CONSERVATION GENETICS OF THE FLORIDA BLACK BEAR

By

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“The bears are yet too numerous; they are a strong creature and prey on fruits of the country.” William Bartram commenting on the abundance of black bears during his trip through Florida (1773-74).

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CONSERVATION GENETICS OF THE FLORIDA BLACK BEAR

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Habitat loss and fragmentation can influence the genetic structure of biological populations. I studied the genetic consequences of historical and contemporary patterns of habitat fragmentation in nine Florida black bear (*Ursus americanus floridanus*) populations. A total of 305 bears from nine populations was genotyped for 12 microsatellite loci to characterize genetic variation and structure. None of the nine populations deviated from Hardy-Weinberg equilibrium. Genetic variation, quantified by mean expected heterozygosity (H_E), ranged from 0.27–0.71, and was substantially lower in smaller populations. Low levels of gene flow (global $F_{ST} = 0.227$; global $R_{ST} = 0.249$) and high values of the likelihood ratio genetic distance (average $D_{LR} = 16.255$) suggest that fragmentation of once-contiguous habitat has resulted in genetically distinct populations. There was no isolation-by-distance relationship among Florida black bear populations. Barriers such as roads, cities, and residential areas limit the dispersal capabilities of black bears in Florida, thereby reducing the probability of gene flow among populations. Regional corridors or translocation of bears may be needed to restore historical levels of genetic variation.

Corridors have been suggested to mitigate the adverse effects of habitat fragmentation, by restoring or maintaining connectivity among once-contiguous populations. However, the role of corridors for large carnivores has rarely been evaluated objectively. I used non-invasive sampling, microsatellite analysis, and population-assignment tests to evaluate the effectiveness of a regional corridor (Osceola-Ocala corridor) in connecting two Florida black bear populations. I sampled 31 bears (28 males, 3 females) within the corridor. Because bear dispersal is male-biased, the gender disparity suggests that the Osceola-Ocala corridor functions as a conduit for dispersal and other seasonal movements. Of the 31 bears sampled in the Osceola-Ocala corridor, 28 had genotypes that were assigned to the Ocala population. I found a mostly unidirectional pattern of movement from Ocala, with a limited mixing of Ocala-assigned individuals with Osceola-assigned individuals in one area of the corridor. I also documented the presence of bears in Osceola assigned to Ocala, and the presence of bears in Osceola that may be Osceola-Ocala hybrids. My results indicate that the Osceola-Ocala corridor provides a conduit for gene flow between these populations. However, residential and industrial development and highways may reduce movements of bears within the Osceola-Ocala corridor. The methods used here may provide a means of evaluating corridor effectiveness, and identifying gaps in connectivity. Regional corridors should be reestablished or maintained where such connectivity occurred in the recent past, to increase the viability of populations, and maintain metapopulation structure.

CHAPTER 1
INTRODUCTION

Habitat fragmentation and loss is one of the greatest threats to the conservation of biodiversity in the world (Harris 1984; Meffe & Carroll 1997). The effect of habitat fragmentation on animal populations can have several demographic and genetic consequences. The reduction of population size and connectivity can create conditions where genetic variation is lost at a rapid rate. The loss of genetic variation within populations may lead to inbreeding depression, a reduction in evolutionary potential, and greater extinction probability (Frankham et al. 2002).

The most serious threat to the continued existence of the Florida black bear (*Ursus americanus floridanus*) is fragmentation and loss of habitat (Wesley 1991; Hellgren & Maehr 1993; Hellgren & Vaughan 1994). Habitat fragmentation and loss is driven by human population growth. An estimated 16.3 million people lived in Florida in 2001. This number is projected to increase to more than 20 million by 2015 (US Census 2000). Roads, and agricultural, commercial and residential developments continue to encroach on (and further degrade) remaining black bear habitat. The distribution of the Florida black bear has been reduced by 83% from its historic distribution (Wooding 1993). Currently, Florida black bears occur in several populations, mostly restricted within the state of Florida (Appendix A) (Pelton & Van Manen 1997).

The reduction of size and connectivity of populations has caused concern regarding the genetic health of Florida black bears. Most extant Florida black bear populations are small compared to historic size, and are relatively isolated. Theory suggests that small, isolated populations are at a higher risk of extinction than large, well-connected populations (Frankham 1995; Meffe & Carroll 1997; Ebert et al. 2002; Frankham et al. 2002). Because Florida black bear populations are fragmented from their original relatively contiguous distribution, the level of gene flow among populations may be important in maintaining levels of genetic variation and evolutionary potential of Florida black bears.

Although aspects of the population genetics of the Florida black bear have been investigated previously (Warrilow et al. 2001; Dobey 2002; Edwards 2002) using microsatellite analyses (Appendix B), these studies did not provide estimates of gene flow among populations, or provide data on the genetic consequences of habitat fragmentation and loss on Florida black bear populations. Little is known about the level of genetic variation within (or gene flow among) populations of the Florida black bear.

It has been suggested that fragmented populations are best managed as a metapopulation, where local populations are functionally connected with corridors that facilitate movement. The large home ranges and long-distance dispersal capabilities of black bears have been used as a rationale for implementation of corridors among populations (Hellgren & Vaughan 1994; Bowker & Jacobson 1995; Hoctor et al. 2000). The Osceola-Ocala corridor has been suggested as the best option in connecting any two of the populations of Florida black bear. However, the efficacy of this corridor or other corridors for large carnivores is relatively unknown.

Objectives

The objectives of my study were to investigate genetic variation and gene flow among Florida black bear populations, and to objectively evaluate the functionality of the Osceola-Ocala corridor in facilitating demographic and genetic connectivity. Chapter 2 discusses the effects of population size on within-population genetic variability, estimates levels of gene flow among populations, and examines relationships among measures of genetic differentiation and geographic distances between pairs of populations. Chapter 3 discusses the effectiveness of a regional corridor in connecting two Florida black bear populations using non-invasive genetic sampling and recently developed population-assignment tests.

Taken together, these chapters provide much-needed data on the genetic variation within (and gene flow among) populations of the Florida black bear; and an objective evaluation of the functionality of the Osceola-Ocala corridor. These data are expected to be important for the formulation and implementation of a management plan to ensure long-term persistence of Florida black bear populations.

CHAPTER 2
GENETIC CONSEQUENCES OF HABITAT FRAGMENTATION AND LOSS

Introduction

Fragmentation and loss of habitat is one of the most serious problems facing the conservation of biodiversity worldwide (Harris 1984; Meffe & Carroll 1997). Habitat fragmentation can increase mortality rates (Jules 1998), reduce abundance (Flather & Bevers 2002), alter movement patterns (Brooker & Brooker 2002), and disrupt the social structure of populations (Ims & Andreassen 1999; Cale 2003); and may reduce the probability of persistence (Harrison & Bruna 1999; Davies et al. 2001). Additionally, habitat fragmentation can influence genetic structure and persistence of populations in several ways. First, isolation and reduction of populations can decrease genetic variation (Hudson et al. 2000; Kuehn et al. 2003), which may reduce the ability of individuals to adapt to a changing environment, cause inbreeding depression (Ebert et al. 2002), reduce survival and reproduction (Frankham 1995; Reed & Frankham 2003), and increase the probability of extinction (Saccheri et al. 1998; Westemeier et al. 1998). Secondly, habitat fragmentation can create dispersal barriers, which can deter gene flow (Hitchings & Beebee 1997; Gerlach & Musolf 2000) or otherwise alter genetic structure of the population (Hale et al. 2001). Thus, efforts to conserve plant and animal populations should take into account the genetic consequences of habitat fragmentation.

Large mammalian carnivores are particularly vulnerable to habitat loss and fragmentation because of their relatively low numbers, large home ranges, and interactions with humans (Noss et al. 1996; Crooks 2002). The Florida panther (*Puma* *concolor coryi*) and giant panda (*Ailuropoda melanoleuca*) are examples of large carnivores that were reduced to small numbers largely because of impacts of habitat fragmentation and loss (Roelke et al. 1993; Lu et al. 2001). Another large carnivore that has been negatively impacted by habitat fragmentation is the Florida black bear (*Ursus americanus floridanus*) (Hellgren & Maehr 1993).

The Florida black bear historically roamed throughout the peninsula of Florida and southern portions of Georgia, Alabama, and Mississippi (Brady & Maehr 1985). From the 1800s to the 1970s, numbers of Florida black bears were significantly reduced by loss and fragmentation of habitat, and unregulated hunting (Cory 1896; Hendry et al. 1982). Only an estimated 300 to 500 bears were left in the state of Florida in the 1970s (McDaniel 1974; Brady & Maehr 1985). Consequently, the Florida Game and Freshwater Fish Commission classified the Florida black bear as a threatened species in most Florida counties, in 1974 (Wooding 1993). Destruction and fragmentation of once-contiguous habitat has reduced the distribution of Florida black bears to nine areas: Eglin (EG), Apalachicola (AP), Aucilla (AU), Osceola (OS), Ocala (OC), St. Johns (SJ), Chassahowitzka (CH), Glades/Highlands (GH), and Big Cypress (BC) (Fig. 1). Fragmentation of populations can reduce genetic variation (Sherwin & Moritz 2000) and increase the probability of extinction (Saccheri et al. 1998; Westemeier et al. 1998), but the genetic consequences of the historical and contemporary patterns of habitat fragmentation on Florida black bear populations are unknown. Using microsatellite analyses, my goal was to investigate the genetic consequences of habitat fragmentation on Florida black bear populations. My specific objectives were to estimate within-population genetic variation, and investigate the level of genetic differentiation among Florida black bear populations. Theory predicts a positive correlation between genetic variation and population size (Frankham 1996), and between genetic differentiation and geographic distance among populations (Slatkin 1993). Thus, I tested these predictions by examining the relationship between measures of genetic variation and recent estimates of population size, and between measures of genetic differentiation and geographic distances among populations.

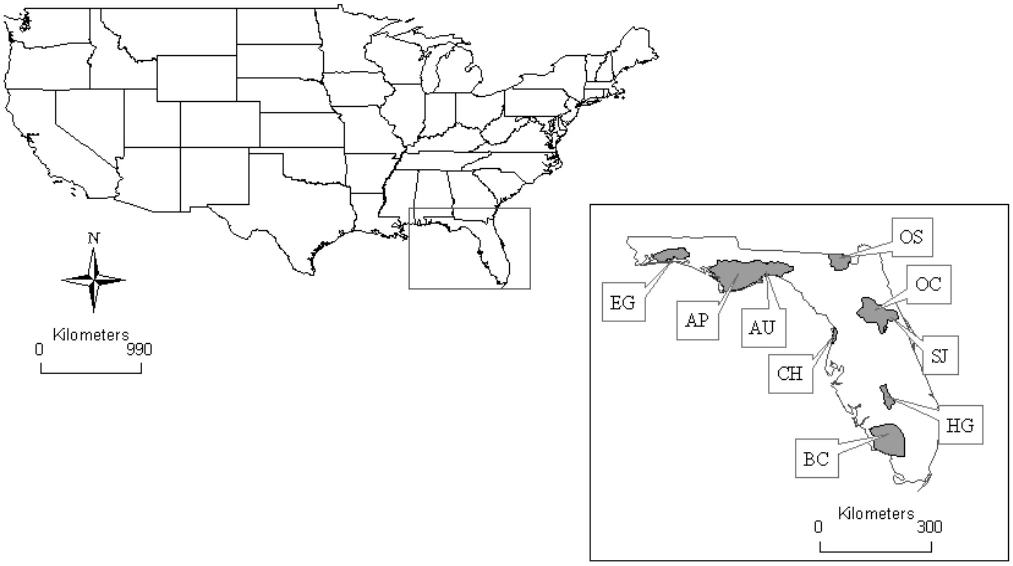

Figure 1. Distribution of black bears in Florida: Eglin (EG), Apalachicola (AP), Aucilla (AU), Osceola (OS), Ocala (OC), St. Johns (SJ), Chassahowitzka (CH), Highlands/Glades (HG), and Big Cypress (BC). The distribution map was compiled by the Florida Fish and Wildlife Conservation Commission.

Methods

Sample Collection

Hair and tissue samples from individual bears were collected from each of the nine Florida black bear populations during 1989-2003. Most samples were collected from field studies, some using non-invasive techniques (Woods et al. 1999); but samples also were collected from translocated animals, and from bears killed on roadways. Hair and tissue samples were sent to Wildlife Genetics International (Nelson, British Columbia, Canada) (www.wildlifegenetics.ca/) for microsatellite analysis. DNA was extracted using QIAGEN's DNeasy Tissue kits (Valencia, California), as per QIAGEN's instructions (http://www.qiagen.com/ literature/genomlit.asp); and microsatellite loci were amplified using polymearse chain reaction (PCR). Each individual was genotyped for 12 microsatellite loci (G1A, G10B, G10C, G1D, G10L, G10M, G10P, G10X, G10H, MU50, MU59, and G10J). Laboratory methods used in my study are described in detail by Paetkau et al. (1995, 1998a, 1998b, 1999) and Paetkau & Strobeck (1994).

Statistical Analyses

Departures from Hardy-Weinberg equilibrium (HWE) were tested using the HWE probability test in Genepop 3.4 (Raymond & Rousset 1995). Exact p-values were computed using the complete enumeration method for loci with fewer than four alleles (Louis & Dempster 1987), and the Markov chain method (dememorization 1,000; batches 100; iterations per batch 1,000) for loci with more than four alleles (Guo & Thompson 1992). Using this same program, linkage-disequilibrium tests were used to test for nonrandom associations among alleles of different loci, using the Markov chain method.

Within each bear population, genetic variation was measured as the observed average heterozygosity (H_O), expected average heterozygosity (H_E), and the average number of alleles per locus (A). Spearman's rank correlation was used to test for the correlation between genetic variation and estimated population size. To characterize nonrandom mating within populations, F_{IS} was calculated according to Weir & Cockerham (1984) in Genepop 3.4 (Raymond & Rousset 1995). Global estimates (across all populations) of F_{IS}, F_{IT} (characterizes nonrandom mating within populations and genetic differentiation among populations), and F_{ST} (characterizes genetic differentiation among populations) were also calculated using these methods.

Genetic differentiation among populations was estimated using Genepop 3.4 (Raymond & Rousset 1995) with pairwise F_{ST} (Weir & Cockerham 1984) and pairwise R_{ST} (Michalakis & Excoffier 1996). The R_{ST} was estimated because microsatellites are thought to conform to the stepwise-mutational model better than to the infinite-alleles model on which F_{ST} is based (Slatkin 1995). The significance of population differentiation was tested using the genic differentiation test in Genepop 3.4 (Raymond & Rousset 1995). The likelihood ratio genetic distance, D_{LR} (Paetkau et al. 1995) was estimated for each pair of populations using the Doh assignment calculator from the website, http://www2.biology.ualberta.ca/jbrzusto/ Doh.php. This genetic distance is based on the ratio of genotype likelihoods between pairs of populations. The software program Phylip 3.5c (Felsenstein 1993) and the subprogram FITCH (Fitch & Margolia 1967) were used to generate an unrooted phylogenetic tree, with branch lengths corresponding to D_{LR} values.

