx 6.5 (Peakall and Smouse 2006). We visualized "clustering" within the data set using STRUCTURE (Pritchard et al. 2000), a Bayesian analysis program that assigns the probability of each individual's inclusion into groups. Allelic frequencies from microsatellites are the basis for determining the number of groups (number of groups is denoted as K). I used an admixture model with 100,000 MCMC iterations and a 100,000 burn-in period.

Phylogenetic Analysis

Sequences were aligned using ESEE and imported into MEGA 5 for tree-building. I built a neighbor-joining tree using the Jukes-Cantor nucleotide substitution model, which assumes equal rates of transitions and transversions. In addition, I built a Bayesian tree in Mr. Bayes 3.2.2 using the HKY-gamma model, as determined by JModelTest (Posado 2008). I also used Arlequin (Excoffier and Lischer 2010) to calculate Φst based on cyt *b* sequences. Since Φst is the nucleotide analogue of Wright's Fst, the same interpretation of differentiation values apply to Φst as to Fst (see Table 6).

Results

In total, I genotyped eighty-five contemporary eastern North America individuals, sixty-one contemporary western North America individuals, twenty-five historic eastern individuals, thirty historic western individuals, and forty-five Swedish individuals (see Table 1.1). Birds were considered "eastern" if they were collected east of the Mississippi River, and similarly, birds were considered "western" if the sample was collected west of the Mississippi. Samples were only included when at least seven out of ten microsatellites amplified. Amplification of all loci was not typically a concern for the contemporary samples, but it was for the historic samples. Thus, this threshold was established to ensure that all individuals included in the analysis (the aforementioned one hundred forty six contemporary birds and fifty-five historic birds) were genotyped to at least 70% completion. No loci showed evidence of allelic dropout. However, multiple loci were out of Hardy-Weinberg equilibrium, and there were differences in historic and contemporary populations (see Table 1.2).

Evaluating Genetic Population Structure of Contemporary Golden Eagles in North America

Using multiple statistical methods, I detected minimal evidence of east-west population structuring of golden eagles in North America. To validate STRUCTURE findings and compare putative populations without *a priori* assumptions, we performed a principal coordinate analysis (PCoA). Neither analyses detected significant distinction between birds from eastern and western North America. Similarly, multiple indices of genetic diversity, including F-statistics and Jost's D, also indicate little differentiation between potential populations (see Table 1.3).

I detected minimal evidence of east-west population structuring of golden eagles in North America using the Bayesian analysis program STRUCTURE. Individual birds are represented as individual bars in the graph, and the color of each bar represents the likelihood that an individual could belong to one group or another. A ΔK analysis of STRUCTURE simulations determined k=6 to be the most probable scenario out of the k values, but k=2 and k=3 showed nearly equally strong support (see Figures 1.2 and Figure 1.3). However, the ΔK method cannot calculate values associated with k=1 (Figure 1.2), and I was concerned that if k=1 should have been the optimal choice, we would not be able to detect it. Thus, to help elucidate the STRUCTURE analysis, we also performed a multivariate principal coordinated analysis (PCoA) on genetic distance based on genotypic data (see Figure 1.4). No major difference in aggregation in eastern versus western was detected with either a two-dimensional graph (Fig 4.a). or a three-dimensional graph (see Appendix B).

Phylogenetic analysis of sequence data further indicated continental homogeneity (see Figure 1.5a and 1.5b). We found 37 total haplotypes out of sixty-two sequenced individuals, and the most common haplotype was shared among 11 western birds and 14 eastern birds. There was an overall average evolutionary divergence of 0.3% between east and west; 0.3% divergence within eastern birds; and 0.2% divergence within western birds. Though sequence-based Φst values range from 0 to 1, Φst between eastern and western birds was -0.002—which is an artifact of Arlequin's calculation algorithm but is interpreted as 0.

Evaluating Genetic Population Structure of Historic Golden Eagles in North America

To determine whether or not the homogeneity of the contemporary golden eagle subpopulation was the result of translocations, we also compared historic populations of eastern and western golden eagles. As with the contemporary birds, we calculated the same indices of diversity (see Table 3) and the inbreeding coefficient between the two populations, and we observed similar values as for the contemporary populations.

Again, we used STRUCTURE to analyzed genotype data from historic birds. This time, ΔK indicated that there was nearly equal support for k=2 and k=3 (see Figures 1.6 and 1.7). A PCoA of historic data did indicate minor structuring between eastern and western populations. Birds from eastern North America show some aggregation compared western birds; however, western birds exhibit a wider range of variation (see Figure 1.8).

Evaluating Genetic Population Structure of Contemporary vs. Historic Golden Eagles in North America

To visualize any shifts in historic versus contemporary allelic frequencies, we also compared contemporary North American golden eagle to historic North American golden eagles. Again, we found no major differentiation (see Figure 1.9).

Evaluating the Effectiveness of Microsatellite Genotyping to Differentiate

To verify that our chosen microsatellites were polymorphic enough to detect differences between known golden eagle subpopulations, we also compared North American golden eagles to Swedish golden eagles (subspecies *Aquila chrysaetos chrysaetos*). STRUCTURE and PCoA all displayed the Swedish individuals as distinct clusters from the North American individuals (see Figures 1.10 and 1.11), and all indices of diversity were roughly twice as high between North America and Sweden as between eastern and western North America (see Table 1.5).

The most probable K value for North American and Swedish golden eagles was k=3 (see Figure 1.11). This is particularly noteworthy given the unclear STRUCTURE results from North American birds alone. A PCoA for North American and Swedish birds also revealed a degree of distinction from each other (see Figure 1.12). Data points representing Swedish individuals cluster closely with little overlap from North American individuals.

Discussion

Population Structure

Our population genetic analyses best supported the idea that there is one continuous genetic population of golden eagles in North America, and that the variation within the populations outweighs the variation between populations. Furthermore, analysis of historical samples suggests that the limited differentiation in present populations is consistent with that observed historically. Thus, there appears to be few impacts of translocation on the population genetics of North American golden eagles.

At a continental scale, it is often expected for populations to exhibit some degree of divergence, though. From some perspectives, it may be surprising that golden eagles exhibit such limited population structuring across North America. It is worth noting that the pattern of increasing numbers in our diversity indices behaved predictably given their relation to each other. F_{ST} and G_{ST} have an established set of ranges of interpretation for of values (see Table 1.6), but these categories do not apply to G'_{ST}, G''_{ST}, and Jost’s D given their differences in calculation. However, these indices all relate to each other in a predictable manner (Meirman and Hedrick 2011), which was reflected in our calculations and reinforces the idea that there is little differentiation between eastern and western golden eagles.

Verification of Marker Selection

To reduce the likelihood that our results were due to low polymorphisms in selected microsatellites, we included a comparison between the North American *A. c. canadensis* and the European *A. c. chrysaetos*. However, we learned that this lack of distinction is not necessarily a result of our selected markers since North American and Swedish golden eagles can be clearly distinguished based on the same analysis methods used for North American specimens only. Though future analyses of North American birds may benefit from a greater number of microsatellites or a suite of SNPs, our selected markers indicated only weak genetic structure across North American birds.

Also, the data suggested possible concerns with selected loci since all showed deviations from Hardy-Weinberg in either historic or contemporary populations. Recently, the genome of the golden eagle was sequenced (Doyle et al. 2014), and it was discovered that some of the loci were near coding regions of their respective chromosomes. In addition, the fact that there are more deviations currently in the eastern population suggest admixture, possibly as a result of the translocations. Future analyses would benefit from a larger number of individuals and more loci, though, and that will soon be a possibility upon genome publication.

Similar Species with Weakly Structured Populations

Factors including migratory behavior, within-season movement, and various aspects of behavioral ecology (i.e., resource partitioning, predator evasion strategies, etc.)

all can play roles in the development of population structure (Langerhans et al. 2007; Ando et al. 2011; Foote et al. 2013; Banks et al. 2013). In North America, some golden eagles are highly migratory whereas other sedentary populations make seasonal non-migratory movements. In similar animal populations where individuals have long-distance movement capabilities, weak genetic structure is not truly a rare phenomenon. Boreal owls and mallards, for example, both are highly vagile demonstrate weak genetic structure continentally and globally, respectively; and both are highly vagile like golden eagles (Kraus et al. 2012; Dean et al. 2013). It follows that varying degrees of gene flow are possible in the absence of (or with the ability to overcome) geographic barriers. This is part of why only marine species tend to be suggested as truly panmictic (Kraus et al. 2012).

Similar Species with Highly Structured Populations

Nevertheless, vagility is not the final deciding factor on the degree of population structure. Red-tailed hawks (*Buteo jamaicensis*) in North America, for example, have similar movement capacity and behavior as golden eagles, but show high levels of population structuring (Hull et al. 2008). However, different populations of red-tailed hawks show strong preference for different habitat types, which is even reflected in adapted phenotypic differences across populations. These preferences are thought to be strong driving factors in divergence and the establishment of population structure (Hull et al 2008). In contrast, golden eagles appear to be much more general in their habitat preference, given that within a clearly single population, some golden eagles may be tree, cliff, or ground-nesters and they may specialize on Corvids, Leporids, or Galliforms.

Thus it seems likely that the degree to which a species is a specialist or generalist may interact with individual vagility to mediate effects on genetic structure.

Other Nesting Across North America

However, the premise that golden eagles are divided into geographically separate populations may not be as straightforward as previously assumed. Within the just past two years, golden eagles have been documented in habitat between these loosely defined "borders," regions not traditionally included in their acknowledged distribution range. Most notably, previously unknown nesting has been observed in both Manitoba and eastern Nunavut in the geographical region between presumed eastern and western golden eagle ranges (Asselin et al. 2013). Also, recent telemetry data from birds wintering in Minnesota have shown the same birds alternating between eastern and western habitat for different breeding seasons (Martell, unpublished data). Thus, it is possible that the two putative populations have never actually been separate at all, and it was a lack of knowledge that led to the presumption of potentially two reproductively separate populations. It is also possible that North American golden eagles were one population in the past, but have been separated to small degree within the last century from population declines and are only now reuniting.

The Impacts of Human Activity on Genetic Structure

In genetic terms, divergence leads to speciation most prominently in two ways: selection and drift. Humans can interfere with either of these processes in a number of ways, both actively and passively. On a more passive level, anthropogenic habitat fragmentation can isolate previously joined populations, halting gene flow and allowing the emergence of genetically distinct populations (Hu et al. 2011). Humans can actively disrupt natural processes through recreational activities such as hunting and fishing (Allendorf and Hard 2009). Since both activities often target specific phenotypes, they are essentially creating selective pressure. Even at the conservation level, such measure as reintroductions, assisted migrations/colonizations, and translocations can shift existing allelic frequencies (the very basis of genetic drift) or introduce new alleles into a population. In the case of golden eagles, there was an introduction of non-local birds into an existing population—more of a population augmentation rather than a true reintroduction. These translocations had the potential to shift the genetic trajectory of the eastern population. However, the effects appear to be neutral since there seems to be very little differentiation between the two populations and the translocations may have been roughly similar to background migrations that maintain gene flow. Given the differences in golden eagles and other species that show more structure, there are a variety of conditions that might make human-assisted migrations more impactful, and possibly detrimental, if rare alleles are lost in the process. The vagility of a species seems to play a role, thus more careful consideration might be required before the translocation of less mobile species. Also, given that it takes only 1-10 migrants per generation to simply maintain gene flow (Mills and Allendorf 1996), generation time is also a worthwhile consideration for number of individuals in translocation efforts.

Conclusion

Based on both nuclear and mitochondrial evidence, we concluded that 1). modern-day golden eagles exhibit little genetic population structure across the continent, 2). prior to the translocations, there was still minimal genetic population structuring across the continent, and 3). a comparison of historic and contemporary birds indicates little to no change in genetic structure over the past century.

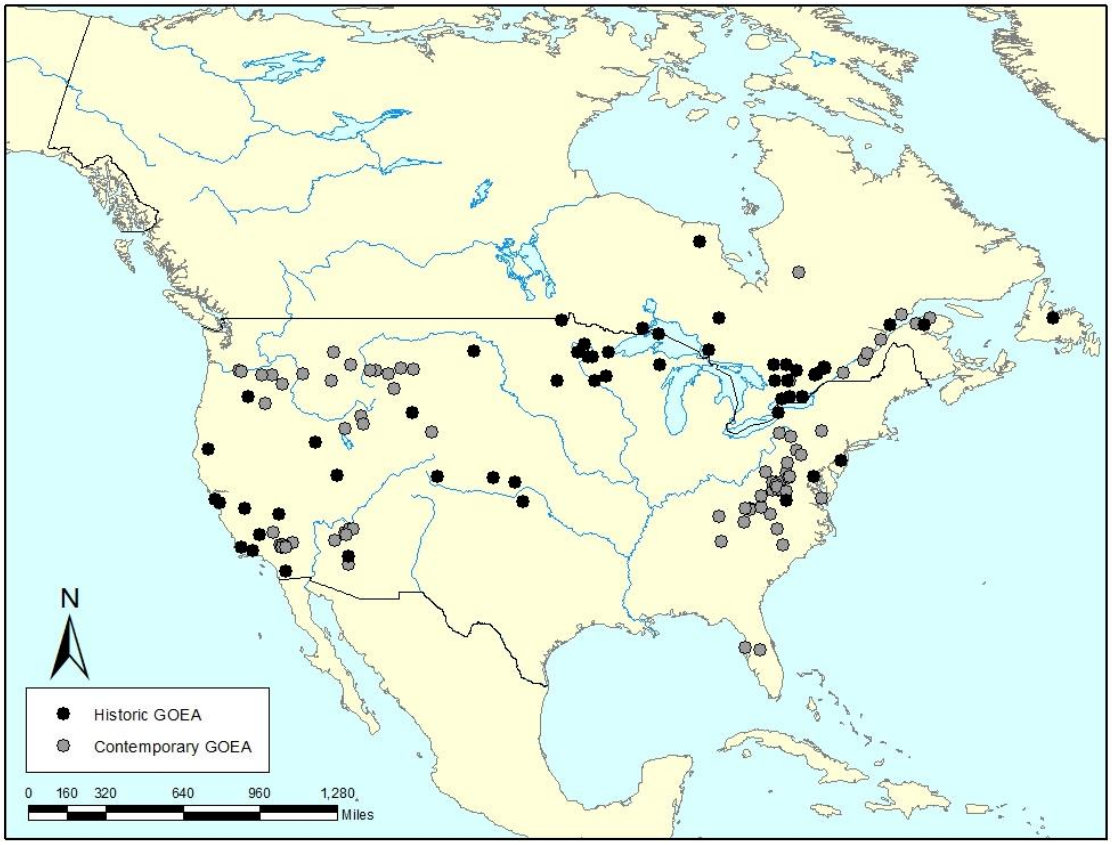


Figure 1.1. Map of all approximate golden eagle sample origins. Produced using an ESRI basemap in ArcGIS 10.

Figure 1.2. K=1-3 for contemporary golden eagles. All individuals were ordered, left to right, most western to most eastern. Therefore, bars (individuals) further are the left came from further west, and samples towards the right came from further east.

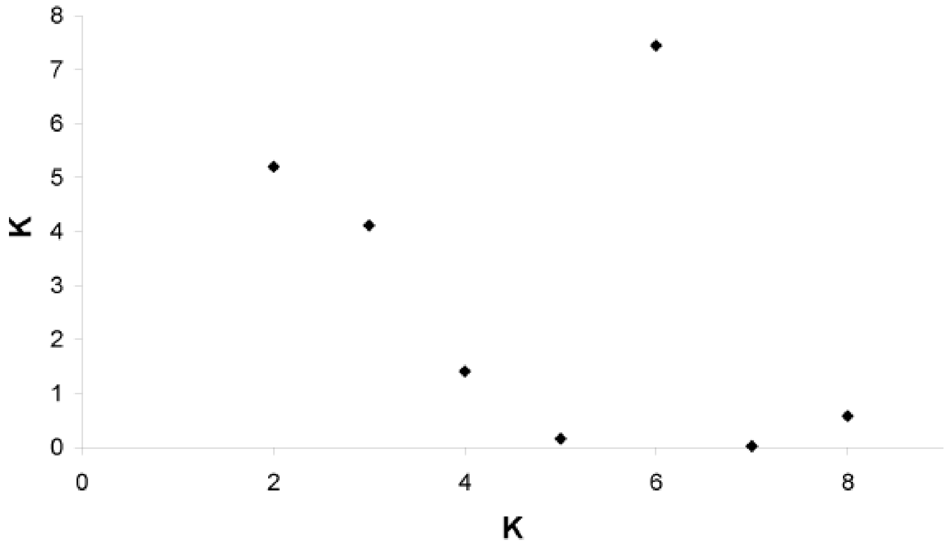


Figure 1.3. ΔK analysis of STRUCTURE simulations determined K=6 to be the most probable model out K=1-8 runs.

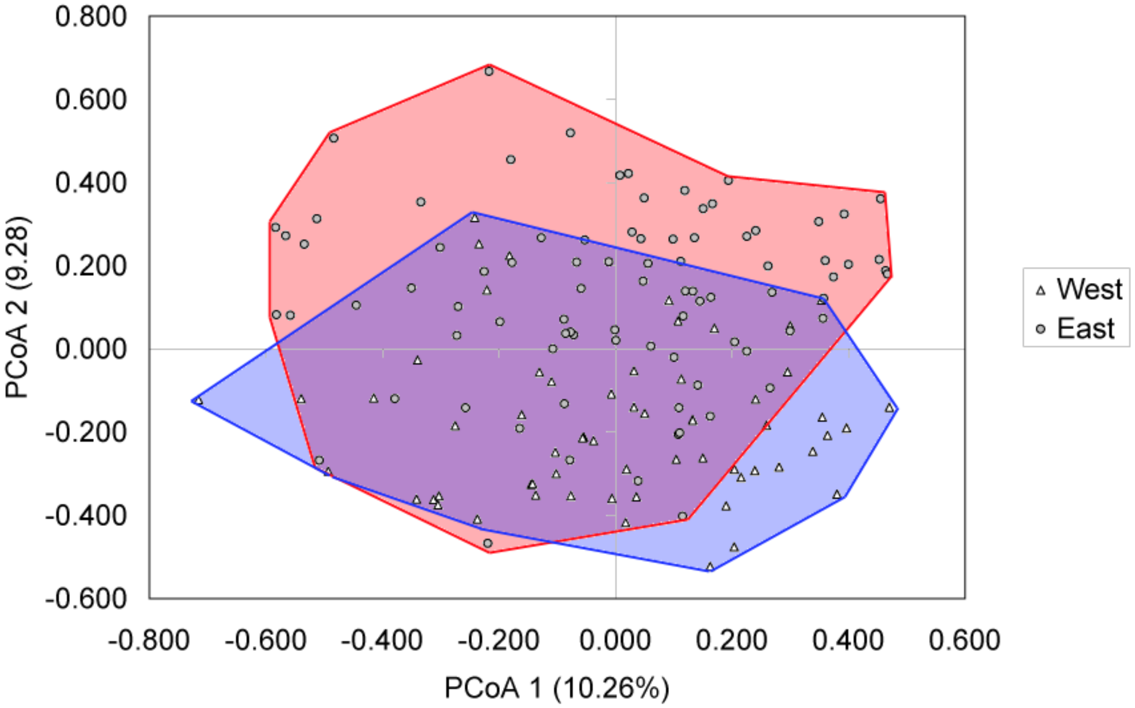


Figure 4. Principal coordinated analysis for contemporary North American individuals. The y-axis represents principal coordinate 1 with an Eigen value of 10.26. The x-axis represents principal coordinate 2 with an Eigen value of 9.28.

Figure 1.5.a. Neighbor-joining tree of all North American golden eagles, Tree was built with the Jukes-Cantor nucleotide substitution model. Western individuals are represented in blue; eastern individuals are in red The outgroup is represented by an imperial eagle (*Aquila heliaca*).

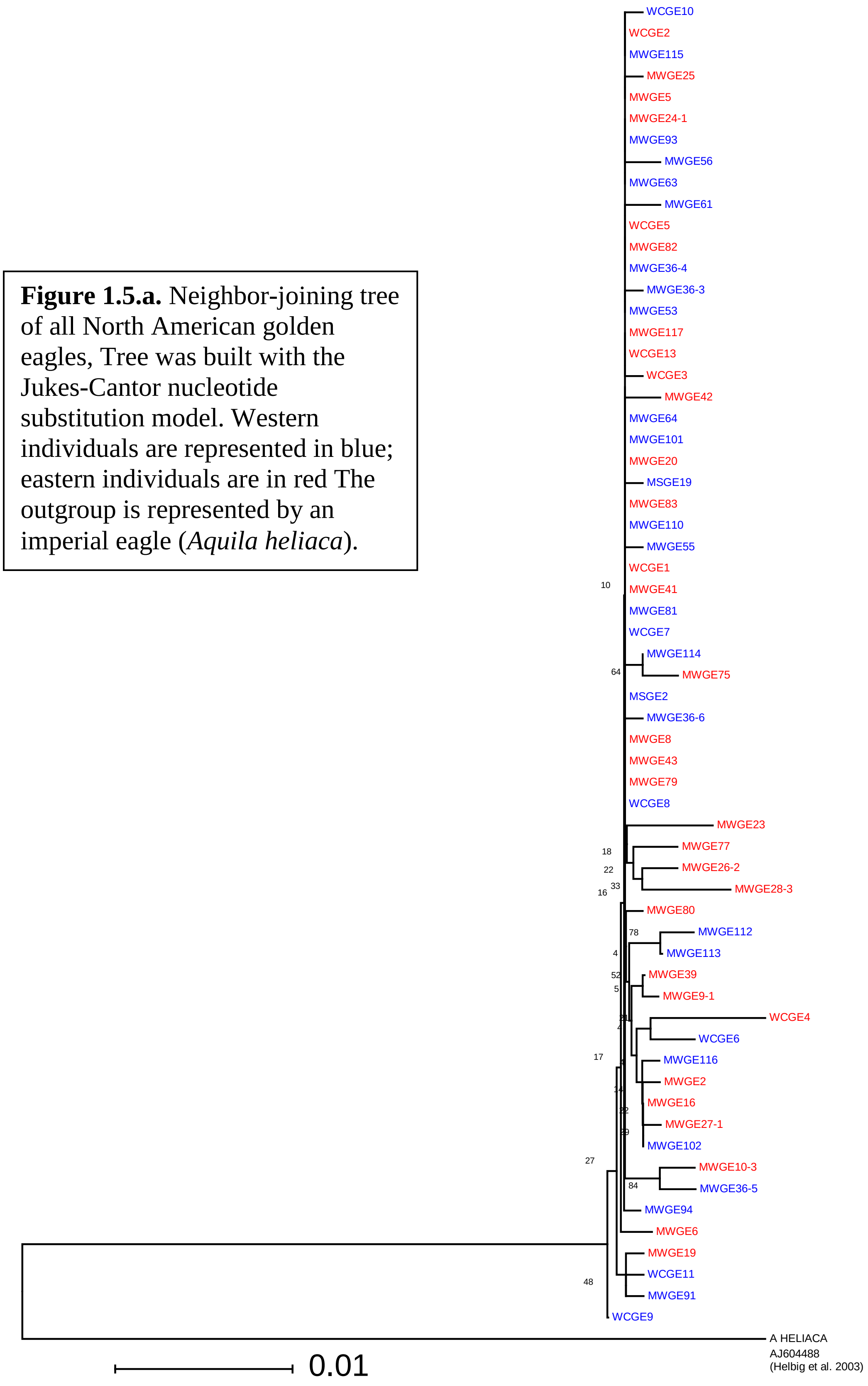
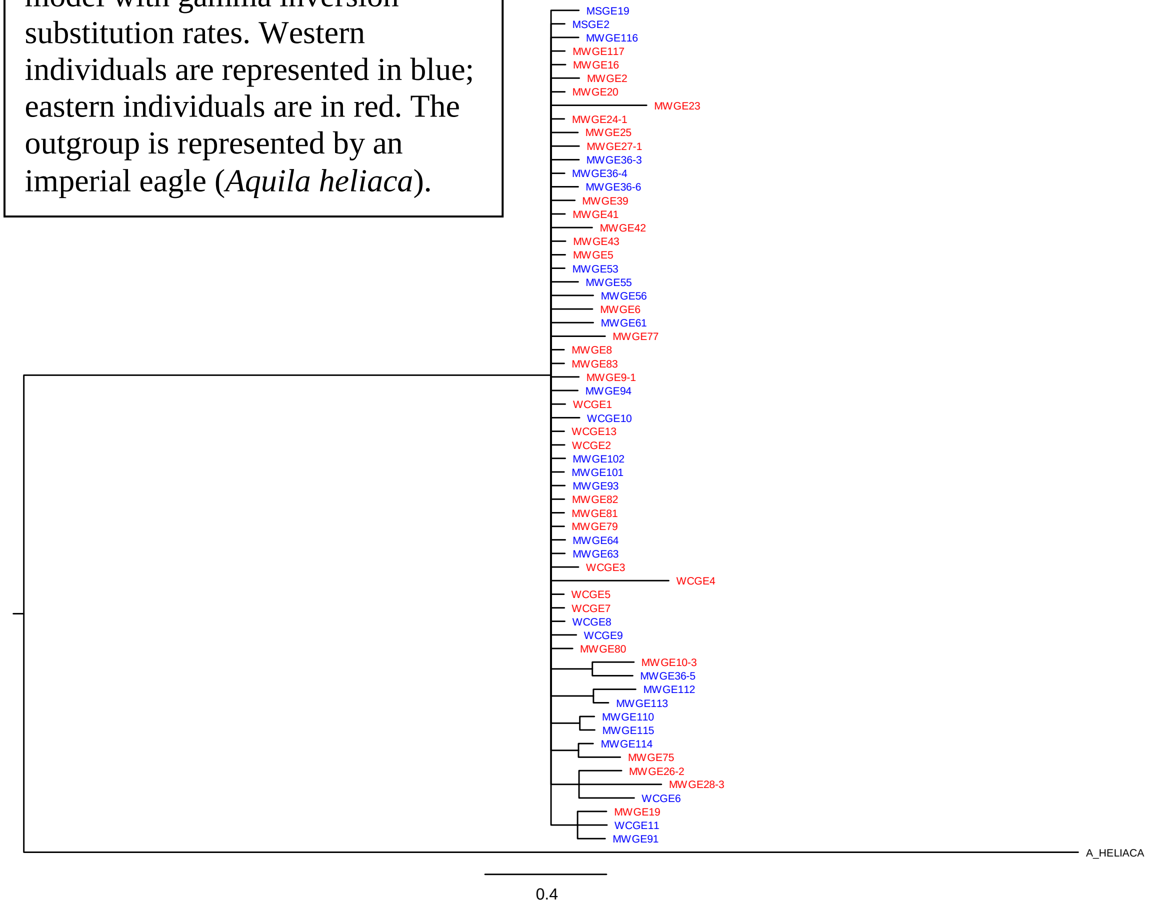


Figure 1.5.b. Bayesian tree of all North American golden eagles, Tree was built using the HKY model with gamma inversion substitution rates. Western individuals are represented in blue; eastern individuals are in red. The outgroup is represented by an imperial eagle (*Aquila heliaca*).



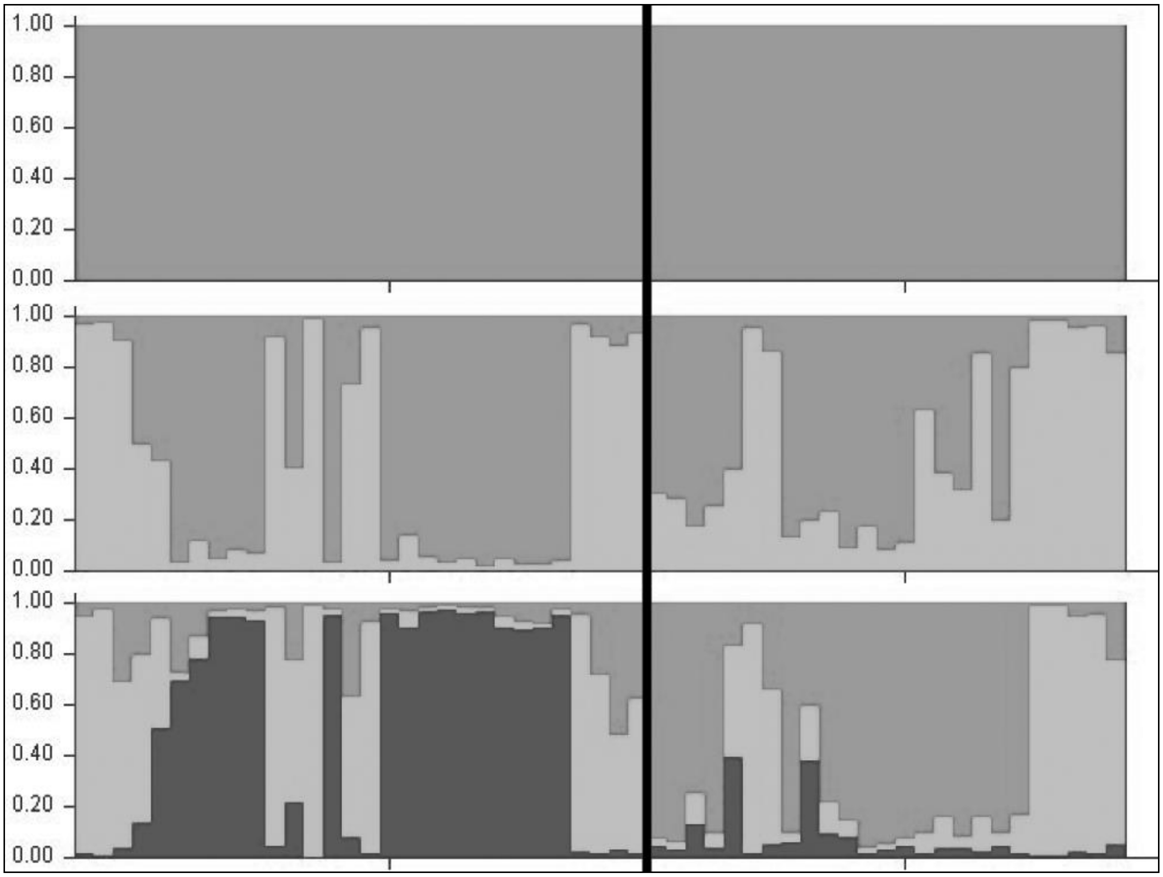


Figure 1.6. K=1-3 for historic golden eagles. All individuals were ordered, left to right, most western to most eastern. Therefore, bars (individuals) further are the left came from further west, and samples towards the right came from further east.

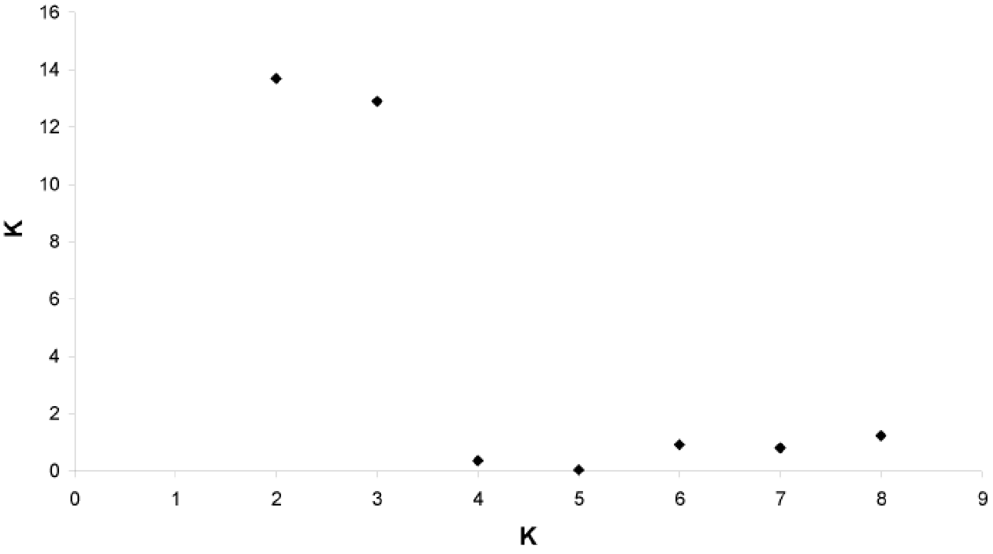


Figure 1.7. ΔK analysis of STRUCTURE simulations determined K=1 to be the most probable model out K=1-8 runs.

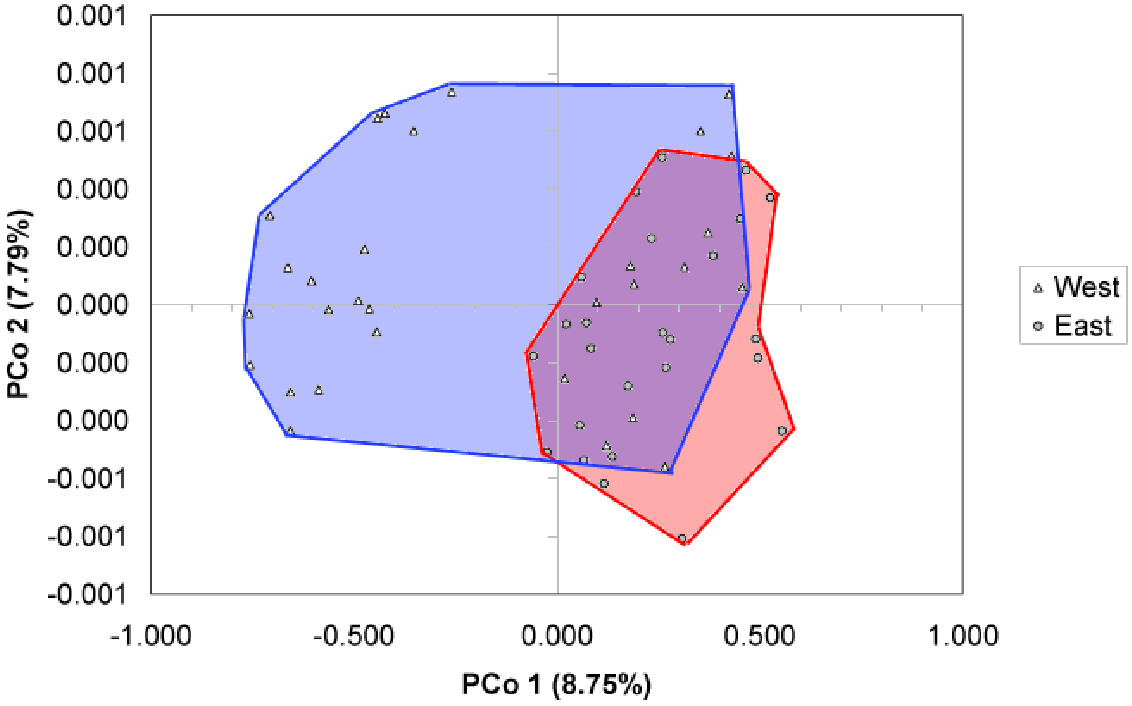


Figure 1.8. Principal coordinated analysis for historic North American individuals. The y-axis represents principal coordinate 1 with an Eigen value of 8.75. The x-axis represents principal coordinate 2 with an Eigen value of 7.79.

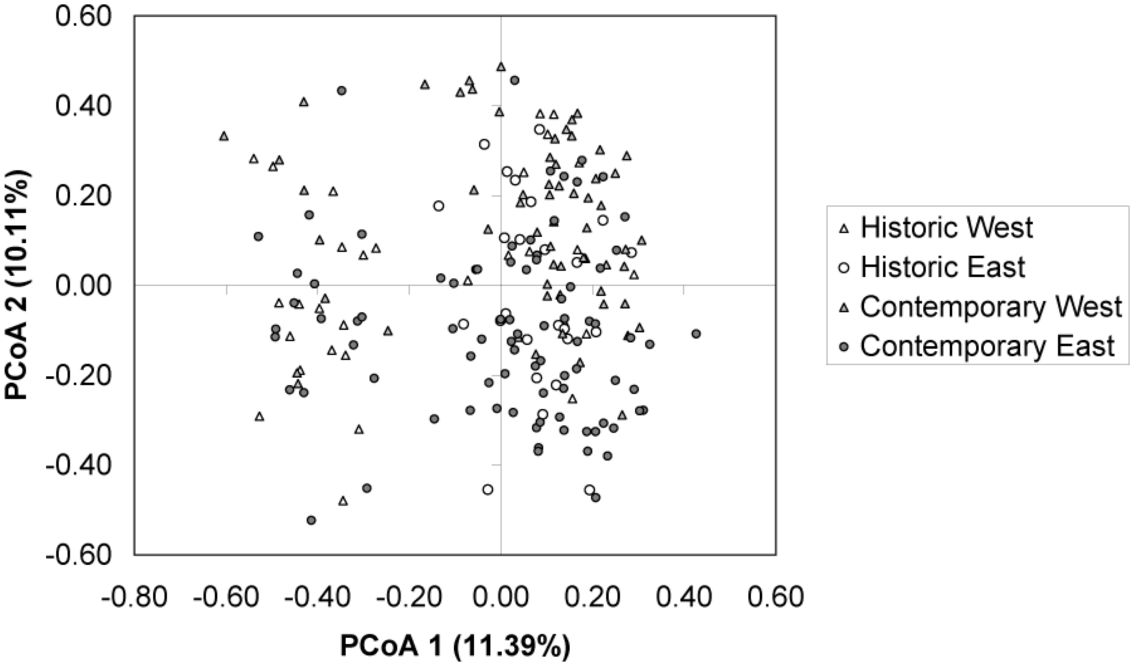


Figure 1.9. Principal coordinate analysis for contemporary and historic North American individuals. The y-axis represents principal coordinate 1 with an Eigen value of 11.39. The x-axis represents principal coordinate 2 with an Eigen value of 10.11.

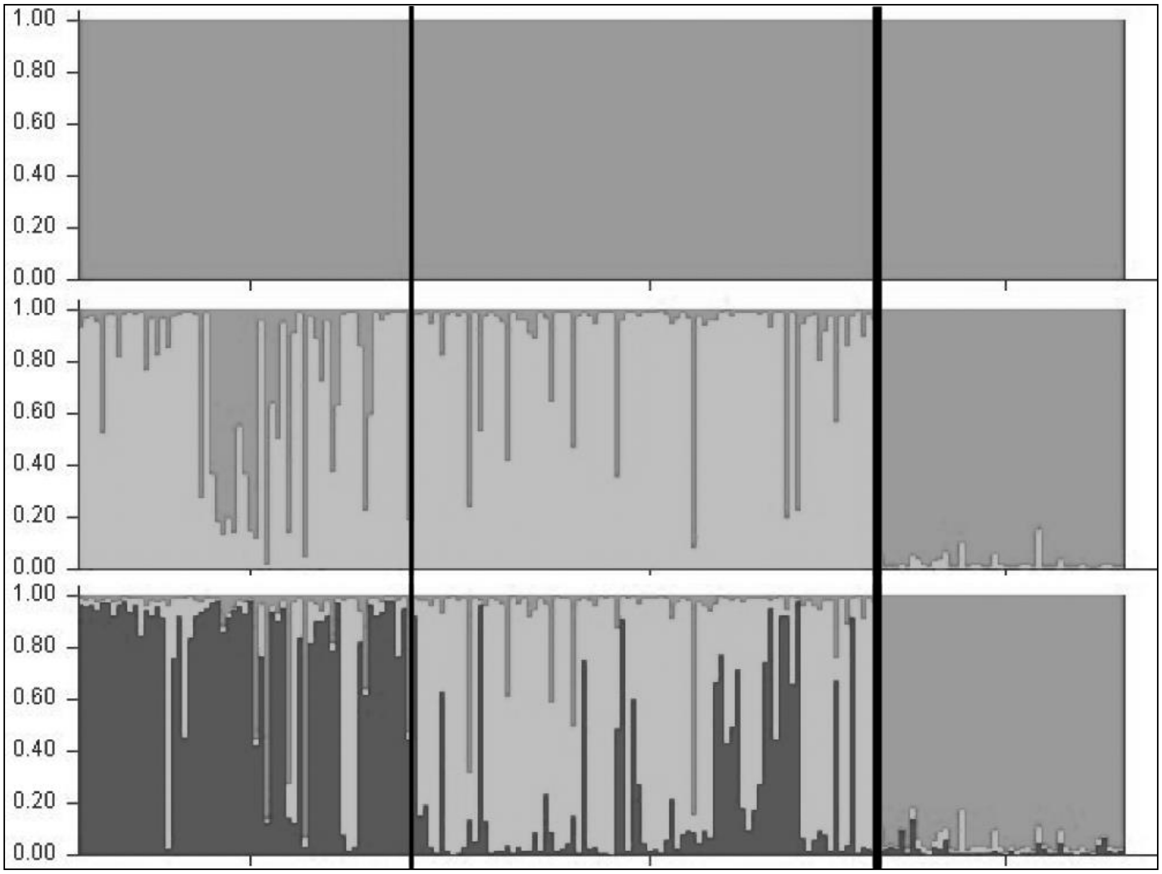


Figure 1.10. K=1-3 with contemporary North American individuals and Swedish individuals. All individuals left of the bolded bar are North American; individuals left of the thin bar are western and to the right of the thin bar are eastern.

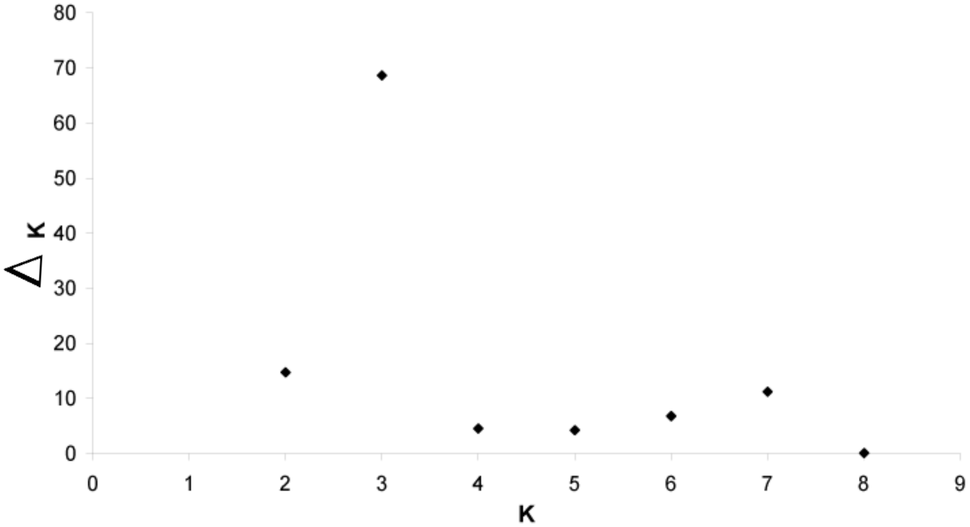


Figure 1.11. ΔK analysis for North American and Swedish birds determined K=3 to be the most probable model out K=1-8 runs.

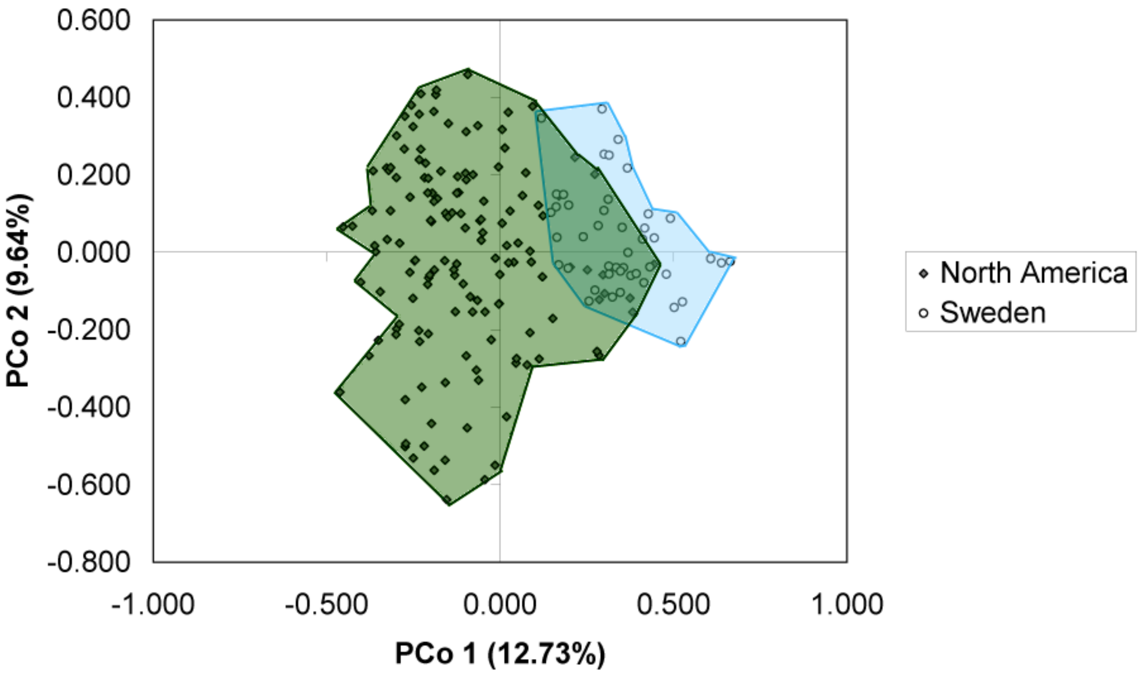


Figure 1.12. Principal coordinated analysis for contemporary North American and Swedish individuals. The y-axis represents principal coordinate 1 with an Eigenvector value of 12.73. The x-axis represents principal coordinate 2 with an Eigenvector value of 9.64.

Table 1.1. Origin of all golden eagle samples

State/Province	Number of Individuals	Era	Category
Alabama	1	Contemporary	East
Florida	2	Contemporary	East
North Carolina	2	Contemporary	East
Pennsylvania	10	Contemporary	East
Tennessee	1	Contemporary	East
Virginia	24	Contemporary	East
West Virginia	10	Contemporary	East
Newfoundland/Labrador	1	Contemporary	East
Ontario	4	Contemporary	East
Quebec	30	Contemporary	East
Arizona	6	Contemporary	West
California	15	Contemporary	West
Idaho	14	Contemporary	West
Montana	7	Contemporary	West
Oregon	7	Contemporary	West
Wyoming	12	Contemporary	West
Quebec	15	Historic	East
Ontario	5	Historic	East
Virginia	3	Historic	East
Maryland	1	Historic	East
New Jersey	1	Historic	East
Alaska	1	Historic	West
Arizona	1	Historic	West
California	10	Historic	West
Colorado	1	Historic	West
Kansas	3	Historic	West
Minnesota	8	Historic	West
North Dakota	1	Historic	West
Nevada	1	Historic	West
Oregon	1	Historic	West
Utah	1	Historic	West
Wisconsin	1	Historic	West
Wyoming	1	Historic	West

Table 1.2. Hardy-Weinberg analysis on microsatellite loci. While there were deviations in both historic and contemporary populations, most contemporary versions of the loci deviated from Hardy-Weinberg.

	Historic Western			**Contemporary Western**			**Historic Eastern**			**Contemporary Eastern**		
Locus	**DF**	**χ^2**	**p-value**	**DF**	**χ^2**	**p-value**	**DF**	**χ^2**	**p-value**	**DF**	**χ^2**	**p-value**
Aa15	10	52.91	0.00*	10	34.72	0.00*	15	33.58	0.004*	6	62.12	0.00*
Aa11	36	76.56	0.00*	45	83.49	0.00*	15	26.84	0.03*	45	250.21	0.00*
Aa12	21	68.11	0.00*	28	265.95	0.00*	10	10.20	0.423	36	394.01	0.00*
Aa36	28	50.03	0.01*	45	80.12	0.00*	15	25.89	0.039*	55	153.34	0.00*
Hal-13	3	1.23	0.75	3	6.84	0.08	3	1.59	0.660	6	22.99	0.00*
IE04	21	36.19	0.02*	45	134.92	0.00*	6	9.95	0.127	55	233.74	0.00*
IE13	3	5.50	0.14	3	58.18	0.00*	3	0.04	0.998	3	96.04	0.00*
Aa27	15	32.62	0.01*	28	145.38	0.00*	6	2.96	0.814	55	309.07	0.00*
IE14	15	60.35	0.00*	10	6.43	0.78	3	3.76	0.289	10	111.11	0.00*
Hal-10	21	34.94	0.03*	55	179.18	0.00*	21	27.41	0.158	66	369.59	0.00*

Table 1.3. Indices of differentiation between contemporary eastern and western golden eagles in North America

Measure	Value	p-value
F_{is}	0.26	-
F_{st}	0.031	<0.001
G_{st}	0.026	<0.001
G'_{st}	0.051	<0.001
G''_{st}	0.158	<0.001
Jost’s D	0.112	<0.001

Table 4. Indices of differentiation between historic eastern and western golden eagles in North America.

Measure	Value	p-value
F_{is}	0.32	-
F_{st}	0.045	<0.001
G_{st}	0.03	<0.001
G'_{st}	0.058	<0.001
G''_{st}	0.165	<0.001
Jost’s D	0.113	<0.001

Table 1.5. Indices of differentiation between golden eagles in North America and Sweden.

Measure	Value	p-value
Fis	0.223	-
Fst	0.064	<0.001
Gst	0.059	<0.001
G´st	0.111	<0.001
G´´st	0.340	<0.001
Jost’s D	0.258	<0.001

Table 1.6. Values for G-related Indices

Fst Values	Meaning in terms of Population Differentiation
0.0	No differentiation
>0.05	Little differentiation
0.05 – 0.15	Moderate differentiation
>0.15	Great differentiation
1.0	Absolute differentiation

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CHAPTER TWO

Changes in Genetic Structure of Bald Eagles (*Haliaeetus leucocephalus*) Before and After the Translocations of the Late Twentieth Century

Conservation translocations are common in management, and they are receiving increasingly more attention as a potential managerial response for global climate change. However, effective conservation management incorporates multiple planning considerations, often including the maintenance of some degree of original genetic structure. To address this subject, we retrospectively investigated one of the world's most well-known translocation projects, that of the bald eagle (*Haliaeetus leucocephalus*) in North America. Methods included sequencing of the mitochondrial cytochrome *b* gene for broad phylogenetic comparison and nuclear DNA microsatellite analysis to determine fine-scale genetic population structure. Contemporary samples came from researchers, zoos and wildlife rehabilitation facilities across the US; and historic populations were represented by preserved museum study skins. Results based on Bayesian analysis of microsallite allelic frequencies demonstrate that bald eagle genotypes exhibit distinct clinal variation from Alaska to Florida, but birds from states with the highest numbers of reintroductions (largely in the eastern US) are a genetic "blend" of origins. This is in contrast to the historic populations demonstrating slight clinal variation. However, total genetic diversity has remained largely unchanged—indicating the reintroductions successfully included a wide variety of translocated birds that established breeding populations.

Introduction

Effective conservation management incorporates multiple planning considerations, often including the maintenance of some degree of original genetic structure. Without this forethought, populations may lose all or some parts of their genetic diversity. This problem has been observed in a variety of reintroduced taxa (Ewing et al. 2008; Barba et al. 2010). In fact, an array of negative consequences can follow a lack of genetic planning, such as inbreeding depression (Keller and Waller 2002; Edmands 2007; Brekke et al. 2010; Jamieson 2011; Spiering et al. 2011), outbreeding depression (Edmands 2007; Huff et al. 2011; Marshall and Spalton 2000), genetic load (Matilla et al. 2012), and loss of variation (Frankham 1995), all of which decrease the overall fitness of individuals.

Conservation Translocations

Translocations are sometimes used to increase genetic diversity within small populations, but in their most basic form, translocations move an organism or group of organisms from one location to another in an effort to augment existing populations, maintain genetic diversity, or recolonize a species' former distribution (Griffith et al. 1989; Sarrazin and Barbault 1996; Seddon 2010; Thomas 2011; IUCN 2013). There is little consensus on a preferred framework for translocation success (Griffith et al. 1989; Armstrong and Seddon 2008; Sandler 2010; Seddon 2010; IUCN 2013; Hoegh-Guldberg et al 2008), although the debate has most recently focused on broader questions focused on cost/benefit analyses, ecosystem services, and habitat connectivity (Lawler and Olden 2011).

The Role of Genetics in Conservation Translocations

Largely absent from the debate over approaches to translocations has been the role of genetics. Only 15% of 515 papers published on reintroductions between 1935 and 2005 discuss the genetics of various translocation projects (Seddon et al. 2007). Furthermore, when genetics is considered, it is most frequently evaluated retrospectively; indicating genetics have been more of an afterthought than a premeditated part of the project planning. Within the most recent literature, though it is becoming a somewhat common suggestion for project managers to consider population genetics for conservation translocations (IUCN 2013), there is little practical guidance or clarity offered. For example, in some suggestions, genetic structure is only discussed in the context of the population that may be augmented but not the source population (Hoeugh-Guldberg et al 2008). This leaves out any possibility of speculation in the matter of how a population will fare with a given reduction (or increase) in genetic diversity.

The lack of attention given to genetics is relevant because of the wide variety of ecological factors that impact genetic population structure. For example, social behavior, feeding strategies, mating systems, and migratory movement work independently or interactively to influence population genetic structure and diversity (DeWoody 2005; Foote et al. 2011; Ficetola et al. 2009; Koopman et al. 2007). Translocations all impact these processes and thus disregarding their consequences may be detrimental to populations involved in translocation plans.

Although it is critical to incorporate genetic considerations into translocation planning, this can also present challenges because the long-term genetic effects of translocation on populations are still not completely understood. To address this problem, we retrospectively investigated one of the world's most well-known translocation projects, that of the bald eagle (*Haliaeetus leucocephalus*) in North America.

Review of Translocation History of Bald Eagles

Beginning in the 1970's, wide-scale bald eagle reintroduction projects were carried out by a variety of state, federal, and non-governmental organizations and agencies. The projects were developed with a sense of urgency and essentially entailed relocating birds from wherever a stable population existed to wherever the birds had been extirpated. There was little capacity or time for thought of the genetics of the efforts. Most sources birds came from Alaska, different parts of Canada, and the Pacific Northwest, where the populations had declined the least. These birds were reintroduced into various parts of eastern US, and the majority of birds were released via hacking—a technique in which nestlings are moved to a new location young enough that they will identify the new site as their natal territory. To a much lesser degree, bald eagle releases continue today through captive breeding efforts by a number of private organizations. A very conservative estimate suggests a minimum of 1300-1700 bald eagles were reintroduced, but due to incomplete records, it is not possible to determine the total number (see Table 3.1).

Through all the efforts, bald eagle reintroductions were immensely successful in terms of sheer population increase. As of 2007, there were 9,789 nesting pairs in the contiguous US (FWS), but their numbers state-by-state have been rising steadily (or doubling in some states) ever since. This renders the most recent total estimate outdated, though a current population number is not known.

Even with this success, however, there have been very few major studies of the population genetics of these birds. Existing population genetics studies have limited by region (Morizot et al. 1985) and were focused on a narrow time span. Thus far, there have been no studies assessing the genetic population structure of bald eagles across the continent or how the structure might have changed since the reintroductions began.

Because of their history, bald eagles present a unique opportunity for a retrospective look at how genetic population structure is impacted by exceptionally large-scale reintroduction efforts. Once numbering as high as 50,000 breeding pairs, this species was almost completely extirpated from much of the area of the US south of Canada, having been reduced to 487 pairs in 1963. Since that time, at least between 1360 and 1750 birds were translocated from breeding areas primarily in Alaska, Canada, and the Pacific Northwest to states across the eastern US.

To better understand the long-term effects of major translocation efforts on population genetics, we compared the pre- and post-translocation populations of bald eagles across the United States (including the contiguous states and Alaska). Specifically, we wanted to determine 1). How were historic populations genetically structured. 2). How are the modern populations structured? 3). What do population genetics indicate about difference between historic and modern populations, and was there an obvious impact from reintroduction? To answer these questions, we focused on cytochrome *b* gene sequencing and microsatellite analysis of historical museums specimens and contemporary eagles sampled from wildlife centers and in the field across the continent. We use these data to make inference about the impact of past translocation activity on modern population structure and discuss how translocation actions could have been altered to result in different genetic outcomes in recovered populations.

Methods

Sample Collection

To understand the changes in genetic population structure of bald eagles before and after the reintroduction, we performed analyses on genetic data of bald eagles that lived across the North American continent before and after the reintroductions. I collected modern samples from five different wildlife centers, state agencies, and eagle biologists from across the US and Canada (see Table 1, Figure 1). To represent historic populations, I collected toe pad tissue from bald eagle study skins at five museums in the US. We only considered study skins prepared prior to 1980 to be representatives of historic populations, as adults before this time should have been native to the region they were collected in.

Sample Collection, Storage, and DNA Extractions

Blood samples were stored at room temperature in a lysis buffer (Rudnick et al. 2005), and from there, DNA was extracted using standard phenol:chloroform protocols (Maniatis et al. 1982). Feather samples were kept in paper envelopes store at room temperature. Extractions from feathers followed the protocol found in Rudnick et al. 2005 (see Appendix 1)., but with the modification of adding both dithiothreitol (DTT) and ProteinaseK just before digestion to reduce degradation of DTT in the buffer during long term buffer storage.

Cytochrome b Gene Amplification and Sequencing

We used the mitochondrial cytochrome *b* gene as an indicator for broad-scale population patterns because it is generally highly conserved but still shows some variability (Farias et al. 2001). PCR was performed in a 50 µL reaction using Fisher buffer B, 2.5 mM $MgCl_2$, 0.8 mM dNTPs, 1.5 units of Taq, 400-700 ng of DNA, and 0.6 mM avian primers H16964 and L14996 (Sorenson et al. 1999). PCR product was purified by Sephadex column-cleaning and sequenced via ABI Big Dye reaction using nested avian primers H15646 and L15560 (Sorenson et al. 1999). Samples were analyzed on an ABI 3130 Genetic Analyzer.

Microsatellites

We optimized PCR settings for nine different microsatellite loci originally developed in other raptor species: amplification techniques for ten different loci originally developed in other species: Aa11, Aa15, Aa27, Aa36 (developed for *Aquila aldaberti;* Martinez-Cruz et al. 2002), Hal-10, Hal-13 (developed for *Haliaeetus albicilla*; Hailer et al. 2005), IEAAAG-04, IE-13, and IEAAAG-14 (Busch et al. 2005; see Table 2). Amplifications were carried out in a 20 µL reaction that included Fisher buffer B, 2.5 mM $MgCl_2$, 1 mM dNTPs, 1 unit of Taq, 50-100 ng of DNA, and 0.6 mM of each primer. Forward primers were labeled with either 6-FAM, VIC, NED, or PET; and genotypes were scored using Peak Scanner v 1.0.

Method Modification for Historic Samples

Extractions from historic tissue were carried out in a dedicated UV hood in a certified forensics teaching lab. To minimize the risk of contamination, neither amplicon nor contemporary bald eagle samples were permitted in the lab. During the extraction process, I added the step of repeating phenol:chloroform step was repeated to ensure the removal of as many PCR inhibitors as possible. PCR reactions for historic samples included the modification of 24 mM BSA.

Population Structure

I used multiple analytical methods to visualize the population structure of bald eagles. My first method was a principal coordinated analysis (PCoA), which is a form of multidimensional scaling based genetic distance, using GenAlEx (Peakall and Smouse 2006). Second we used the Bayesian analysis program STRUCTURE (Pritchard et al. 2000) set as an admixture model with 100,000 MCMC iterations and a 100,000 burn-in period, and to determine K, we used ΔK (Evanno et al. 2005). To measure variation between small subpopulations within the total population, I used GenAlEx to determine pairwise F_{ST} values across the each state's individuals. I tested historic bald eagle populations for isolation-by-distance using a Mantel test based on genetic distance and latitude and longitude coordinates.

There was a potential that my results could have been confounded by seasonal migrant eagles. My samples were collected throughout the year, which means that there was a chance that a bird's true origin may not have been the same as where it was collected. To verify this wasn't creating issues in the interpretation of my data, I also ran an AMOVA and a PCoA on sixty-five birds that were known to be in their identified region during the breeding season, which we defined as April-October based on Laing et al. (2005). During the rest of the year (November-March), there is a possibility that a bird observed in a particular area is actually a migrant from another region.

Phylogenetic Analysis

Sequences of the *cyt b* gene were aligned using ESEE and imported into MEGA 5 for tree-building. I built both a neighbor-joining tree, using the Jukes-Cantor nucleotide substitution model, and a Bayesian tree using the program Mr. Bayes. I calculated Φst values based on cyt b sequences using Arlequin 1.0.

Impact of Translocations

We performed comparative analyses on historic versus contemporary populations of bald eagles to determine how the genetic population structure is different as a result of the reintroductions. Specifically, we used Microsatellite Analyser (Dieringer and Schlotterer 2003) to compute global G_{st} over 10,000 permutations, Nei's D (1978; corrected for population size), and chord distance D_A (Nei et al 1983). Also, I used GenAlEx to compare the number of alleles, effective number of alleles and total and locus-specific heterozygosity. Lastly, we used STRUCTURE to compare historic and contemporary Alaskan and Florida populations, to verify that two large source populations were not significantly different in modern birds compared to historic birds. Alaska was chosen alone as a comparison, since it is unlikely that any individuals from other parts of the country have been translocated to Alaska, whereas even states without any organized reintroduction (e.g. Virginia) may include reintroduced birds that dispersed after release.

Results

Genetic Structure of Contemporary Bald Eagles

In total, we genotyped 105 birds from across the US. Of these birds, eighty-two samples represented the contemporary, post-translocation population; and twenty-three preserved specimens of bald eagles from museums represented the historic, pre-reintroduction population.

Within contemporary populations, I determined there were deviations from Hardy-Weinberg in five of the nine microsatellite loci that we used (Table 2). Also, we calculated expected and observed heterozygosity in individuals from each region (Table 3) and pairwise F_{ST} between each region (Table 4) to determine the levels of differentiation between subpopulations. The greatest divergence was between Alaskan birds and Florida birds, followed by Alaskan individuals and birds from the eastern US.

Eagle populations showed evidence of underlying spatial genetic structure. Bayesian STRUCTURE runs revealed some clustering based on location (Figure 2), and a ΔK determination of ideal K values (Evanno et. al 2005) suggested a most likely scenario of K=2 (Figure 3), a result possibly derived from the fact that ΔK cannot calculate a K value of 1, which is suggested by the standard L(K) from Pritchard et al (2000). Similarly, a genetic distance PCoA indicated little divergence within the total population, but showed some clustering within possible subpopulations (Figure 4).

We were also able to verify that the observed structure was not being affected by migrants. Pairwise Fst values from an AMOVA indicated the same patterns of differentiation between the different regions (Table 5), and the same scatter pattern was observed in the PCoA (Figure 5).

Phylogenetic analysis revealed little molecular diversity in bald eagles from across the US. We sequenced 993 nucleotides of the cytochrome *b* gene from thirty-nine individuals, and detected only 0.1% nucleotide divergence (pairwise distances) across all individuals. Between potential subpopulations, Φst values indicated the greatest distinction between eagles from Alaska and Florida (Table 6). A Jukes-Cantor Neighbor-joining tree (Figure 6) and a maximum likelihood tree (Figure 7) both indicated differentiation of most Florida bald eagles from individuals in other parts of the country, but these differences were not significant by bootstrapping or posterior probability.

Genetic Structure of Historic Bald Eagles

Historically, it appears that bald eagles demonstrated clinal variation in allelic frequencies over a geographic gradient. This trend can be visualized by STRUCTURE images (Figure 8), though a ΔK analysis designated $K=6$ as the optimal scenario (Figure 9). A PCoA similarly revealed a general trend of structure across geographic regions (Figure 10). To determine if bald eagles historically showed a trend of isolation-by-distance, we also performed a Mantel test based on genetic distance and geographic coordinates (Figure 11) and detected a positive trend.

Impact of Reintroduction

We detected moderate impact of translocations in the modern population of bald eagles. Comparing contemporary and historic data as temporally separate populations indicates little loss in diversity since the reintroductions. Contemporary and historic numbers of alleles and effective alleles for each locus were comparable, and I included an analysis of “private alleles” between historic and contemporary populations. Though these are generally used in comparisons of populations that coincide temporally, I wanted to determine if there was a major loss of alleles after the reintroduction. However, private alleles appeared in similar numbers between historic and modern populations (Table 7). To compare variation between historic and contemporary populations, we used Microsatellite Analyser (Dieringer and Schlötterer 2003) to calculate global G_{st} (Weir and

Cockerham 1984), Nei's D corrected for population size (Nei 1978), and Nei's chord distance D_A (Nei et al. 1983; Table 8). Values did not indicate major distinction between the total pre- and post-translocation populations. There is, however, a notable loss of clinal variation in historic and modern populations. The original northwest-southeast gradual shift in structure that is seen in historic samples is not present in today's bald eagles (Figures 1 and 5).