Geographic distances among populations were estimated as the shortest land distance between population centroids using least-cost path analysis in ArcGIS 8.1.2 (McCoy & Johnston 2000). Centroids were estimated as the harmonic mean of the sample collection locations in each study site. The subprogram ISOLDE in Genepop 3.4 (Raymond & Rousset 1995) was used to test for a relationship between geographic distances, and F_{ST}, R_{ST}, and D_{LR} values. Statistical significance of these relationships was tested using a Mantel (1967) test with 10,000 permutations.

Results

A total of 305 individual bears was genotyped for 12 microsatellite loci in nine Florida black bear populations (Table 1). There were no significant departures from HWE for any locus or population ($p > 0.05$). The linkage disequilibrium test indicated that only 15% of loci pairings had significant nonrandom associations ($p \leq 0.05$). Loci used in this analysis were found to be independent (D. Paetkau, pers. comm.). Thus, any significant linkage observed among loci pairs may be a result of nonrandom mating, sampling bias, recent admixture, or genetic drift (Frankham et al. 2002).

The population with the highest mean number of alleles per locus (A) was Osceola (mean ± 1SE; 6.667 ± 0.225); whereas Chassahowitzka had the lowest value (2.250 ± 0.179). Observed average heterozygosity (H_O) ranged from 0.287 ± 0.058 in Chassahowitzka to 0.705 ± 0.030 in Osceola. Similarly, expected average heterozygosity (H_E) ranged from 0.271 ± 0.054 in Chassahowitzka to 0.713 ± 0.027 in Osceola (Table 1). Estimated population sizes ranged from 20 in Chassahowitzka to 830 in Osceola (Kasbohm & Bentzein 1998; Maehr et al. 2001; Florida Fish and Wildlife Conservation Commission (FWC), unpublished data). All three measures of genetic variation were positively correlated with estimated population size (A: $r_s = 0.845$, $p = 0.004$; H_O: $r_s = 0.778$, $p = 0.014$; H_E: $r_s = 0.728$, $p = 0.026$) (Fig. 2).

Table 1. Measures of genetic variation (mean ± 1 SE) at 12 microsatellite loci in nine Florida black bear populations (sample sizes are in parentheses). Measures of genetic variation are: observed average heterozygosity (H_O), expected average heterozygosity (H_E), and mean alleles per locus (A). Values of F_{IS} (a measure of nonrandom mating within populations) ± 1 SE are also given.

Population	H_O	H_E	A	F_{IS}
Apalachicola (38)	0.686 ± 0.036	0.706 ± 0.031	5.92 ± 0.358	0.027 ± 0.025
Aucilla (9)	0.556 ± 0.063	0.616 ± 0.054	3.83 ± 0.322	0.097 ± 0.062
Big Cypress (41)	0.642 ± 0.036	0.650 ± 0.026	5.50 ± 0.435	0.013 ± 0.034
Chassahowitzka (29)	0.287 ± 0.058	0.271 ± 0.054	2.25 ± 0.179	-0.057 ± 0.028
Eglin (40)	0.613 ± 0.071	0.537 ± 0.062	4.08 ± 0.379	-0.141 ± 0.024
Highlands/Glades (27)	0.327 ± 0.049	0.385 ± 0.051	2.75 ± 0.250	0.149 ± 0.059
Ocala (40)	0.579 ± 0.045	0.610 ± 0.045	4.75 ± 0.305	0.051 ± 0.024
Osceola (41)	0.705 ± 0.030	0.713 ± 0.027	6.67 ± 0.225	0.010 ± 0.033
St. Johns (40)	0.650 ± 0.048	0.663 ± 0.041	5.58 ± 0.379	0.020 ± 0.028

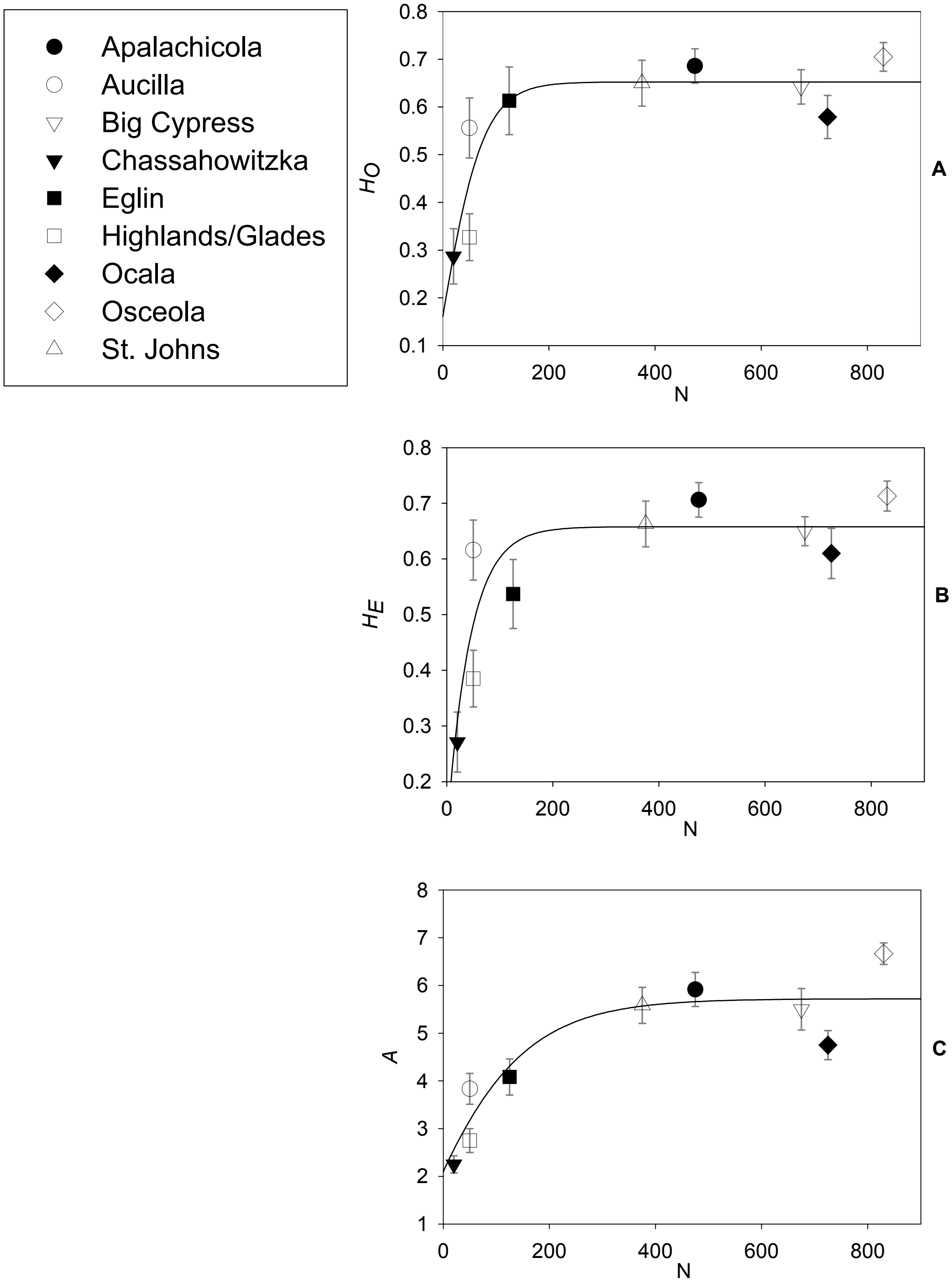

Figure 2. Relationship between estimated population size (N) and measures of genetic variation (mean ± 1 SE) in nine Florida black bear populations. A) N and Observed average heterozygosity (H_O), B) N and Expected average heterozygosity (H_E), and C) N and Average alleles per locus (A). Curves were fitted using a sigmoid 4-parameter regression in Sigmaplot.

F_{IS} ranged from -0.141 ± 0.024 in Eglin to 0.149 ± 0.059 in Highlands/Glades (Table 1). These results give evidence of random mating within these populations. The global estimate of F_{IS} was 0.010 and the global estimate of F_{IT} was 0.235. The relatively high F_{IT} values encompass relatively insubstantial effects of mating between close relatives within populations; and also the extensive effects of restricted gene flow among the populations (Hartl & Clark 1997).

Global $F_{ST,}$ the measure of population subdivision across all populations, was 0.227. Estimates of F_{ST} ranged from 0.009 to 0.574 and R_{ST} ranged from 0.010 to 0.629. The pairwise comparisons between Ocala and St. Johns had highest levels of gene flow whereas Highlands/Glades and Chassahowitzka had the lowest levels of gene flow (Table 2). All tests of genic differentiation among populations were highly significant ($p < 0.001$).

Table 2. Pairwise F_{ST} (below diagonal) and R_{ST} (above diagonal) estimates for nine Florida black bear populations (standard errors are in parentheses). Populations are: Apalachicola (AP), Aucilla (AU), Big Cypress (BC), Chassahowitzka (CH), Eglin (EG), Highlands/Glades (HG), Ocala (OC), Osceola (OS), and St. Johns (SJ). Fig. 1 contains the geographic locations of these populations.

	AP	AU	BC	CH	EG	HG	OC	OS	SJ
AP		0.0546 (±0.034)	0.1356 (±0.034)	0.3427 (±0.067)	0.1572 (±0.063)	0.4197 (±0.046)	0.2017 (±0.050)	0.0727 (±0.044)	0.2225 (±0.049)
AU	0.1223 (±0.019)		0.2073 (±0.053)	0.5953 (±0.101)	0.1946 (±0.066)	0.4966 (±0.097)	0.2348 (±0.065)	0.1388 (±0.054)	0.2714 (±0.062)
BC	0.1379 (±0.026)	0.2010 (±0.018)		0.3342 (±0.074)	0.3026 (±0.073)	0.2435 (±0.062)	0.1053 (±0.050)	0.1422 (±0.051)	0.0848 (±0.037)
CH	0.3609 (±0.041)	0.4449 (±0.061)	0.3748 (±0.046)		0.5472 (±0.087)	0.6292 (±0.075)	0.3723 (±0.087)	0.3443 (±0.078)	0.3449 (±0.061)
EG	0.1653 (±0.029)	0.1961 (±0.026)	0.2348 (±0.032)	0.4846 (±0.065)		0.5176 (±0.088)	0.2847 (±0.071)	0.1477 (±0.055)	0.3207 (±0.073)
HG	0.2972 (±0.038)	0.3841 (±0.064)	0.2431 (±0.038)	0.5737 (±0.064)	0.4000 (±0.068)		0.2269 (±0.056)	0.3787 (±0.050)	0.1576 (±0.049)
OC	0.1617 (±0.030)	0.1960 (±0.036)	0.1360 (±0.029)	0.3906 (±0.067)	0.2299 (±0.034)	0.2707 (±0.035)		0.0842 (±0.014)	0.0101 (±0.029)
OS	0.1167 (±0.022)	0.1463 (±0.023)	0.1277 (±0.032)	0.3483 (±0.049)	0.1792 (±0.032)	0.3050 (±0.036)	0.1062 (±0.029)		0.1351 (±0.042)
SJ	0.1419 (±0.033)	0.1790 (±0.042)	0.1212 (±0.018)	0.3585 (±0.052)	0.2240 (±0.035)	0.2232 (±0.036)	0.0099 (±0.005)	0.0942 (±0.028)	

An unrooted phylogenetic tree based on D_{LR} values suggested that the Ocala and St. Johns populations were closely related, whereas Chassahowitzka, Highlands/Glades, and Eglin were the most divergent of all the populations (Fig. 3). There was no significant relationship between geographic distance and measures of genetic differentiation [F_{ST} ($p = 0.211$), R_{ST} ($p = 0.104$), or D_{LR} ($p = 0.073$)].

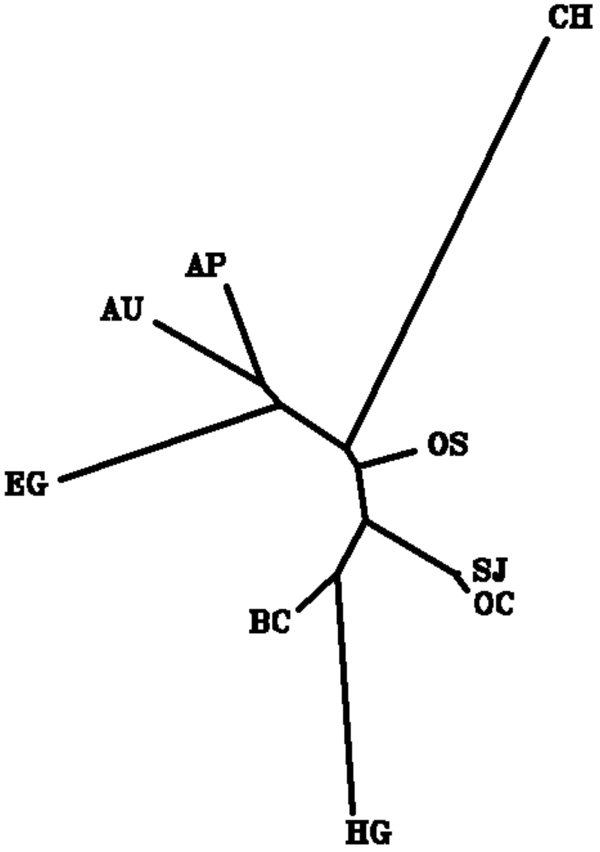

Figure 3. An unrooted phylogenetic tree depicting the genetic relationships among Florida black bear populations. Branch lengths correspond to the likelihood ratio genetic distance, D_{LR}. Populations are: Eglin (EG), Apalachicola (AP), Aucilla (AU), Osceola (OS), Ocala (OC), St. Johns (SJ), Chassahowitzka (CH), Highlands/Glades (HG), and Big Cypress (BC).

Discussion

Genetic Variation

Habitat fragmentation can reduce genetic variation, which can adversely influence fitness [e.g., the Florida panther (Roelke et al. 1993) and lion *(Panthera leo)*], increase susceptibility to disease [e.g., cheetah (*Acinonyx jubatus*) (O'Brien et al. 1994)], and decrease population viability (Sherwin & Moritz 2000). Habitat fragmentation and hunting are thought to be responsible for losses in genetic variation in wolverines (*Gulo gulo*) (Kyle & Strobeck 2001), lynx (*Lynx lynx*) (Spong & Hellborg 2002), mountain lions (*Puma concolor*) (Ernest et al. 2003), Ethiopian wolves (*Canis simenesis*) (Gottelli et al. 1994) and brown bears (*U. arctos*) (Miller & Waits 2003). Large carnivores may be much more susceptible than other taxa to losses in genetic variation due to habitat fragmentation because of their large home ranges and low population densities (Paetkau & Strobeck 1994).

The measures of genetic variation reported for most Florida black bear populations were within the range of other populations of bears using 8 of the same microsatellite loci (Waits et al. 2000) . However, genetic variation in Chassahowitzka and Highlands/Glades are among the lowest reported for any bear population (Appendix C, Table 4). The three measures of genetic variation for Florida black bear populations were positively correlated with population size. Chassahowitzka was characterized by a small population size, and accordingly, this population had the lowest level of genetic diversity. Osceola was characterized by a large population size because of its connection with the Okefenokee National Wildlife Refuge, and had the highest levels of genetic diversity. Presumably, the effects of genetic drift on loss of genetic variation are much greater in

Chassahowitzka and Highlands/Glades because of small population sizes, whereas the effects of genetic drift are not as substantial in the larger populations.