Finally, to examine the possibility of significant pre- and post-reintroduction genetic drift biasing our results, we compared historic and contemporary Alaskan individuals using STRUCTURE, but did not detect any major shift in the population (Figure 12).

Discussion

Genetic Structure of Contemporary Bald Eagles

Current populations of bald eagles across the US exhibit some degree of population structuring. However, this population structure is not distinct enough clustering to be verified by a ΔK analysis following Bayesian analysis. In addition, overall low heterozygosity indicates little variation across bald eagle populations.

According to STRUCTURE results pairwise F_{ST} values, bald eagles in West Virginia cluster separately from the rest of their geographic region. Part of the reason behind this could be the rapid increase in population pairs within the past decade. In 2007, West Virginia had only 19 nesting pairs in the state (FWS); however, as of 2012, there were between 40 and 50 active nests (O'Malley WV-DNR, pers. comm.). This rapid doubling in size from a small population could be demonstrating a small founder's effect and be responsible for the relatedness observed in these birds compared to the rest of the country, particularly if the birds exhibit some degree of natal philopatry as bald eagles in other regions do (Laing et al. 2005; Wood 2009).

Though Florida and Virginia both suffered population declines until the mid twentieth century, neither state has record of any reintroductions. Currently the two most populous states in the eastern half of the US (www.dgif.virginia.gov, www.fl.audubon.org), individuals from these states show little divergence from each other, which could be due to two different factors. First, Florida bald eagles, particularly sub-adults and juveniles, are known to have a northward migration in the spring and summer (Broley 1947). Since our VA samples were collected year round, it is possible that there are native Florida birds included in the Virginia data set—though our analyses that excluded winter birds lowered the potential for bias. Also, as mentioned earlier, some bald eagles have shown low natal dispersal, but others show a higher degree of it—particularly females—by moving into areas less densely populated than around their natal territory (Harmata 1999). Such ongoing gene flow would limit the potential structure between the two states in spite of the distance, as is the case in other taxa (Ando et al. 2011; Dohms and Burg 2013).

Bald eagles are more abundant in Alaska than they are anywhere else in the US with an estimated 30,000 individuals (AK-DFG), and they were among the source populations for many of the reintroduction efforts in the Lower 48 states. In our comparisons, though, Alaskan eagles clustered separately in a PCoA based on genetic distance, and F_{ST} values marked them as increasingly differentiated from other regions with increasing distance. We considered this as possible product of genetic drift in the reintroduced populations since our comparison of historic and contemporary bald eagles indicates no major genetic difference between Alaskan bald eagles over the past century. A similar situation has been seen in the genetic population structure found in Alpine ibex. After a series of reintroductions from a single source population over the course of less than a century, at least three genetically distinct populations of ibex exist today; and the divergence between the three populations is most likely due to drift alone (Biebach and Keller 2009).

Genetic Structure of Historic Bald Eagles

Prior to the bald eagles' population crash and subsequent releases, the U.S. population exhibited a trend of clinal variation along a geographic gradient. Both STRUCTURE and PCoA analyses revealed slight shifts in similarity with greater distance, suggesting gradual isolation by distance as has been seen in a wide variety of taxa (Zieritz et al. 2010; Petrou et al. 2013). In theory, the distinction between bald eagles from the southeast versus the northwest could have prompted concerns of outbreeding depression, a decrease in fitness due to the disruption of co-adapted genes in F_2 hybrids. However, phenotypic evidence of this occurring in bald eagles have not been recorded in the literature.

I determined that genetic drift has most likely not been a factor in the interpretation of my results. This was important to demonstrate as it has been shown that refuge populations—populations managed as a source for future reintroductions—can exhibit evolutionary divergence in morphology after a single generation (Collyer et al. 2011). If stable bald eagle populations were undergoing drift while the reintroductions were going on, that could have been a source of misinterpretation of population structure when comparing my historic and contemporary populations. However, the modern population of Alaskan bald eagles is not genetically distinct from historic populations of Alaskan bald eagles. This suggests that over the past century, drift has likely not been a significant player in population structuring of bald eagle populations.

Impact of Reintroduction

Indices of diversity corrected for population size indicate little overall difference between contemporary and historic populations (Table 8). Although the p-value for G_{ST} indicated non-significance, this was possibly due to unequal sample size between historic and contemporary. Overall, results suggest that during the bald eagles' reintroduction efforts, the broad assortment of birds that were translocated were diverse enough to maintain large-scale diversity. However, today there is some observable clustering between modern subpopulations across the country. This indicates that the original genetic structure of bald eagles across continent appears to have been lost since the reintroductions. The low heterozygosity seen in total North American birds may be a sign of the Wahlund effect masking metapopulation structure (Williams and Scribner 2010), or this structuring could be a form of founder's effect acting in multiple regions.

We considered genetic drift as a factor in the present population structuring since drift has been cited as a potential cause behind structuring in populations of other reintroduced species (Grueber et al 2013; Pelizza and Britten 2002; Smulders et al. 2000; Fitzsimmons et al 1997), and it is one of many interactions whose impacts have been modeled in translocation success/failure simulations (Thrimawithana et al 2013; Robert 2009). Genetic drift has even been documented to counteract natural selection in other reintroduced avian species (Grueber et al. 2013). If gene flow between bald eagle subpopulations in states is low, it would make sense that the current genetic structure seen is a mild founder's effect occurring simultaneously in the rising subpopulations.

Implications for Translocation in the Future

At the time of the bald eagle population crisis and managerial response, there was little precedence for how best to manage the situation (aside from peregrine falcons, which faced a similar conservation issue; Tordoff and Redig 2001). It is known that at least 1359 (or 1749, see note in Table 1), bald eagles have been released since the 1970's; though it is likely that this number is in reality much higher due to varying methods of record keeping. However, what is apparent is that bald eagles are in the midst of great population growth, and exhibit levels of genetic diversity that are comparable to their historic counterparts. Future planning of broad-scale conservation translocations of other species would do well to mirror the inclusion of diversity. To yield the best results, incorporating a preliminary genetic population analysis into management plans would reveal basal structure and diversity we wish to preserve.

Table 2.1. Bald eagle sample localities, number of individuals, and sample provider.

State/Province	Number of Individuals	Category	Sample Source
Alaska	7	Historic	CAS, UAM, CMNH
Florida	4	Historic	OSU-VM
Maryland	1	Historic	PANS
New Jersey	1	Historic	PANS
Ohio	3	Historic	OSU-VM
Pennsylvania	3	Historic	CMNH
Washington, D.C.	1	Historic	OSU-VM
West Virginia	1	Historic	CAS
British Columbia (Canada)	2	Historic	PANS
Alaska	30	Contemporary	Rehab, ARC
Florida	22	Contemporary	Rehab, ACBP
Montana	3	Contemporary	Rehab, MRCC
Virginia	21	Contemporary	Wild, VA-DGIF
Washington	6	Contemporary	Rehab, WHWRC
West Virginia	10	Contemporary	Wild, WV-DNR

**CAS is the California Academy of Sciences; UAM is the University of Alaska Museum; CMNH is the Carnegie Museum of Natural History; PANS is the Philadelphia Academy of Natural Sciences; OSU-VM is The Ohio State University-Vertebrate Museum; ARC is the Alaska Raptor Center; ACBP is the Audubon Center for Birds of Prey; MRCC is the Montana Raptor Conservation Center; VA-DGIF is the Virginia Department of Game and Inland Fisheries; WHWRC is the Wolf Hollow Wildlife Rehabilitation Center; and WV-DNR is the West Virginia Division of Natural Resources.*

Table 2.2. Characterization of the nine microsatellite loci. All were developed in other species and summarized by Bourke and Dawson (2006) for use in golden eagles (*Aquila chrysaetos*). A (*) indicates significant deviation from Hardy-Weinberg.

Locus	EMBL Accession no.	Primer sequence	Repeat motif in source species	*A*	*Ho*	*He*	*p-value*
Aa15	AF469499	F: TCACTGACCTGCCCTCTACA R: CCAACCCTCTAGTCGTCCAC	(CA)13	2	0.133	0.124	0.28
Aa11	AF469497	F: ACGAGCTTATCTTTGACCAAGC R: CTTTGTTTCAGCTGTTCCAGG	(CA)11	3	0.016*	0.156	0.00
Aa36	AF469504	F: ACAGGCCAGCACCAAGAG R: TTTGGAGCCATTGTTACCGT	(AC)16	4	0.071*	0.389	0.00
Hal-13	AY817052	F: CCACTCAGTAAGGAGCTTTGC R: CTTTGTGTTTGCTGCAGATG	(GT)17	4	0.328*	0.429	0.00
IE04	AY631063	F: GCATGTAACAAGTTTAATGTTGATGG R: GTTGGAAACAGGACATGTTAAGC	(AAAG)6 (AAAC)4 (AAAG)6	6	0.706	0.639	0.53
IE13	AY631068	F: GAATACCACAATAAGAGGCAGAGTG R: GTCTAAAATGAAGTGAATCTGTAAGACAG	(AAAG)3 (RAAG)13 (AAAG)16	2	0.141	0.129	0.27
Aa27	AF469502	F: GAGATGTCTTCACAGCTTGGC R:AAGTCTCAGAGACTGACGGACC	(CA)11	4	0.585*	0.583	0.02
IE14	AY631069	F: GTCCAGATTCCCTGCTAGAAAGC R: GTTGGAGAGTCTAAGCACTGAATCAG	(AAAG)18	2	0.481	0.413	0.64
Hal-10	AY817049	F: CATGCACGCTGTGAATCAG R: ACCCACCAACGTTACCAGTG	(CA)12	5	0.203*	0.394	0.00

A refers to the number of alleles found at each locus; *Ho* is the observed heterozygosity; *He* is the expected heterozygosity; and the *p-value* refers to significant or non-significant deviations from Hardy-Weinberg.

Table 2.3. Expected and observed heterozygosities across all loci for each region (contemporary). Eastern States represent states in the eastern US that are likely all descendents of reintroduced birds. Northwestern States represent Montana and Washington.

State	*Ho*	*He*
Florida	0.237	0.332
Eastern States	0.226	0.38
Northwestern States	0.361	0.482
Alaska	0.259	0.278
All Populations	0.296	0.362

Table 2.4. Pairwise F_{ST} values between all contemporary bald eagle populations. Associated p-values were all lower than 0.01.

	Florida	Eastern States	Northwestern States	Alaska
Florida	-	-	-	-
Eastern States	0.046	-	-	-
Northwestern States	0.078	0.082	-	-
Alaska	0.153	0.185	0.059	-

Table 2.5. Pairwise F_{ST} values between all contemporary populations with samples collected only in the summer. Associated p-values were all lower than 0.01 unless denoted by a (*).

	Florida	Eastern States	Northwestern States	Alaska
Florida	-	-	-	-
Eastern States	0.049	-	-	-
Northwestern States	0.066	0.068	-	-
Alaska	0.160	0.172	0.0*	-

Table 2.6. Pairwise Φ_{ST} values between all contemporary populations. Associated p-values are above the diagonal. A (*) represents non-significant p-values.

	Florida	Virginia	West Virginia	Washington	Alaska
Florida	-	0.081*	<0.001	0.036	<0.001
Virginia	0.28	-	0.56*	0.11*	0.022
West Virginia	0.22	0	-	0.49*	0.07*
Washington	0.4	0.11	0.026	-	0.99*
Alaska	0.37	0.02	0.115	0	-

Table 2.7. Comparison of contemporary and historic allelic diversity by locus.

Locus	Historic *A*	Current *A*	Historic n_e	Current n_e	Historic "Private" Alleles	Current "Private" Alleles
Aa11	1	3	1	1.243	2	0
Aa15	2	2	1.55	1.215	1	1
Aa27	3	4	2.13	2.43	1	0
Aa36	4	4	1.37	1.72	1	1
Hal-10	4	5	1.57	1.69	2	3
Hal-13	4	4	2.315	1.99	0	0
IE-04	5	6	2.471	2.81	0	0
IE-13	3	2	1.258	1.18	0	0
IE-14	3	2	1.97	1.73	0	1
Average	**3.22**	**3.56**	**1.74**	**1.78**	**0.78**	**0.67**

A, the total number of alleles for a given locus; n_e, the effective number of alleles at a given locus

Table 2.8. Diversity indices between historic and contemporary populations of bald eagles suggest there are little genetic differentiation between historic and contemporary populations. This suggests the comparable levels of diversity and composition exist today and historically.

Index	Value	P-value
Nei's D	0.071	N/A
D_A	0.216	N/A
Gst	0.036	0.12

Nei's D (corrected for sample size, 1978), D_A is the chord distance of Nei et al (1983)

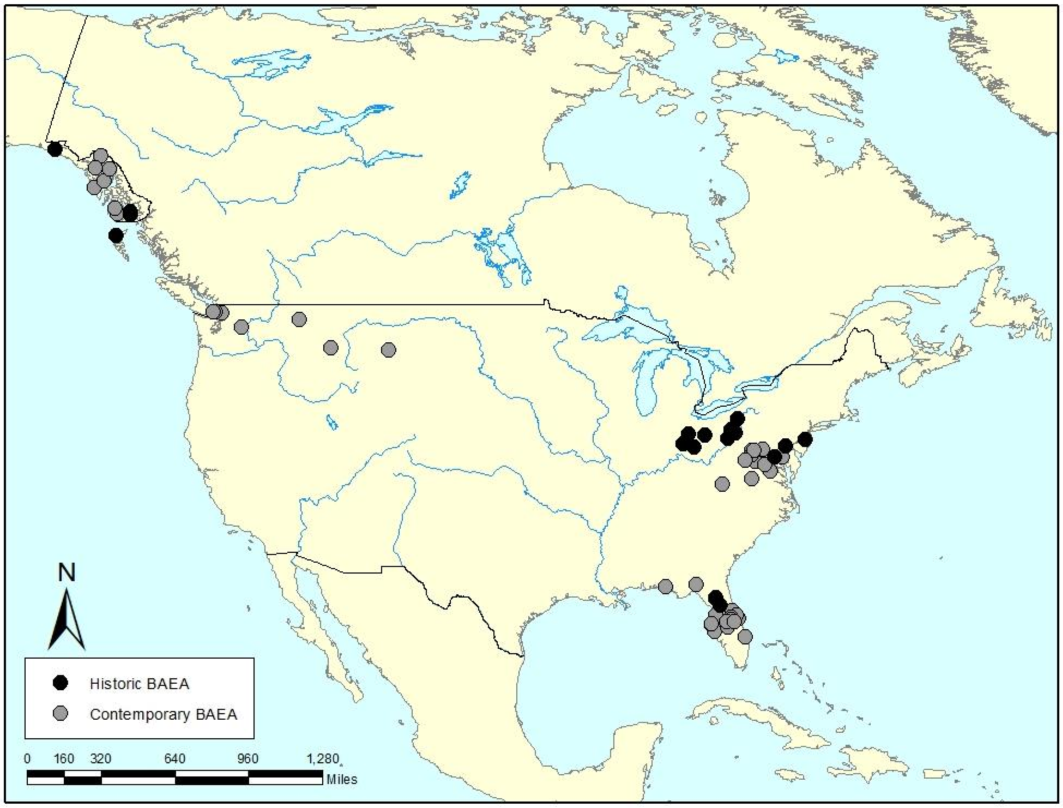

Figure 2.1. Map of sampling locations of bald eagles across North America. Produced using an ESRI basemap in ArcGIS 10.

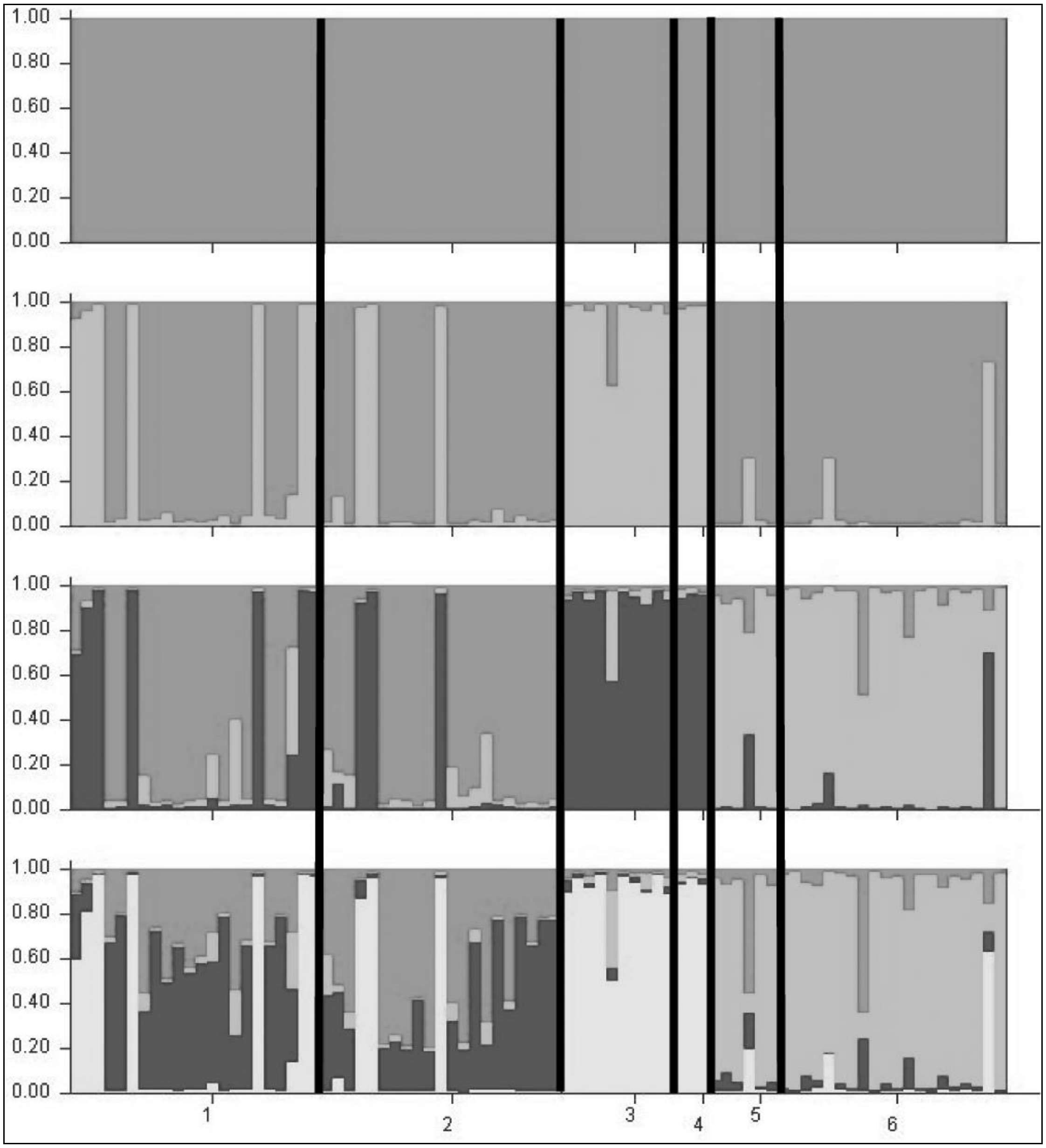

Figure 2.2. Contemporary individuals are arranged (left-right) east to west. Group 1 individuals are from Florida, group 2 are from Virginia, group 3 are from West Virginia, group 4 are Montana, group 5 are Washington state, and group 6 are from Alaska.

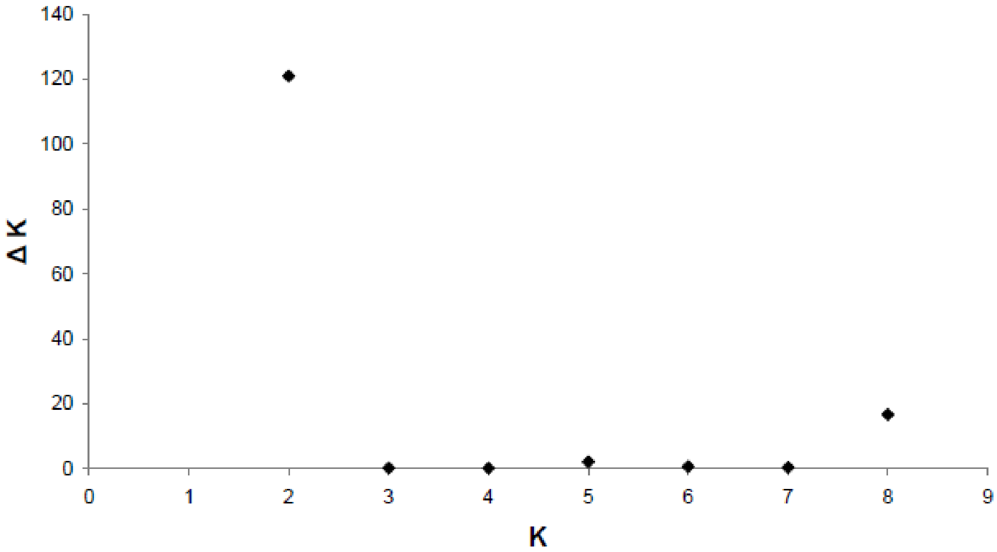

Figure 2.3. Determination of ideal K-value based on Evanno (2005) suggests a most likely K of 1 (one population cluster of contemporary bald eagles).

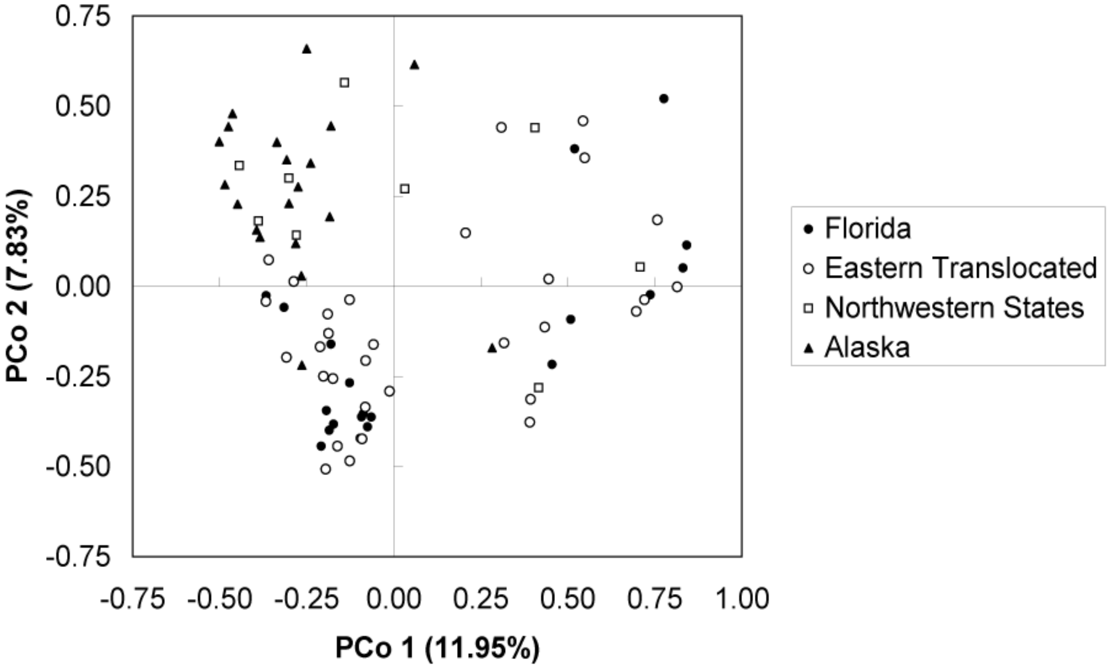

Figure 2.4. Principal coordinated analysis of contemporary bald eagles. Moderate clustering can be seen in individuals from different states, eastern translocated individuals are fairly scattered.

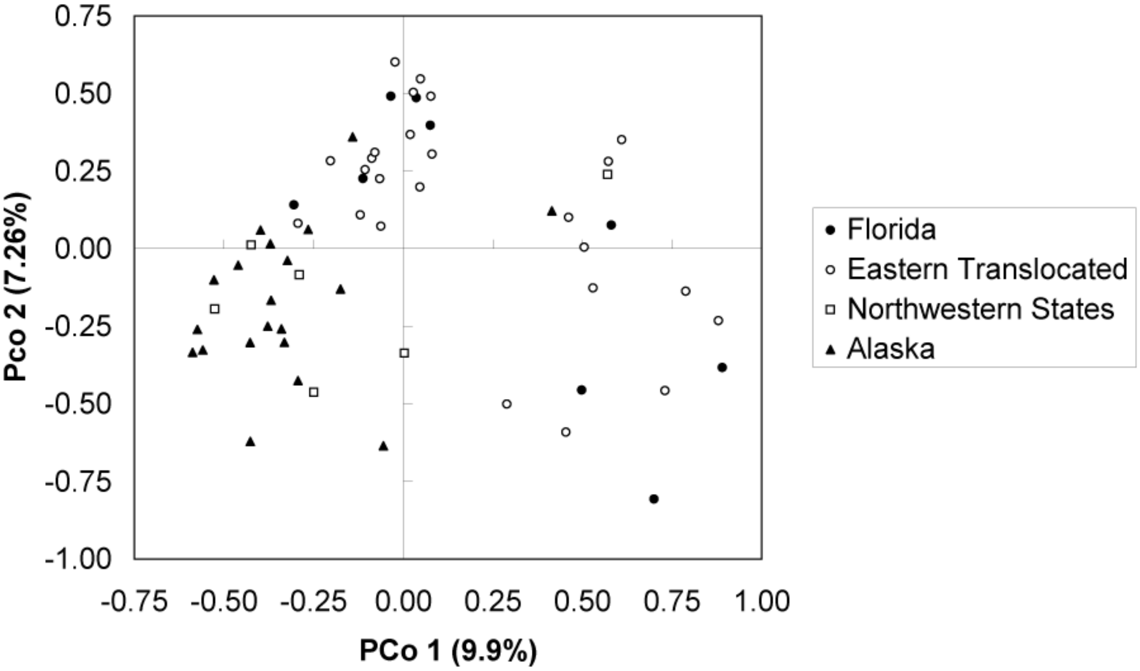

Figure 2.5. Principal coordinated analysis of contemporary bald eagles collected during the summer breeding season.

Figure 2.6. Jukes-Cantor neighbor-joining phylogenetic tree with contemporary bald eagles.

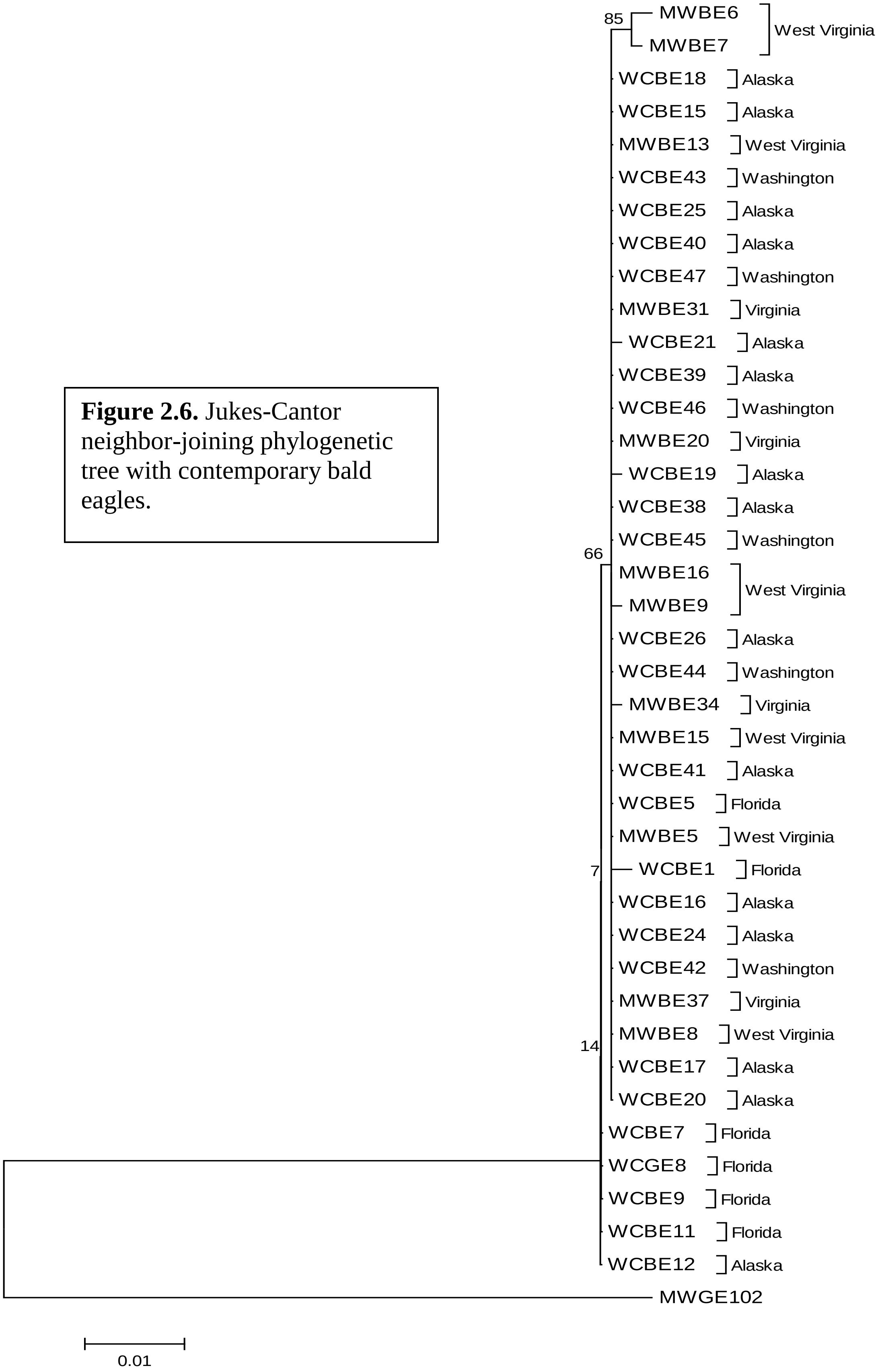

Figure 2.7. Maximum likelihood phylogenetic tree of contemporary bald eagles.

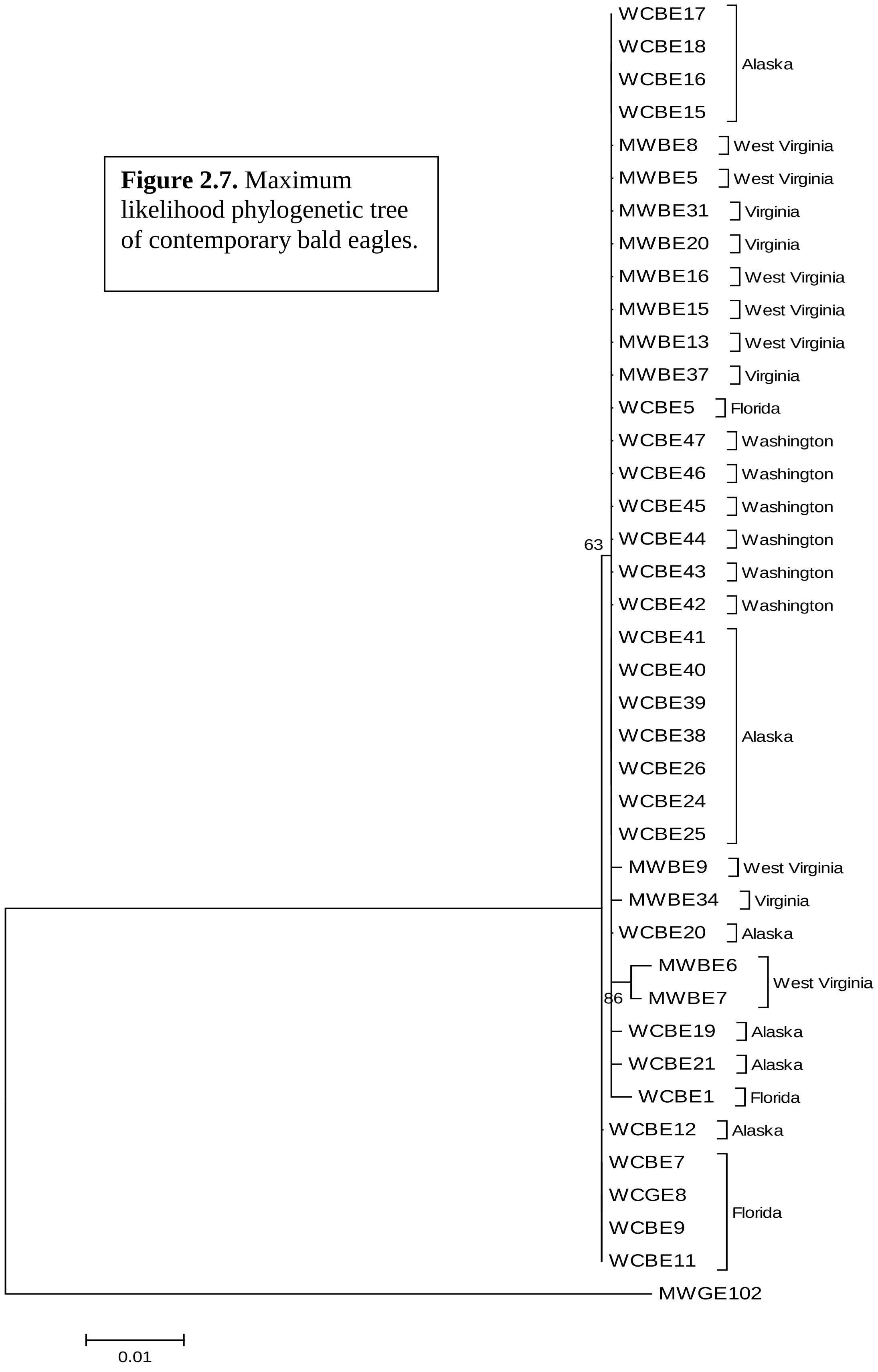

Figure 2.8. STRUCTURE bar graph representing historic bald eagles. Group 1 represents birds from Florida; Group 2 represents individuals from New England; Group 3 represents West Virginia, Ohio, and Pennsylvania birds; and Group 4 represent Alaska birds.