One of the only bear populations that have a reported genetic variation lower than Chassahowitzka is that of brown bears on Kodiak Island, Alaska. Kodiak bears have remained isolated from the mainland brown bear populations for >10,000 years (Paetkau et al. 1998b). The Chassahowitzka and Highlands/Glades populations are thought to have remained isolated from other Florida black bear populations for a longer period than any other Florida black bear populations. The isolation of these populations is remarkable because it has resulted in the substantial loss of genetic variation that has occurred in presumably < 100 years.

The declines in local abundance and genetic variability of Chassahowitzka and Highlands/Glades bear populations raise the possibility that inbreeding depression could reduce fitness, survival, and evolutionary potential (Reed & Frankham 2003), and that these populations may face an increased risk of local extinction (Frankham 1995; Ebert et al. 2002). Although not within these populations, some characteristic signs of inbreeding depression were observed in Florida black bears in the western panhandle of Florida (Dunbar et al. 1996) and southern Alabama (Kasbohm & Bentzien 1998). However, low F_{IS} values and lack of deviations from Hardy-Weinberg Equilibrium suggest that random mating is operating within studied populations of the Florida black bear.

Genetic Structure

The tests of genetic differentiation, F_{ST}, R_{ST}, and D_{LR} indicated that there was extensive differentiation among Florida black bear populations. This differentiation was most evident with pairwise comparisons of Chassahowitzka, Highlands/Glades, or Eglin with any other population. The high rate of genetic drift within these populations most likely contributed to the extensive genetic differentiation among populations. The level of genetic differentiation between Florida black bear populations was substantially greater than between other large carnivore populations (e.g., bears: (Paetkau et al. 1997), the Asian black bear [*U. thibetanus*]: (Saitoh et al. 2001), mountain lions: (Ernest et al. 2003) wolverines: (Kyle & Strobeck 2001; Walker et al. 2001) and lynx: (Hellborg et al. 2002; Schwartz et al. 2002).

The global estimate of F_{ST}, the measure of population subdivision across all populations, was 0.227. This degree of subdivision is expected if there are on average 0.85 successful migrants [$Nm = (1/F_{ST}-1)/4$] entering each population per generation (approximately 8 years for black bears) assuming an island model of migration (Frankham et al. 2002). Therefore, on average, across all Florida black bear populations, there is one successful migrant every 10 years, a relatively low level of gene flow.

There have been dozens of bear translocations among populations due to management activities during the last 20 years (T. Eason, pers. comm.). Due to the relatively recent history of these artificial movements, it is unknown what effects they will have on the genetic structure of these populations. Some studies suggest that most translocations of carnivores are unsuccessful, and probably do not contribute to the gene pool of the population in which they were released (Linnell et al. 1997).

In large natural populations occupying a mostly contiguous habitat, a pattern of isolation by distance is expected (Wright 1931). This relationship has been reported for other bear populations (Paetkau et al. 1997). However, there was no relationship between geographic distance and measures of genetic differentiation among Florida black bear populations. However, nearly significant relationships of pairwise R_{ST} and D_{LR} values with geographic distances suggest that exclusion of values associated with small populations (i.e., Chassahowitzka and Highlands/Glades) may generate a significant isolation-by-distance relationship among "larger" populations of Florida black bears. Interestingly, two pairs of populations separated by comparable geographic distances (Ocala-St. Johns and Apalachicola-Aucilla) had very different F_{ST} values, 0.009 and 0.122 respectively, suggesting that there is a high level of gene flow between Ocala and St. Johns, but not between Apalachicola and Aucilla.

The genetic differentiation among Florida black bears was substantial, although the average distance between nearest neighboring populations (134 km) is within the dispersal capabilities of black bears (Rogers 1987; Maehr et al. 1988). Dispersal of bears is sex-biased, and males typically disperse farther than females, who tend to establish home ranges near their mother's home range (Rogers 1987; Schwartz & Franzmann 1992). It has been suggested that dispersing black bears may be able to maintain connectivity among populations even when populations are fragmented (Noss et al. 1996; Maehr et al. 2001). Why, then, was there such a high level of genetic differentiation among Florida black bear populations? Furthermore, why did I fail to find isolation-by-distance relationship in Florida black bears, which has been reported for other black bear populations occupying contiguous habitat? I suggest that the substantial genetic differentiation and the lack of isolation-by-distance relationship among Florida black bear populations is primarily due to the reduction of bear numbers by habitat fragmentation, and by human-made barriers to dispersal.

The presence of natural barriers, such as mountain ranges or large rivers, has historically determined the limits of species distribution (Chesser 1983). Habitat fragmentation in the form of anthropogenic barriers such as roads or other human development can further limit species distribution and gene flow (Mader 1984). The separation of populations with roads reduced the level of gene flow in the moor frog (*Rana arvalis*) (Vos et al. 2001), ground beetle (*Carabus violaceus*) (Keller & Largiader 2003), and bank vole (*Clethrionomys glareolus*) (Gerlach & Musolf 2000). Additionally, habitat fragmentation is responsible for altering the genetic structure of the red squirrel (*Sciurus vulgaris*) (Hale et al. 2001) and black grouse (*Tetrao tetrix*) (Caizergues et al. 2003). Although large carnivores are thought to be highly vagile (Paetkau et al. 1999; Schwartz et al. 2002), some studies suggest they may be limited in distribution because of anthropogenic barriers (Kyle & Strobeck 2001; Sinclair et al. 2001; Walker et al. 2001; Ernest et al. 2003; Miller & Waits 2003). Black bear movement does not seem to be limited by topographical features of the native Floridian landscape; however, human-made barriers such as roads, cities, and residential areas, appear to limit the successful dispersal of black bears (Brody & Pelton 1989; Hellgren & Maehr 1993) in Florida.

Although bears are able to cross some highways (McCown et al. 2001), the impact of highways on mortality of bears can be detrimental. From 2000 to 2002, 346 bears were documented as killed on roads in Florida. Most of these were young males that may have been attempting dispersal or migration to distant populations (FWC, unpublished data). Additionally, highways and development can act as partial or complete barriers. Some bears may avoid interstate highways (Brody & Pelton 1989; Proctor et al. 2002), and other forms of human development may alter movement patterns (Maehr et al. 2003), further decreasing the probability of movement of bears among populations.

Given the unprecedented rate of human population growth in Florida, wildlife habitat will continue to be converted for commercial or residential purposes. Consequently, further fragmentation or isolation of Florida black bears and other wildlife population is likely. My results indicate that habitat fragmentation and human-made dispersal barriers may have substantially altered the genetic structure of Florida black bears. The effects of habitat fragmentation and isolation are likely to be even greater in species with limited dispersal capabilities. It is imperative that management plans for the conservation of black bears in Florida consider measures to mitigate genetic (and most likely, demographic) consequences of habitat fragmentation and anthropogenic dispersal barriers.

Conclusion

I conclude that the loss and fragmentation of once contiguous habitat has caused the loss of genetic variation in the Florida black bear, and that genetic variation in smaller populations is among the lowest reported for any species of bear. This substantial loss of genetic variation has contributed to extensive genetic differentiation among populations. Additionally, roads with high traffic volume and commercial and residential developments apparently act as barriers to gene flow, contributing to genetic differentiation among populations.

Loss of genetic variation is a concern for the long-term survival and adaptation of Florida black bears. What constitutes historical levels of genetic variation for Florida black bear populations? Evidence suggests that at one time Florida black bears were distributed throughout the state (Brady & Maehr 1985). Most contiguous mainland populations of black bears have high levels of genetic variation ($H_E \sim 0.76$) (Paetkau et al. 1998b). Thus, efforts should be made to restore historic levels of genetic variation within Florida black bear populations, using mainland figures as a baseline.

To prevent the further loss of genetic variation, efforts should be made to increase the size of Florida black bear populations. It has been suggested that a minimum of 50 effective breeders is needed to prevent inbreeding depression and population levels in the hundreds or thousands to maintain evolutionary potential (Franklin 1980; Lande 1995). However, keeping bears at high population levels may be increasingly difficult due to the rapid rate of development over much of the state.

Given that Florida black bear populations have been reduced in size, gene flow among bear populations is needed to restore and maintain genetic variation (Waits 1999). A minimum of one and a maximum of ten successful migrants per generation have been suggested as a rule of thumb to maintain levels of genetic variation (Mills & Allendorf 1996). I suggest that Florida black bear populations should be managed as a metapopulation so that gene flow can occur among populations connected with conservation corridors (Craighead & Vyse 1996; Maehr et al. 2001; Larkin et al. 2004). However, the effectiveness of corridors in maintaining gene flow among populations of carnivores is not well understood (Beier & Noss 1998). Recent data suggest that one such corridor between the Ocala and Osceola populations may facilitate gene flow between these populations (FWC, unpublished data).

Additionally, wildlife crossing structures may be needed to allow safe passage of bears across roadways that pose significant barriers to bear movement (Foster & Humphrey 1995). In situations where population connection via corridors is impractical, artificial translocation of animals should be considered (Griffith et al. 1989).

Translocation of animals has been successful in curbing some effects of inbreeding depression and increasing levels of genetic variation in some animal populations (Mansfield & Land 2002). Conservation biologists should be cognizant of the fact that the effects of translocated animals on population structure and hierarchy are not understood. Finally, further reduction or fragmentation of habitat likely will have detrimental impact on demographic and genetic health of the Florida black bear populations, and efforts to conserve remaining habitat cannot be overemphasized.

CHAPTER 3
EVALUATING THE EFFECTIVENESS OF A REGIONAL BLACK BEAR CORRIDOR

Introduction

The effect of habitat fragmentation on natural populations is one of the greatest threats to biodiversity conservation (Fahrig & Merriam 1994; Meffe & Carroll 1997; Fahrig 2001). Habitat fragmentation can subdivide and isolate populations, reduce genetic diversity, and increase the chances of local extinction (Harris 1984; Saccheri et al. 1998; Westemeier et al. 1998). Because most wildlife populations in human-dominated landscapes occur in fragmented habitats, attempts have been made to identify measures that can reduce the adverse influences of habitat fragmentation. Corridors have been proposed to mitigate the negative effects of habitat fragmentation by connecting once isolated populations (Noss & Harris 1986). Corridors can increase movement of organisms among patches (Hass 1995; Aars & Ims 1999; Haddad 1999; Sieving et al. 2000; Mech & Hallett 2001; Haddad et al. 2003; Kirchner et al. 2003), thereby providing additional habitat (Perault & Lomolino 2000), facilitate plant-animal interactions (Tewksbury et al. 2002), and increase recolonization potential (Hale et al. 2001), survival (Coffman et al. 2001), gene flow (Harris & Gallagher 1989) and the probability of persistence (Fahrig & Merriam 1985; Beier 1993). The use of corridors in conservation stems from the equilibrium theory of island biogeography (MacArthur & Wilson 1967), landscape ecology (Forman & Godron 1986), and the metapopulation paradigm (Levins 1970; Hanski 1994). Several authors have suggested that conservation of fragmented populations requires a metapopulation approach (Hanski & Simberloff 1997; Dobson et al. 1999). Managing fragmented or spatially-structured populations requires functional corridors that permit exchange of individuals among populations.

Discussions regarding the role of corridors in conservation biology is confused by the many definitions of this concept (Rosenberg et al. 1997; Beier & Noss 1998; Hess & Fischer 2001). Corridors range in scale from small transects linking patches of habitat to regional complexes linking ecosystems and watersheds. Noss et al. (1996) suggested that "connectivity will be best provided by broad, heterogeneous landscapes, not narrow, strictly defined corridors." Thus, evaluating the effectiveness of corridors requires a consideration of the entire landscape mosaic and the functional/structural aspects of the corridor for the focal species.

Large carnivores are highly susceptible to the effects of habitat fragmentation, because of the potential for conflicts with humans, large home ranges, and low population densities (Noss et al. 1996; Crooks 2002). Many populations of large carnivores exist within fragmented habitats, encompassing areas much too small to support viable populations (Woodroffe & Ginsberg 1998). Additionally, the conservation of large carnivores that are flagship and umbrella species provides a means of protecting biodiversity at smaller scales (Cox et al. 1994; Noss et al. 1996). It has been suggested that carnivore populations in fragmented habitats operate as metapopulations (Poole 1997; Ferreras 2001; Palomares 2001). For many carnivore species, movement among populations is vital for metapopulation persistence (e.g., lynx [*Lynx spp.*]: Ferreras 2001; Ganona et al. 1998; Palomares 2001; and brown bears [*Ursus arctos*]: Craighead & Vyse 1996).

The long-distance movements of large carnivores suggest that they are more likely to use corridors for movements than species with limited dispersal capabilities (Lidicker & Koenig 1996; Harrison & Voller 1998). Corridors were recommended as management tools for connecting populations of lynx (Poole 1997; Ferreras 2001; Palomares 2001), cougars (*Puma concolor*) (Beier 1995; Ernest et al. 2003), wolves (*Canis lupus*) (Duke et al. 2001), brown bears (Picton 1987; Craighead & Vyse 1996; Weaver et al. 1996), and black bears (*U. americanus*) (Cox et al. 1994; Hoctor 2003; Larkin et al. 2004). However, the effectiveness of corridors for large carnivores has not been tested on a regional scale.

One challenge in testing the effectiveness of regional corridors for carnivores using traditional techniques, such as radio telemetry, is that the long-distance movements of carnivores make it difficult to locate and observe animals. In many species, long-distance dispersal is often rare, and there is no guarantee that the sample of radio-instrumented animals will contain dispersing animals (Koenig et al. 1996). Moreover, the dispersal of an animal from population to population does not indicate effective dispersal; genetic data are much more suited to provide that information (Frankham et al. 2002). The use of relatively inexpensive, non-invasive sampling techniques, such as hair snares, and genetic analyses may help overcome these limitations of radio telemetry-based studies. Such techniques provide data necessary for evaluation of the functionality of corridors by elucidating genetic structure and effective dispersal (Foran et al. 1997). Recent advances in genetic analyses and statistical techniques (e.g., population-assignment tests) have made it possible to identify the origin of animals by assigning them to a population based on their multilocus genotypes (Paetkau et al. 1995;

Waser & Strobeck 1998; Waser et al. 2001). Population-assignment tests have been used to identify immigrants within populations of cougars (Ernest et al. 2003), otters (*Lutra lutra*) (Dallas et al. 2002), wolves (Flagstad et al. 2003; Vila et al. 2003), marten (*Martes americana*) (Small et al. 2003), wolverines (*Gulo gulo*) (Cegelski et al. 2003), and bears (Paetkau et al. 1995). These techniques can identify dispersal patterns and cryptic boundaries, which may indicate breaks in the gene flow across populations or the reconnection of once isolated populations (Manel et al. 2003). Additionally, some assignment tests detect not only immigrants into a population, but also their offspring, which enables researchers to directly detect and monitor gene flow (Rannala & Mountain 1997; Pritchard et al. 2000).