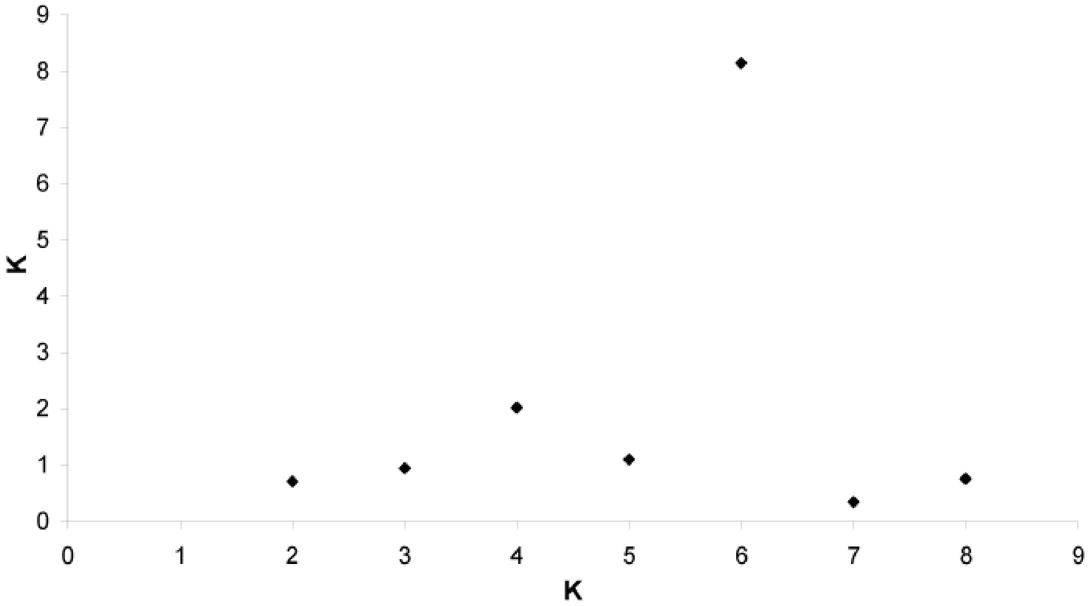

Figure 2.9. Determination of ideal K-value based on Evanno (2005) suggests a most likely K of 1 (one population cluster of historic bald eagles).

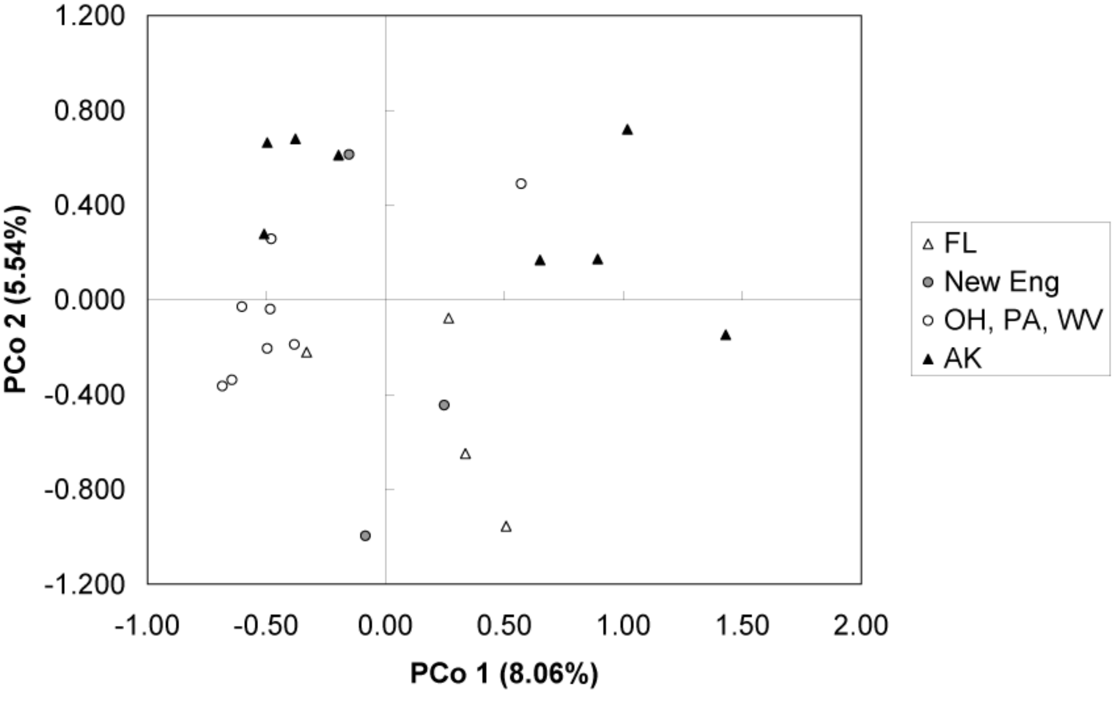

Figure 2.10. Principal coordinated analysis of historic bald eagles. Moderate grouping of individuals from similar geographic locations can be seen.

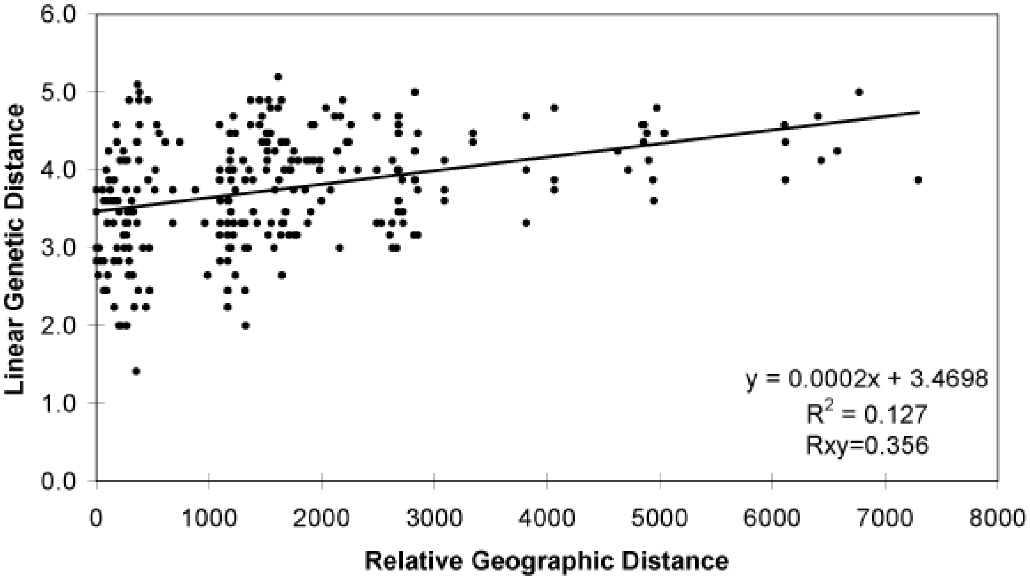

Figure 2.11. A Mantel test of historic bald eagles indicates a degree of isolation by distance.

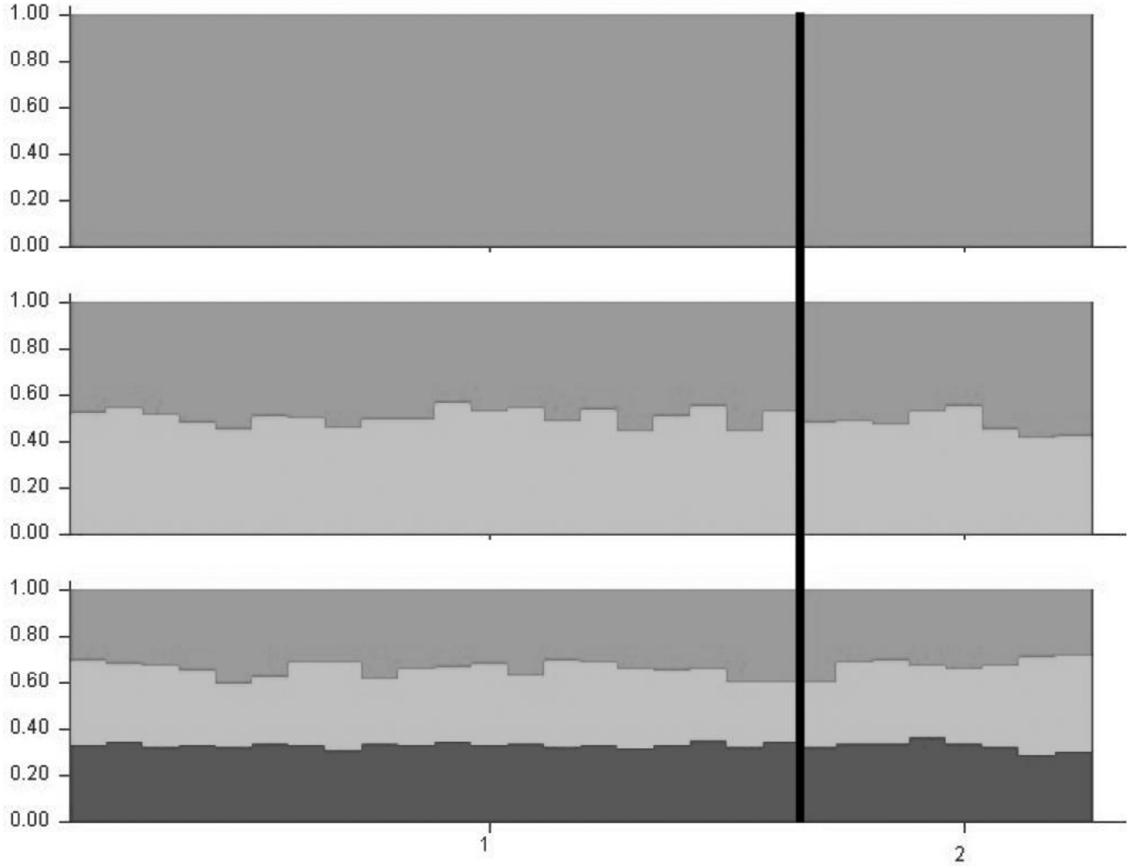

Figure 12. STRUCTURE analysis of contemporary (Group 1) versus historic (Group 2) Alaskan individuals indicated no difference between extant and historic populations.

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CHAPTER THREE

A Heuristic Evaluation of the Role of Population Genetics in Reintroduction and Conservation Translocations

Release of individuals into ecosystems where the species is either not present or occurs at low density is commonplace for conservation management. The two most common mechanisms for such releases are reintroduction and translocation. This transfer of new genotypes or new alleles can have dramatic consequences at multiple levels of organization. These processes can also have dramatically different outcomes depending on the context in which they occur. To better understand these consequences, we compared the genetic impact of reintroduction and translocation on two raptors with similar life histories. In the past half-century, the bald eagle (*Haliaeetus leucocephalus*) and the North American golden eagle (*Aquila chrysaetos canadensis*) were the subjects of dramatically different broad-scale translocation and reintroduction methods. The goal of our study was to determine the genetic consequenses of these two reintroduction strategies using mtDNA cytochrome *b* and 10 nuclear microsatellite loci. We sampled both modern North American birds and preserved musuem study skins. Results indicate that translocations did not impact the genetic structure of golden eagles since their genetic structure across the continent implies some degree of panmixia. Bald eagles, on the other, demonstrate a pre-reintroduction clinal trend in genetic variation. This population structure, however, was lost during the reintroduction process, though the current bald eagle population is thriving and in exponential population growth. These contrasting results highlight a need for preliminary genetic surveying of translocation candidate species since there is not a clear reason why the pre-management genetic structures of bald eagles and golden eagles would be different.

Introduction

Over the past few decades, the conservation practices of reintroduction and translocation have become increasingly common (Seddon et al. 2010). Both of these management techniques involve releasing individuals into the wild, but the purpose and outcomes of the releases vary dramatically (Kleiman 1989; Marshall and Spalton 2000; Lockwood et al. 2005; Stamps and Swaigood 2007; Ricciardi and Simberloff 2008; Hedrick and Fredrickson 2012). However, as these practices become more common and are being considered for novel uses in response to climate change (Lawler and Olden 2011), it is important that we understand the potential impacts of these management actions. In particular, the role of genetics has been given relatively little attention when compared to all of the factors that must be considered in a wildlife relocation plan (Seddon et al. 2007). Our goal is to draw attention to this subject with a review of recent wildlife relocation history. In particular, we will focus on a post-hoc comparison of the reintroduction and translocation efforts of North America’s two species of eagles—both of which have been the subject of conservation management over the last half-century.

Translocations and Reintroduction in Conservation Management

Translocations are conservation management tool that, by definition, move an organism or group of organisms from one location to another (Griffith et al. 1989; Sarrazin and Barbault 1996; Seddon 2010; Thomas 2011; IUCN 2013). Within this broad category, variations on the theme abound throughout conservation literature and include assisted colonization, assisted migration, and managed relocation. Some of these terms are used interchangeably while others have a unique definition. Managed relocation encompasses assisted migration and assisted colonization—both of which involve attempting to establish a population in an area not formerly a part of the organism's typical geographic range (Ricciardi and Simberloff 2008; Minteer and Collins 2010; Seddon 2010). For our purposes, we will use the term "translocation" in reference to moving a group of organisms to either augment an existing population or to intentionally introduce a group of organisms into a completely new environment for the species for conservation management purposes.

Reintroductions are a form of conservation restoration and involve releasing organisms (either wild or captive-bred) specifically into a former range from which they were extirpated (IUCN 2013). Here, we will restrict the use of the word "reintroduction" to situations where a species has been completely extirpated from a particular region—as a consequence of either natural or anthropogenic factors—and either wild-caught or captive individuals are being released in former territory.

Context, Concerns, and Outcomes: Differences Between Reintroduction and Translocation

The context for a reintroduction project versus a translocation project varies. Since the primary definition of a reintroduction is to "reintroduce" a species into a part of its former habitat, in most examples, the species has undergone a local extinction. Thus, the goal of reintroduction is to establish a population capable of self-sustaining persistence. An example of this would be the hugely successful American bison (*Bison bison*) reintroductions in the USA. After approaching extinction in the US, a handful of reintroductions began in 1907 and established populations of thousands of bison across the Great Plains that persist even today (Kleiman 1989).

Alternately, translocations have been used to address a wider variety of circumstances. They have been used to augment the number of individuals in existing populations (Kleiman 1989), increase genotypic and phenotypic diversity (Haye et al. 2012), decrease genetic load (Pimm et al. 2006), establish refuge populations for future conservation (Collyer et al. 2011), and relocate populations as response to climate change (Willis et al. 2009). Thus, the goals of a translocation can vary greatly depending on the context and need of a given situation. For example, translocations have been used in "genetic rescue." (Pimm et al. 2006; Hedrick and Fredrickson 2012; Heber et al. 2013). In these situations, inbreeding has led to a build-up of deleterious alleles and threatens the viability of a population, but the addition of new alleles from a translocation group of individuals relieves low diversity (Miller et al. 2012).

A prominent example of genetic rescue is the Florida panther (*Puma concolor*). A small population of these cats persisted in southern Florida, but they were impacted by a genetic load that severely reduced male fitness. As a management response, a few individual panthers were translocated from Texas to Florida, which successfully increased the genetic diversity of the Florida population and reducing the effect of genetic load in hybrid offspring (Pimm et al. 2006; Hedrick and Frederickson 2008; Hedrick and Frederickson 2010). Another example of genetic rescue is the translocations of New Zealand South Island robins. In this case, members of one population were relocated to the range of an inbred population to offset the effects of a severe bottleneck (Heber et al. 2013). In a variation of genetic rescue, a captive breeding program of endangered hamsters in the Netherlands benefited from the introduction of hamsters from neighboring populations. These donor populations showed greater genetic diversity than the rescue population, and the addition increased litter size in the captive breeders (Haye et al. 2012).

In some cases, long term management may involve both reintroductions and translocations, and it is fairly common for translocations to subsequently be used to reinforce a population that was reintroduced. For example, populations of reintroduced North American elk (*Cervus elaphus*) and Laysan teals (*Anas laysanensis*) both required population augmentations following reintroductions (Conrad et al. 2010; Reynolds et al. 2012). In a more unique situation, roughly ten years after golden lion tamarins (*Leontopithecus rosalia*) were successfully reintroduced to their native habitat in Brazil, several groups of them were found outside of protected forest and had to be translocated to new habitat (Kierulff et al. 2012).

Regardless of the context of a reintroduction or translocation project, there are a number of concerns that must be addressed prior to the release of individuals. Among the foremost concerns in reintroduction is ensuring that the original cause of a species population decline has been managed. For instance, in Guam, the majority of avian species on the island has either been extirpated or has undergone severe population declines over the past ~60 years because of the introduction of the brown tree snake (*Boiga irregularis*; Wiles et al. 2003). In spite of the severity of the situation, attempting to reintroduce any of the extirpated species would likely meet with little success until the brown tree snakes are under control.

However, translocations in the form of assisted migration or assisted colonization bring about entirely different concerns. These types of translocations have been suggested as a response to climate change and involve moving groups of organisms into potentially new habitat types ahead of warming climates. The benefits and risks are currently hotly debated largely because of the incredible impact such translocations could have. For example, Lawler and Olden (2011) pointed out that assisted colonization risks changing a habitat's existing ecosystem services output. Kreyling et al. (2011) even suggested that it may not even be feasible to introduce just one species without also translocating other ecosystem symbiont species.

As with virtually any form of wildlife management, there is the potential for unintended consequences with reintroductions and translocations. These unintended consequences can be excessive stresses on the wildlife involved, unexpected behaviors from the wildlife involved, or negative impacts on the environment. For example, it has been noted in a variety of taxa that the handling and transportation involved in both reintroductions and translocations can significantly alter the animals' stress responses, even years after the event (Dickens et al. 2009; Jachowski et al, 2013). This ultimately can have a negative impact on the animal's ability to survive in their new environment (Dickens et al. 2009; Jachowski et al, 2013). Disease transmission has also been a serious concern in translocations (Chipman et al. 2008). If infected organisms are translocated into a new population, they can bring the disease with them. Such has been the case with rabies in translocated raccoons (Slate et al. 2009).There have also been situations in smaller reintroduced populations where a single male dominates the siring opportunities in a population (Barba et al. 2011). This reduces the effective population size and jeopardizes population persistence. Other possible unintended outcomes of reintroduction have included human-wildlife conflict (Gusset et al. 2008)—though, ironically, translocations have also been used to relieve human-carnivore tension (Goodrich and Miquelle 2005).

Because translocations can involve moving groups of organisms into completely new habitat, it is possible that they may even have a greater assortment of unintended consequences than reintroduction. Most of the potential concerns of reintroduction also apply to translocations (i.e., diseases transmission, human-wildlife conflict, disruption of mating systems, etc)., but translocations may also include an entirely new array of unforeseen results. For an example, the endangered North Island Kōkako (*Callaeas wilsoni*) began showing signs of assortative mating following a series of multi-source translocations in New Zealand. Translocated birds formed pairs only with other translocated birds, and native birds bred only with other native birds (Bradley et al. 2013). This prompted concerns about a low effective population number and a reduced overall success of the translocation project. On an even larger scale, though, it has been suggested that translocations could potentially have the ability to alter entire ecosystems with shifting abundance of various wildlife or plant life (Lawler and Olden 2011).

In part because of this possibility for unintended consequences, the use of assisted colonization as a management tool for climate change in particular has stirred great debates. For example, to determine when assisted colonizations would be a viable option for a species Hoegh-Guldberg et al (2008) developed a "decision framework" focused on determining whether or not there were any other management options available before initiating a plan to move individuals of a species to a suitable location.

Defining the Success of Translocations

In spite of all of the energy and resources dedicated to translocations, the success rates of translocation and reintroduction projects have typically been reported as low (Stamps and Swaigood 2007). However, the criteria for defining a translocation "success" are not always clear and hardly universal. The most basic explanation defines success as "establishment, re-establishment, or augmentation of a wild population" (Wolf et al. 1998). In some sense, the definition of success will depend on an individual project's stated objectives, and it may take multiple generations of the translocated organisms to determine whether or not the project met its goals. For example McPhee and McPhee (2012) discuss the success of reintroduction primarily in terms of population establishment and persistence. Alternately, populations may already exist before a translocation, but the introduction of new individuals is meant to offset an existing genetic load within the population (Hedrick and Fredrickson 2010; Haye et al. 2012).

Other descriptions constituting "success" also appear in the literature. In the upper peninsula of Michigan, USA, the once-extirpated American marten (*Martes americana*) now flourishes (Williams and Scribner 2010). This new widespread distribution—rather than the number of individuals in the population—was presented as the definition of success for this project. In another study that modeled that majors factors in avian reintroduction failure or success, the specific definition of what constituted either success or failure was never directly stated. However, it was implied that success was defined as some margin of population growth and reproductive success (Taylor et al 2005).

Alternately, reintroduction and translocations can fail to meet their project goals for a variety of reasons. Reintroduced individuals may face predation (Moseby et al. 2011; Grey-Ross et al. 2009; Moorhouse et al. 2009), threatening environmental conditions (Hamilton-FWS 2013), human-wildlife conflict (Chipman et al. 2008), behavioral attributes of captivity—all of which have been large enough barriers to cause total reintroduction failure. In particular, it has been observed that habitat quality has been a large factor in the failure or success of reintroduction (Fustec et al. 2001; Hebblewhite et al. 2011; Osborne and Seddon 2012), suggesting that released wildlife can reject some subtle landscape attributes in spite of conservation managers' best efforts to take habitat into account (Stamps and Swaigood 2007). In contrast, reintroduced organisms may settle in habitat that was restored specifically for their reintroduction, but the area may still bear signs of disturbance. This can impact the behavior of wildlife. Such was the case of failed brown treecreeper (*Climacteris picumnus*) reintroduction in Australia. Prior to the birds' release, their habitat underwent extensive restoration. However, after the birds were reintroduced, they suffered higher rates of predation in comparison to reference sites, and it was determined that differences tree and shrubbery types caused differences the reintroduced birds' ability to escape predators (Bennett et al. 2013).

In the past, some longstanding knowledge gaps in the science of reintroductions have been attributed to a lack of an experimental approach (Seddon et al. 2007). However, more recent efforts have included experimental components in an attempt to elucidate possible reasons for the repeated failures (Roe et al. 2010; Bernardo et al. 2011; Smyser et al. 2013; Walters and Reynolds 2013). In the United Kingdom, for instance, one water vole (*Arvicola terrestris*) reintroduction project included the release of multiple groups of cohorts in slightly varying habitats and locations (Moorhouse et al. 2009). Because of the methods, the authors were able to establish mortality from predation as a major factor in the failure of their reintroduction projects, which allowed them to optimize habitat selection for future efforts. Similarly, houbara bustard reintroductions in Saudi Arabia included close monitoring from program inception in 1991. Data collected since then have been used in habitat selection analyses and home range models to maximize the success of ongoing reintroductions (Islam et al. 2013). In other situations, reintroductions may continually fail, but the reasons behind the failure are not understood. For example, endangered Attwater's prairie chickens (*Tympanuchus cupido attwateri*) have been the focus of numerous reintroduction efforts since 1967. For still unknown reasons, the release efforts have repeatedly demonstrated very poor success rates (Lockwood et al. 2005). This shows a need for a greater understanding of the various factors involved in translocations—especially given the time and resources involved.

However, scholarly literature often is not a great source for documentation of failed reintroductions and translocations. Unsuccessful projects often go unpublished. This is problematic not only in the short term for urgent projects that require immediate solutions, but there is much to be learned in the long term from failed experiences.

The Role of Genetics in Translocations

The role of population genetics in reintroduction or translocation has received comparatively little consideration (Seddon et al. 2007), though over the past several years, the role of genetics is gaining more attention in the literature. Still, with rising interest in the use of various forms of conservation translocations as a managerial response to climate change, understanding the impact of genetics is crucial.

Two significant issues that could arise as a result of neglecting genetics in the planning stages are inbreeding depression and outbreeding depression. Inbreeding depression is a decrease in fitness due to reproduction between genetically similar individuals (Charlesworth and Willis 2009). In contrast, outbreeding depression is a decrease in fitness in offspring because of disruption of co-adapted genes from the parental generation (Waser et al. 2000). Both inbreeding and outbreeding depression have been observed in populations after management-related translocations; but in particular, examples of inbreeding following reintroductions and translocations abound (Keller and Waller 2002; Edmands 2007; Brekke et al. 2010; Jamieson 2011; Spiering et al. 2011). Outbreeding depression, however, is less prevalent in the literature, possibly because the effects may not appear until successive generations after the translocation event (Edmands 2007). Nevertheless, documentation of outbreeding depression following translocations has indeed been observed (Huff et al. 2011). Also, reintroduced populations of Arabian oryx (*Oryx leucoryx*) have undergone both inbreeding and outbreeding depression simultaneously (Marshall and Spalton 2000).

However, over the past several decades, little consideration has been given to the animals' origins, which jeopardizes locally adapted traits or overall genetic variation and adaption potential. In fact, between 1979 and 2005, as few as 15 % of reintroduction studies in the literature placed on emphasis on genetics as opposed to behavior, ecosystems effects, general management, and population dynamics (Seddon et al 2007). This shows a clear need for genetic analyses of modern populations that are the product of reintroductions to ensure we are not setting up a population to become homogenized and vulnerable.

The Translocations of Golden Eagles and Bald Eagles in North America

To better understand the factors involved in successful translocation projects, we conducted a comparative retrospective analysis on two large-scale conservation relocation projects. Within a relatively similar time span, two raptors with similar life histories, the bald eagle (*Haliaeetus leucocephalus*) and the North American golden eagle (*Aquila chrysaetos canadensis*) both were the subjects of broad-scale projects involving either reintroduction or translocation. The goal of this study is to determine how the respective methods of reintroduction impacted the genetics of the modern populations.

To understand the genetic consequences of moving individuals into established ecosystems, we compared and contrasted the translocation and reintroduction programs of bald and golden eagles into eastern North America over the last half century. Specifically, 1). We evaluated the genetic similarity of the populations before and after the reintroductions, 2). We determined the degree of differentiation between the historic and modern populations of each species and 3). We compared the degree of change between respective species in light of their respective translocation strategies.

<u>Methods</u>

Respective Translocation and Reintroduction Strategies

To determine the full extent of the reintroductions and translocation of the two respective species, we contacted state agencies across the US and searched the literature for documentation of private release efforts. The quality of record-keeping varied, but we were able to develop what we believe to be a largely comprehensive list of the majority of the releases through 2010 (Tables 1 and 2). However, bald eagle captive breeding and releases are ongoing still, and it has not been possible to get a completely accurate tally of these.

Bald eagle reintroduction strategies generally involved moving birds from sustainable populations to anywhere in the US that had faced significant declines or complete extirpation. This meant that populations predominantly in Canada, Alaska, and the Pacific Northwest became donors for a large portion of the US. In addition, captive breeding was (and still is) a source of numerous reintroduced birds. For a full list of translocations, see Table 1.

Alternately, golden eagle translocations were much smaller efforts. From 1981-2006, a minimum of roughly 200 birds from the western population were released into various eastern states (Touchstone 1997, C. McGrath, pers. comm., S. Somershoe, pers. comm). In spite of the small number of relocated birds, the size of the eastern population is unknown but has been estimated to be as low as 2000 individuals (Katzner et al. 2012). If that is indeed the case, the translocations would have equaled roughly 10% of the total size of the population. This would be enough to have introduced significant change in the genetic structure of the eastern population if eastern and western birds were reproductively isolated. For a full list of translocations, see Table 2.

Sample Acquisition and Genotyping

To compare and contrast the pre- and post-reintroduction or translocation changes in genetic population structure of each of these species, we focused on analyses based on allelic frequency and genetic distance of genotypes. We collected blood, tissue, or feather samples from extant golden eagles and bald eagles to represent the modern populations, and we collected toe pad tissue from museum study skins of species to represent historic populations. Following DNA extraction, samples were genotyped using ten different microsatellite loci (for complete lab methods, see Chapters 1 and 2).

Statistical Analyses

We first determined the degree of change between the historic and modern populations of each species. Then, to determine which strategy had more significant genetic consequences, we compared how much change there was between the historic and the contemporary of each species. To accomplish this, we performed an AMOVA, a Principal Coordinated Analysis (PCoA), and calculated five indices of genetic diversity (F_{ST}, G_{ST}, G'_{ST}, G''_{ST}, and Jost's D) on the genotype data sets using GenAlEx (Peakall and Smouse 2006).

Results

Golden Eagles

A PCoA based on genetic distance indicated no difference in golden eagles from historic populations compared to golden eagles in modern populations (Figure 1). Historic and modern birds do not form separate clusters as we would expect them to if they were genetically differentiated. Similarly, an AMOVA detected no major differentiation between historic populations and the modern populations. The values of five different indices of genetic diversity between modern and historic populations were low (Table 3), and the associated p-values were all non-significant—indicating the index values were not significantly greater than 0. Together, these indicate a lack of change between historic and modern populations in the time since the translocations.

Bald Eagles

Results of an AMOVA indicate that the patterns of total diversity between historic and contemporary populations have not been significantly altered. In both pre-reintroduction and post-reintroduction populations, the vast majority of molecular variance in the populations was within individuals (57% for contemporary birds, and 46% for historic) rather than between potential subpopulations (11% in contemporary birds, 12% in historic). I also determined that allelic richness is comparable between historic and modern populations in spite of the discrepancy in samples size (see chapter 2, Table 8). This indicates that overall, little diversity was lost during the reintroductions.

However, pairwise F_{ST} between subpopulations (Tables 4 and 5) indicate stronger genetic structure historically than in modern populations. Also, a PCoA indicates that the genetic population structure of pre- and post-reintroduction bald eagles differs (Figure 2). This demonstrates that overall genetic structure of bald eagles across the US is currently different than it was before the reintroductions.

Discussion

Our results indicate that prior to translocations, bald eagles populations across the continent were highly structured but golden eagle populations exhibited very little structure. These differences in genetic structure then influenced the respective outcomes of each species translocation efforts. Our results suggest that even though two species may share a great deal of similarities, they can have very different genetic trajectories—something that should be considered in conservation translocations.

Different Population Structures

We noticed immediately that there is a difference in population structure between these two species of eagles across the same land area. While bald eagles historically showed geographic clinal population structure (see also: Chapter Two), that structure has largely been lost post-reintroduction. Alternately, golden eagles show relatively little structure in either pre- or post-translocation populations—exhibiting very little genetic differentiation in eastern versus western North America (see also: Chapter One). This raises the question why are balds and goldens not similar in patterns of genetic population structure. Both species are capable of long distance migration, and both species have migrant and non-migrant populations (Kochert and Steenhoff 2002; Millsap et al. 2004; Laing et al. 2005; Katzner et al. 2012). A possible explanation could lie in the species' respective colonizations of North America, which is largely unknown. Golden eagles are dispersed throughout the Northern Hemisphere (Watson 2010), and may have arrived later on the continent than bald eagles did. This could have allowed divergence time and, thus, less population structure.