A carnivore species that could benefit from the implementation of regional corridors is the Florida black bear (*U. a. floridanus*). The Florida black bear was once distributed throughout Florida, and the southern portions of Georgia, Alabama, and Mississippi. Human activities significantly reduced the number of black bears from the 1850s to the 1970s through extensive fragmentation of habitat and excessive hunting (Brady & Maehr 1985). Consequently, Florida black bears now occur in fragmented populations. The long-term isolation of populations could lead to a loss of genetic variation and evolutionary potential, and may also reduce population viability (Harris 1984; Frankham 1995; Reed & Frankham 2003). However, some populations are expanding as bears recolonize suitable vacant habitat (Eason 2000). Black bears have large home ranges and dispersing bears can travel hundreds of kilometers from their natal home range (Alt 1979; Rogers 1987; Maehr et al. 1988; Wooding & Hardisky 1992; Hellgren & Maehr 1993; McCown et al. 2001; Lee & Vaughan 2003). However, development throughout much of the state of Florida has created formidable obstacles to movements such as towns, commercial/residential developments, and major highways (Brody & Pelton 1989; Maehr et al. 2003). Consequently, regional corridors may be needed to mitigate the detrimental demographic and genetic effects of habitat fragmentation in Florida black bear populations (Harris & Scheck 1991; Noss 1993).

Documented dispersal and movement of individual bears (Florida Fish and Wildlife Conservation Commission (FWC), unpublished data) and Geographic Information Systems (GIS) analysis (Hoctor 2003) suggest that the Osceola-Ocala regional corridor may be the best option for connecting two of the largest Florida black bear populations. The Osceola-Ocala corridor is a patchwork of public and private lands within a matrix of roads and development stretching for 90 km from the Ocala National Forest to Osceola National Forest (Fig. 4). This proposed corridor contains a mosaic of flatwoods, pine plantations, forested wetlands, riparian hammocks, scrub, and sandhill covering over 80,000 ha (Maehr et al. 2001). Osceola and Ocala are two of the largest populations of Florida black bear (Eason 2000), and establishing or maintaining connectivity between these populations may be necessary to ensure the long-term persistence of the Florida black bear.

The goal of my study was to evaluate the effectiveness of the Osceola-Ocala corridor for the Florida black bear. I used non-invasive sampling to obtain genetic material from bears within the Osceola-Ocala corridor and genotyped bears for 12 microsatellite loci. I also sampled bears from the Osceola and Ocala populations and from seven other areas throughout Florida. I used population-assignment tests to assign individuals sampled from the corridor to a population of origin (Osceola or Ocala) based on their multilocus genotypes. These techniques allowed me to characterize the dispersal of bears from the source populations, and identify gaps in connectivity within the Osceola-Ocala corridor.

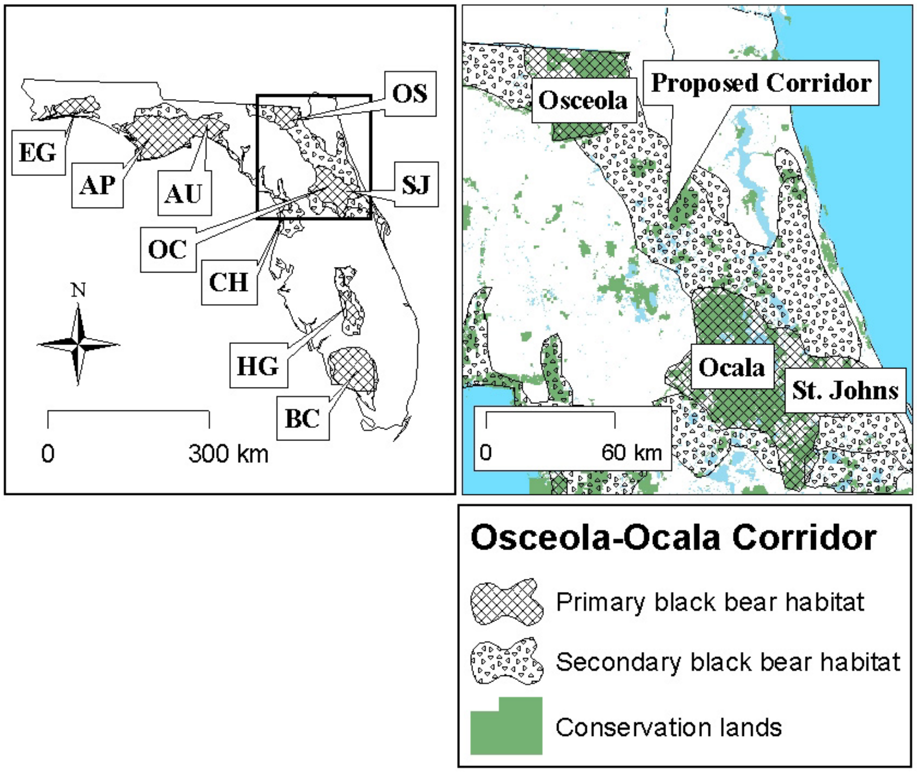

Figure 4. Area proposed as a regional corridor between the Ocala and Osceola black bear populations. Crosshatched areas represent primary black bear habitat (presence of breeding females) and stippled areas represent secondary black bear habitat from a recent distribution map (Florida Fish and Wildlife Conservation Commission (FWC), unpublished data). Populations are abbreviated as: Eglin (EG), Apalachicola (AP), Aucilla (AU), Osceola (OS), Ocala (OC), St. Johns (SJ), Chassahowitzka (CH), Highlands/Glades (HG), and Big Cypress (BC).

Methods

I used a map of secondary black bear habitat (FWC, unpublished data; Fig. 4) and results from a least-cost path analysis (Hoctor 2003) to identify areas that might serve as a potential regional corridor between Ocala and Osceola. These habitat patches represented areas that bears most likely travel through to avoid commercial and residential development. I overlaid a grid of 20 km^2 cells on a map of available lands within the potential corridor and placed at least one hair snare (Woods et al. 1999) within each cell.

Each hair snare was constructed of two strands of standard 4-prong barbed wire at heights of approximately 30 cm and 55 cm, attached to a perimeter of three or more trees encompassing a total area of 10-30 m^2. I baited the center of the snare with pastries and corn, and placed two attractants (pastries and raspberry extract) $\geq$ 2.44 m above the snare. As bears entered the hair snare, the barbed wire snagged hair samples that were used in genetic analyses. I operated each hair snare for an average of seven times with a mean period of 26 days between baiting and sampling from May to November of 2002 and May to August of 2003. I collected hair samples using the protocol of Eason et al. (2001). Additionally, I collected hair samples within the corridor opportunistically from a complementary hair snare project in Osceola (May-August, 2002-03), existing fences (2001-03) and bears killed on roads (1998-2003).

Black bear tissue and hair samples collected from previous research studies and highway mortalities during 1989-2003 were available for the Osceola and Ocala populations (n = 41 and n = 40 individual bears, respectively). To provide comparative data, individuals also were sampled from other Florida black bear populations: Apalachicola (n = 40), Aucilla (n = 9), Big Cypress (n = 41), Chassahowitzka (n = 29), Eglin (n = 40), Highlands/Glades (n = 28), and St. Johns (n = 40).

I sent hair and tissue samples to Wildlife Genetics International (Nelson, British Columbia, Canada) (http://www.wildlifegenetics.ca/), where individuals were genotyped using microsatellite analysis. DNA was extracted using QIAGEN's DNeasy Tissue kits (Valencia, California), as per QIAGEN's instructions (http://www.qiagen.com/literature/genomlit.asp). Microsatellite loci were amplified using polymerase chain reaction (PCR) primers (G1A, G10B, G10C, G1D, G10L, G10M, G10P, G10X, G10H, MU50, MU59, and G10J). The gender of each bear was determined using the length polymorphism in the amelogenin gene (D. Paetkau, pers. comm.). Laboratory analyses were performed as described in Paetkau et al. (1995, 1998a, 1998b, 1999) and Paetkau & Strobeck (1994).

I used the software program STRUCTURE to assign individuals to a population of origin using Bayesian clustering techniques (Pritchard et al. 2000). STRUCTURE assumes Hardy-Weinberg equilibrium (HWE) within populations and linkage equilibrium between loci. I used Genepop 3.4 (Raymond & Rousset 1995) to test for deviations from Hardy-Weinberg equilibrium (HWE). For loci with fewer than four alleles, exact p-values were computed using the complete enumeration method (Louis & Dempster 1987), and for loci with more than four alleles the Markov chain method (dememorization 1,000; batches 100; iterations per batch 1,000) was used (Guo & Thompson 1992). Using Genepop 3.4, I used linkage disequilibrium tests to identify nonrandom association between alleles of different loci using the Markov chain method.

I assigned bears sampled from the corridor and from other populations to a cluster or population based on their genotypes, without regard to where the samples were collected, using the program STRUCTURE. I used the admixture model, which assumes that each individual draws some proportion of membership (q) from each of K clusters.

Allele frequencies were assumed independent and analyses were conducted with a 100,000 burn-in period and 100,000 repetitions of Markov Chain - Monte Carlo.

I conducted population-assignment tests using STRUCTURE at two levels. For comparative purposes, the first analysis was conducted on the statewide level with individuals sampled from the nine populations and the corridor ($K = 8$ clusters). A second analysis was conducted on a regional level; only individuals sampled from Ocala, Osceola, and the corridor were included ($K = 2$ clusters). An individual bear was placed into a cluster if $q > 0.85$ for that cluster. If $q > 0.40$ for both clusters, the genotype profile indicated mixed ancestry, suggesting the individual may be an offspring of a mating between the two clusters. I plotted the assigned individuals on a map of north-central Florida using ArcGIS 8.1.2 to examine the geographic patterns of congruence (Ormsby et al. 2001).

Results

A total of 598 hair samples was collected at 44 out of 86 hair snare sites within the Osceola-Ocala corridor (Fig. 5). Overall, trap success for hair snares was 23.33%, with substantially lower trapping success towards the center of the corridor (Fig. 6). Within the corridor, 31 black bears were sampled at 50 locations; 11 of the 31 bears were sampled at multiple locations. Only three of the 31 bears sampled in the corridor were females, and these were within 20 km of the Ocala population.

There were no significant departures from HWE for any locus or population ($p > 0.05$), and the linkage disequilibrium test indicated that 10% of loci pairings had significant nonrandom associations ($p \leq 0.05$). These significant loci pairings may be a result of nonrandom mating, sampling bias, recent admixture, or genetic drift (Frankham et al. 2002).

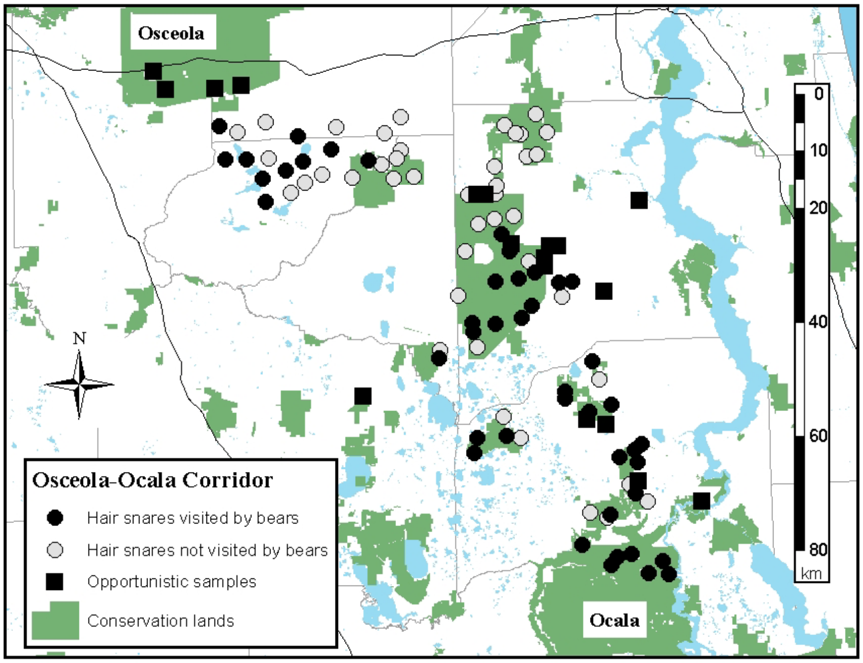

Figure 5. Locations of samples collected in the Osceola-Ocala corridor. Dark circles represent hair snares visited by bears, whereas open circles represent hair snares not visited by bears. Squares represent samples collected opportunistically.

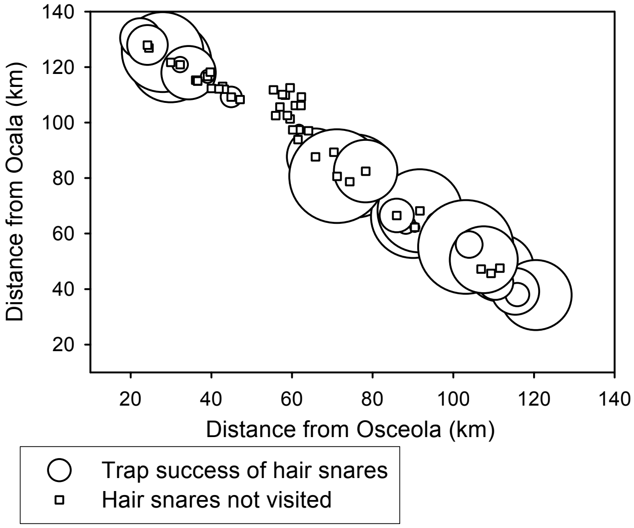

Figure 6. Bubble plot of trap success in the Osceola-Ocala corridor. The size of the bubble represents the number of bear visits relative to the number of trapping sessions. Squares represent hair snares not visited by bears. The distance was estimated as the linear distance from the population's centroids (the harmonic mean of sample locations in the Ocala and Osceola populations) to the hair snare sites in the corridor.

For the statewide analysis, the 31 individuals sampled in the corridor, along with the 308 individuals sampled statewide, were analyzed using STRUCTURE. The 10 predefined populations had 79% or more of their membership assigned to a single cluster. Individuals sampled from Ocala, St. Johns and the Osceola-Ocala corridor were assigned to the same cluster ($q > 0.85$), suggesting no significant genetic differentiation among these three populations (Table 3).

Table 3. Assignment of individuals using the Bayesian clustering technique using the program STRUCTURE (Pritchard et al. 2000) without any prior information on population of origin. The average proportion of membership for individuals sampled in predefined populations for each of 8 clusters (highest average proportion of membership assigned to a single cluster is in bold italics). Sample sizes are in parentheses.

	Average proportion of membership in 8 clusters							
Population	1	2	3	4	5	6	7	8
Apalachicola (40)	***0.846***	0.088	0.013	0.006	0.021	0.007	0.011	0.009
Aucilla (9)	0.121	***0.835***	0.008	0.009	0.007	0.006	0.006	0.008
Big Cypress (41)	0.012	0.006	***0.887***	0.006	0.010	0.021	0.045	0.012
Chassahowitzka (29)	0.002	0.004	0.004	***0.977***	0.003	0.004	0.004	0.003
Eglin (40)	0.010	0.006	0.010	0.005	***0.947***	0.007	0.006	0.010
Highlands/Glades (28)	0.003	0.003	0.024	0.004	0.003	***0.954***	0.006	0.003
Ocala (40)	0.006	0.005	0.010	0.004	0.008	0.011	***0.947***	0.009
Corridor (31)	0.008	0.007	0.009	0.006	0.009	0.008	***0.848***	0.105
Osceola (41)	0.019	0.016	0.035	0.014	0.015	0.020	0.085	***0.796***
St. Johns (40)	0.019	0.021	0.024	0.014	0.009	0.035	***0.853***	0.025

For the regional analysis, I conducted population-assignment tests including only individuals sampled from Ocala, Osceola, and the corridor, and estimated the proportion of membership of each bear to the two clusters (Ocala and Osceola). All bears sampled in Ocala were assigned to cluster 1 ($q > 0.90$), indicating that no immigrants from Osceola were sampled in Ocala. Bears sampled in Osceola had ancestry in both clusters, with 36 of the 41 bears assigned to cluster 2 ($q > 0.85$). Two individuals sampled in Osceola (OS31 and OS41) were assigned to cluster 1 ($q > 0.99$), suggesting they were immigrants from Ocala. Additionally, two bears sampled in the Osceola population

(OS14 and OS20) were assigned to both clusters (q > 0.40), indicating that these individuals were offspring from an Osceola and Ocala mating (Fig. 7).