Case Study Outcomes

In short, though, the outcomes of each conservation relocation strategy relate back to the initial state of these two considered species. Golden eagles did not show a change in population structure, but that was largely the result of little genetic structure before the translocations. Alternately, bald eagles showed a great deal change in structure, but they were highly structured before the population crash. Given the similarity in life history and distribution between the two species, it is not immediately obvious that they should have had such a difference in genetic structure. There is a possibility that behavioral differences (such as migratory versus non-migratory subpopulations or feeding strategies) may have influenced the outcome. However, the variable factors involved in genetic structure demonstrate how crucial preliminary genetic surveys are to conservation management planning.

At their lowest documented population number, bald eagles were reduced to approximately 480 nesting pairs in the lower 48 states in 1963 (FWS). Today, there are upwards of 10,000 breeding pairs (as of a 2007 FWS estimate). However, this most likely underestimating the actual tally given that bald eagles are currently in exponential population growth. They are also widely distributed across the US for both breeding and wintering (pers. comm. various state agencies).

Thus, it appears that even if the original population structure of bald eagles was disrupted, it has not impacted their ability to flourish. They still show remnants of isolation-by-distance, with high F_{ST} values corresponding to increasing expansive geographic distance (i.e., Alaskan birds compared to Florida birds), but they have lost the trend of isolation-by-distance that was present historically (see chapter 2). Their historical genetic population structure suggests there could have been a possibility of outbreeding depression as a results of the mixed-source populations (Huff et al 2011), but this remains to be seen. It is also clear that the combined reintroduction efforts successfully maintained historic levels of genetic diversity.

While bald eagles appeared to have been highly structured, golden eagles historically did not exhibit a distinct population structure across the continent, and that lack of differentiation did not change with translocations. There is no certainty that any of the translocated individuals ever joined the eastern breeding population; however, various indices of diversity indicate minimal levels of differentiation between contemporary and historic populations of golden eagles. This suggests some degree of gene flow between the two populations even without the translocations.

Other Factors in Translocation and Reintroduction, Including Outside of Genetics

Beyond the genetic origin of a captive lineage, another genetic concern with captive breeding and release is the concept of relaxed selection. In nature, selective pressure is a constant; but in captive situations, there is nowhere near the pressure on alleles that in the wild might be deleterious to individual fitness or survivorship. Thus, the offspring of generations of captive animals may not be fit enough for release to the wild. To counter this, modeling programs that predict captive breeding outcomes are becoming increasingly of interest (Robert 2009, McPhee and McPhee 2012, Fiumera et al. 2004) and their results may aid in guiding long-term reintroduction strategies.

Although genetic structure and variation have indeed been shown to be highly influential to fitness and population persistence (Tarpy 2003, Lamont 1998, Spielman et al. 2004), it is by no means the sole factor in conservation success. Indeed many populations persist with minimal genetic variation (Groomsbridge et al. 2000, Tucker et al. 2012, Kok et al. 2012, Reed 2010). As stated by Reed (2010), in a study that reviewed numerous examples of population persistence with low genetic variability, "genetic effects do not operate in a vacuum." Rather, they act synergistically or antagonistically alongside environmental, reproductive, and demographic factors that may be completely situation-dependent. Thus, a wide variety of other factors need to be considered as well in conservation translocations and reintroduction.

Conclusion: Lessons Learned

Currently, scientific literature contains numerous variations of guidelines and frameworks for reintroduction and conservation translocations. Recommendation publications tend to cover issues such as when or if to consider a translocation and what principles to keep in mind during the project development process (Griffith et al. 1989;

Armstrong and Seddon 2008; Sandler 2010; Seddon 2010; Kreyling et al. 2011; IUCN 2013). However, our results show that two species that share a great deal of similarities can still have very different genetic trajectories. Thus, with the advancement of conservation management projects such as reintroduction and conservation translocations, it is now more important than ever to take population genetics into account before implementing new actions.

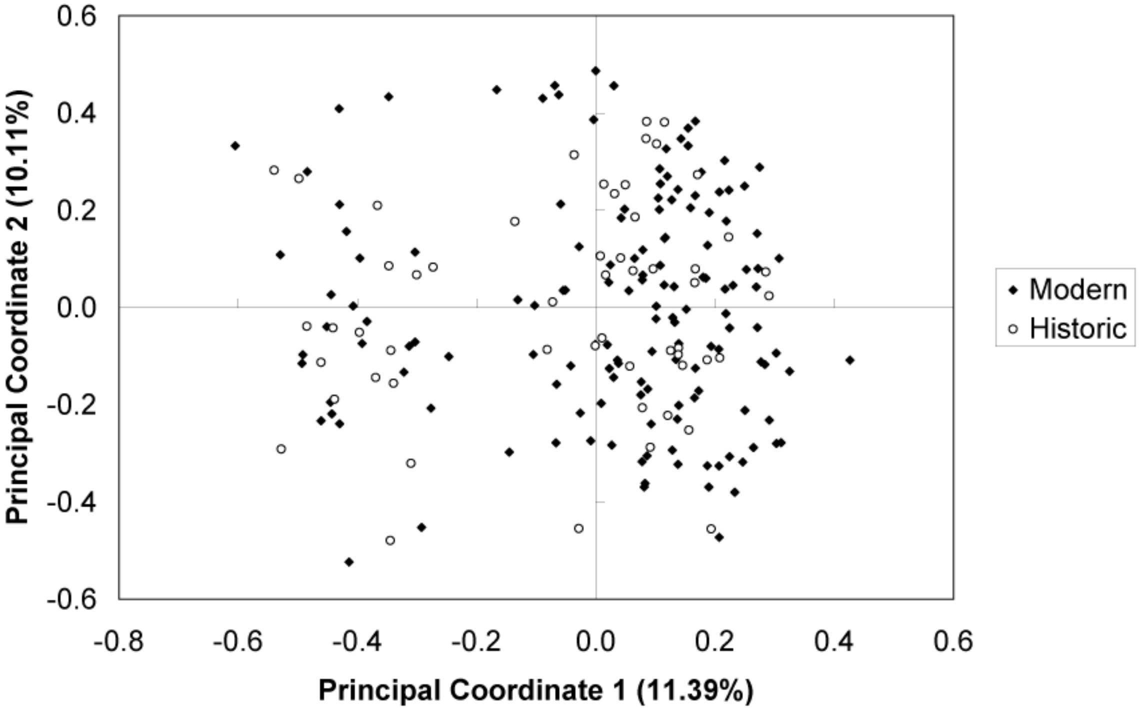

Figure 3.1. Principal coordinated analysis of contemporary and historic populations of golden eagles. Eigen values calculated from genetic distance of microsatellite data.

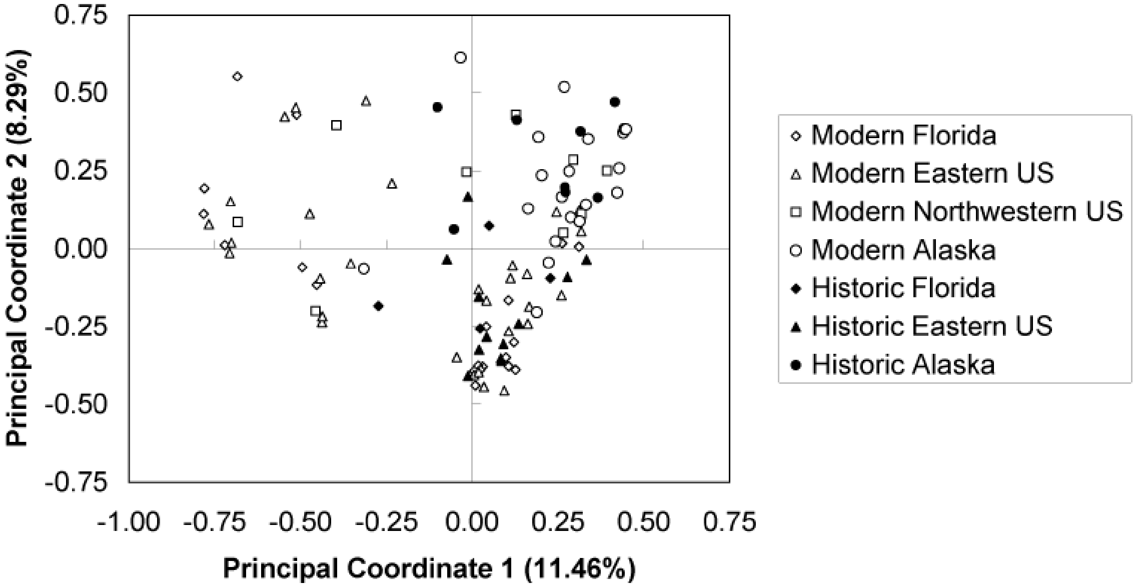

Figure 3.2. Principal coordinated analysis of contemporary and historic populations of bald eagles. Eigen values calculated from genetic distance of microsatellite data.

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Table 3.1. Accounting of known bald eagle reintroductions. All of the following were either discovered or verified by personal communication with respective state agencies.

State	Source	Time period	Origin for Hacked Birds	Number of Birds
*CA,OK, AR, MO, TN, AL, GA, IN, PA, NY, MA, NJ, NC, and Ontario	multiple	1976 -1985	AK, Canada, Great Lakes & Pacific Northwest States	390
PA	PA GC	1980's	Mostly Saskatchewan	88
OH	ODNR	-	No records kept	Birds reintroduced, no records kept
Oklahoma	Sutton Center Records	1980's-1990's	Florida	275
Maine	MDIFW	Unk	Unk	Unk
Indiana	Nature Conservancy	1985-1989	Wisconsin, Alaska	73
Tennessee	TWRA	1980-2010	Captive-bred, AK, WI, MN, Canada, few others	337
North Carolina	NCWRC	1983-1988	AK, VA, FL, MD, captivity & unknown origins	29 or 33, some records lost
New Jersey	NJDEP DFW	1983-1990	Canada	60
New York	NYDEC	1976-1988	Not clear	198
Georgia	GA DNR WRD	1979-1995	Captive breeding & multiple states	89

Table 3.1. Continued.

State	Source	Time period	Origin for Hacked Birds	Number of Birds
Missouri	MDC, Dickerson Park Zoo	1981-1990	Captive breeding & multiple states	74
Alabama	ADCNR	1985-1991	Origins unknown	91
Massachusetts	MDFW	1982-1988	Michigan, Canada	41

*Summary from Nye 1988. It is unknown if the birds in this tally are included in any other state estimates. Thus, the final count of a possible 1749 could be 1359.

Abbreviations: PA GC, Pennsylvania Game Commission; ODNR, Ohio Department of Natural Resources; MDIFW, Maine Department of Inland Fisheries and Wildlife; TWRA, Tennessee Wildlife Resources Agency; NCWRC, North Carolina Wildlife Resources Commission; NJDEP DFW, New Jersey Department of Environmental Protection, Division of Fish and Wildlife; NYDEC, New York Department of Environmental Conservation; GDNR WRD, Georgia Department of Natural Resources, Wildlife Resources Division; MDC, Missouri Department of Conservation; ADCNR, Alabama Department of Conservation and Natural Resources; MDFW, Massachusetts Division of Fisheries and Wildlife

Table 3.2. Accounting of known golden eagle translocations. Information came largely from personal communication with state agency officials.

State	Source	Time period	Origin for Hacked Birds	Number of Birds
Georgia	Touchstone Ecosystems	1980-90s	Primarily Wyoming	111
North Carolina	TVA, FWS, NCWRC	1980-1986	Origins unknown	26
Pennsylvania	Private effort	1983-1990	Western US	6
Tennessee	Private effort	1995-2006	Captive bred	47

Abbreviations: TVA, Tennessee Valley Authority; FWS, Fish and Wildlife Service; NCWRC, North Carolina Wildlife Resources Commission.

Table 3.3. Indices of differentiation between contemporary and historic golden eagles in North America

Measure	Value	p-value
Fst	0.013	0.098
Gst	0.008	0.107
G´st	0.016	0.107
G´´st	0.050	0.113
Jost’s D	0.035	0.113

Table 3.4. Pairwise F_{ST} values between all contemporary bald eagle populations. Associated p-values were all lower than 0.01.

	Florida	Eastern States	Northwestern States	Alaska
Florida	-	-	-	-
Eastern States	0.046	-	-	-
Northwestern States	0.078	0.082	-	-
Alaska	0.153	0.185	0.059	-

Table 3.5. Pairwise F_{ST} values between all historic bald eagle populations. Associated p-values were all lower than 0.05.

	Florida	Eastern States	Alaska
Florida	-	-	-
Eastern States	0.108	-	-
Alaska	0.098	0.108	-

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APPENDIX A

Expanded Methods

DNA Extraction Buffers

Buffer used to store tissue or blood samples prior to phenol:chloroform extractions

ABI Lysis Buffer:	**to mix up 250mL:**
0.1 M Tris	25mL of 1M stock
4.0 M Urea	60.06g dry
0.2 M NaCl	10mL 5M stock
0.01 M CDTA	0.866g dry
0.5% n-Laurylsarcosine	1.25g dry
RO water to 250mL	

Buffers used in DNA extractions from feathers

Digestion Buffer – for 1 digestion
600 µl 1x TNE (see below)
60 µl 1M Tris Cl (pH 8.0)
10 µl 25% (w/v) SDS
5 µl Proteinase K (10mg/mL) *
5 µl 1M DTT*
24 µl ddH_2O

TNE, Tris, and SDS can be mixed and stored, but do not add DTT or Proteinase K to the buffer if it will be left in storage. Add both directly to individual reactions at the time of digestion. DTT will denature if left in buffer, and ProtK will digest itself eventually. Also do not refrigerate buffer or SDS will come out of solution. Also, using primary feathers or multiple feather tips may need 10-15 µl of Prot K

250 mL 1x TNE
1.461 g NaCl (100mM)
1.51375 g Tris (50mM)
2.3265 g EDTA (25mM)
Bring to pH 7.5 w/HCl
Bring volume to 250ml

PCR

Molarity for all PCR set-ups are included in the chapters, but here are the following recipes used throughout the project.

Cytochrome B amplification

	1x
buffer	5
MgCl2	5
dNTPs	8
L14996	1.5
H 16964	1.5
Taq	1.5
H20	24.5
DNA	3
Total volume	**50**

Big Dye Sequencing reaction

	1x
Big Dye	2
2.5X buffer	6
primer	2
DNA dil.	10
Total volume	**20**

Microsatellite amplification

	1x
buffer	2
MgCl2	2
dNTPs	4
for primer	0.5
rev primer	0.5
Taq	0.5
H20	9.5
DNA	1
Total volume	20

Microsatellite amplification with BSA

	1x
buffer	2
MgCl2	2
dNTPs	4
for primer	0.5
rev primer	0.5
Taq	0.5
BSA	2
H20	7.5
DNA	1
Total volume	20

Cytochrome b amplification with BSA

	1x
buffer	5
MgCl2	5
dNTPs	8
L14996	1.5
H 16964	1.5
Taq	1.5
H20	21.5
BSA	3
DNA	3
Total volume	50

Appendix B

Expanded Results

The following are all sequenced golden eagles and bald eagles used in the study. The IDs provided correspond to a master list that contains band numbers, telemetry numbers, and full capture data, if available. Lower case bases represent ambiguous base assignments.

<u>All Golden Eagle *cyt b* Sequences</u>

MSGE19 (West)
CAAATCCTAACCGGcCTTCTATTAGCCATACACTACACCGCAGACACCACCCT
AGCCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTAA
TCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTT
CACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAA
ACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTAT
GTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACC
TATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGG
TGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTT
ACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGtACTAATACTACT
CCCACTAACAACTCTAGcTCtATTcTCACCtAACCtGCtAGGCGACCCAGAAAAC
TTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGAT
ACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGA
GTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCAT
AAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTG
GACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTA
GAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCAC
CCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACC
ACTAA

MSGE2 (West)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCAGACACCACCC
TAGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTAC
TCCCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAA
AACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAAT
GATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGA
GGAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTC
CATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATT
CTGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCA

GTAGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTC
CACCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCA
ACCACTAA

MWGE10-3 (East)
CaAATcCTAACCGGCCTCCTATTAGCCATACAaTACACcGCAGACACCACCCTA
GcCTTcTCATCcGTcGCCCACACATGTCGGAACGTACAGTACGGCTGACTAATC
CGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTCA
CATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAAC
ACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGT
CCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTA
TTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTG
GATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTAC
TTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATT
CCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACTCC
CACTAACAACTCTAGCTcTAtTcTCACCTaACCtGcTAGGCGACCCAGAAAACTT
CACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATAC
TTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGT
GCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATCC
GTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGA
CCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGA
ACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTCCTTCTCCACCCT
CCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACT
AA

MWGE110 (West)
CAAATCCtAACCGGCCTCCTATTAGCCATACAcTACACCGCAGACACCACCCT
AGCCTTCTCATCCGTcGCCCACACATGTCGGAACGTACAGTACGGCTGAcTAA
TCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTT
CACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAA
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GTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACC
TATT?TCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGT
GGATTCTCTGTAGATAACCCCACCCTCACTCGCTTcTTCGCCCTACATTTTTTA
CTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGA
GTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCA
TTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTcGTACTAATACTACTC
CCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAA
ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA

CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

MWGE112 (West)
CAAATCcTAACCGGCcTCcTATTAGCCATACAcTACACcGCAGACACCACCCTA
GcCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGAcTAATC
CGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTCA
CATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAAC
ACAGGAATCATTcTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTC
CTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTAT
TCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGG
ATTCTCTGTAGATAACCCCACCCTCACTCGcTtcTTCGCCCTACATTTTTTACTT
CCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGTC
CGGATCAAACAaTCCCcTAGGAATTATCTCAAACtGtGACAAATTCCCGTTCCA
CCCCTACTTCTCCCTAAAAGaCATCCTAGGATTCGTACTAATACTACTCCCACT
AACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCA
CCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTC
CTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCT
AGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTC
CAAACAACGGACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCC
TAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACA
CCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCT
AATCCTCTTCCCCCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE113 (West)
CAAATCcTAACCGGCcTCcTATTAGCCATACAcTACACCGCAGACACCACCCTA
GcCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTAAT
CCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTC
ACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAA
CACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATG
TCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCT
ATTcTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTG
GATTCTCTGTAGATAACCCCACCCTCACTCGCTTcTTCGCCCTACATTTTTTAC
TTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAtTCCCgTTC
CACCCcTACTTCTCCCTAAAAGACaTCcTAGGATTCGtACTAaTACTACTCCCAC
TAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTC
ACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACT
TCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTG
CTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAG
TCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGAC
CCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAA
CACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTC
CTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTA
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MWGE114 (West)
CAAATCcTAACCGGCcTCcTATTAGCCATACAcTACACCGCAGACACCACCcTA
GcCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGcTGACTAAT
CCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTC
ACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAA
CACAGGAATCATTcTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGT
CCTCCCATGAGGACAGATATCCTTcTGAGGAGCCACAGTCATCACCAACCTAT
TcTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGG
ATTCTCTGTAGATAACCCCACCCTCACTCGCTTGTTCGCCCTACATTTTTTACT
TCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAaTCCCATTC
CACCCCTACTTCTCCCTAAAAGACaTCCTAGGATTCGTACTAaTACTACTCCCA
cTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTT
CACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATAC
TTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGT
GCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAA
GTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGA
CCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGA
ACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCC
TCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCAC
TAA

MWGE115 (West)
CAAaTCcTAACCGGCcTCcTATTAGCCATACAcTACACCGCAGACACCACCCTA
GCcTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGcTGAcTAATC
CGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTCA
CATCGGCCGAGGACTcTAcTACGGCTCATACCTTTATAAAGAGACCTGAAACA
CAGGAATCATTcTCcTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTCC
TcCCAtGAGGACAGATATCCTTcTGAGGAGCCACAGTCATCACCAACcTATTGT
CAGCAATCCCATACATCGGACAAACCcTCGTAGAGTGGGCCTGAGGTGGATT
CTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCcTACATTTTTTACTTCC
AtTCCTTATcGCAAgCCTTACCCTAATCCACcTTACCTTCCTACAcGAGTCCGGA
TCAAACaATCCCCTAGGAaTTaTcTCAAACtGtGACaAAATCCCaTTCCACCCCtAC
TTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACTCCCACTAACAAC
TCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCACCCCAG
CAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCCTATTT
GCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCTAGCTC
TAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTCCAAA
CAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCCTAAT
CGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACACCCG
TTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCTAATC
CTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE116 (West)
CAAATCcTAACCGGCcTCcTATTAGCCATACATTACACCGCAGACACCACCCT
AGcCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGcTGAcTAAT

CCGCAACCTACATGCCAACGGAGcATCCTTCTTCTTCATCTGCATTTACCTTCA
CATCGGCCGAGGACTCTAcTACGGCTCATACCTTTATAAAGAGACCTGAAACA
CAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTC
CTCCCAtGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTATT
CTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGGA
TTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTACTT
CCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGTC
CGGATCAAACaATCCCCTAGgaATTATCTCAAACTgTgACAAAATCCCaTTCCAC
CCCtACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACTCCCACTA
ACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCAC
CCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCC
TATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCT
AGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTC
CAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCC
TAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACA
CCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCT
AATCCTCTTCCCCCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE117 (East)
CAAATCcTAACCGGCcTCcTATTAGCCATACAcTACACcGCAGACACCACCCTA
GCcTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGAcTAAT
CCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTC
ACATCGGCCGAGGACTCTAcTACGGCTCATACCTTTATAAAGAGACCTGAAAC
ACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGT
CCTCCCAtGAGGACAGATATCCTTcTGAGGAGCCACAGTCATCACCAACCTAT
TcTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGG
ATTCTCTGTAGATAACCCCACCCTCACTCGCTTcTTCGCCCTACATTTTTTACT
TCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATCAAACAATCCCcTAGGAATTATCTCAAACtGtGACAAAATCCCATTCC
ACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGtACTAATACTAcTCCCAC
TAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTC
ACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACT
TCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTG
CTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAG
TCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGAC
CCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAA
CACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTC
CTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTA
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MWGE16 (East)
CAAATCCTAACCGGCCTCCTATTAGCCATACAcTACACCGCAGACACCACCCT
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TCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTT
CACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAA
ACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTAT

GTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACC
TATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGG
TGGATTCTCTGTAGATAAcCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTT
ACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTAC
TCCCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAA
AACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAAT
GATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGA
GGAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTC
CATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATT
CTGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCA
GTAGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTC
CACCCTCCTAATCCTCTTCCCCCTAATTGGAGCCCTCGAAAATAAAATGCTCA
ACCACTAA

MWGE19 (East)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACAACGCAGACACCACCC
TAGCCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATccTAGGATTCGTACTAATACTACT
CCCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAA
ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTACTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA
CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

MWGE2 (East)
CAAATCCTaaCCGGCCTCcTaTTAGCCATACAcTACaCCGcAGACACCACCCTAG
CcTTATCATCcGTCGCCCACACATGTcgGAACGTACAGTACGGCtGACTAATCC
GCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACcTTCACA
TCGGCCGAGGACTCTAcTACGGcTCATACCTTTATAAAGAGACCTGAAACACA
GGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTCCT
CCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTATTC
TCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGGAT

TCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTACTTC
CATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGTCC
GGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATTCC
ACCCCTACTTCTCCCTAAAAGACATCctAGGATTCGTACTAATACTACTCCCAC
TAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTC
ACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACT
TCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTG
CTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAG
TCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGAC
CCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAA
CACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTC
CTAATCCTCTTCCCCCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTA
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MWGE20 (East)
CaAATCCTAaCcGGCCTCCTATTAGCCATACAcTACACCGCAGACACCACCCTA
GCcTTcTCATCCGTCGcCCACACATGTCGGAACGTACAGTACGGCTGACTAATC
CGCAACcTACATGCCAAcGGAGCATCCTTcTTCTTCATcTGCATTTACCTTCACA
TCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAACAC
AGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTCC
TCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTATT
CTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGGA
TTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTACTT
CCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGTC
CGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATTC
CACCCCTACTTCTCCCTAAAAGACATcctAGGATTCGTACTAATACTACTCCCA
CTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTT
CACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATAC
TTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGT
GCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAA
GTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGA
CCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGA
ACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCC
TCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCAC
TAA

MWGE23 (East)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCAGACaCCACCcT
AGCCTTCTCATCCGTCGCCcACaCaTGTCGGAACGtaCAGtACGGCTGACTAATC
CGCAACcTACATGCCAACGGAGCATCCTTcTTCTTCATCtGCATTTACcTTCACA
TCGGCCGAGGACTcTACTACGGATCATACCTTTATAAAGAGACCTGAAACAA
CGGAATCATTcTCCTAcTTACCCTTAtAGCAACCGCCTTtGTAGGcTATGTCCTC
CCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACcTATTTCca
GCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCcTGAGGTGGATTCTC
TGTAGATAACCCCACCCTCACTCGCTTcTTCGCCcTACATTTtTTAcTTCCATTCc
TTATCGCAAGCcTTACCcTAATCCACCtTACCtTCATACaCGAGTCCGGATCAAA

CAATCCCCTAGGAATTATCTCAAACTGTgACAAAATCCCATTCCACCCCTACT
TctCCcTAAAAGACATCCTAGGATTCGtACTAATActACtccCActAACAACTCtAGc
TCTaTTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCACCCCAGCAAACC
CCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCCTATTTGCATAC
GCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCTAGCTCTAGCTG
CCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTCCAAACAACGC
ACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCCTAATCGCCAA
CCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACACCCGTTCATTA
TCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCTAATCCTCTTCC
CTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE24-1 (East)
CAAATCCTAACCGGCCTCcTATTAGCCATACAcTACACcGCAGACACCACCCT
AGCCTTcTCATCCGTCGcCCACACATGTCGGAACGTACAGTACGGCTGACTAA
TCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTT
CACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAA
ACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTAT
GTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACC
TATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGG
TGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTT
ACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACtGTGACAAAATCCCA
TTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACT
CCCACTAACAACTCTAGCTCTatTcTCACCTAACCTGCTAGGCGACCCAGAAAA
CTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGAT
ACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGA
GTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCAT
AAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTG
GACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTA
GAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCAC
CCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACC
ACTAA

MWGE25 (East)
CAAATCCTAACCGGCcTCcTATTaGCCATACAcTACACCGCaGACACCACCCTA
GCCTTcTCATCCGTCGCCCACACATGTcGGAACGTACAGTACGGCTGAcTAATC
CGCAACcTACATGCCAACGGAGCATCCTTcTTCTTCATCtGCATTTACCTTCAC
ATCGGCCGAGGACTcTACTACGGCTCATACCTTTATAAAGAGACCTGAAACAC
AGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTCC
TCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACcTATTC
TCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGGAT
TCTCTGTAGATAACCCCACCCTCACTCGcTTCTTCGCCCTACATTTTTTACTTC
CATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGTCC
GGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATTCC
ACCCCTACTTCTCCCTAAAAGAcatccTAGGATTCGTACTAATACTACTCCCAcT
AACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCA

CCCCAGCAGACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTC
CTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCT
AGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTC
CAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCC
TAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACA
CCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCT
AATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE26-2 (East)
CaAATCCTAACCGGCcTCcTATTAGCCATACAcTACACcGCAGACACCACCcTA
GCcTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGAaTAATC
CGCAACCTACATGCCAACGGAGCATCcTTCTTCtTCATATGCATTTACCTTCAC
aTCGGCCGAGGAcTcTACTACGGCTCATACCTTTATAAAGAGACcTGAAACACA
GGAATCATTCTCGTAcTTACCcTTATAGCAACCGCCTTTGTAGGCTATGTCCTC
CCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACcTATTCTC
AGCAATCCCATACATcGGACAAACCCTCGTAGAGTGGGCCTGAGGTGGATTC
TCtGTAGATAACCCCACCCTCACTCGCTTCTTCGCCcTACATTTTTTACTTCCAT
TCCTTATCGCAAGCCTTACCcTAATCCACCTTACCTTCCTACACGAGTCCGGAT
CAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATTCCACCC
CTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACTCCCAcTAA
CAACTCTAGCTCTaTTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCACC
CCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCCT
ATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCTA
GCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTCC
AAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCCT
AATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACAC
CCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCTA
ATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE27-1 (East)
CAAATCcTAACcGGCcTCcTATTAGCCATACAcTACACcGCAGACACCACCcTAG
cCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGcTGAcTAATCC
GCAACcTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTCACA
TCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAACAC
AGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTCC
TCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTATT
CTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGGA
TTCTCTGTAGATAACCCCACCCTCACTCGcTTCTTCGCCCTACATTTTTTACTTC
CATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGTCC
GGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAaATCCCaTTCCA
CCCCTACTTCTCCCTAAAAGACGTCCTAGGaTTCGTACTAaTACTAcTCCCACT
AACaACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCA
CCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTC
CTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCT
AGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTC
CAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCC

TAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACA
CCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCT
AATCCTCTTCCCCCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE28-3 (East)
CAAATCcTAACCGGCCTCcTATTAGcCATACAcTACACcGCaGACAcCACCcTAG
CcTTcTCATCcGTcGCCCACACAtGTCGGAAcGTACAGTACGGCTGAATAATCCG
CAACCTACATgCCAACGGAGCATCCTTCTTcTTCATCTGCATTTACCTTCACaTC
GgCCGAGGACTcTACTACGGCTCATACCTTtATAAAGAGACCtGAAACaCAGGA
ATCATTCTCcTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTCCTcCCAt
GAGGACAGATATCCtTCTGAGGAGCCACAGTCATCACCAACcTATTCTCAGCA
ATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGtGGATTCTCtGT
AGATAACCCCACCCTCACTCGCTTCTTCGCCaTACATTTTTTACTTCCATTCCtT
ATcGCAAGCCTTACCGTAATCCACCTTACCtTCGGACACGAGTCCGGATCAAA
CAATcCCcTAGGAATTATCTCAAACTgTGACAAAAGCCCATTcCACCCCTACTT
CTCCcTAAAAGACATCCTAGGATTCGTACTAATACtACtcCCACTAACAACTCT
AGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCACCCCAGCA
AACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCCTATTTGC
ATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCTAGCTCTA
GCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTCCAAACA
ACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCCTAATCG
CCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACACCCGTT
CATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCTAATCCT
CTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE36-3 (West)
CAAATCCTAAcCGGCcTCCTaTTaGCCATACAcTACACCGCAGACACCACCCTA
GCCTTcTCATCGGTCGCCCACACATGTcGGAACGTACAGTACGGCTGAcTAATC
CGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTCA
CATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAAC
ACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGT
CCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTA
TTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTG
GATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACAttTTTTACT
TCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATT
CCACCCCTACTTCTCCCTAAAAGACATCctaGGATTCGTAcTAATAcTAcTCCCA
CTAACAACTcTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTT
CACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATAC
TTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGT
GCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAA
GTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGA
CCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGA
ACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCC
TCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCAC
TAA

MWGE36-4 (West)
CAAATCCTAACCGGCCTCCTATTAGCCATACAcTACACcGCAGACACCACCCT
AGCcTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTAA
TCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTT
CACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAA
ACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTAT
GTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACC
TATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGG
TGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTT
ACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCcTAGGATTCGTACTAATACTACT
CCCACTAACAACTCTAGCTcTAtTcTCACCTAACCTGCTAGGCGACCCAGAAAA
CTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGAT
ACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGA
GTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCAT
AAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTG
GACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTA
GAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCAC
CCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACC
ACTAA

MWGE36-5 (West)
CAAATCCTAACCGGCCTCCTATTAGCCATtCaCTACACAGCAgAcAccACCctAGc
CTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTaATCC
GCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTCAC
ATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAACA
CAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTC
CTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTAT
TCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGG
ATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTaCATTTTTTACTT
CCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGTC
CGGATCAAACAATcCCCTAGGAATTATCTCaaactgtGACAAAATCCCATTCCACC
CCTACTTCTCCCTAAAAGACAtcctAGGATTCGTACTAATACTACTCCCACTAAC
AACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCACCC
CAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCCTA
TTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCTAG
CTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATCCGTCCA
AACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCCTA
ATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACACC
CGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCTAA
TCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE36-6 (West)

CAAATCCTAACCGGCCTCCTaTTAGCCATACAcTACACCGCAGACACCACCCT
AGCCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGcTGAcTAAT
CCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTC
ACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAA
CACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATG
TCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCT
ATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGT
GGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTA
CTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGA
GTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCA
TTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACT
CCCACTAACAACTcTAGCTcTATTcTCACcTAACCTGCTAGGCGACCCAGAAAA
CTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGAT
ACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGA
GTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCAT
AAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACGCCTATTCTG
GACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTA
GAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCAC
CCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACC
ACTAA