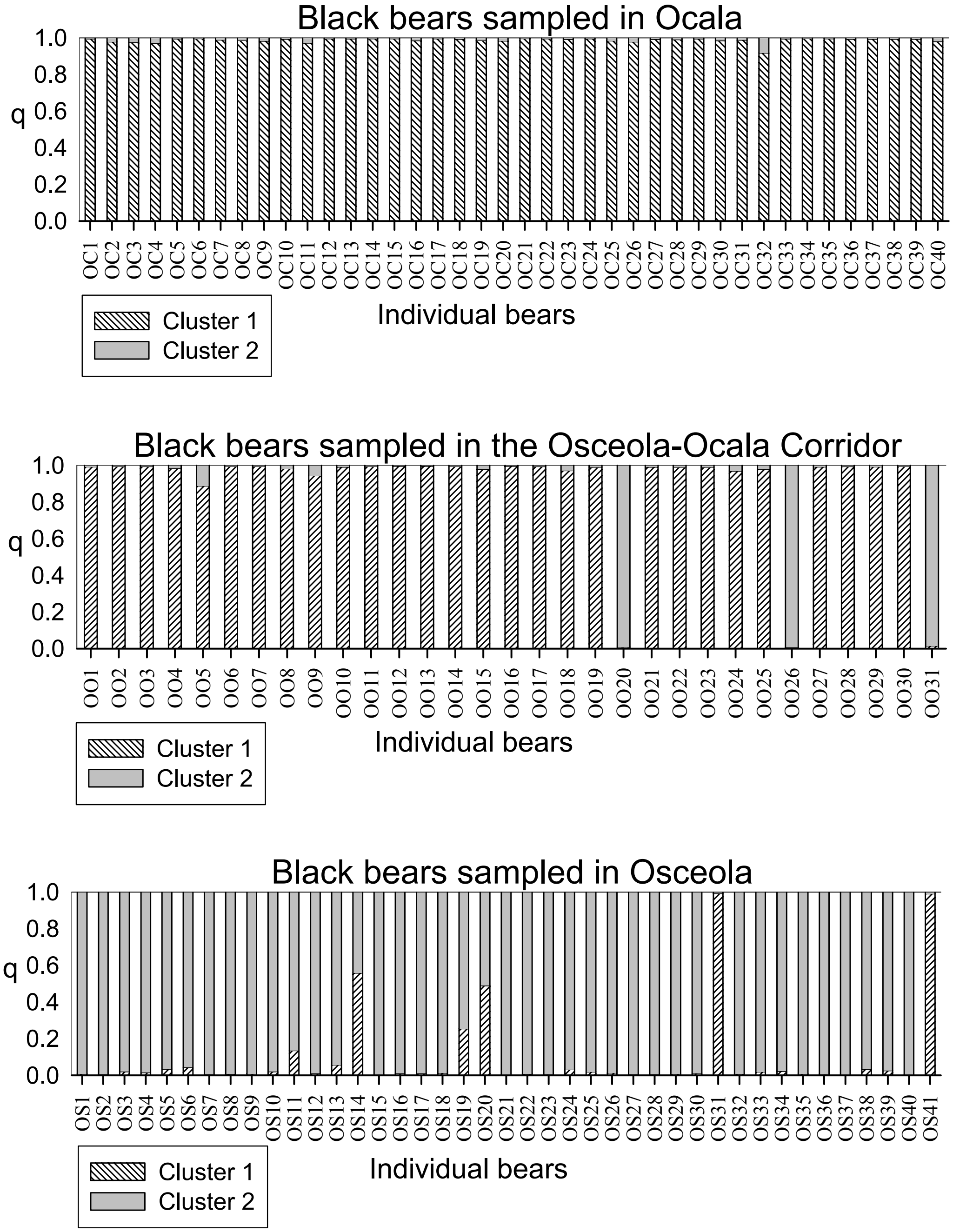

Figure 7. Assignment of black bears to a population of origin without regard to sample locations using STRUCTURE (Pritchard et al. 2000). Each individual bear sampled in Ocala, Osceola and the corridor is represented by a single vertical line, which is partitioned into segments that represent that individual's proportion of membership (q) in the two clusters.

Of the 31 black bears sampled in the corridor, 28 were assigned to cluster 1 (Ocala) with $q > 0.85$, suggesting a predominately one-way movement by bears from Ocala into the corridor. However, there were three individuals sampled in the corridor (OO20, OO26, and OO31) that were assigned to cluster 2 ($q > 0.98$), suggestive of origins in the Osceola population (Fig. 7). The sample locations of these bears plotted on a map of north-central Florida revealed a spatial pattern in the distribution of genotypes with limited mixing of Osceola and Ocala bears within the corridor (Fig. 8).

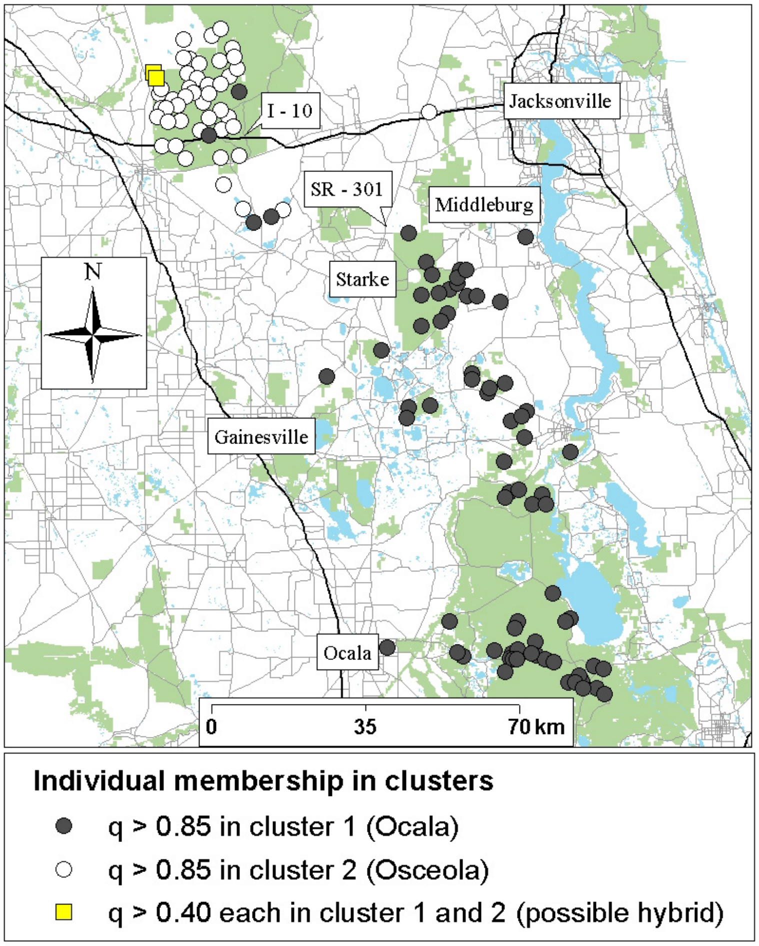

Figure 8. Spatial pattern of the proportion of membership (q) for bears sampled in Osceola, Ocala and the Osceola-Ocala corridor using the program STRUCTURE (Pritchard et al. 2000). For Osceola and Ocala, 41 and 40 individuals respectively, are displayed. Within the Osceola-Ocala corridor, 31 bears sampled at 50 different locations are displayed. Black bears with $q > 0.85$ in a cluster are labeled as belonging to that cluster. Individuals with mixed ancestry have $q > 0.40$ in both clusters.

Discussion

The role of corridors in conservation planning has been controversial, due largely to the lack of empirical studies evaluating the effectiveness of corridors (Simberloff & Cox 1987; Simberloff et al. 1992; Rosenberg et al. 1997; Niemela 2001). Despite the paucity of data supporting the function of corridors, many conservation biologists argue that corridors should be reestablished or maintained where such connectivity occurred in the recent past (Noss & Harris 1986; Noss 1987; Beier & Noss 1998). Nowhere has the corridor controversy been more intense than in the state of Florida (Noss 1987; Simberloff & Cox 1987; Simberloff et al. 1992). Plans for a regional network of connected lands have been undertaken with little knowledge of the efficiency of corridors in facilitating movements of animals (Noss & Harris 1986; Hoctor et al. 2000; Larkin et al. 2004). The effectiveness of corridors in connecting carnivore populations is a question of considerable conservation importance. Large carnivores provide flagship and umbrella mechanisms for conservation and are sensitive to the effects of habitat fragmentation (Noss et al. 1996; Woodroffe & Ginsberg 1998). Thus, corridors that provide connectivity among large carnivore populations are likely to be beneficial to other species with smaller home ranges.

I documented the presence of black bears throughout the Osceola-Ocala corridor, indicating that perhaps a small population inhabits this area. Male black bears disperse long distances due to competition for resources (Rogers 1987; Schwartz & Franzmann 1992), and the substantial disparity in the sex ratio of bears (28 males, 3 females) sampled in the Osceola-Ocala corridor suggests that the corridor is primarily used as a conduit for gender-biased dispersal.

For a dispersal corridor to be functional, the distance between populations should be within dispersal capabilities of the focal species. The average dispersal distance observed for male black bears is roughly half the distance of the Osceola-Ocala corridor (Alt 1979; Rogers 1987; Maehr et al. 1988; Schwartz & Franzmann 1992; Wooding & Hardisky 1992; Wertz et al. 2001; Lee & Vaughan 2003). However, black bears can move great distances, occasionally dispersing > 100 km (Alt 1979; Rogers 1987; Maehr et al. 1988). Long-distance dispersal is difficult to measure and often underestimated (Koenig et al. 1996). However, the range of dispersal distances for black bears suggest that it is possible for bears to travel the length of the Osceola-Ocala corridor.

The effectiveness of a dispersal corridor would require that animals use the area for natal dispersal, seasonal migration, foraging or searching for a mate (Harris & Scheck 1991; Noss 1993; Rosenberg et al. 1997; Hess & Fischer 2001). Many studies suggest that there are directional patterns of dispersal related to the presence of habitat suitable for dispersal corridors (Smith 1993; Poole 1997; McLellan & Hovey 2001; Wertz et al. 2001; Maehr et al. 2002; Lee & Vaughan 2003). For instance, bears used the Osceola-Ocala corridor for dispersal because there is available habitat in which to disperse. Additionally, the presence of the bears, including some females, in multiple locations suggests that some individuals may be residents with home ranges within the corridor. Although there were only three females sampled, a reproducing population within the corridor would better facilitate movement among populations (Noss 1993; Noss et al. 1996; Rosenberg et al. 1997; Beier & Noss 1998).

Most individuals were assigned to the population in which they were sampled, verifying the validity of using population-assignment tests for Florida black bears (Table

3). However, two male bears sampled in Osceola had genotype combinations most consistent with those assigned to Ocala. Additionally, two individuals had genotypes assigned as hybrids, indicating that bears born in Ocala may have bred successfully in Osceola. There is a possibility that some bears identified as immigrants within the Osceola population may be nuisance bears that were translocated from Ocala. However, the relatively small number of documented translocations and the known fates of most of these translocated bears suggests that one or both bears sampled in Osceola that were assigned to Ocala are dispersers from the latter population that used the corridor for movement.

Most bears sampled within the Osceola-Ocala corridor were assigned to Ocala, with a predominantly unidirectional pattern of movement. There was a limited mixing of Ocala-assigned individuals with Osceola-assigned individuals in one area of the corridor (Fig. 8). Three of the Ocala-assigned bears were previously sampled in the Ocala population; these are clear examples of long-distance dispersal (30-100 km) into the corridor and further validate the accuracy of assignment tests. The use of the Osceola-Ocala corridor by bears has increased in recent years (J. Garrison, pers. comm.), a pattern similar to recolonization rates of black bears in the Trans-Pecos (Mexico-Texas border) (Onorato & Hellgren 2001) and red squirrels (*Sciurus vulgaris*) in Scotland (Hale et al. 2001). Expansion of the Ocala population into the Osceola-Ocala corridor likely will continue as long as habitat is available and there are no significant barriers to movement.

The spatial pattern of trap success of the hair snares (Fig. 5) and assignment tests (Fig. 8) indicated a limited gap in connectivity. This gap may have been caused by a significant habitat bottleneck caused by residential development and a four-lane highway (S.R. 301). Development near the city of Starke, the expansion of unincorporated areas of Jacksonville (especially near Middleburg) and extensive surface mines in those areas may also have contributed to a break in connectivity (Hoctor 2003). Extensive habitat alteration by residential and industrial developments have been identified as potential deterrents for bear dispersal (McLellan & Shackleton 1988; Maehr et al. 2003), and this may be the situation for bears in the Osceola-Ocala corridor. However, there remains a possibility that bears have not had sufficient time to recolonize these areas.

Only three bears with Osceola genotypes were sampled south of the interstate highway (I-10), despite the large population of bears (Osceola) just north of I-10. One of those three bears also was sampled north of I-10 (FWC, unpublished data) suggesting that while the highway is not a complete barrier to movement, it may represent a significant filter allowing only a few individuals to cross successfully. Large, high-speed highways have been known to alter movement patterns of bears (Brody & Pelton 1989; Wertz et al. 2001; Proctor et al. 2002; Kaczensky et al. 2003). My results were consistent with the hypothesis that high-speed interstate highways can significantly reduce movements of Florida black bears.

Roads can have a more significant effect on bear movements within the corridor. From 1979 to 2002, 32 bears (28 males, 3 females, 1 unknown) were documented as killed on highways within the Osceola-Ocala corridor. High mortality rates of dispersing carnivores are not uncommon (e.g., San Joaquin kit foxes [*Vulpes macrotis mutica*]: Koopman et al. 2000; tigers [*Panthera tigris*]: Smith 1993; brown bears: McLellan & Hovey 2001; and black bears: Alt 1979, Schwartz & Franzmann 1992). Clearly, maintaining or restoring effective connectivity between the Osceola and Ocala populations will require measures to reduce mortality of dispersing animals.

Taken together, my results show that the Osceola-Ocala corridor is functional. My study provides one of the first empirical evaluations of the effectiveness of a regional corridor in connecting populations of a large carnivore. The methods used in my study provide a framework for using non-invasive sampling and genetic analysis for evaluating the effectiveness of corridors in providing demographic and genetic connectivity between wildlife populations. These techniques allow researchers to identify the genetic signatures of connectivity by identifying immigrants and hybrids, and these methods should be useful in evaluating the effectiveness of other potential corridors for connecting wildlife populations.