MWGE39 (East)
CAAATCCTAACCGGCCTCCTATTAGCCATACAcTACACcGCAGACAcCAcccTA
GCAtTcTCATCcGTCGCCCACACATGTCGGAACGTACAGTACGGCTGAcTAATC
CGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTCA
CATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAAC
ACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGT
CCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTA
TTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTG
GATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTAC
TTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATCAAACAATCCCCTAGGAATTATCTCAAActGTGACAAAATCCCATTC
CACCCCTACTTCTCCCTAAAAGACATcctaGGATTCGTACTAATACTACTCCCAC
TAACAACTCTAGCTCtAtTcTCACCtAACCTGCTAGGCGACCCAGAAAACTTCA
CCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTC
CTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCT
AGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTC
CAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCC
TAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACA
CCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCT
AATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE41 (East)
CAAATCCTAACcGGCCTCCTATTAGCCATACAcTACACCGCAGACACCACCCT
AGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT

TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACAtccTAGGATTCGTACTAATACTACT
CCCACTAACAACTCTAGCTcTATTcTcACCtAACCTGCTAGGCGACCCAGAAAA
CTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGAT
ACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGA
GTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCAT
AAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTG
GACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTA
GAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCAC
CCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACC
ACTAA

MWGE42 (East)
CAAATCCTAACCGGCCTCcTATTAGCCATACAcTACACCGCAGACACCACCCT
AGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTa
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAGACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATcctAGGATTCGTACTAATACTACT
TCCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAA
ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA
CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

MWGE43 (East)
CAAATCCTAACCGGCCTCCTATTAGCCATACAcTACACCGCAGACACCACCCT
AGCCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTAA
TCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTT
CACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAA
ACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTAT

GTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACC
TATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGG
TGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTT
ACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGtACTAAtACTACT
CCCACTAACAACTCTAGcTCTAtTctCACcTAaCCTGCTAGGCGACCCAGAAAAC
TTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGAT
ACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGA
GTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCAT
AAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTG
GACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTA
GAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCAC
CCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACC
ACTAA

MWGE5 (East)
CAAATCCTAACCGGCcTCCTATTaGCCATACACTACACCGCAGACACCACCcT
AGCcTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGAcTAAT
CCGCAACcTACATGCCAACGGAGCATCcTTCTTcTTCATCTGCATTTACCTTCA
CATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAAC
ACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGT
CCTCCCATGAGGACAGATATCCTTcTGAGGAGCCACAGTCATCACCAACCTAT
TCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGG
ATTCTCTGTAGATAACCCCACCCTCACTCGCTTcTTCGCCCTACATTTTTTACT
TCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATCAAACAATCCCCTAGGAATTATCTCAAACTgTGACAAAATCCCATTC
CACCCCTACTTCtcCCTAAAAGACATCCTAGGAtTCGtACTAAtACTACTCCCAC
TAACAaCTCTAGcTCtAtTCTCACCtAaCCTGCTAGGCGACCCAGAAAACTTCAC
CCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCC
TATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCT
AGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTC
CAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCC
TAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACA
CCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCT
AATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE53 (West)
CAAaTCCTAACCGGCcTCcTATTAGCCATACAcTACACcGCAGACACCACCCTA
GCcTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGcTGAcTAATC
CGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTCA
CATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAAC
ACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGT
CCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTA
TTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTG
GATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTAC

TTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATT
CCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACTCC
CACTAACAACTCTAGcTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAAC
TTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGAT
ACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGA
GTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCAT
AAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTG
GACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTA
GAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCAC
CCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACC
ACTAA

MWGE55 (West)
cAAATCcTAACCGGCCTCCTATTAGCCATACAcTACACCGCAGACACCACCcTA
GCcTTcTCaTCCGTCGCCCACACATGTCGGAACGTACAGTACGGcTGAcTAATC
CGCAACcTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTCAC
ATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAACA
CAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTC
CTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTAT
TCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGG
ATTCTCTGTAGATAACCCCACCCTCACTCGcTTCTTCGCCCTACATTTTTTACT
TCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATT
CCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACTCC
CACTAACAAcTCTAGcTCTAtTcTCAcCTAACCTGCTAGGCGACCCAGAAAACTT
CACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATAC
TTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGT
GCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAA
GTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGA
CCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGA
ACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCC
TCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAGTGCTCAACCAC
TAA

MWGE56 (West)
cAAATCcTAACCGGcCTCCTATTAGCCATACAcTACACCGCAGACACCACCCTA
GCcTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGcTGAcTAATC
CGCAACCTACATGCCAACGGAGCATCCTTTTTCTTCATCTGCATTTACCTTCA
CATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAAC
ACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGT
CCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTA
TTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTG
GATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTAC
TTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATT

CCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTcGTACTAATACTACTCC
CACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAA
CTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGAT
ACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGA
GTGCTAGCTCTAGGTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCAT
AAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTG
GACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTA
GAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCAC
CCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACC
ACTAA

MWGE6 (West)
CAAATCCTAAACGGCCTCCTATTAGCCATACAcTACACcGCAGACACCACCCT
AGCCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTAA
TCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTT
CACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAA
ACACAGGAATCATTCTCcTACTTACCCTTATAGCAACCGCCTTTGTAGGCTAT
GTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACC
TATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGG
TGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTT
ACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTAC
TCCCACTAACAACTCTAGCTCTATTcTCACCtAACCTGCTAGGCGACCCAGAA
AACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAAT
GATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGA
GGAGTGCTAGCCCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCT
CCATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTAT
TCTGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCA
GTAGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTC
CACCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCA
ACCACTAA

MWGE61 (West)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCACACACCACCCT
AGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGAcTAA
TCCGCAACCTACATGCCAaCGGAGCATcCTTCTTCTTCATCTGCATTTACCTTC
ACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAA
CACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATG
TCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCAcCAACcTA
TTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTG
GATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTAC
TTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATcAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATTC
CACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACTCCC
ACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGAGACCCAGAAAAC

TTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGAT
ACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGA
GTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCAt
AAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTG
GACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAg
AACACCCGTTCATTATCATCGGCCAACTCGCCTcCCTCACCTACTTCTCCAcCC
TCCTAATCCTCTTcCCTCTAATTGGAGCCCTCgAAAAtAAAATGCTCaAcCaCTA
A

MWGE75 (East)
CAAATCCTAACCGGCCTCCTATTAGCCATACAcTACACCGCAGACACCACCCT
AGCCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTAA
TccGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTC
ACATCGGCCGAGGACTCTAcTACGGCTCATACCTTTATAAAGAGACcTGAAAC
ACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGT
CcTCCCATGAGGACAGATATCCTTcTGAGGAGCCACAGTCATCcCCAACcTATT
cTCAGCAATCCCATACATCGGACAAACCcTCGTAGAGTGGGCCTGAGGTGGAT
TcTcTGTAGATAACCCCACCCTCACTCGGTTGTTCGCCCTACATTTTTTAcTTCC
AtTCCTTATcGCAAGCCTTACCCTAATCCACcTtACCTTcCTACaCGAGTCcGGAT
CAAACAATCCCcTAGGAAttATCTCaAACTGTGACAAAATCcCATTCCACCCCTA
CTTcTCCcTAAAAGACATCCTAGGATTCGTACTAATACTACTCCCACTAACAAC
TCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCACCCCAG
CAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCCTATTT
GCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCTAGCTC
TAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTCCAAA
CAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCCTAAT
CGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACACCCG
TTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCTAATC
CTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE77 (East)
CAAATCCTAACCGGCCTCcTATTAGCCATACACTACACCGCAGACACCACCCT
AGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGAcTAA
TccGcAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTC
ACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAA
CACAGGAATCATTcTCATAcTTACCcTTATAGCAACCGCCTTTGTAGGCTATGT
CcTCCCATGAGGACAGATATCCtTcTGAGGAGCCACAGTCATCACCAACcTATT
cTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGGA
TTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCTTACATTTTTTAcTTC
CAtTCCTTATTGCAAGCCTTACCCTAATCCACcTTACCTTcCTACacGAGTCcGGA
TCAAACAATCCCcTAGGAAttATCTCAAACTGTGACAAAATCCCATTCCACCCC
TACTTcTCCcTAAAAGACATCCTAGGATTCGTAcTAATAcTAcTCCCACTAACAA
CTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCACCCCA
GCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCCTATT
TGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCTAGCT
CTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTCCAA

ACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCCTAA
TCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACACCC
GTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCTAAT
CCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE8 (East)
CAAATCCTAACCGGCCTCcTATTAGCCATACAcTACACCGCAGACACCACCCT
AGCCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTAA
TCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATcTGCATTTACCTTC
ACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAA
CACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATG
TCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCT
ATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGT
GGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTA
CTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGA
GTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCA
TtcCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACTC
CCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAA
ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA
CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

MWGE83 (East)
CAAATCCTAACCGGCcTCCTaTTAGCCATACAcTACACCGCAGACACCACCCT
AGCCTTcTCATCCGTcGCCCACACATGTCGGAACGTACAGTACGGCTGACTAA
TCcGcAAcctAcATGCCAACGGAGCATCCTTCTTCTTCATcTGCATTTACCTTCAC
ATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAACA
CAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTC
CTCCCATGAGGACAGATATCCTTcTGAGGAGCCACAGTCATCACCAACCTATT
CTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGGA
TTCTCTGTAGATAACCCCACCCTCACTCGcTTCTTCGCCCTACATTTTTTAcTTC
CATTCCTTATcGCAAGCCTTACCCTAATCCACCTTACCTTCCTACaCGAGTCCG
GATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATTCCA
CCCCTACTTCTCCCTAAAAGACATCCTaGGaTTCGTACTAATACTACTCCCACT
AACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCA
CCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTC
CTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCT
AGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTC
CAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCC
TAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACA

CCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCT
AATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE9-1 (East)
CAAATCCTaACcGGCCTCCTATTaGCCATACAcTACACCGCaGACACCAccctAGC
ATTcTCATCCGTCGCCCACACATGTcGGAACGTACAGTACGGcTGACTAATCCG
CAACCTACATGCCAaCGGAGCATCCTTCTTcTTCATCTGCATTTACCTTCACAT
CGGCCGAGGACTcTACTACGGCTCATACCTTTATAAAGAGACCTGAAACACA
GGAATCATTCTCcTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTCCTC
CCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTATTCT
CAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGGATT
CTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACAtttttTACTTCCATT
CCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGTCCGGAT
CAAACAATCCCCTAGGAATTATCTCAAactGTGACAAAATCCCATTCCACCCCT
ACTTCTCCCTAAAAGACATcCtAGGATTCGTACTAATACTACTCCCACTAACAA
CTctAGCTCTaTTCtCACCtAACCTGCTAGGCGACCCAGAAAACTTCACCCCAGC
AAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCCTATTTG
CATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCTAGCTCT
AGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTCCAAAC
AACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCCTAATC
GCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACACCCGT
TCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCTAATCC
TCTTCCCCCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

MWGE94 (West)
CAAATCCTAACCGGCCTCcTATTAGCCATACAcTACACCGCAGACACCACCcT
AGCcTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGAcTAAT
CcGcAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTCA
CATCGGCCGAGGACTCTAcTACGGCTCATACCTTTATAAAGAGACCTGAAACA
CAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTC
CTCCCATGAGGACAGATATCCTTctGAGGAGCCACAGTCATCACCAACcTATTc
TCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGGAT
TCTCTGTAGATAACCCCACCCTCACTCGCTTcTTCGCCCTACATTTTTTACTTC
CATTCCTTATcGCAAGCCTTACCCTAATCCACcTTACCTTCCTACAcGAGTCCG
GATCAAACAATCCCCTAGGAAttATCTCAAACTGTGACAAAATCCCATTCCAC
CCCTACTTCTCCcTAAAAGACATCCTaGGATTCGTAcTAATAcTACTCCCAcTAA
CAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCACC
CCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCCT
ATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCTA
GCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTCC
AAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCCT
AATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACAC
CCGTTCATTATCATCGGCCAAGTCGCCTCCCTCACCTACTTCTCCACCCTCCTA
ATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

WCGE1 (East)

CAAATCcTAACCGGCcTCcTATTAGCCATACACTACACCGCAGACACCACCCT
AGCcTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGcTGAcTAAT
CCGCAACCTACATGCCAACGGAGCATCcTTCTTCTTCATCTGCATTTACCTTCA
CATCGGCCgAGGACTcTAcTACGGCTCATACCTTTATAAAGAGACCTGAAACA
CAGGAATCATtctcctAcTTACCCTTATAGCAACCGCCTTTGTAgGcTATGTCCTCC
CATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTATTCTC
AGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGGATTC
TCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTACTTCCA
TTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGTCCGG
ATCAAACAATCCCCTAGGAATTATCTCAAACTGtGACAAAATCCCATTCCACC
CCTACTTCTCCCTAAAAGACATccTAGGATTCGtACTAATACTACTCCCACTAA
CAACTCTAGcTctATTcTCACCTAACCTGCTAGGCGACCCAGAAAACTTCACCC
CAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCCTA
TTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCTAG
CTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTCCA
AACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCCTA
ATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACACC
CGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCTAA
TCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

WCGE10 (West)
CAAATCcTAACCGGCCTCcTATTAGCCATACAcTACACCGCAGACACCACCCT
AGcCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGAcTAAT
CCGCAACcTACATGCCAACGGAGCATCCTTCTTcTTCATCTGCATTTACCTTCA
CATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAAC
ACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGT
CCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTA
TTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTG
GATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTAC
TTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATT
CCACCCCTACTTCTCCCTAAAAGACATCcTAGGATTCGtACTAATACTACTCCC
ACTAACAACTCTAGcTCtATtcTCAcCTaAcCTGCTAGGCGACCCAGAAAACTTC
ACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACT
TCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTG
CTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAG
TCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGAC
CCTAATCGCCAACCTCATCATCCTCACATGGATTGGCAGCCAACCAGTAGAA
CACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTC
CTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTA
A

WCGE11 (West)
CAAATCCTAACCGGCCTCCTaTTAGCCATACAcTACACcGCAGACACCACCCT
AGCCTTcTCATCcGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTAA
TCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTT

CACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAA
ACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTAT
GTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACC
TATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGG
TGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTT
ACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTAC
TCCCACTAACAACTcTAGCTcTATTcTcACCtAACCTGCTAGGCGACCCAGAAA
ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTACTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
CGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA
CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

WCGE13 (East)
CaAATCCTAAcCGGCCTCcTAtTAGcCATACAcTACACcGCAGACACCACCcTAG
CCTTcTCATCcGTCGCCCACACATGTcGGAACGTACAGTACGGCTGAcTAATCC
GCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTCAC
ATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAACA
CAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTC
CTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTAT
TCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGG
ATTCTcTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCcTACATTTTTTACTT
CCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGTC
CGGATCAAACAATCCCcTAGGAATTATCTCAAACTGTGACAAAATCCCATTCC
ACCCCTACTTCTCCCTAAAAGACAtccTAGGATTCGTACTAATACTACTCCCAcT
AACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCA
CCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTC
CTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCT
AGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTC
CAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCC
TAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACA
CCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCT
AATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

WCGE2 (East)
CAAATCCTAACcGGCcTCCTATTAGCCATACAcTACACCGCAGACACCACCCT
AGCCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGcTGACTAA
TCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTT
CACATCGGCCGAGGACTcTACTACGGCTCATACCTTTATAAAGAGACCTGAAA
CACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATG
TCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCT

ATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGT
GGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTA
CTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGA
GTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCA
TTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTcGtACTAATACTACTC
CCACTAACAACTctAGcTCtAtTcTcACCTAACCTGCTAGGCGACCCAGAAAACTT
CACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATAC
TTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGT
GCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAA
GTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGA
CCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGA
ACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCC
TCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCAC
TAA

MWGE102 (West)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCAGACACCACCC
TAGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACtGTGACAAAATCCCA
TTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACT
CCCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAA
ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA
CCCTCCTAATCCTCTTCCCCCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

MWGE101 (West)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCAGACACCACCC
TAGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT

TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTAC
TCCCACTAACAACTCTAGCTCTAtTCTCACCTAACCTGCTAGGCGACCCAGAA
AACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAAT
GATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGA
GGAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTC
CATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATT
CTGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCA
GTAGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTC
CACCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCA
ACCACTAA

MWGE93 (West)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCAGACACCACCC
TAGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATcctAGGATTCGTACTAATACTACT
CCCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAA
ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA
CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

MWGE91 (West)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCAGACACCACCC
TAGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC

ATTCCACCCCTACTTCTCCCTAAAAGACATCcTAGGATTCGTACTAATACTACT
CCCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCACAAA
ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTACTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA
CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

MWGE82 (East)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCAGACACCACCC
TAGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCctAGGATTCGTACTAATACTACT
CCCACTAACAACTCTAGCTCTAtTCTCACCTAACCTGCTAGGCGACCCAGAAA
ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA
CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

MWGE81 (East)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCAGACACCACCC
TAGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCcTAGGATTCGTACTAATACTACT
CCCACTAACAACTCTAGCTCTAtTCTCACCTAACCTGCTAGGCGACCCAGAAA

ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA
CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

MWGE79 (East)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCAGACACCACCC
TAGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTAC
TCCCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAA
AACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAAT
GATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGA
GGAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTC
CATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATT
CTGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCA
GTAGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTC
CACCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCA
ACCACTAA

MWGE64 (West)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCAGACACCACCC
TAGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTAC
TCCCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAA
AACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAAT
GATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGA

GGAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTC
CATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATT
CTGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCA
GTAGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTC
CACCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCA
ACCACTAA

MWGE63 (West)
CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCAGACACCACCC
TAGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTAC
TCCCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAA
AACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAAT
GATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGA
GGAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTC
CATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATT
CTGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCA
GTAGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTC
CACCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCA
ACCACTAA

WCGE3 (East)
CAAATCCTAACCGGCcTCCTATTAGCCATACAcTACACCGCAGACACCACCCT
AGcCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTAA
TCCGCAACCTACATGCCAACGGAGCATCCtTCTTCTTCATCTGCATTTACCTTC
ACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAA
CACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATG
TCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCT
ATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGT
GGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTA
CTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGA
GTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCA
TTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACT
CCCACTAACAACTCTAGcTCTaTtCTCACcTAACCTGCTAGGCGACCCAGAAAA
CTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGAT
ACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGA
GTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCAT
AAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTG

GACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTA
GAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCAC
CCTCCTAATCTTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACC
ACTAA

WCGE4 (East)
CAAATCCTAACCGGCcTCCTATTAGCCATACATTACACCGCAGACACCACCCT
AGCtTTATCATCcGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTAA
TCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTT
CACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAA
ACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTAT
GTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACC
TATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGG
TGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTT
ACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCGtAGGATTCGTACTAATACTACT
CCCACTAACAACTCTAGCTCtATTcTCACCtaAcCtGcTAGGCGACCCAGAAAACT
TCACCCCAGCAAACCCCCTACTCACACCCCCTCATATCAAACCAGAATGATA
CTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAATCTGGGAGGAG
TGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATA
AGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGG
ACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAG
AACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACT
CTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCA
CTAA

WCGE5 (East)
CAAATCCTaACCGGCCTCCTATTAGCCATACAcTACACcGCAGACACCACCCT
AGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTAC
TCCCACTAACAACTCTAGCTcTAtTcTCACCTAACCTGCTAGGCGACCCAGAAA
ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA

CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

WCGE6 (West)
CAAATcCTAACcGGCcTCcTATTAGCCATACATTACACcGCAGACACCACCcTA
GCcTTTTCATCcGTCGCCCACACATGTcGGAACGTACAGTAcGGcTGAaTaATCC
GCAACcTACATGCCAAcGGAGCATCcTTcTTCTTCATCtGCATTTACcTTCACATc
GGCGGAGGACTcTAcTAcGGCTCATACCTTTATAAAGAGACcTGAAACACAGG
AATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGTCCTCCC
ATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACcTATTCTCAG
CAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTGGATTCTC
TGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTACTTCCATT
CCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGTCCGGAT
CAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATTCCACCC
CTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTACTCCCACTAA
CAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACTTCACC
CCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATACTTCCT
ATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAGTGCTA
GCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATAAGTCC
AAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGGACCCT
AATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAGAACAC
CCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACCCTCCTA
ATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCACTAA

WCGE7 (West)
CAaATCCTAACCGGCCTCCTATTAGCCATACAcTACACCGCAGACACCACCCT
AGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTAC
TCCCACTAACAACTcTAGCTcTATTcTCACCtAACCTGCTAGGCGACCCAGAAA
ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA
CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

WCGE8 (West)
CAAATCcTAACCGGCCTCCTaTTAGCCATACACTACACcGCAGACACCACCCT
AGCCTTcTCATCCGTcGCCCACACATGTCGGAACGTACAGTACGGCTGACTAA
TCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTT
CACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAA
ACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTAT
GTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACC
TATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGG
TGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTT
ACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCTAGGATTCGTACTAATACTAC
TCCCACTAACAACTcTAGCTcTATTcTCACCTAACCTGCTAGGCGACCCAGAAA
ACTTCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA
CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

WCGE9 (West)
CAAATCCTAACCGGCcTCcTATTAGCCATACAcTACACcGCAGACACCACCcTA
GcCTTcTCATCCGTCGCCCACACATGTCGGAACGTACAGTATGGCTGAcTAATC
CGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCTTCA
CATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGAAAC
ACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTATGT
CCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAACCTA
TTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAGGTG
GATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTTTAC
TTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACGAGT
CCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCCATT
CCACCCCTACTTCTCCCTAAAAGACATCcTAGGATTCGtACTAATACTACTCCC
ACTAACAACTCtAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAAACT
TCACCCCAGCAAACCCCCTAGTTACACCCCCTCATATCAAACCAGAATGATA
CTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAGGAG
TGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCCATA
AGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTCTGG
ACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGTAG
AACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCACC
CTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAACCA
CTAA

MWGE80 (East)

CAAATCCTAACCGGCCTCCTATTAGCCATACACTACACCGCAGACACCACCC
TAGCCTTCTCATCCGTCGCCCACACATGTCGGAACGTACAGTACGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCCTTCTTCTTCATCTGCATTTACCT
TCACATCGGCCGAGGACTCTACTACGGCTCATACCTTTATAAAGAGACCTGA
AACACAGGAATCATTCTCCTACTTACCCTTATAGCAACCGCCTTTGTAGGCTA
TGTCCTCCCATGAGGACAGATATCCTTCTGAGGAGCCACAGTCATCACCAAC
CTATTCTCAGCAATCCCATACATCGGACAAACCCTCGTAGAGTGGGCCTGAG
GTGGATTCTCTGTAGATAACCCCACCCTCACTCGCTTCTTCGCCCTACATTTTT
TACTTCCATTCCTTATCGCAAGCCTTACCCTAATCCACCTTACCTTCCTACACG
AGTCCGGATCAAACAATCCCCTAGGAATTATCTCAAACTGTGACAAAATCCC
ATTCCACCCCTACTTCTCCCTAAAAGACATCCtaGGATTCGTACTAATACTACT
CCCACTAACAACTCTAGCTCTATTCTCACCTAACCTGCTAGGCGACCCAGAAA
ACTTCACCCCAGCAAACCCCCTAGTCACACCCCCTCATATCAAACCAGAATG
ATACTTCCTATTTGCATACGCCATCCTACGTTCAATCCCAAACAAGCTGGGAG
GAGTGCTAGCTCTAGCTGCCTCAGTACTGATCCTATTCCTTATCCCCTTCCTCC
ATAAGTCCAAACAACGCACAATAACCTTTCGACCCCTCTCCCAACTCCTATTC
TGGACCCTAATCGCCAACCTCCTCATCCTCACATGGATTGGCAGCCAACCAGT
AGAACACCCGTTCATTATCATCGGCCAACTCGCCTCCCTCACCTACTTCTCCA
CCCTCCTAATCCTCTTCCCTCTAATTGGAGCCCTCGAAAATAAAATGCTCAAC
CACTAA

All Bald Eagle cyt b Sequences

WCBE24 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCtcAAACTGTGACAAAATTCCA
TTCCACCCATacTTCTCCCTAAAAGatatCCTAGGATTTACACTAATGCTACTCCC
ACTAATAACCTtAGCCCTAtTCTCACCTAACCTGTTAGGAGACCCGGAAAACTT
CACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGATAC
TTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGGAG
TACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCACA
AGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCTGA
ACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGTAG
AACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCATC
CTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAACCA
CTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE25 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCTTAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAA
AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATT
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE26 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGAtATCCTAGGATTTACACTAATGCTACT
CCCACTAATAACCTTAGCCCTATTCtCACCTAACCTGttAGGAGACCCGGAAAA
CTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGA
TACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGG
AGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCA
CAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCT
GAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE38 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCTTAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAA
AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATT
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE39 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA

AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCTtAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAA
AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATT
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE40 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCTtAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAA
AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATT
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE41 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC

TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCTtAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAA
AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATT
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE42 (Washington)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCTtAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAA
AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATT
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE43 (Washington)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCTtAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAA

AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATT
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE44 (Washington)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGAcTA
ATCCGCAACcTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCTA
CACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGAA
ACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCcttcGTAGGCTACGT
ACTTCCATGAggCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATTTAT
TCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGGGGG
ATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCCTACT
CCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACGAAT
CCGGTTCAAACAACCCCCTAGGtatcaTCTCAAACTGTGAcAAAATTCCATTCCA
CCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTACTCCCAC
TAAtAACCTTAGCCCTatTcTCACCTAACCTGTTAGGAGACCCGGAAAACTTCA
CCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGATACTT
CCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGGAGTA
CTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCACAAG
TCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCTGAAC
CCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGTAGAA
CACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCATCCTT
CTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAACCACTA
ATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE45 (Washington)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATtTACACTAATGCTACT
CCCACTAAtAACCtTAGCCCTAtTCTCACCtAACCTGTTAGGAGACCCGGAAAA
CTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGA
TACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGG
AGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCA
CAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCT

GAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTC???CCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAACC
ACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE46 (Washington)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATtTACACTAATGCTACT
CCCACTAAtAACCTtAgcCCTATtctCACCTAACCTGTTAGGAGACCCGGAAAACT
TCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGATA
CTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGGA
GTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCAC
AAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCTG
AACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGTA
GAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCAT
CCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAACC
ACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE47 (Washington)
TAGCcTTTTCATCcGTAGcCCATACATGTcGAAAcGTACAGTATGGcTGAcTAAT
CCGCAACcTACATGCCAACGGAGCATCTTTcTTcTTCATcTGCATcTACcTACAC
ATTGGCCGAGGGcTATATTATGGCTCATACCTATATAAAGAAACTTGAAACAC
AGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTACGTAC
TTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATTTATTC
TCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGGGGGAT
TTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCCTACTCC
CATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACGAATCC
GGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCCATTCCA
CCCATACTTCTCCCTAAAAGATATCCTAGGATtTACACTAATGcTACTCCCACT
AAtAACCTtAgcCCtaTTCTCACCTAACCTGTTAGGAGACCCGGAAAACTTCACC
CCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGATACTTCC
TATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGGAGTACT
AGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCACAAGTC
CAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCTGAACCC
TAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGTAGAACA
CCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCATCCTTCT
AGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAACCACTAAT
ACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE1(Alaska)
TAGCctTTTCATCcGTAGCCCATACATGTCGAAACGTACAGTATGGcTGACTAA
TCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATGTGCATCTACCTA
CACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGAA
ACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTAC
GTACTTCCATGAGGCCAGATATCCTTTTGAGGAGCCACAGTCATCACCAATTT
ATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGGG
GGATtTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCCTA
CTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACGA
ATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCCAT
TCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTACTC
CCACTAATAACCTTAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAAA
ACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATG
ATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAG
GAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTC
ACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTC
TGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE5 (West Virginia)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGcTGAcTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAAcCCCACCCTCACTCGATTCTTTGCCCTACACTTCCT
ACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCAcGA
ATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCCAT
TCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTACTC
CCACTAATAACCTTAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAAA
ACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATG
ATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAG
GAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTC
ACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTC
TGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE7 (West Virginia)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT

ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCtaGGATTTACACTAATGCTACT
CCCACTAATAACCtTAGCCCTAtTCTCACCTAACCTGTTAGGAGACCCGGAAA
ACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATG
ATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAG
GAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTC
ACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTC
TGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGCCTTGT

MWBE34 (Virginia)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCGACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCTtAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAA
AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATT
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

MWBE37 (Virginia)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG

GGGATTTTCCGTAGACAACcCCACCCTCACTCGATTCTTTGCCCTACACTTCCT
ACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCcTAAAAGATATCCTAGGATTTACACTAATGCTACT
CCCACTAATAACCtTAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAAA
ACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATG
ATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAG
GAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTC
ACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTC
TGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

MWBE13 (West Virginia)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCTTAGCCCTATTCTCACCtaACCTGTTAGGaGACCCGGAAA
ACTTCACCCCAGCAAACCCCCTAGCCaCACCACCCCATATCAAACCGGAATG
ATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAG
GAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTC
ACAAGTCCAAAcAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTC
TGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

MWBE15 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC

TCCCACTAATAACCTtAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAA
AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATT
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

MWBE16 (West Virginia)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGAtatCCTAGGATTTACACTAATGCTACTC
CCACTAATAACCTTAGCCCTATTCtCACCTAACCtGttAGGAGACCCGGAAAACT
TCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGATA
CTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGGA
GTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCAC
AAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCTG
AACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGTA
GAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCAT
CCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAACC
ACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

MWBE20 (Virginia)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGAtaTCCTAGGATTTACACTAATGCTACT
CCCACTAATAACCTTAGCCCTATTCtCACCTAACCTGtTAGGAGACCCGGAAA
ACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATG
ATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAG
GAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTC

ACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTC
TGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

MWBE31 (Virginia)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGctGACTAA
TCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCTA
CACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGAA
ACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTAC
GTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATTT
ATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGGG
GGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCCT
ACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCtTAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAA
AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATT
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

MWBE5 (West Virginia)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGcTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGaTaTCCTAGGATTTACACTAaTGCTACT
CCCACTAATAACCTTAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAAA
ACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATG
ATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAG
GAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTC
ACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTC
TGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA

TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

MWBE6 (West Virginia)
TAGcCTTTTCATCCGTAGCCCATACATGTcGAAACGTACAGTATGGcTGAcTAA
TCCGCAACcTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCTAC
ACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGAAA
CACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCATAGGCTACG
TACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATTTA
TTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGGGG
GATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCCTA
CTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACGA
ATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTgTgACAAAATTCCAT
TCCACCCATACTTCTCCCTaAAAGATATCCTAGGATTTACACTAaTGCTACTCC
CACTAATAACCTTAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAAAA
CTTCACCTTAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGA
TACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGG
AGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCA
CAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCT
GAACCCTAATCGCTAATCTCCTAATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

MWBE7 (West Virginia)
TAGCcTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGcTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATaTCCTAGGATTTACACTAaTGCTACT
CCCACTAaTAACCTtAgcCCTATTCTCACCTAACCTGTTAGGAGACCCGGAAAA
CTTCACTTTAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGA
TACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGG
AGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCA
CAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCT
GAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

MWBE8 (West Virginia)

TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCTTAgcCCTATTCTCACCTAACCTGTTAGGAGACCCGGAA
AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATT
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

MWBE9 (Florida)
TAGCcTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGcTGAcTAA
TCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCTA
CACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGAA
ACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGcTAC
GTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATTT
ATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGGG
GGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCCT
ACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATtTACACTAATGcTACT
CCCACTAAtAACCtTAgcCCTatTCTCACCTAACCTGTGAGGAGACCCGGAAAAC
TTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGAT
ACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGG
AGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCA
CAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCT
GAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCGE8 (Florida)
taGCCTTTTCaTCCGTAGCCCaTaCATGtCGAAAcGTACAGTATGGCTGACTAATC
CGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCTACA
CATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGAAAC
ACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTACGT

ACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATTTAT
TCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGGGGG
ATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCCTACT
CCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACGAAT
CCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCCATTC
CACCCATACTTCTCCCTAAAAGATATCCtaGGATtTACACTAATGCTACTCCCA
CTAATAACCTTAGCCCTATTcTCACCTaACCTGTTAGGAGACCCGGAAAACTTC
ACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGATACT
TCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGGAGT
ACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCACAA
GTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCTGAA
CCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGTAGA
ACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCATCCT
TCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAACCACT
AATACTCTAATAGTTTATAAAAAACATTGGCCTTGT