Conclusion

My results suggest that the Ocala and Osceola black bear populations were recently re-connected, primarily through unidirectional movement of bears from Ocala to Osceola, and that some of the dispersers may have successfully reproduced. Moreover, I found a small black bear population currently inhabits the Osceola-Ocala corridor itself. Based on these results, I conclude that the Osceola-Ocala corridor is functional, and provides genetic and demographic connectivity between Ocala and Osceola black bear populations. The connection of the Osceola and Ocala populations allows gene flow between these populations through male-mediated dispersal, the maintenance of metapopulation structure, and may increase population viability. However, increasing development pressure in this regional corridor may thwart functional connectivity of these populations if the habitat within the corridor is not protected.

Maintaining or restoring connectivity may require multiple strategies including encouraging recolonization of the corridor by maintaining high densities in the source populations, minimizing habitat loss and fragmentation, and managing for a high quality habitat. Very short distances separate most of Osceola and Ocala bears within the corridor; these breaks in connectivity should be minimized such that a bear could cross the area in a single dispersal event (Beier & Loe 1992). However, sufficient habitat for recolonization requires easements, purchasing conservation lands, fostering agreements with private landowners, and reducing human activity (Beier 1995; Duke et al. 2001). Providing connectivity may also require retrofitting highways to allow safe passage of bears (Foster & Humphrey 1995).

I found that the use of non-invasive hair snares and population-assignment tests could serve as an appropriate and efficient method for evaluating the effectiveness of a regional corridor. Although my study was not replicated, it did provide useful insights into the functionality of a regional corridor for large carnivores. A fully replicated, experimental approach is rarely practical in conservation settings. Design limitations aside, I do view consistent use of a corridor as sufficient evidence to justify the conservation value of these areas (Beier & Noss 1998). Given the rapid pace of development in Florida, the connection of populations with corridors may be the best option in mitigating the adverse impacts of habitat fragmentation on black bears and other wildlife.

CHAPTER 4
CONCLUSIONS AND MANAGEMENT RECOMMENDATIONS

In my study, I used microsatellite analysis of complete 12-locus genotypes of 339 bears to investigate the conservation genetics of Florida black bear populations (Appendix D, Table 5). Allele frequencies for these bears varied substantially across 10 study areas (Appendix D, Table 6). I used these microsatellite data to investigate the genetic consequences of habitat fragmentation and to examine the functionality of the Osceola-Ocala corridor.

Conclusions

Genetic variation is an important consideration for the long-term survival and adaptation of Florida black bears. My results indicate that most Florida black bear populations had genetic variation within the range reported for other bear populations (Appendix C, Table 3). However, Florida black bear populations with < 200 individuals were characterized by low levels of genetic variation. The level of genetic variation within the Chassahowitzka and Highlands/Glades populations are among the lowest reported for any species or population of bears (Appendix C, Table 3). The reduction of genetic variation in the Chassahowitzka and Highlands/Glades populations could adversely influence evolutionary potential and increase inbreeding depression, which may lead to the eventual extirpation of these populations.

My results indicated low levels of gene flow among most populations of the Florida black bear. However, there was a high level of gene flow between the St. Johns and

Ocala populations, and for genetic management, these populations could be considered as the same population unit.

Genetic differentiation among Florida black bear populations is greater than that reported for other bear populations separated by greater geographic distances (Paetkau et al. 1998b; Paetkau et al. 1999; Waits et al. 2000; Lu et al. 2001; Saitoh et al. 2001; Warrillow et al. 2001; Marshall & Ritland 2002). Additionally, there was no significant pattern of isolation by distance in Florida black bear populations. This pattern has been observed among other populations of bears (Paetkau et al. 1997). Roads with high traffic volume and anthropogenic development apparently act as barriers to gene flow among populations of bears in Florida.

Data presented in Chapter 3 clearly indicate that the Osceola-Ocala corridor provides demographic and genetic connectivity between two of the largest bear populations via unidirectional movement of bears from Ocala into Osceola. I documented the presence of bears in Osceola with Ocala genotypes and others that may be Osceola-Ocala hybrids. There was a preponderance of male bears within the Osceola-Ocala corridor, suggesting that the corridor is primarily used as a conduit for dispersal. The recolonization of the corridor likely will continue as long as sufficient habitat is available and there are no significant barriers to movement. However, there were some gaps in black bear distribution within the corridor, possibly due to barriers such as residential and industrial development. The methods used in my study provide a framework for evaluating functionality of corridors for connecting other wildlife populations.

Management Recommendations

Efforts should be made to restore historic levels of genetic variation within Florida black bear populations. For the smaller, more isolated populations (i.e., Chassahowitzka and Highlands/Glades) to persist into the foreseeable future, it may be necessary to increase levels of genetic variation within these populations.

I recommend two ways to increase or maintain genetic variation in Florida black bear populations. The first is to increase the size of the populations, and to prevent further loss and fragmentation of their habitat. Efforts should be made to maintain or increase populations to > 200 individuals to prevent substantial loss of genetic variation. The increase in population size would minimize the loss of genetic variation due to genetic drift, and would increase the number of dispersers, potentially increasing the level of gene flow among populations.

My second recommendation is to increase gene flow among populations. This may be accomplished in two ways: genetic augmentation and the connection of populations with corridors. Genetic augmentation would require the translocation of bears among populations. For augmentation to be successful, these bears must mate with members of the target population.

The Florida Fish and Wildlife Conservation Commission has a policy that requires the movement of nuisance bears among populations. A study is needed to determine the fate and reproductive success of these translocated bears. If the findings suggest that translocated nuisance bears successfully breed, this method could be used to genetically augment populations. Translocation of pregnant female bears may be a better option than nuisance bears because they have a higher probability of staying in the area where they are released (Eastridge & Clark 2001). Additionally, the stocking of bears in the Big

Bend of Florida (north of Chassahowitzka and east of Aucilla) would increase the probability of gene flow into the Chassahowitzka and Aucilla populations (Wooding & Roof 1996).

Gene flow among populations via natural dispersal would require the connection of populations with conservation corridors. This method is preferred because it would restore historical connectivity, increase probability of long-term persistence, and maintenance of metapopulation structure. However, little habitat that could potentially serve as corridors is available because of the high rate of commercial and residential development throughout much of the state of Florida.

The Osceola-Ocala corridor may be the only corridor that can provide demographic and genetic connectivity of the Florida black bear. As noted above, this corridor is functional, and efforts should be made to enhance the quality of habitat and minimize the effects of potential barriers. The protection and conservation of lands within the Osceola-Ocala corridor will be needed to ensure functional connectivity between these populations. The large number of landowners requires a consortium to manage these lands effectively. Management actions to reduce mortality and increase safe movement across highways also may include the installation of wildlife underpasses and/or overpasses (Foster & Humphrey 1995; Roof & Wooding 1996). Additionally, a reproducing population within the Osceola-Ocala corridor would provide a better means of facilitating movement of bears between the Osceola and Ocala populations. Therefore, efforts should be made to encourage female recolonization of the corridor.

Recommendations for Further Research

Genetic monitoring of Florida black bear populations is needed to examine changes in levels of genetic variation over time. These investigations could be coordinated with the statewide population monitoring program of the Florida Fish and Wildlife Conservation Commission (Eason et al. 2001).

A relatedness analysis using microsatellites would help clarify the relationships among individuals within a populations (Schenk et al. 1998; Spong et al. 2002). This method could be used to create a pedigree of sampled individuals in a population, thereby determining the levels of inbreeding.

A comprehensive mitochondrial DNA (mtDNA) study is needed for a better understanding of the genetic status of these populations. These investigations could better elucidate female dispersal and population structure.

Finally, comprehensive demographic studies are needed to conduct a population viability analysis (PVA). These analyses could be used to predict the impact of further habitat fragmentation and loss on the viability of Florida black bear populations.

APPENDIX A
HISTORY OF THE FLORIDA BLACK BEAR

General

The American black bear (*Ursus americanus*) has maintained a broad distribution throughout much of its history, and fossil evidence indicates that black bears have been present in North America for at least 3 million years (Kurten & Anderson 1980). The Florida black bear (*U. a. floridanus*) is one of three subspecies of North American black bears, and was first described in Key Biscayne by Merriam (1896). The Florida black bear historically ranged throughout Florida and southern portions of Georgia, Alabama, and Mississippi (Hall 1981) (Fig. 9).

Black bears have large body size and need considerable expanses of land to maintain home ranges. They use a wide variety of habitats, including pine flatwoods, hardwood swamp, cypress swamp, cabbage palm forest, sand pine scrub, and mixed hardwood hammock (Maehr et al. 2001). The omnivorous diet of black bears includes mostly plant and some animal material (Maehr & Brady 1984).

Seminole Indians hunted black bears in Florida, using meat, skin and fat for various consumptive, ornamental, and traditional purposes (Bartram 1980; Bakeless 1989). In the past, cattle ranchers and beekeepers considered the Florida black bear a nuisance; consequently, the shooting and poisoning of bears was common (Hendry et al. 1982). Hunting for sport and food was intensive and unregulated prior to 1950 (Cory 1896). Regulated bear hunting was initiated in Florida in 1950 (Wooding 1993), but was stopped in most counties in 1971 and in all counties in 1993 (Maehr et al. 2001).

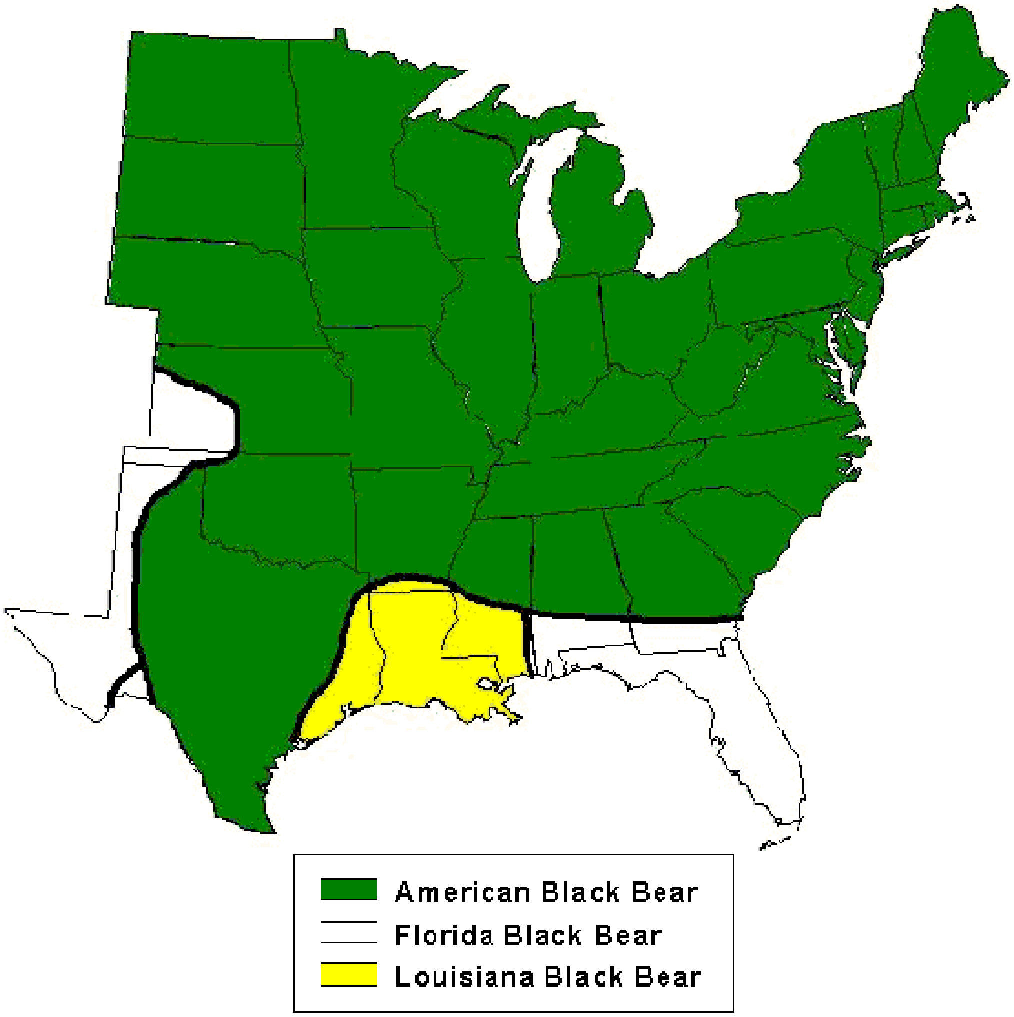

Figure 9. Historic distribution of black bears in the southeastern United States (after Eason 1995)

The greatest reduction of Florida black bear was a result of extensive habitat loss and fragmentation during the 19th century (Wesley 1991; Pelton & Van Manen 1997). Forests were cleared for timber and agriculture, wetlands were drained, and large areas were mined (Myers & Ewel 1991). In the 1970's, there were only an estimated 300-500 bears in Florida (McDaniel 1974; Brady & Maehr 1985). Under the assumption that bears once occupied nearly all the state's land area (34.5 million acres), they have been eliminated from approximately 83% of their range (Wooding 1993).

Currently, Florida black bears occur in several populations that are mostly relegated to public lands within Florida (Apalachicola, Aucilla, Big Cypress, Chassahowitzka, Eglin, Highlands/Glades, Ocala, Osceola, and St. Johns), Georgia (Okefenokee), and Alabama (South Alabama) (Fig. 10).

Regulations

The Florida Game and Freshwater Fish Commission classified the Florida black bear as a threatened species in most Florida counties in 1974 (Wooding 1993). Florida black bears in Georgia are considered a game animal and are subject to a limited hunting season, but are listed as an endangered species on the state-level in Alabama (Pelton & Van Manen 1997; Kasbohm 2004).

The U.S. Fish and Wildlife Service (USFWS) was petitioned in 1990 to list the Florida black bear as a federally threatened species under the Endangered Species Act of 1973. The USFWS findings of 1991 concluded that the petition to list the Florida black bear was warranted, but was precluded by work on other species having higher priority for listing (Wesley 1991). A subsequent reexamination by the USFWS in 1998 concluded that listing the Florida black bear as federally threatened or endangered was not warranted based on existing data (Bentzien 1998). This decision was challenged in court by several conservation organizations, and the USFWS was ordered to clarify the documentation of the adequacy of existing regulatory mechanisms to protect the Florida black bear. The findings concluded that the existing regulatory mechanisms were sufficient and that listing the Florida black bear as a threatened or endangered species was not warranted (Kasbohm 2004).

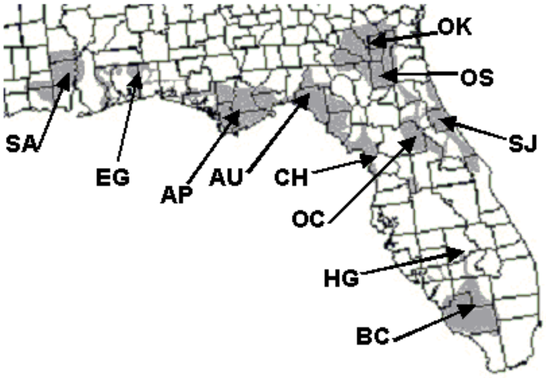

Figure 10. Current populations of the Florida black bear (*Ursus americanus floridanus*). Abbreviations are as follows: SA (South Alabama), EG (Eglin), AP (Apalachicola), AU (Aucilla), CH (Chassahowitzka), OC (Ocala), HG (Highlands/Glades), BC (Big Cypress), SJ (St. Johns), OS (Osceola), and OK (Okefenokee) (after Pelton and van Manen 1997).

APPENDIX B
MICROSATELLITE ANALYSIS

Microsatellites are a class of nuclear DNA markers that have a rapid mutation rate and are ideal for studies of genetic consequences of habitat fragmentation (Lindenmayer & Peakall 2000). Microsatellites consist of a variety of tandem repeat loci that involve a base motif of 1-6 base pairs repeated up to 100 times. Microsatellites are abundant, widely disbursed in eukaryotic genomes, and are highly polymorphic. Individual loci are amplified using polymearse chain reaction (PCR). This allows resolution of alleles that differ by as little as 1 base pair, and several loci can be analyzed simultaneously (Hedrick 2000).

Microsatellite analysis has frequently been used in conservation studies for estimating within-population genetic variation and gene flow among populations of black bears (*Ursus americanus*) (Paetkau & Strobeck 1994; Saitoh et al. 2001; Warrillow et al. 2001; Marshall & Ritland 2002; Csiki et al. 2003), brown bears (*U. arctos*) (Kohn et al. 1995; Taberlet et al. 1997; Paetkau et al. 1998a; Paetkau et al. 1998b; Waits et al. 2000; Miller & Waits 2003), polar bears (*U. maritimus*) (Paetkau et al. 1995; Paetkau et al. 1999), spectacled bears (*Tremarctos ornatus*) (Ruiz-Garcia 2003) and giant pandas (*Ailuropoda melanoleuca*) (Lu et al. 2001). Microsatellite analysis has also been used to estimate population density of black and brown bear populations using mark-recapture models (Woods et al. 1999; Mowat & Strobeck 2000; Boerson et al. 2003).

APPENDIX C
GENETIC VARIATION AMONG BEAR POPULATIONS

Table 4. Microsatellite genetic variation in bear populations. Sample size (n), observed average heterozygosity (H_O), expected average heterozygosity (H_E), mean alleles per locus (A), and number of loci used in the study (L).

Species	**Population**	**n**	**H_O**	**H_E**	**A**	**L**	**Citation**
Florida black bear	Apalachicola	40	0.690	0.708	5.92	12	my study
(Ursus americanus floridanus)	Aucilla	9	0.556	0.616	3.83	12	my study
	Big Cypress	41	0.642	0.650	5.50	12	my study
	Chassahowitzka	29	0.287	0.271	2.25	12	my study
	Eglin	40	0.613	0.537	4.08	12	my study
	Highlands/Glades	28	0.327	0.384	2.75	12	my study
	Ocala	40	0.579	0.610	4.75	12	my study
	Osceola	41	0.705	0.713	6.67	12	my study
	St. Johns	40	0.650	0.663	5.58	12	my study
	Osceola/Ocala Corridor	31	0.629	0.629	5.42	12	my study
	Mobile River	13	0.390	0.350	2.88	7	Warrilow et al. 2001
	South Alabama	19	0.316	N/A	2.88	8	Edwards 2002
	Okefenokee	39	0.663	N/A	6.13	8	Dobey 2002
	Osceola	37	0.679	N/A	5.75	8	Dobey 2002
Louisiana black bear	Pointe Coupee Parish	16	0.546	0.686	5.60	5	Csiki et al. 2003
(Ursus americanus luteolus)	Southern Coastal Louisiana	20	0.380	0.428	4.20	5	Csiki et al. 2003
	Tensas River	14	0.530	0.480	3.57	7	Warrilow et al. 2001
	Upper Atchafalaya Basin	20	0.550	0.660	6.00	7	Warrilow et al. 2001
	Tensas River	36	0.576	N/A	3.80	12	Boersen et al. 2003
	Lower Atchafalaya Basin	26	0.420	0.540	6.14	7	Warrilow et al. 2001
American black bear	North Carolina (treatment)	66	0.667	N/A	6.00	10	Thompson 2003
(Ursus americanus)	North Carolina (control)	115	0.664	N/A	6.90	10	Thompson 2003
	Ozarks	13	0.723	0.761	5.80	5	Csiki et al. 2003
	Ouachitas	6	0.733	0.754	4.60	5	Csiki et al. 2003

Table 4. Continued

Species	**Population**	**n**	**H_O**	**H_E**	**A**	**L**	**Citation**
American black bear	White River	18	0.447	0.317	1.80	5	Csiki et al. 2003
(Ursus americanus)	Minnesota	10	0.576	0.772	5.60	5	Csiki et al. 2003
	Cook County	36	0.540	0.770	8.71	7	Warrilow et al. 2001
	Ozarks	14	0.540	0.730	6.00	7	Warrilow et al. 2001
	Ouachitas	6	0.560	0.730	4.86	7	Warrilow et al. 2001
	White River	22	0.380	0.330	2.43	7	Warrilow et al. 2001
	La Mauricie	32	0.783	0.800	8.75	4	Paetkau & Strobeck 1994
	Banff (West Slope)	31	0.801	0.800	8.00	4	Paetkau & Strobeck 1994
	Terra Nova	23	0.360	0.360	2.25	4	Paetkau & Strobeck 1994
	West Slope	116	0.800	0.806	9.50	8	Paetkau et al. 1998b
	Newfoundland Island	33	0.427	0.414	3.00	8	Paetkau et al. 1998b
	Nimpkish	19	N/A	0.621	4.40	10	Marshall et al. 2002
	Hawkesbury Island	20	N/A	0.699	5.70	10	Marshall et al. 2002
	Gribbell Island	16	N/A	0.664	5.40	10	Marshall et al. 2002
	Princess Royal Island	50	N/A	0.707	6.50	10	Marshall et al. 2002
	Roderick Island	11	N/A	0.668	4.80	10	Marshall et al. 2002
	Pooley Island	10	N/A	0.692	5.00	10	Marshall et al. 2002
	Yeo Island	10	N/A	0.725	5.10	10	Marshall et al. 2002
	West of Hawkesbury	6	N/A	0.724	4.20	10	Marshall et al. 2002
	East of Princess Royal	21	N/A	0.747	6.30	10	Marshall et al. 2002
	North of Roderick	13	N/A	0.673	6.60	10	Marshall et al. 2002
	Don Peninsula	23	N/A	0.667	5.90	10	Marshall et al. 2002
	Terrace	17	N/A	0.793	7.50	10	Marshall et al. 2002
brown bear	NN	29	0.660	0.660	5.50	19	Waits et al. 2000
(Ursus arctos)	NS	108	0.660	0.660	6.20	19	Waits et al. 2000
	M	88	0.650	0.660	5.80	19	Waits et al. 2000

Table 4. Continued

Species	**Population**	**n**	**H_O**	**H_E**	**A**	**L**	**Citation**
	S	155	0.710	0.660	6.80	19	Waits et al. 2000
brown bear	Kluane	50	0.788	0.761	7.38	8	Paetkau et al. 1998b
(Ursus arctos)	Richardson Mountains	119	0.766	0.755	7.50	8	Paetkau et al. 1998b
	Brooks Range	148	0.774	0.749	7.63	8	Paetkau et al. 1998b
	Flathead River	40	0.694	0.694	6.50	8	Paetkau et al. 1998b
	Kushoskim Range	55	0.700	0.682	6.13	8	Paetkau et al. 1998b
	West Slope	41	0.668	0.678	6.38	8	Paetkau et al. 1998b
	East Slope	45	0.644	0.670	7.00	8	Paetkau et al. 1998b
	Paulatuk	58	0.657	0.650	5.75	8	Paetkau et al. 1998b
	Coppermine	36	0.611	0.605	5.75	8	Paetkau et al. 1998b
	Yellowstone	57	0.553	0.554	4.38	8	Paetkau et al. 1998b
	Kodiak Island	34	0.298	0.265	2.13	8	Paetkau et al. 1998b
	Admirality Island	30	0.646	0.628	n/a	17	Paetkau et al. 1998a
	Alaska Range	28	0.759	0.779	n/a	17	Paetkau et al. 1998a
	Baranof and Chicagof Island	35	0.493	0.496	n/a	17	Paetkau et al. 1998a
	Yellowstone	136	N/A	0.560	5.50	8	Miller & Waits 2003
polar bear	Western Hudson Bay	33	N/A	0.670	6.00	16	Paetkau et al. 1999
(Ursus maritimus)	Foxe Basin	30	N/A	0.660	6.00	16	Paetkau et al. 1999
	Davis Strait-Labrador	30	N/A	0.630	6.30	16	Paetkau et al. 1999
	Baffin Bay	31	N/A	0.680	6.30	16	Paetkau et al. 1999
	Kane Basin	30	N/A	0.710	6.70	16	Paetkau et al. 1999
	Lancaster Sound	30	N/A	0.700	6.90	16	Paetkau et al. 1999
	Gulf of Boothia	30	N/A	0.720	6.70	16	Paetkau et al. 1999
	M'Clintock Channel	15	N/A	0.680	5.50	16	Paetkau et al. 1999
	Viscount Melville Sound	30	N/A	0.660	6.30	16	Paetkau et al. 1999
	Norwegian Bay	30	N/A	0.670	6.20	16	Paetkau et al. 1999

Table 4. Continued

Species	Population	n	H_O	H_E	A	L	Citation
	Northern Beaufort Sea	30	N/A	0.700	6.80	16	Paetkau et al. 1999
	Southern Beaufort Sea	30	N/A	0.690	6.40	16	Paetkau et al. 1999
	Chukchi Sea	30	N/A	0.700	6.80	16	Paetkau et al. 1999
	Franz Josef L.- Novaja Z.	32	N/A	0.660	6.70	16	Paetkau et al. 1999
	Svalbard	31	N/A	0.690	6.90	16	Paetkau et al. 1999
	East Greenland	31	N/A	0.690	6.80	16	Paetkau et al. 1999
spectacled bear	Venezula	8	N/A	0.607	2.00	4	Ruiz-Garcia 2003
(Tremarctos oranatus)	Colombia	32	N/A	0.392	2.80	4	Ruiz-Garcia 2003
	Ecuador	42	N/A	0.245	3.00	4	Ruiz-Garcia 2003
Asian black bear	Western Chugoku	52	0.272	0.300	2.00	6*	Saitoh et al. 2001
(Ursus thibetanus)	Eastern Chugoku	24	0.243	0.301	2.50	6*	Saitoh et al. 2001
	Western N. Kinki	66	0.311	0.324	3.33	6*	Saitoh et al. 2001
	Eastern N. Kinki	67	0.445	0.450	4.17	6*	Saitoh et al. 2001
giant panda	Qinling	14	0.570	n/a	3.30	18*	Lu et al. 2001
(Ailuropoda melanoleuca)	Minshan	7	0.580	n/a	3.50	18*	Lu et al. 2001
	Qionglai	15	0.490	n/a	4.30	18*	Lu et al. 2001

*Suite of microsatellite markers different than other studies

APPENDIX D
MICROSATELLITE DATA FOR FLORIDA BLACK BEARS

Table 5. Individual 12-loci genotypes for black bears sampled in Florida, 1989-2003.

Apalachicola	*Loci*											
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
A1	194 200	156 156	211 211	186 186	241 241	187 203	135 157	212 212	155 163	147 147	124 138	239 239
A2	190 198	160 162	211 211	176 188	239 241	187 187	153 153	212 216	151 159	147 155	124 124	243 243
A3	190 198	158 162	215 215	188 190	241 253	187 199	151 157	206 212	157 157	141 149	122 122	239 239
A4	190 198	156 156	215 215	176 182	241 241	187 187	135 157	214 216	159 163	149 151	124 138	239 239
A5	196 200	156 156	209 215	186 190	241 241	187 203	135 155	214 216	163 163	149 149	124 138	239 243
A6	190 202	160 164	209 209	176 186	241 241	185 187	155 157	212 216	159 163	149 155	138 142	239 243
A7	190 198	156 164	211 211	176 176	241 253	187 187	143 157	214 214	155 159	147 155	124 138	231 239
A8	190 194	156 156	211 211	186 188	251 253	187 199	135 157	214 216	159 159	141 149	124 124	231 239
A9	190 190	156 156	207 209	176 176	241 253	203 203	155 155	214 216	155 161	149 155	126 138	239 239
A10	200 200	160 160	215 215	176 182	241 241	203 203	153 155	212 214	161 163	147 149	126 138	243 243
A11	200 202	156 156	209 209	176 190	241 241	185 187	155 155	206 206	159 163	141 149	126 126	239 243
A12	194 200	156 156	209 209	176 176	241 251	187 203	157 157	206 214	159 161	141 147	124 138	239 239
A13	194 194	156 160	209 215	176 190	241 251	187 203	153 157	206 214	155 159	147 147	124 138	239 243
A14	190 196	156 156	209 215	176 186	241 241	203 203	135 157	216 216	163 163	147 149	126 138	239 243
A15	190 200	156 156	215 215	176 188	241 241	187 187	135 157	216 218	159 159	141 155	124 138	239 243
A16	200 202	160 164	209 209	176 182	241 241	203 203	135 155	206 218	163 163	139 155	126 142	239 243
A17	200 200	156 156	209 211	176 188	241 241	185 199	153 155	218 218	159 161	147 149	124 126	239 241
A18	198 200	162 162	211 215	188 190	239 253	187 187	143 157	214 214	155 157	141 147	124 124	243 243
A19	198 200	156 162	207 215	176 190	241 241	187 203	135 143	212 214	157 159	147 155	126 126	239 243
A20	200 202	160 162	207 215	176 186	239 241	187 203	143 153	214 214	151 155	155 155	124 138	239 243
A21	198 202	156 156	215 215	176 186	239 247	187 203	157 157	214 216	151 155	141 149	124 126	239 243

Table 5. Continued

Apalachicola						*Loci*						
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
A22	190 200	156 162	211 215	176 188	241 251	187 199	135 153	212 214	155 159	149 155	124 124	239 243
A23	194 198	156 160	209 215	188 190	241 241	203 203	135 153	206 214	155 159	147 149	124 138	239 239
A24	190 200	156 160	211 215	176 186	239 241	187 187	153 157	212 214	155 159	147 147	122 124	243 243
A25	196 200	156 156	209 209	176 176	241 241	203 203	153 157	214 216	151 163	149 149	124 126	239 243
A26	202 202	156 160	215 215	186 188	241 249	199 199	135 143	214 214	155 155	137 149	124 138	239 239
A27	196 200	160 162	215 215	176 182	239 241	187 199	153 157	214 218	155 159	137 155	124 128	239 243
A28	192 200	156 162	207 215	176 182	239 241	187 203	135 153	214 218	159 163	137 155	128 136	239 243
A29	190 198	158 160	205 211	172 188	241 241	187 199	143 157	206 212	163 163	137 141	122 122	239 243
A30	190 200	160 162	209 211	176 186	241 253	203 203	153 153	212 216	151 155	141 147	122 128	239 243
A31	190 192	156 156	209 215	182 186	241 241	187 187	143 157	214 216	155 155	137 141	124 124	239 239
A32	196 200	156 162	209 211	182 188	239 241	187 187	143 153	212 214	155 163	141 149	124 128	243 243
A33	190 198	156 162	205 209	182 184	241 241	185 187	141 157	212 216	155 157	137 141	124 124	239 239
A34	196 200	162 164	211 211	176 176	241 241	187 199	135 157	214 216	151 159	147 149	128 138	239 239
A35	198 198	156 156	209 215	176 186	239 241	187 203	157 157	216 216	159 159	147 149	124 124	239 239
A36	200 202	156 160	207 215	186 186	241 241	187 199	141 153	212 216	155 159	137 147	124 126	243 243
A37	194 198	156 160	211 215	188 190	241 241	187 203	157 157	206 214	155 159	147 147	122 124	239 243
A38	194 198	160 164	209 215	176 182	241 252	187 203	153 157	212 214	155 159	147 155	124 138	239 243
A39	194 198	156 160	211 215	182 190	241 251	199 203	153 157	214 214	155 163	141 147	124 124	239 243
A40	192 194	162 162	205 215	184 190	241 241	185 187	141 143	212 214	157 157	141 155	124 138	239 239