WCBE9 (Florida)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTaGGATTTACACTAATGCTACT
CCCACTAATAACCTTAGCCCTAtTCTCACCTAACCTGTTAGGAGACCCGGAAA
ACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATG
ATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAG
GAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTC
ACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTC
TGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGCCTTGT

WCBE11 (Florida)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG

AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTaGGATTTACACTAATGCTACT
CCCAcTAATAaCCTTAGCCCTATtcTCACCTAACCtgtTAGGAGACCCGGAAAACT
TCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGATA
CTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGGA
GTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCAC
AAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCTG
AACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGTA
GAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCAT
CCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAACC
ACTAATACTCTAATAGTTTATAAAAAACATTGGCCTTGT

WCBE12 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTtACACTAATGCTACT
CCCACTAATAACCTTAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAAA
ACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATG
ATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAG
GAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTC
ACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTC
TGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGCCTTGT

WCBE15 (West Virginia)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATtTACACTAATGCTACT
CCCACTAATAACCTtAGCCCTAtTcTCACCTAaCCtGTTAGGAGACCCGGAAAAC
TTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGAT

ACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGG
AGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCA
CAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCT
GAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE16 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCtaGGATTTACACTAATGCTACT
CCCACTAATAACCTTAGCCCTATTctCACCTAACCtgTTAGGAGACCCGGAAAA
CTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATGA
TACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAGG
AGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTCA
CAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTCT
GAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE17 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATtTACACTAATGCTACT
CCCACTAATAACCTtAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAAA
ACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATG
ATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAG
GAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTC
ACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTC
TGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT

AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE18 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCtTAGCCCTATtCTCACCtAACCTGTTAGGAGACCCGGAAA
ACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATG
ATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAG
GAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTC
ACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATTC
TGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE19 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATtTACACTAATGCTACT
CCCACTAATAACCTTAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAAA
ACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAATG
ATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGAG
GAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTTC
ACAAGTCCAAACAACGAAGCATAACCTTTCGACCCTTCTCCCAACTACTATTC
TGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAGT
AGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTCA
TCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAAC
CACTAAtACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE20 (Alaska)
TAGCCTTTTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTCTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGG
GGGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCC
TACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCTTAGCCCTATTcTCACCTAaCCTGTTAGGAGACCCGGAA
AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATT
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

WCBE21 (Alaska)
TAGCCTTtTCATCCGTAGCCCATACATGTCGAAACGTACAGTATGGCTGACTA
ATCCGCAACCTACATGCCAACGGAGCATCTTTCTTCTTCATCTGCATCTACCT
ACACATTGGCCGAGGGCTATATTATGGCTCATACCTATATAAAGAAACTTGA
AACACAGGAATCATTCTATTACTCACCCTCATGGCAACTGCCTTCGTAGGCTA
CGTACTTCCATGAGGCCAGATATCCTTCTGAGGAGCCACAGTCATCACCAATT
TATTcTCAGCCATCCCATACATCGGACAAACCATCGTAGAATGAGCCTGAGGG
GGATTTTCCGTAGACAACCCCACCCTCACTCGATTCTTTGCCCTACACTTCCT
ACTCCCATTTCTAATCGCAGGCTTCACCCTAATCCACCTTACCTTCCTCCACG
AATCCGGTTCAAACAACCCCCTAGGTATCATCTCAAACTGTGACAAAATTCC
ATTCCACCCATACTTCTCCCTAAAAGATATCCTAGGATTTACACTAATGCTAC
TCCCACTAATAACCTTAGCCCTATTCTCACCTAACCTGTTAGGAGACCCGGAA
AACTTCACCCCAGCAAACCCCCTAGCCACACCACCCCATATCAAACCGGAAT
GATACTTCCTATTCGCATACGCCATCCTACGCTCAATCCCAAACAAACTAGGA
GGAGTACTAGCCCTAGCTGCCTCCGTACTAATTCTATTCCTAGTCCCCTTTCTT
CACAAGTCCAAACAACGAACCATAACCTTTCGACCCTTCTCCCAACTACTATG
CTGAACCCTAATCGCTAATCTCCTCATTCTCACGTGAATCGGAAGCCAACCAG
TAGAACACCCATTCATTATCATTGGCCAAGTAGCCTCCCTTACCTACTTCCTC
ATCCTTCTAGCCCTCTTCCCCCTAACTGGAGCCCTAGAAAACAAACTTCTCAA
CCACTAATACTCTAATAGTTTATAAAAAACATTGGTCTTGT

All Genotypes Included in Analyses

Table A.1. Contemporary Golden Eagle Genotypes

Sample ID	Population	Aa15	Aa15	Aa11	Aa11	Aa12	Aa12
MWGE101	**Western North America**	187	201	259	269	152	154
MWGE102	**Western North America**	185	201	249	261	152	154
MWGE110	**Western North America**	201	201	259	269	0	0
MWGE111	**Western North America**	189	201	267	267	154	154
MWGE112	**Western North America**	185	201	249	269	150	150
MWGE113	**Western North America**	189	201	259	261	154	154
MWGE114	**Western North America**	201	201	249	269	154	154
MWGE115	**Western North America**	185	201	249	259	0	0
MWGE116	**Western North America**	185	201	259	261	154	154
MWGE90	**Western North America**	185	201	249	269	150	154
MWGE91	**Western North America**	187	201	259	271	154	154
MWGE92	**Western North America**	185	201	259	269	154	154
MWGE93	**Western North America**	185	201	249	259	152	152
MWGE94	**Western North America**	185	201	269	269	152	152
WCGE12	**Western North America**	185	199	261	265	160	160
WCGE16	**Western North America**	199	199	261	269	150	154
WCGE21	**Western North America**	189	201	249	267	152	152
WCGE22	**Western North America**	199	207	249	263	154	154
WCGE24	**Western North America**	199	199	263	263	154	154
WCGE25	**Western North America**	199	199	249	249	154	154
WCGE26	**Western North America**	185	199	249	249	154	154
WCGE7	**Western North America**	185	201	261	269	154	154
MWGE35-11	**Western North America**	185	201	259	271	146	146
MWGE35-5	**Western North America**	185	185	0	0	0	0
MWGE35-9	**Western North America**	185	189	249	259	0	0
MWGE36-1	**Western North America**	187	199	249	269	146	146
MWGE36-2	**Western North America**	187	199	249	269	0	0
MWGE36-3	**Western North America**	201	201	259	267	0	0
MWGE36-4	**Western North America**	187	199	249	269	148	162
MWGE36-5	**Western North America**	199	199	251	251	152	154
MWGE36-6	**Western North America**	189	199	249	269	154	154
MWGE36-7	**Western North America**	199	199	259	263	146	146
MWGE50	**Western North America**	199	199	249	267	152	154
MWGE53	**Western North America**	0	0	259	261	154	154
MWGE54	**Western North America**	199	199	249	249	158	158
MWGE55	**Western North America**	185	199	259	269	150	150
MWGE56	**Western North America**	187	199	259	271	150	150

Sample ID	Population	Aa15	Aa15	Aa11	Aa11	Aa12	Aa12
MWGE57	**Western North America**	185	199	269	269	154	154
MWGE58	**Western North America**	0	0	249	265	150	154
MWGE60	**Western North America**	185	199	265	265	152	154
MWGE61	**Western North America**	187	199	269	269	154	154
MWGE62	**Western North America**	199	199	259	259	150	150
MWGE63	**Western North America**	199	199	269	269	152	154
MWGE64	**Western North America**	199	199	259	269	154	154
MWGE65	**Western North America**	185	199	259	269	150	150
WCGE10	**Western North America**	185	199	241	261	152	152
WCGE11	**Western North America**	189	207	261	269	150	150
WCGE14	**Western North America**	185	199	259	265	162	162
WCGE15	**Western North America**	201	201	249	249	152	154
WCGE17	**Western North America**	201	201	249	249	152	152
WCGE18	**Western North America**	201	201	249	249	152	154
WCGE19	**Western North America**	201	201	263	269	150	150
WCGE8	**Western North America**	185	201	251	267	148	148
WCGE9	**Western North America**	187	199	249	269	0	0
MWGE103	**Western North America**	185	201	259	265	154	154
MWGE104	**Western North America**	201	201	259	259	154	154
MWGE105	**Western North America**	185	201	249	249	154	154
MWGE106	**Western North America**	185	201	249	259	154	154
MWGE107	**Western North America**	189	201	249	259	152	152
MWGE108	**Western North America**	185	201	249	269	154	154
WCGE6	**Western North America**	199	205	259	265	154	154
MWGE117	**Eastern North America**	185	185	259	259	0	0
MWGE121	**Eastern North America**	199	199	261	269	152	154
MWGE122	**Eastern North America**	199	199	261	261	152	152
MWGE123	**Eastern North America**	199	199	261	261	152	152
MWGE124	**Eastern North America**	199	199	261	267	152	154
MWGE22-1	**Eastern North America**	185	185	0	0	0	0
MWGE23-1	**Eastern North America**	199	201	259	259	0	0
MWGE24-1	**Eastern North America**	201	201	261	261	0	0
MWGE25	**Eastern North America**	189	199	261	267	154	154
MWGE26-2	**Eastern North America**	199	199	261	271	152	154
MWGE38	**Eastern North America**	185	201	267	267	152	154
MWGE40	**Eastern North America**	201	201	249	271	0	0
WCGE5	**Eastern North America**	187	199	249	259	154	154
CAN24	**Eastern North America**	0	0	0	0	152	154
CAN25	**Eastern North America**	189	201	249	267	152	152
CAN26	**Eastern North America**	189	201	265	265	0	0

Sample ID	**Population**	Aa15	Aa15	Aa11	Aa11	Aa12	Aa12
CAN27	**Eastern North America**	201	201	249	259	152	152
CAN28	**Eastern North America**	0	0	259	259	156	156
CAN29	**Eastern North America**	0	0	265	269	152	152
CAN30	**Eastern North America**	201	201	249	259	152	152
CAN31	**Eastern North America**	201	201	265	269	152	156
CAN32	**Eastern North America**	201	201	259	267	152	154
CAN33	**Eastern North America**	0	0	265	265	0	0
CAN34	**Eastern North America**	201	201	259	259	0	0
CAN35	**Eastern North America**	201	201	259	269	152	154
CAN36	**Eastern North America**	0	0	261	265	0	0
CAN37	**Eastern North America**	0	0	261	271	152	152
CAN38	**Eastern North America**	201	201	267	269	154	154
CAN4	**Eastern North America**	0	0	249	249	152	154
CAN5	**Eastern North America**	0	0	259	259	150	152
CAN7	**Eastern North America**	201	201	259	267	152	152
CAN75	**Eastern North America**	201	201	261	269	154	154
CAN77	**Eastern North America**	201	201	265	265	154	154
CAN78	**Eastern North America**	201	201	0	0	152	154
MWGE28-1	**Eastern North America**	189	199	0	0	152	152
MWGE28-2	**Eastern North America**	189	201	0	0	152	152
MWGE28-3	**Eastern North America**	199	201	259	259	152	152
MWGE29-1	**Eastern North America**	0	0	241	241	0	0
MWGE30-1	**Eastern North America**	185	185	0	0	154	154
MWGE39	**Eastern North America**	189	199	261	269	152	154
MWGE41	**Eastern North America**	201	201	261	261	154	154
MWGE42	**Eastern North America**	199	199	261	261	152	154
MWGE43	**Eastern North America**	199	199	261	261	152	154
MWGE44	**Eastern North America**	199	199	261	261	152	152
MWGE45	**Eastern North America**	189	199	267	269	154	154
MWGE46	**Eastern North America**	189	199	261	267	152	154
MWGE47	**Eastern North America**	189	199	261	269	0	0
MWGE49	**Eastern North America**	199	199	249	261	152	154
MWGE51	**Eastern North America**	199	199	259	259	152	152
MWGE67	**Eastern North America**	0	0	259	269	154	154
MWGE68	**Eastern North America**	187	199	259	269	152	152
MWGE69	**Eastern North America**	199	199	259	259	150	150
MWGE70	**Eastern North America**	199	199	259	265	152	154
MWGE71	**Eastern North America**	187	199	0	0	148	152
MWGE72	**Eastern North America**	199	199	0	0	150	154
MWGE73	**Eastern North America**	187	199	259	259	152	152

Sample ID	Population	Aa15	Aa15	Aa11	Aa11	Aa12	Aa12
MWGE74	**Eastern North America**	189	201	261	261	154	160
MWGE75	**Eastern North America**	185	201	261	269	152	152
MWGE76	**Eastern North America**	185	201	259	259	152	152
MWGE77	**Eastern North America**	185	201	261	261	154	154
MWGE78	**Eastern North America**	201	201	267	269	152	152
MWGE79	**Eastern North America**	201	201	259	269	152	152
MWGE80	**Eastern North America**	185	201	259	269	152	154
MWGE81	**Eastern North America**	185	201	257	269	152	154
MWGE82	**Eastern North America**	185	185	261	269	152	152
MWGE83	**Eastern North America**	185	201	265	265	150	150
MWGE84	**Eastern North America**	189	201	259	265	152	154
WCGE1	**Eastern North America**	185	201	249	249	152	160
WCGE13	**Eastern North America**	185	199	265	269	162	162
WCGE3	**Eastern North America**	199	201	249	261	154	154
WCGE4	**Eastern North America**	185	199	289	289	148	154
CAN10	**Eastern North America**	201	201	259	259	0	0
CAN11	**Eastern North America**	201	201	259	259	154	154
CAN12	**Eastern North America**	201	201	265	269	150	150
CAN13	**Eastern North America**	0	0	241	241	0	0
CAN14	**Eastern North America**	0	0	241	261	152	154
CAN15	**Eastern North America**	0	0	269	269	152	152
CAN16	**Eastern North America**	0	0	0	0	0	0
CAN2	**Eastern North America**	0	0	261	261	0	0
CAN3	**Eastern North America**	0	0	249	259	152	152
CAN43	**Eastern North America**	201	201	265	269	154	154
CAN6	**Eastern North America**	0	0	261	271	152	154
CAN79	**Eastern North America**	201	201	0	0	150	152
CAN8	**Eastern North America**	201	201	259	259	152	152
CAN9	**Eastern North America**	201	201	259	259	152	154
SWE1	**Sweden**	201	201	259	265	0	0
SWE10	**Sweden**	199	199	259	269	0	0
SWE11	**Sweden**	205	205	259	265	150	154
SWE12	**Sweden**	199	199	249	259	0	0
SWE13	**Sweden**	199	199	249	249	0	0
SWE14	**Sweden**	199	199	259	259	0	0
SWE15	**Sweden**	199	207	0	0	0	0
SWE16	**Sweden**	201	201	249	265	0	0
SWE18	**Sweden**	203	203	249	259	0	0
SWE19	**Sweden**	201	205	259	259	152	152
SWE2	**Sweden**	201	207	249	259	0	0

Sample ID	Population	Aa15	Aa15	Aa11	Aa11	Aa12	Aa12
SWE20	**Sweden**	199	205	261	265	148	150
SWE21	**Sweden**	199	199	249	261	150	150
SWE22	**Sweden**	201	205	259	267	150	150
SWE23	**Sweden**	199	199	259	259	150	150
SWE24	**Sweden**	199	201	0	0	152	152
SWE25	**Sweden**	199	205	259	267	152	152
SWE26	**Sweden**	201	201	259	265	0	0
SWE27	**Sweden**	205	205	259	259	148	150
SWE28	**Sweden**	205	205	241	259	152	154
SWE29	**Sweden**	199	199	245	265	152	152
SWE3	**Sweden**	201	201	259	267	152	152
SWE30	**Sweden**	201	201	259	267	0	0
SWE31	**Sweden**	199	199	259	267	152	152
SWE32	**Sweden**	199	199	259	269	148	150
SWE33	**Sweden**	199	199	259	267	152	152
SWE34	**Sweden**	201	205	249	259	150	150
SWE35	**Sweden**	199	201	259	267	152	152
SWE36	**Sweden**	199	205	259	267	0	0
SWE37	**Sweden**	199	199	259	265	152	152
SWE38	**Sweden**	199	199	259	269	152	152
SWE39	**Sweden**	201	207	259	259	152	158
SWE40	**Sweden**	199	199	259	259	148	148
SWE41	**Sweden**	199	201	259	259	152	152
SWE43	**Sweden**	199	199	259	265	150	150
SWE44	**Sweden**	199	199	249	249	148	148
SWE45	**Sweden**	199	205	0	0	152	152
SWE46	**Sweden**	199	201	259	259	152	152
SWE47	**Sweden**	199	205	249	259	0	0
SWE48	**Sweden**	199	203	259	259	152	152
SWE49	**Sweden**	199	205	259	275	0	0
SWE5	**Sweden**	199	205	259	267	0	0
SWE50	**Sweden**	199	199	259	267	148	154
SWE51	**Sweden**	199	199	249	259	152	152
SWE6	**Sweden**	199	199	259	267	0	0

Table A.1. continued Contemporary Golden Eagle Genotypes

Sample ID	Hal-13	Hal-13	IE04	IE04	IE13	IE13	Aa27	Aa27	IE14	IE14
MWGE101	154	154	212	230	241	245	90	92	203	203
MWGE102	154	154	230	234	241	241	84	90	199	203
MWGE110	154	156	230	230	241	241	82	90	199	203
MWGE111	154	154	230	234	241	245	82	90	203	203
MWGE112	154	154	230	238	245	245	90	90	199	203
MWGE113	154	156	230	234	241	245	82	90	203	203
MWGE114	154	154	230	242	241	241	82	90	203	203
MWGE115	154	156	234	234	241	241	90	90	199	199
MWGE116	154	156	230	234	241	241	90	90	199	203
MWGE90	154	156	230	238	241	241	82	90	199	203
MWGE91	154	154	230	238	241	245	82	82	199	203
MWGE92	156	156	234	238	241	241	92	94	195	199
MWGE93	154	154	230	234	241	241	90	90	199	199
MWGE94	154	154	212	224	241	241	0	0	203	203
WCGE12	152	154	230	230	241	241	92	94	0	0
WCGE16	154	156	230	238	241	241	92	92	199	199
WCGE21	154	154	238	238	239	239	84	92	199	199
WCGE22	156	156	238	238	243	243	92	92	199	199
WCGE24	154	154	230	230	243	243	92	92	195	199
WCGE25	154	154	238	238	243	243	92	92	199	203
WCGE26	154	154	234	238	243	243	92	92	199	203
WCGE7	154	156	230	234	241	241	84	84	203	203
MWGE35-11	154	156	230	238	241	245	96	96	187	203
MWGE35-5	154	156	230	234	241	241	92	92	199	203
MWGE35-9	152	154	220	220	0	0	104	104	199	199
MWGE36-1	0	0	216	220	241	241	82	90	199	199
MWGE36-2	0	0	216	220	241	241	84	92	199	199
MWGE36-3	154	154	216	220	241	245	84	90	199	203
MWGE36-4	154	154	216	220	241	241	84	92	199	199
MWGE36-5	154	154	220	224	241	241	92	92	203	203
MWGE36-6	154	154	216	220	0	0	92	92	199	199
MWGE36-7	0	0	212	216	235	235	90	90	199	203
MWGE50	154	154	230	230	241	241	84	92	199	203
MWGE53	152	156	242	242	241	245	92	92	199	203
MWGE54	152	152	230	234	241	241	92	92	199	199
MWGE55	154	156	0	0	241	245	92	94	203	203
MWGE56	152	156	230	234	241	241	94	94	199	199
MWGE57	154	156	230	234	241	245	84	92	199	199
MWGE58	152	154	238	238	241	245	84	84	203	203

Sample ID	Hal-13	Hal-13	IE04	IE04	IE13	IE13	Aa27	Aa27	IE14	IE14
MWGE60	152	152	234	238	241	241	92	94	199	203
MWGE61	152	154	230	238	241	241	92	92	195	203
MWGE62	0	0	0	0	241	245	94	94	199	203
MWGE63	154	156	230	234	241	241	92	94	199	203
MWGE64	154	156	230	234	241	245	92	92	199	199
MWGE65	152	156	230	242	241	241	92	92	199	203
WCGE10	154	154	230	230	241	241	82	82	203	203
WCGE11	154	156	212	220	241	241	84	88	195	203
WCGE14	154	154	230	238	241	241	90	92	199	203
WCGE15	154	156	230	238	243	247	92	92	199	203
WCGE17	154	156	238	242	243	243	92	92	199	203
WCGE18	154	156	234	238	243	243	84	92	199	203
WCGE19	154	156	238	246	243	243	90	92	199	199
WCGE8	154	156	212	226	241	245	84	94	203	203
WCGE9	154	156	216	220	241	245	94	94	203	203
MWGE103	154	154	234	238	241	241	82	82	203	203
MWGE104	154	154	230	230	241	241	0	0	203	203
MWGE105	154	156	230	234	241	241	90	90	199	203
MWGE106	154	154	230	230	241	241	82	90	203	203
MWGE107	154	156	230	234	241	241	90	92	203	203
MWGE108	154	154	238	238	241	241	82	90	199	203
WCGE6	154	154	230	242	241	245	84	92	0	0
MWGE117	154	156	220	220	241	241	82	82	195	203
MWGE121	154	154	238	238	243	243	84	92	199	203
MWGE122	156	156	230	238	241	241	92	92	199	203
MWGE123	152	152	238	238	241	241	92	92	199	203
MWGE124	154	156	238	238	243	243	94	94	199	203
MWGE22-1	152	154	0	0	241	241	84	92	199	203
MWGE23-1	154	156	238	238	241	241	92	98	203	203
MWGE24-1	154	156	238	238	243	247	92	94	203	203
MWGE25	154	156	238	238	243	243	84	84	195	203
MWGE26-2	156	156	234	242	243	243	94	94	199	203
MWGE38	154	156	226	234	241	241	94	94	0	0
MWGE40	154	156	238	238	241	241	92	94	203	203
WCGE5	154	154	234	238	241	241	96	96	0	0
CAN24	154	154	238	238	241	245	92	92	203	203
CAN25	154	154	238	238	241	241	92	92	199	203
CAN26	154	154	234	238	241	241	84	94	203	203
CAN27	154	154	234	242	241	241	82	92	203	203
CAN28	156	156	230	238	241	241	84	94	199	203

Sample ID	Hal-13	Hal-13	IE04	IE04	IE13	IE13	Aa27	Aa27	IE14	IE14
CAN29	154	156	238	238	241	241	92	94	195	195
CAN30	154	154	234	234	241	241	82	92	203	203
CAN31	154	156	0	0	0	0	92	94	195	195
CAN32	154	154	238	238	241	245	92	92	203	203
CAN33	154	154	234	238	241	241	84	94	203	203
CAN34	154	156	238	242	241	241	82	92	203	203
CAN35	154	156	230	242	241	241	84	92	199	203
CAN36	154	156	230	230	241	241	84	94	195	199
CAN37	154	156	238	238	241	241	92	94	203	203
CAN38	0	0	238	238	241	241	84	92	195	203
CAN4	154	154	238	238	241	241	92	92	203	203
CAN5	154	154	0	0	241	241	82	92	203	203
CAN7	154	154	238	242	241	241	92	92	199	203
CAN75	154	156	230	238	241	241	84	90	203	203
CAN77	154	156	238	238	241	241	86	94	199	199
CAN78	154	154	238	238	241	241	84	92	199	199
MWGE28-1	154	156	238	238	243	243	92	94	199	203
MWGE28-2	154	156	238	238	0	0	94	94	199	203
MWGE28-3	154	156	238	238	243	243	92	94	203	203
MWGE29-1	0	0	0	0	0	0	96	96	203	203
MWGE30-1	154	156	0	0	243	243	94	104	199	199
MWGE39	152	154	238	242	241	241	92	94	203	203
MWGE41	154	154	220	238	241	241	92	92	199	203
MWGE42	154	154	230	242	241	241	92	94	199	203
MWGE43	154	156	0	0	241	241	94	94	195	203
MWGE44	0	0	234	238	243	243	92	94	199	203
MWGE45	154	154	238	238	243	243	92	94	199	199
MWGE46	154	154	238	238	243	243	92	94	203	203
MWGE47	154	156	220	238	241	241	94	94	199	203
MWGE49	156	156	0	0	241	245	84	94	195	203
MWGE51	154	156	238	238	241	241	92	94	203	203
MWGE67	154	156	234	238	241	241	92	92	199	203
MWGE68	156	156	238	238	241	241	92	92	199	203
MWGE69	152	156	238	238	241	241	90	90	199	199
MWGE70	156	156	238	238	241	241	92	94	199	203
MWGE71	152	156	238	238	243	243	92	92	195	203
MWGE72	152	152	238	238	243	243	94	94	203	203
MWGE73	156	156	230	238	241	241	92	94	195	203
MWGE74	154	156	220	238	241	241	90	92	199	203
MWGE75	154	156	238	242	243	243	82	90	199	203

Sample ID	Hal-13	Hal-13	IE04	IE04	IE13	IE13	Aa27	Aa27	IE14	IE14
MWGE76	154	154	220	238	241	241	90	92	203	203
MWGE77	154	154	230	238	243	243	82	90	195	199
MWGE78	154	156	230	238	241	241	94	94	203	203
MWGE79	156	156	234	238	241	241	92	94	199	203
MWGE80	154	156	238	238	241	241	92	92	199	199
MWGE81	154	154	224	242	243	243	94	94	195	203
MWGE82	154	156	212	224	241	241	94	94	203	203
MWGE83	154	156	230	238	241	241	92	92	199	203
MWGE84	154	154	220	238	241	241	90	92	203	203
WCGE1	154	154	230	230	243	243	92	92	203	203
WCGE13	154	156	0	0	241	241	96	104	199	199
WCGE3	154	156	212	212	243	243	90	92	199	203
WCGE4	154	154	220	220	0	0	90	90	199	199
CAN10	154	154	238	238	241	241	84	84	203	203
CAN11	154	156	238	238	241	241	92	94	199	203
CAN12	156	156	230	242	241	241	92	94	195	203
CAN13	154	154	234	234	241	241	92	92	0	0
CAN14	154	154	238	242	241	241	92	94	199	199
CAN15	156	156	238	242	241	241	86	94	195	203
CAN16	154	154	230	230	241	241	84	94	199	199
CAN2	154	154	238	238	241	241	84	92	195	195
CAN3	154	154	234	242	241	241	82	92	203	203
CAN43	154	154	234	238	241	241	0	0	199	199
CAN6	154	154	238	242	241	241	92	92	203	203
CAN79	154	154	238	238	241	241	92	92	199	203
CAN8	154	154	234	238	241	241	82	84	203	203
CAN9	154	154	238	238	241	241	84	84	203	203
SWE1	154	158	226	234	241	241	84	92	195	199
SWE10	154	154	226	226	241	245	84	90	191	191
SWE11	152	156	226	242	241	245	84	90	199	199
SWE12	152	156	0	0	241	241	84	90	199	199
SWE13	152	156	224	250	241	245	84	84	199	203
SWE14	152	156	234	246	241	245	84	84	199	199
SWE15	152	158	234	238	241	241	84	84	199	203
SWE16	152	158	0	0	241	241	84	92	199	199
SWE18	0	0	234	246	241	245	84	84	199	203
SWE19	156	156	226	226	241	250	84	84	199	199
SWE2	152	158	230	250	241	241	84	84	199	203
SWE20	154	154	226	230	241	241	86	86	199	199
SWE21	154	154	226	230	241	241	84	92	195	199

Sample ID	Hal-13	Hal-13	IE04	IE04	IE13	IE13	Aa27	Aa27	IE14	IE14
SWE22	154	154	226	246	241	245	94	94	191	199
SWE23	0	0	226	230	241	241	88	88	199	199
SWE24	0	0	230	242	241	241	86	86	199	199
SWE25	0	0	230	246	241	245	84	84	199	203
SWE26	154	154	226	242	241	245	84	94	199	199
SWE27	154	158	230	234	241	241	84	92	199	203
SWE28	158	158	226	250	241	245	88	88	199	203
SWE29	0	0	226	230	241	250	84	84	199	199
SWE3	154	154	230	238	241	241	84	84	191	199
SWE30	154	158	234	242	241	245	0	0	199	199
SWE31	154	158	234	246	241	245	84	84	191	199
SWE32	154	158	226	226	0	0	84	88	195	203
SWE33	158	158	230	250	241	247	84	84	0	0
SWE34	152	156	242	242	241	245	84	92	191	203
SWE35	154	158	226	234	241	241	88	88	199	203
SWE36	154	158	226	234	245	250	84	84	199	199
SWE37	154	154	226	230	241	241	84	94	199	203
SWE38	158	158	226	230	241	245	84	96	199	199
SWE39	0	0	226	242	241	245	84	92	199	199
SWE40	152	152	226	250	241	245	0	0	199	203
SWE41	154	158	0	0	241	241	92	94	199	203
SWE43	154	158	242	246	241	241	84	84	187	203
SWE44	154	154	226	230	241	245	84	84	199	203
SWE45	154	156	226	226	241	245	84	94	0	0
SWE46	154	158	0	0	241	245	84	94	199	203
SWE47	154	154	226	226	241	245	84	92	199	199
SWE48	0	0	226	226	241	245	84	84	199	199
SWE49	154	158	226	242	241	247	92	96	199	199
SWE5	154	154	226	226	241	245	84	90	199	203
SWE50	154	154	226	230	0	0	84	84	199	203
SWE51	154	158	226	250	241	245	84	94	199	203
SWE6	152	158	226	242	241	241	84	92	199	203

Table A.1. continued. All Contemporary Golden Eagle Genotypes.

Sample ID	Hal-10	Hal-10	Aa36	Aa36
MWGE101	234	240	92	100
MWGE102	234	234	90	92
MWGE110	232	240	92	96
MWGE111	228	240	90	92
MWGE112	232	238	92	92
MWGE113	228	240	92	92
MWGE114	230	240	90	94
MWGE115	228	232	90	98
MWGE116	228	232	92	92
MWGE90	230	240	96	96
MWGE91	228	234	92	98
MWGE92	240	240	92	98
MWGE93	232	240	90	98
MWGE94	240	240	90	96
WCGE12	228	238	90	90
WCGE16	0	0	92	92
WCGE21	230	240	96	100
WCGE22	234	234	92	98
WCGE24	230	240	90	98
WCGE25	0	0	92	92
WCGE26	230	234	86	90
WCGE7	228	230	90	98
MWGE35-11	0	0	96	96
MWGE35-5	0	0	98	98
MWGE35-9	0	0	82	92
MWGE36-1	228	242	88	96
MWGE36-2	228	242	94	100
MWGE36-3	228	228	92	92
MWGE36-4	228	242	0	0
MWGE36-5	232	238	92	92
MWGE36-6	228	242	94	100
MWGE36-7	232	238	88	96
MWGE50	224	224	92	92
MWGE53	228	230	84	84
MWGE54	224	224	0	0
MWGE55	238	238	84	92
MWGE56	228	234	84	92
MWGE57	230	230	0	0
MWGE58	224	232	90	94

Sample ID	Hal-10	Hal-10	Aa36	Aa36
MWGE60	236	236	88	88
MWGE61	228	236	84	92
MWGE62	228	228	0	0
MWGE63	228	232	92	98
MWGE64	228	240	88	96
MWGE65	228	232	84	86
WCGE10	228	240	82	90
WCGE11	236	240	90	92
WCGE14	230	232	92	92
WCGE15	0	0	96	100
WCGE17	228	230	92	96
WCGE18	230	240	96	96
WCGE19	232	240	96	98
WCGE8	230	230	90	90
WCGE9	230	234	90	92
MWGE103	232	232	92	100
MWGE104	240	240	90	96
MWGE105	228	232	92	92
MWGE106	228	234	92	98
MWGE107	230	240	92	98
MWGE108	232	240	92	96
WCGE6	228	238	92	92
MWGE117	230	234	96	96
MWGE121	240	240	92	96
MWGE122	234	234	98	98
MWGE123	232	238	88	96
MWGE124	230	232	96	100
MWGE22-1	228	228	96	96
MWGE23-1	230	230	96	96
MWGE24-1	230	236	96	96
MWGE25	228	228	94	96
MWGE26-2	232	232	96	98
MWGE38	232	240	94	94
MWGE40	230	240	92	96
WCGE5	232	238	92	98
CAN24	228	234	94	98
CAN25	230	230	96	100
CAN26	228	228	96	96
CAN27	226	230	94	94
CAN28	232	232	94	96

Sample ID	Hal-10	Hal-10	Aa36	Aa36
CAN29	228	228	96	96
CAN30	226	230	94	94
CAN31	228	228	96	96
CAN32	228	236	94	94
CAN33	228	228	0	0
CAN34	226	236	96	96
CAN35	226	228	82	96
CAN36	226	238	94	94
CAN37	228	228	0	0
CAN38	230	240	96	96
CAN4	228	228	96	98
CAN5	0	0	94	94
CAN7	0	0	96	96
CAN75	228	228	98	98
CAN77	0	0	96	96
CAN78	228	228	94	98
MWGE28-1	228	230	96	96
MWGE28-2	228	228	96	96
MWGE28-3	230	230	96	96
MWGE29-1	0	0	96	96
MWGE30-1	0	0	88	88
MWGE39	0	0	96	96
MWGE41	228	228	92	98
MWGE42	228	232	92	96
MWGE43	228	228	92	96
MWGE44	230	234	88	96
MWGE45	230	234	96	96
MWGE46	230	230	98	98
MWGE47	236	236	96	96
MWGE49	234	234	96	98
MWGE51	226	238	92	100
MWGE67	230	236	88	96
MWGE68	230	236	86	94
MWGE69	232	236	94	94
MWGE70	228	240	0	0
MWGE71	232	236	98	98
MWGE72	232	238	96	98
MWGE73	228	228	84	90
MWGE74	234	240	96	96
MWGE75	0	0	92	96

Sample ID	Hal-10	Hal-10	Aa36	Aa36
MWGE76	228	232	96	96
MWGE77	238	238	94	96
MWGE78	232	240	92	98
MWGE79	228	232	92	98
MWGE80	230	236	92	96
MWGE81	232	238	96	96
MWGE82	228	228	98	98
MWGE83	240	240	92	92
MWGE84	230	230	98	98
WCGE1	230	234	84	84
WCGE13	228	240	94	96
WCGE3	226	230	98	98
WCGE4	228	228	88	88
CAN10	228	234	88	98
CAN11	230	230	94	94
CAN12	226	226	96	96
CAN13	230	236	94	96
CAN14	0	0	96	116
CAN15	230	238	96	96
CAN16	230	238	92	96
CAN2	220	228	96	96
CAN3	226	232	94	94
CAN43	232	238	92	92
CAN6	226	226	96	96
CAN79	0	0	94	94
CAN8	230	230	88	96
CAN9	228	236	88	98
SWE1	236	236	94	94
SWE10	236	238	90	94
SWE11	232	232	90	90
SWE12	238	238	94	94
SWE13	228	232	90	90
SWE14	230	238	94	94
SWE15	228	238	92	92
SWE16	228	234	94	94
SWE18	0	0	96	96
SWE19	240	240	94	100
SWE2	238	238	98	98
SWE20	228	232	96	96
SWE21	234	240	94	94

Sample ID	Hal-10	Hal-10	Aa36	Aa36
SWE22	232	240	92	94
SWE23	0	0	96	122
SWE24	0	0	94	96
SWE25	232	240	110	122
SWE26	0	0	94	122
SWE27	232	232	96	96
SWE28	232	240	96	96
SWE29	0	0	94	98
SWE3	228	228	94	94
SWE30	228	232	94	94
SWE31	228	240	94	96
SWE32	228	236	94	124
SWE33	230	240	94	94
SWE34	228	228	94	122
SWE35	0	0	100	100
SWE36	228	234	96	96
SWE37	228	240	98	98
SWE38	228	230	94	94
SWE39	0	0	94	94
SWE40	228	228	96	96
SWE41	240	242	94	94
SWE43	236	240	96	96
SWE44	228	234	94	94
SWE45	232	240	94	94
SWE46	234	238	94	94
SWE47	240	240	94	94
SWE48	228	232	94	94
SWE49	232	240	92	96
SWE5	234	238	92	98
SWE50	228	240	94	94
SWE51	232	240	96	100
SWE6	228	238	90	90

Table A.2. All Historic Golden Eagle Genotypes

Sample ID	Population	Aa15	Aa15	Aa11	Aa11	Aa12	Aa12
MSGE81	**Western North America**	199	199	249	259	150	154
MSGE60	**Western North America**	0	0	0	0	148	148
MSGE85	**Western North America**	187	187	0	0	0	0
MSGE91	**Western North America**	205	205	0	0	0	0
MSGE92	**Western North America**	201	201	259	259	152	154
MSGE93	**Western North America**	201	201	249	269	154	154
MSGE94	**Western North America**	201	201	0	0	154	160
MSGE95	**Western North America**	201	201	267	267	152	152
MSGE96	**Western North America**	201	201	245	245	0	0
MSGE97	**Western North America**	201	201	0	0	0	0
MSGE46	**Western North America**	199	205	0	0	0	0
MSGE51	**Western North America**	199	199	261	271	0	0
MSGE11	**Western North America**	185	199	259	265	148	148
MSGE119	**Western North America**	201	201	261	267	154	154
MSGE33	**Western North America**	201	201	0	0	154	154
MSGE80	**Western North America**	199	201	249	269	154	154
MSGE108	**Western North America**	201	201	0	0	154	154
MSGE111	**Western North America**	199	199	251	261	154	154
MSGE112	**Western North America**	201	201	261	267	150	150
MSGE113	**Western North America**	201	201	267	267	0	0
MSGE114	**Western North America**	199	199	261	261	0	0
MSGE115	**Western North America**	201	201	261	261	152	152
MSGE117	**Western North America**	201	205	271	271	152	154
MSGE118	**Western North America**	201	201	249	271	152	154
MSGE121	**Western North America**	201	201	261	261	152	152
MSGE122	**Western North America**	199	199	261	267	0	0
MSGE15-1	**Western North America**	199	199	0	0	146	146
MSGE19	**Western North America**	185	201	261	261	146	160
MSGE20	**Western North America**	185	201	261	261	160	160
MSGE21	**Western North America**	185	199	251	265	162	162
CAN44	**Eastern North America**	201	201	265	269	154	154
CAN45	**Eastern North America**	201	201	261	269	152	152
CAN52	**Eastern North America**	0	0	0	0	152	154
CAN53	**Eastern North America**	0	0	261	261	154	154
CAN54	**Eastern North America**	0	0	249	261	152	152
CAN57	**Eastern North America**	197	207	0	0	152	154
CAN58	**Eastern North America**	185	201	0	0	0	0
CAN59	**Eastern North America**	201	201	0	0	154	154
CAN60	**Eastern North America**	201	211	261	261	154	154

Sample ID	**Population**	Aa15	Aa15	Aa11	Aa11	Aa12	Aa12
CAN67	**Eastern North America**	201	201	0	0	154	154
CAN39	**Eastern North America**	0	0	261	261	152	154
CAN40	**Eastern North America**	0	0	261	269	154	154
CAN47	**Eastern North America**	201	201	261	269	152	152
CAN48	**Eastern North America**	0	0	261	269	152	152
CAN49	**Eastern North America**	0	0	261	261	152	162
CAN68	**Eastern North America**	197	201	0	0	154	154
CAN69	**Eastern North America**	201	201	265	265	154	154
CAN72	**Eastern North America**	201	201	269	269	154	162
CAN73	**Eastern North America**	201	201	261	261	152	158
CAN74	**Eastern North America**	201	201	269	269	0	0
MSGE65	**Eastern North America**	199	201	0	0	150	150
MSGE66	**Eastern North America**	199	199	269	269	160	160
MSGE67	**Eastern North America**	201	201	0	0	0	0
MSGE69	**Eastern North America**	199	199	259	261	0	0
MSGE73	**Eastern North America**	201	201	261	261	150	154

Table A.2. continued. Historic Golden Eagle Genotypes.

Sample ID	Hal-13	Hal-13	IE04	IE04	IE13	IE13	Aa27	Aa27	IE14	IE14
MSGE81	96	96	152	154	220	238	241	241	84	94
MSGE60	96	98	154	154	0	0	239	241	84	92
MSGE85	88	96	154	154	230	230	241	241	92	92
MSGE91	94	98	154	156	230	238	241	241	92	92
MSGE92	92	92	154	156	230	238	243	247	92	92
MSGE93	96	96	154	154	230	238	243	243	92	94
MSGE94	90	96	156	156	230	234	243	243	92	92
MSGE95	92	100	154	156	234	238	243	243	84	94
MSGE96	92	96	154	154	230	242	243	243	92	92
MSGE97	92	98	154	154	230	238	243	243	92	92
MSGE46	94	98	154	154	0	0	241	241	82	90
MSGE51	0	0	154	154	230	242	241	241	84	92
MSGE11	84	88	154	156	212	212	245	245	96	104
MSGE119	94	94	154	154	234	238	243	243	92	94
MSGE33	92	92	154	154	230	242	241	241	90	90
MSGE80	90	96	152	156	230	234	241	245	90	92
MSGE108	98	98	154	154	230	230	243	243	92	92
MSGE111	96	100	154	156	238	242	243	243	84	92
MSGE112	96	96	154	156	230	242	243	243	92	92
MSGE113	94	94	154	154	238	242	243	243	92	92
MSGE114	96	98	156	156	238	242	243	243	84	92
MSGE115	92	98	154	154	230	238	243	243	92	92
MSGE117	96	96	154	156	230	230	243	243	92	92
MSGE118	96	96	156	156	238	242	243	243	92	92
MSGE121	96	96	154	156	230	242	243	243	84	94
MSGE122	92	96	156	156	238	242	243	243	94	94
MSGE15-1	96	96	154	154	0	0	0	0	96	96
MSGE19	90	96	154	154	220	238	241	241	94	96
MSGE20	92	96	154	154	238	238	241	241	84	92
MSGE21	0	0	154	156	230	234	241	241	92	92
CAN44	96	96	156	156	238	238	241	241	0	0
CAN45	96	96	154	154	230	238	241	241	0	0
CAN52	96	96	154	154	230	230	241	241	0	0
CAN53	92	96	154	154	238	238	241	241	0	0
CAN54	98	98	154	156	230	238	241	245	92	92
CAN57	0	0	154	154	234	238	239	241	90	90
CAN58	92	96	152	154	230	230	241	241	92	92
CAN59	0	0	154	156	238	238	241	241	94	94
CAN60	98	98	154	156	238	238	241	241	92	92

Sample ID	Hal-13	Hal-13	IE04	IE04	IE13	IE13	Aa27	Aa27	IE14	IE14
CAN67	90	98	154	154	234	238	241	241	94	94
CAN39	92	96	154	156	234	242	241	241	92	92
CAN40	96	96	154	154	230	238	241	241	92	94
CAN47	96	96	154	156	234	242	241	241	0	0
CAN48	96	96	154	156	234	242	241	241	92	92
CAN49	96	96	154	156	238	238	241	241	0	0
CAN68	96	96	154	156	230	234	241	241	84	94
CAN69	0	0	154	156	230	238	241	241	92	92
CAN72	96	100	154	154	238	238	241	241	84	92
CAN73	96	96	154	156	238	238	241	241	92	94
CAN74	96	96	154	154	230	238	241	241	86	92
MSGE65	80	92	154	156	230	234	239	239	82	90
MSGE66	94	94	0	0	230	230	245	245	90	90
MSGE67	92	98	154	156	242	242	241	241	82	90
MSGE69	98	100	154	154	234	238	241	241	90	92
MSGE73	94	96	152	156	238	242	241	241	90	92

Table A.2. continued. Historic Golden Eagle Genotypes.

Sample ID	Hal-10	Hal-10	Aa36	Aa36
MSGE81	203	203	228	228
MSGE60	209	209	228	228
MSGE85	199	199	0	0
MSGE91	195	199	0	0
MSGE92	195	199	234	242
MSGE93	199	203	232	232
MSGE94	199	199	0	0
MSGE95	203	203	0	0
MSGE96	199	199	0	0
MSGE97	199	203	240	240
MSGE46	203	203	230	240
MSGE51	199	199	232	238
MSGE11	203	203	0	0
MSGE119	203	203	234	234
MSGE33	199	203	0	0
MSGE80	203	203	228	228
MSGE108	203	203	0	0
MSGE111	199	199	234	234
MSGE112	199	203	230	234
MSGE113	199	203	230	232
MSGE114	203	203	230	230
MSGE115	199	199	230	230
MSGE117	199	203	230	238
MSGE118	195	203	230	232
MSGE121	203	203	230	238
MSGE122	203	203	232	234
MSGE15-1	203	203	0	0
MSGE19	199	203	232	238
MSGE20	203	203	228	238
MSGE21	195	199	232	236
CAN44	195	199	228	234
CAN45	203	203	228	232
CAN52	195	203	230	238
CAN53	195	203	0	0
CAN54	199	203	230	236
CAN57	199	203	0	0
CAN58	203	203	0	0
CAN59	203	203	0	0
CAN60	199	199	234	240

Sample ID	Hal-10	Hal-10	Aa36	Aa36
CAN67	199	199	0	0
CAN39	195	199	0	0
CAN40	195	199	0	0
CAN47	195	199	232	238
CAN48	195	199	0	0
CAN49	199	203	236	236
CAN68	199	199	0	0
CAN69	199	199	0	0
CAN72	199	203	228	228
CAN73	203	203	0	0
CAN74	199	203	226	238
MSGE65	203	203	228	228
MSGE66	191	195	228	228
MSGE67	191	191	228	228
MSGE69	199	203	228	228
MSGE73	203	203	228	228

Table A.3. All Contemporary Bald Eagle Genotypes

Sample ID	**Population**	Aa15	Aa15	Aa11	Aa11	Aa36	Aa36
WCBE10	Florida	195	195	239	239	99	99
WCBE11	Florida	195	195	239	239	99	99
WCBE4	Florida	195	195	239	239	97	97
WCBE48	Florida	195	195	241	241	99	99
WCBE49	Florida	195	195	241	241	99	99
WCBE5	Florida	195	195	239	239	97	97
WCBE50	Florida	195	195	241	241	99	99
WCBE51	Florida	195	195	241	241	99	99
WCBE52	Florida	195	195	241	241	99	99
WCBE53	Florida	195	195	241	241	99	99
WCBE54	Florida	195	195	241	241	99	99
WCBE55	Florida	195	195	241	241	99	99
WCBE56	Florida	195	195	241	241	99	99
WCBE57	Florida	195	195	241	241	99	99
WCBE58	Florida	195	195	241	241	99	99
WCBE59	Florida	195	195	241	241	99	99
WCBE6	Florida	195	195	239	239	97	97
WCBE60	Florida	195	195	241	241	99	99
WCBE61	Florida	195	195	241	241	99	99
WCBE7	Florida	195	195	241	241	99	99
WCBE8	Florida	195	195	239	239	97	97
WCBE9	Florida	195	195	239	239	97	97
MWBE12	Eastern Translocated	195	195	239	239	99	99
MWBE13	Eastern Translocated	195	195	239	239	97	97
MWBE15	Eastern Translocated	195	195	239	239	99	99
MWBE16	Eastern Translocated	195	195	239	239	97	97
MWBE2	Eastern Translocated	195	195	239	239	99	99
MWBE5	Eastern Translocated	195	195	239	239	97	97
MWBE6	Eastern Translocated	195	195	239	239	99	99
MWBE7	Eastern Translocated	195	195	0	0	97	97
MWBE8	Eastern Translocated	195	195	239	239	97	97
MWBE9	Eastern Translocated	195	195	0	0	97	97
MWBE19-1	Eastern Translocated	195	195	241	241	99	101
MWBE19-2	Eastern Translocated	195	195	241	241	97	99
MWBE19-3	Eastern Translocated	195	195	241	241	99	101
MWBE20	Eastern Translocated	195	195	239	239	99	99
MWBE21	Eastern Translocated	195	195	239	239	97	97
MWBE22	Eastern Translocated	195	195	241	243	95	99
MWBE23	Eastern Translocated	195	195	241	241	99	99

Sample ID	**Population**	Aa15	Aa15	Aa11	Aa11	Aa36	Aa36
MWBE24	Eastern Translocated	195	195	241	241	95	99
MWBE25-1	Eastern Translocated	195	195	241	241	95	99
MWBE25-2	Eastern Translocated	195	195	241	241	95	95
MWBE26	Eastern Translocated	195	195	239	239	97	97
MWBE27-1	Eastern Translocated	195	195	241	241	99	99
MWBE27-2	Eastern Translocated	0	0	241	241	95	99
MWBE29	Eastern Translocated	195	195	241	241	99	99
MWBE30	Eastern Translocated	195	195	241	243	99	99
MWBE31	Eastern Translocated	195	195	241	241	99	99
MWBE33	Eastern Translocated	195	195	241	241	95	99
MWBE34	Eastern Translocated	195	195	241	241	99	99
MWBE35	Eastern Translocated	195	195	241	241	95	99
MWBE36	Eastern Translocated	0	0	241	241	99	99
MWBE37	Eastern Translocated	195	195	241	241	99	99
WCBE1	MT and WA	195	195	239	239	97	97
WCBE2	MT and WA	195	195	239	239	0	0
WCBE3	MT and WA	195	195	239	239	99	99
WCBE42	MT and WA	180	195	241	241	99	99
WCBE43	MT and WA	195	195	241	241	99	99
WCBE44	MT and WA	180	195	241	241	99	99
WCBE45	MT and WA	195	195	241	241	97	97
WCBE46	MT and WA	180	180	241	241	0	0
WCBE47	MT and WA	180	195	241	241	0	0
WCBE22	Alaska	195	195	241	241	99	99
WCBE23	Alaska	180	195	241	241	99	99
WCBE24	Alaska	180	195	241	241	99	99
WCBE25	Alaska	195	195	241	241	99	99
WCBE26	Alaska	195	195	239	239	99	99
WCBE27	Alaska	195	195	241	241	99	99
WCBE28	Alaska	180	195	241	241	99	99
WCBE29	Alaska	180	195	241	241	99	99
WCBE30	Alaska	195	195	241	241	99	99
WCBE31	Alaska	180	195	241	241	99	99
WCBE32	Alaska	195	195	241	241	99	99
WCBE33	Alaska	195	195	241	241	99	99
WCBE34	Alaska	195	195	241	241	99	99
WCBE35	Alaska	195	195	241	241	101	101
WCBE36	Alaska	195	195	241	241	99	99
WCBE37	Alaska	180	195	241	241	99	99
WCBE38	Alaska	195	195	241	241	99	99

Sample ID	**Population**	Aa15	Aa15	Aa11	Aa11	Aa36	Aa36
WCBE39	Alaska	195	195	241	241	99	99
WCBE40	Alaska	195	195	239	239	99	99
WCBE41	Alaska	195	195	241	241	99	99

Table A.3. All Contemporary Bald Eagle Genotypes

Sample ID	Hal-13	Hal-13	IE04	IE04	IE13	IE13	Aa27	Aa27
WCBE10	154	154	210	210	212	212	88	92
WCBE11	158	158	210	218	212	212	88	88
WCBE4	158	158	218	218	0	0	88	90
WCBE48	158	158	214	214	212	212	88	94
WCBE49	158	158	210	214	212	212	88	88
WCBE5	158	158	214	218	212	212	90	92
WCBE50	154	158	214	218	212	212	92	94
WCBE51	154	158	210	214	212	212	88	92
WCBE52	154	158	214	214	212	212	92	92
WCBE53	154	158	214	214	212	212	88	94
WCBE54	158	158	214	214	212	212	92	94
WCBE55	154	158	214	218	212	212	88	94
WCBE56	154	158	214	218	212	212	88	88
WCBE57	152	158	210	214	212	212	88	88
WCBE58	154	158	214	218	212	212	94	94
WCBE59	158	158	214	214	212	212	88	92
WCBE6	154	158	210	214	212	212	90	92
WCBE60	158	158	214	214	212	212	88	92
WCBE61	158	158	210	214	212	212	88	88
WCBE7	156	156	218	226	212	212	88	88
WCBE8	158	158	214	226	212	212	88	92
WCBE9	158	158	214	218	212	212	88	88
MWBE12	152	152	214	214	212	212	92	92
MWBE13	154	158	210	218	212	212	88	92
MWBE15	154	158	214	214	212	212	90	92
MWBE16	152	152	214	226	212	212	88	92
MWBE2	156	156	214	222	212	216	92	92
MWBE5	158	158	218	218	212	212	88	88
MWBE6	158	158	218	226	212	212	88	92
MWBE7	152	156	214	214	212	212	90	92
MWBE8	158	158	214	214	212	212	88	90
MWBE9	152	158	214	218	212	212	88	92
MWBE19-1	152	158	210	210	212	212	94	94
MWBE19-2	152	154	210	214	212	212	94	94
MWBE19-3	154	158	214	214	212	212	94	94
MWBE20	152	158	210	214	212	212	92	92
MWBE21	158	158	210	214	212	212	88	92
MWBE22	154	158	214	214	212	212	88	94
MWBE23	158	158	214	214	212	212	92	94

Sample ID	Hal-13	Hal-13	IE04	IE04	IE13	IE13	Aa27	Aa27
MWBE24	158	158	214	214	212	212	92	94
MWBE25-1	154	154	214	214	212	212	88	94
MWBE25-2	154	154	214	222	212	212	92	94
MWBE26	154	158	214	218	212	212	88	88
MWBE27-1	154	158	214	230	212	216	88	94
MWBE27-2	154	154	214	222	212	212	94	94
MWBE29	158	158	210	218	212	212	88	94
MWBE30	154	156	214	214	212	212	92	94
MWBE31	152	158	210	214	212	212	88	92
MWBE33	152	158	210	218	212	212	94	94
MWBE34	152	154	210	214	212	212	88	88
MWBE35	158	158	210	214	212	212	88	88
MWBE36	154	154	210	214	212	212	88	88
MWBE37	158	158	210	214	212	212	88	88
WCBE1	158	158	214	222	212	212	90	92
WCBE2	158	158	214	226	212	212	88	92
WCBE3	158	158	214	226	212	212	92	92
WCBE42	158	158	210	214	212	212	88	94
WCBE43	156	158	210	214	212	216	88	94
WCBE44	154	156	210	222	212	212	88	94
WCBE45	158	158	218	218	212	212	94	94
WCBE46	158	158	210	218	212	216	92	92
WCBE47	158	158	210	214	212	216	94	94
WCBE22	158	158	222	222	212	212	88	94
WCBE23	158	158	218	222	212	212	94	94
WCBE24	158	158	214	214	212	212	88	94
WCBE25	158	158	214	218	212	216	92	92
WCBE26	156	156	218	222	216	216	88	94
WCBE27	156	158	218	218	212	212	88	88
WCBE28	158	158	214	214	212	216	94	94
WCBE29	158	158	214	214	212	212	92	94
WCBE30	156	156	210	218	212	212	94	94
WCBE31	156	158	218	218	212	212	88	94
WCBE32	158	158	214	222	212	212	94	94
WCBE33	158	158	214	222	212	212	88	94
WCBE34	156	158	214	222	212	212	94	94
WCBE35	156	158	222	222	212	216	88	94
WCBE36	158	158	222	222	212	212	88	94
WCBE37	156	158	210	214	212	216	92	94
WCBE38	158	158	210	218	212	212	92	94

Sample ID	Hal-13	Hal-13	IE04	IE04	IE13	IE13	Aa27	Aa27
WCBE39	158	158	218	222	212	212	0	0
WCBE40	156	158	214	218	212	212	92	94
WCBE41	156	156	218	222	212	212	94	94

Table A.3. continued. All Contemporary Bald Eagle Genotypes

Sample ID	IE14	IE14	Hal-10	Hal-10
WCBE10	0	0	240	240
WCBE11	0	0	240	240
WCBE4	0	0	238	240
WCBE48	176	176	240	240
WCBE49	176	176	240	240
WCBE5	0	0	240	240
WCBE50	176	176	0	0
WCBE51	172	176	240	240
WCBE52	172	176	240	240
WCBE53	176	176	240	240
WCBE54	176	176	240	240
WCBE55	176	176	240	240
WCBE56	176	176	238	240
WCBE57	172	176	240	240
WCBE58	176	176	238	240
WCBE59	172	176	240	240
WCBE6	176	176	238	238
WCBE60	172	176	240	240
WCBE61	176	176	240	240
WCBE7	176	176	240	240
WCBE8	172	176	240	240
WCBE9	0	0	240	240
MWBE12	176	176	240	240
MWBE13	176	176	240	240
MWBE15	176	176	238	238
MWBE16	176	176	238	238
MWBE2	176	176	240	240
MWBE5	172	172	240	240
MWBE6	172	176	240	240
MWBE7	172	176	238	238
MWBE8	0	0	240	240
MWBE9	176	176	236	240
MWBE19-1	176	176	0	0
MWBE19-2	176	176	0	0
MWBE19-3	176	176	0	0
MWBE20	176	176	240	240
MWBE21	172	176	240	240
MWBE22	172	176	240	242
MWBE23	172	176	240	242

Sample ID	IE14	IE14	Hal-10	Hal-10
MWBE24	172	172	240	242
MWBE25-1	176	176	240	240
MWBE25-2	172	176	240	240
MWBE26	172	176	238	238
MWBE27-1	172	176	240	240
MWBE27-2	172	176	240	240
MWBE29	176	176	240	240
MWBE30	176	176	238	240
MWBE31	176	176	240	240
MWBE33	172	176	240	240
MWBE34	176	176	240	240
MWBE35	172	176	240	240
MWBE36	176	176	240	240
MWBE37	172	176	240	240
WCBE1	172	176	240	240
WCBE2	172	176	238	238
WCBE3	176	176	240	240
WCBE42	176	176	238	238
WCBE43	172	172	238	240
WCBE44	172	176	238	238
WCBE45	172	176	240	244
WCBE46	172	176	238	238
WCBE47	172	176	0	0
WCBE22	172	172	236	236
WCBE23	172	176	238	238
WCBE24	176	176	238	238
WCBE25	172	176	236	238
WCBE26	172	176	238	238
WCBE27	172	176	238	238
WCBE28	172	176	236	238
WCBE29	176	176	240	244
WCBE30	172	176	238	238
WCBE31	172	172	238	240
WCBE32	0	0	238	238
WCBE33	172	176	238	240
WCBE34	176	176	238	238
WCBE35	172	172	238	238
WCBE36	172	176	238	240
WCBE37	176	176	236	238
WCBE38	172	176	238	238

Sample ID	IE14	IE14	Hal-10	Hal-10
WCBE39	0	0	238	238
WCBE40	176	176	240	240
WCBE41	176	176	238	238

Table A.4. All Historic Bald Eagle Genotypes

Sample ID	**Population**	Aa15	Aa15	Aa11	Aa11	Aa36	Aa36
MSBE9	Alaska	195	195	0	0	99	99
MSBE66	Alaska	195	195	241	241	99	99
MSBE65	Alaska	195	195	241	241	99	99
MSBE64	Alaska	195	195	241	241	99	99
MSBE63	Alaska	195	195	241	241	99	99
MSBE31	Alaska	195	195	0	0	99	101
MSBE80	Alaska	189	189	0	0	97	99
MSBE79	Alaska	189	189	241	241	99	101
MSBE71	OH, PA, WV, New Eng	189	189	241	241	99	99
MSBE68	OH, PA, WV, New Eng	189	189	0	0	99	99
MSBE58	OH, PA, WV, New Eng	195	195	241	241	99	99
MSBE60	OH, PA, WV, New Eng	195	195	241	241	99	99
MSBE57	OH, PA, WV, New Eng	195	195	241	241	99	99
MSBE56	OH, PA, WV, New Eng	195	195	0	0	99	99
MSBE54	OH, PA, WV, New Eng	195	195	241	241	99	99
MSBE30	OH, PA, WV, New Eng	195	195	241	241	99	99
MSBE19	OH, PA, WV, New Eng	195	195	241	241	99	99
MSBE13	OH, PA, WV, New Eng	195	195	241	241	99	99
MSBE2	OH, PA, WV, New Eng	195	195	241	241	97	99
MSBE47	Florida	189	189	241	241	99	99
MSBE46	Florida	0	0	241	241	91	99
MSBE45	Florida	189	189	0	0	91	99
MSBE41	Florida	195	195	241	241	91	99

Table A.4. continued. All Historic Bald Eagle Genotypes

Sample ID	Hal-13	Hal-13	IE04	IE04	IE13	IE13	Aa27	Aa27
MSBE9	156	156	214	214	212	212	88	92
MSBE66	154	158	214	218	212	216	94	94
MSBE65	154	158	214	218	216	216	94	94
MSBE64	158	158	218	218	212	216	94	94
MSBE63	158	158	214	222	212	212	0	0
MSBE31	154	156	0	0	212	216	94	94
MSBE80	154	156	0	0	212	212	88	94
MSBE79	154	158	0	0	208	212	94	94
MSBE71	154	158	210	210	212	212	88	88
MSBE68	154	158	214	218	212	212	92	94
MSBE58	152	158	214	214	212	212	94	94
MSBE60	158	158	214	214	212	212	92	92
MSBE57	154	158	210	222	212	212	92	92
MSBE56	152	158	0	0	212	212	92	94
MSBE54	158	158	210	210	212	212	88	94
MSBE30	154	158	214	214	212	212	0	0
MSBE19	152	156	214	222	212	212	94	94
MSBE13	158	158	210	214	212	212	88	92
MSBE2	154	158	210	222	212	212	88	94
MSBE47	154	158	210	214	212	212	88	88
MSBE46	158	158	214	214	212	212	92	92
MSBE45	158	158	210	226	212	212	88	88
MSBE41	154	158	214	214	212	212	88	88

Table A.4. continued. All Historic Bald Eagle Genotypes

Sample ID	IE14	IE14	Hal-10	Hal-10
MSBE9	176	176	0	0
MSBE66	0	0	238	240
MSBE65	172	176	238	240
MSBE64	172	172	238	238
MSBE63	172	176	238	238
MSBE31	176	176	0	0
MSBE80	0	0	0	0
MSBE79	0	0	0	0
MSBE71	172	176	240	240
MSBE68	172	172	240	240
MSBE58	176	176	234	234
MSBE60	176	176	240	240
MSBE57	172	176	240	240
MSBE56	176	176	234	234
MSBE54	172	172	240	240
MSBE30	172	180	240	240
MSBE19	172	172	240	240
MSBE13	172	172	240	240
MSBE2	172	176	240	240
MSBE47	172	176	0	0
MSBE46	0	0	0	0
MSBE45	176	176	240	240
MSBE41	172	176	232	240

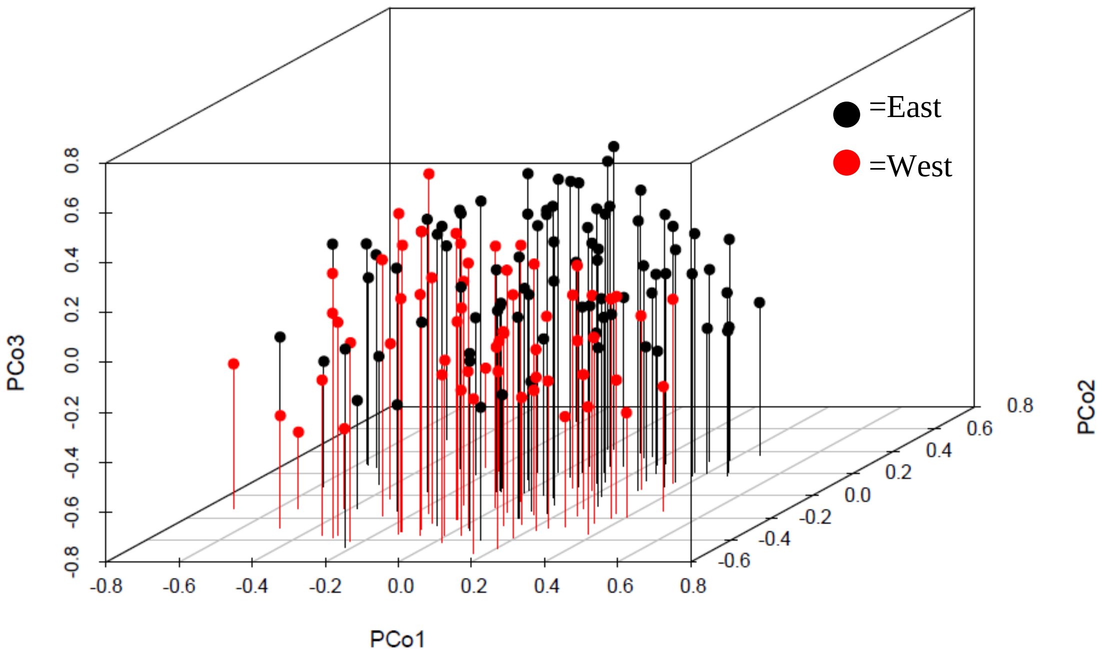

Figure A.1. Three-dimensional PCoA of Contemporary Golden Eagles Reveals No More Clustering Than Two-dimensional Structuring.