Table 5. Continued

Aucilla

	Loci											
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
AU1	190 190	156 158	205 215	180 188	235 241	187 187	151 151	206 216	159 163	141 147	122 126	239 239
AU2	198 200	158 162	215 215	180 188	235 241	187 199	143 157	206 206	159 163	137 149	122 126	239 239
AU3	198 198	158 162	205 205	172 176	241 241	187 199	151 151	212 212	163 163	155 155	122 122	239 239
AU4	198 200	158 164	215 215	180 190	235 241	187 187	141 151	212 212	157 157	141 141	122 124	239 239
AU5	198 200	162 162	205 205	172 180	241 241	199 199	143 151	206 212	157 157	147 155	122 122	239 239
AU6	198 200	156 158	205 215	190 190	241 241	191 191	143 151	212 212	157 157	141 149	122 124	239 239
AU7	194 198	156 164	211 215	176 188	241 251	187 199	135 153	212 214	159 159	149 155	124 124	239 243
AU8	190 200	158 164	215 215	180 190	235 241	187 187	141 143	212 212	157 157	141 147	122 124	239 239
AU9	198 200	158 158	207 215	180 188	241 241	187 191	151 151	206 212	157 159	141 141	122 122	239 239

Big Cypress

Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
B1	190 198	164 164	207 207	176 184	253 253	187 199	139 139	212 214	159 163	147 149	134 134	231 243
B2	190 190	152 154	207 213	172 176	241 253	187 199	153 161	212 214	161 163	149 151	134 134	239 239
B3	190 198	152 164	207 207	176 176	253 261	185 199	135 139	212 214	147 163	141 147	134 134	239 239
B4	198 198	154 164	207 215	186 188	235 253	199 199	139 155	214 214	163 163	141 149	134 134	239 243
B5	190 190	156 156	207 207	176 186	249 253	187 199	139 155	212 214	159 159	149 149	122 134	239 247
B6	190 190	156 156	207 215	172 184	241 241	187 199	155 155	210 210	159 161	147 149	134 134	239 243
B7	190 190	156 156	207 215	178 184	241 253	199 199	139 157	212 214	147 163	149 149	126 134	239 243
B8	190 192	152 164	207 215	176 176	253 261	185 199	135 155	214 214	147 163	141 147	134 134	239 239
B9	190 200	152 154	207 207	186 186	241 253	185 187	135 157	212 214	147 159	141 149	122 134	235 239
B10	200 200	152 156	207 207	176 186	235 253	199 199	153 155	212 214	147 159	149 149	134 134	243 243
B11	190 194	156 160	207 215	176 186	235 249	185 199	139 139	212 212	159 163	141 149	122 122	243 243

Table 5. Continued

Big Cypress	*Loci*											
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
B12	190 198	154 156	207 207	176 184	235 253	187 199	139 157	212 214	147 159	149 149	126 126	239 239
B13	190 200	152 152	207 215	176 176	253 259	185 203	139 153	210 212	147 159	143 149	134 134	243 243
B14	190 200	156 160	207 207	176 186	253 253	185 187	139 157	212 212	147 163	147 149	126 126	241 243
B15	190 190	152 156	207 207	178 186	253 253	199 199	153 157	212 214	159 163	147 149	122 134	243 243
B16	190 190	154 156	207 207	176 176	253 253	185 199	139 157	214 214	147 163	141 147	126 134	239 243
B17	190 200	152 154	207 215	176 188	253 253	199 199	139 157	212 212	147 163	141 149	122 134	239 243
B18	190 200	154 160	207 215	176 184	241 253	185 199	135 139	212 212	147 147	149 149	122 134	243 243
B19	190 198	154 154	207 207	176 184	235 253	187 187	155 155	210 214	159 163	149 149	122 122	239 243
B20	190 190	152 156	207 207	176 184	241 241	187 199	155 155	210 212	159 163	149 149	122 134	239 239
B21	190 190	154 160	207 215	176 188	253 253	185 199	135 153	212 214	163 163	149 149	126 134	239 243
B22	190 196	156 158	207 213	176 186	251 253	185 199	135 157	212 214	163 163	141 157	122 134	241 243
B23	190 190	152 160	215 215	176 186	249 253	187 203	139 161	210 214	159 163	149 149	134 134	243 243
B24	190 190	156 164	207 213	176 186	243 249	185 187	139 153	210 212	147 159	149 149	122 126	239 239
B25	190 200	152 152	213 215	176 178	241 253	187 199	139 139	212 212	147 147	147 149	134 134	243 243
B26	192 200	152 164	207 207	176 186	235 261	185 187	135 141	212 214	147 163	149 149	122 126	239 239
B27	190 190	154 154	207 215	176 184	241 253	187 203	135 139	210 212	159 163	149 149	122 126	239 239
B28	190 190	156 164	215 215	176 184	253 253	187 199	153 153	212 214	163 163	149 149	134 134	231 239
B29	190 190	156 160	215 215	186 190	241 253	185 187	157 157	214 216	159 163	141 149	122 134	231 239
B30	198 200	156 164	207 215	176 184	253 253	187 187	139 153	210 212	159 163	149 149	134 134	231 239
B31	190 192	152 152	207 215	176 186	241 253	187 199	139 139	214 214	159 163	149 149	134 134	235 235
B32	190 200	154 156	207 215	184 186	235 253	187 187	139 153	210 214	159 159	149 149	134 134	239 239
B33	190 200	154 164	215 215	176 186	241 253	187 199	139 155	212 214	147 161	141 149	122 134	243 243

Table 5. Continued

Big Cypress

	Loci											
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
B34	190 196	152 156	207 207	176 184	241 253	187 187	157 161	214 214	159 163	149 149	122 126	239 241
B35	190 200	156 164	207 215	186 186	241 253	187 199	135 157	214 214	163 163	147 149	122 134	239 243
B36	190 198	152 154	207 207	176 184	241 241	185 187	139 153	212 214	163 163	147 149	122 122	239 239
B37	190 190	152 156	213 215	184 186	241 253	187 199	155 157	212 212	163 163	147 149	122 126	239 239
B38	190 190	160 160	207 215	176 186	235 241	185 187	139 157	212 214	147 163	149 149	126 126	239 243
B39	194 200	154 156	207 207	184 186	253 253	185 203	155 157	212 212	147 159	149 149	126 134	243 243
B40	190 190	154 156	215 215	172 184	253 253	185 187	139 157	212 214	163 163	147 149	122 134	239 243
B41	194 198	154 156	215 215	184 184	241 241	187 203	139 139	206 212	159 163	141 149	122 128	239 239

Chassahowitzka

Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
C1	198 198	154 156	211 213	172 172	241 247	187 199	137 149	212 212	159 159	149 149	140 140	239 239
C2	198 198	156 156	207 211	172 184	241 241	187 199	139 149	212 212	157 159	141 149	140 140	239 239
C3	198 198	154 156	207 211	172 172	241 247	199 199	137 149	212 212	159 159	141 149	140 140	239 239
C4	198 198	156 156	211 211	172 172	247 247	199 199	137 149	212 212	159 159	141 149	140 140	239 239
C5	190 198	154 156	211 211	172 172	241 241	199 199	137 149	212 212	157 159	141 149	140 140	239 239
C6	198 198	156 156	207 211	172 184	241 247	199 199	139 149	212 212	159 159	149 149	140 140	239 239
C7	198 198	154 156	207 211	172 184	241 241	199 199	139 139	212 212	159 159	149 149	140 140	239 239
C8	198 198	154 156	211 211	172 172	241 247	199 199	149 149	212 212	159 159	149 149	140 140	239 239
C9	198 198	156 156	211 211	172 186	241 247	199 199	149 149	212 212	159 159	141 149	140 140	239 239
C10	198 198	156 156	211 211	184 186	241 247	199 199	139 149	212 212	159 159	149 149	140 140	239 239

Table 5. Continued

Chassahowitzka

	Loci											
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
C11	190 198	156 156	211 211	172 172	241 247	199 199	137 149	212 212	157 159	141 141	140 140	239 239
C12	198 198	156 156	207 211	172 184	241 241	187 199	149 149	212 212	157 157	141 141	140 140	239 239
C13	198 198	156 156	211 211	172 184	241 241	199 199	149 149	212 212	157 159	141 149	140 140	239 239
C14	198 198	156 156	207 211	172 184	241 247	199 199	149 149	212 212	159 159	149 149	140 140	239 239
C15	198 198	154 156	211 211	172 184	241 247	199 199	139 149	212 212	159 159	149 149	140 140	239 239
C16	198 198	156 156	207 211	172 184	247 247	199 199	139 149	212 212	159 159	141 149	140 140	239 239
C17	198 198	156 156	207 211	172 172	241 247	199 199	139 149	212 212	159 159	149 149	140 140	239 239
C18	198 198	156 156	211 211	172 172	241 247	199 199	149 149	212 212	159 159	141 149	140 140	231 239
C19	198 198	154 156	207 211	172 172	241 247	199 199	149 149	212 212	159 159	149 149	140 140	239 239
C20	198 198	154 154	207 211	172 172	247 247	199 199	137 149	212 212	159 159	141 149	140 140	239 239
C21	190 198	156 156	211 211	172 172	241 241	199 199	137 149	212 212	159 159	149 149	140 140	239 239
C22	190 198	156 156	211 211	172 172	247 247	199 199	149 149	212 212	159 159	141 141	140 140	239 239
C23	198 198	154 156	207 211	172 184	241 241	199 199	139 149	210 212	159 159	149 149	140 140	239 239
C24	198 198	156 156	211 211	172 184	241 247	199 199	139 149	212 212	159 159	149 149	140 140	239 239
C25	198 198	156 156	211 211	172 186	241 247	199 199	149 149	212 212	159 163	149 149	140 140	231 239
C26	198 198	154 156	211 211	172 172	241 247	199 199	149 149	212 212	159 159	141 149	140 140	239 239
C27	190 198	154 156	211 211	172 172	241 247	199 199	137 137	212 212	157 159	149 149	140 140	239 239
C28	198 198	154 156	211 211	184 186	241 241	199 199	139 149	212 212	159 159	149 149	140 140	239 239
C29	198 198	156 156	207 211	172 172	247 247	199 199	149 149	212 212	159 163	141 149	140 140	231 239

Table 5. Continued

Eglin	*Loci*											
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
E1	196 200	160 164	215 217	178 190	247 247	187 199	153 157	214 218	163 163	139 141	122 142	239 239
E2	190 196	156 160	215 217	186 190	241 241	187 199	153 155	214 214	155 163	137 139	122 122	239 239
E3	196 200	160 164	217 217	176 176	241 241	187 187	149 155	210 214	159 163	139 139	122 122	239 239
E4	200 202	160 160	215 217	178 190	241 255	187 199	151 155	210 218	163 163	137 149	122 142	239 239
E5	196 202	160 160	215 217	176 186	241 241	187 187	153 155	210 214	155 163	141 141	122 142	239 239
E6	200 200	160 164	215 215	178 186	241 247	187 187	149 153	206 210	159 163	139 141	122 122	239 239
E7	196 200	156 160	209 215	178 190	241 247	187 187	155 155	210 214	163 163	137 139	122 142	239 239
E8	196 200	160 164	215 217	178 186	241 241	187 187	153 155	206 214	159 163	137 141	122 142	239 239
E9	196 202	156 160	215 217	176 176	241 247	187 199	153 155	210 214	155 163	139 141	122 124	239 239
E10	196 196	156 164	209 217	186 190	241 241	187 187	153 153	214 218	163 163	137 139	122 142	239 239
E11	200 200	156 164	215 215	190 190	241 247	199 199	153 157	214 216	163 163	139 141	122 142	239 239
E12	190 200	156 164	215 215	176 186	241 241	187 199	151 153	206 214	159 163	137 137	122 142	239 239
E13	200 202	156 164	215 217	186 190	241 247	187 187	153 155	206 214	155 163	137 139	122 124	239 239
E14	196 196	160 164	215 217	178 190	241 241	187 187	151 153	210 214	163 163	137 139	122 122	239 239
E15	196 202	156 164	215 217	186 190	241 247	187 187	153 153	206 214	155 163	137 141	122 142	239 239
E16	196 200	160 160	215 217	190 190	241 241	187 199	151 153	210 218	155 163	137 139	122 142	239 239
E17	196 200	156 164	215 217	178 190	241 241	187 187	155 155	212 218	163 163	137 139	122 122	239 243
E18	196 200	160 164	215 217	176 186	241 247	187 187	153 155	214 214	163 163	137 139	122 122	239 239
E19	190 196	156 164	215 217	186 190	241 247	187 199	153 153	210 218	163 163	137 139	122 126	239 239
E20	196 202	156 160	215 215	178 190	241 247	187 199	153 153	214 216	163 163	139 141	142 142	239 239
E21	196 200	156 160	215 217	176 186	241 247	187 187	151 153	206 214	159 163	139 141	122 142	239 239
E22	194 196	160 164	215 217	178 190	241 241	187 187	149 155	210 214	163 163	137 137	122 126	239 239

Table 5. Continued

Eglin	*Loci*											
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
E23	196 196	156 156	209 215	186 190	241 241	187 187	151 153	206 214	163 163	137 141	122 142	239 239
E24	196 200	156 164	215 215	178 190	241 241	187 187	153 155	212 214	163 163	139 149	122 122	239 239
E25	196 196	160 164	215 217	178 190	241 241	187 187	153 155	210 218	163 163	137 139	122 122	239 239
E26	196 196	160 164	215 215	176 186	241 247	187 187	149 153	214 214	159 163	137 139	122 122	239 239
E27	196 200	160 164	215 215	176 178	241 247	187 199	135 155	206 214	159 163	139 149	122 142	239 239
E28	198 200	160 160	215 215	190 190	241 241	199 205	153 155	216 218	163 163	139 149	122 122	239 239
E29	196 196	160 164	215 217	176 190	241 241	187 187	149 155	214 214	159 163	139 141	122 142	239 239
E30	196 196	156 164	215 217	178 178	241 241	187 205	153 155	212 218	159 163	137 149	122 126	239 239
E31	196 200	152 160	215 217	176 178	241 241	187 187	155 157	210 214	163 163	137 141	122 122	239 239
E32	196 202	156 160	215 215	176 186	241 241	187 205	149 155	210 218	155 159	139 141	122 122	239 239
E33	190 196	156 164	215 215	186 190	241 247	187 199	153 155	214 218	155 163	139 141	122 142	239 239
E34	200 200	156 160	215 215	178 190	241 241	187 199	157 157	212 216	159 163	137 141	122 122	239 239
E35	200 200	160 160	215 217	176 178	241 253	187 199	135 149	210 214	159 163	139 149	122 142	239 239
E36	196 200	156 164	215 215	176 178	241 247	187 187	153 155	214 214	159 163	137 141	122 122	239 239
E37	196 196	160 164	215 217	178 186	241 241	187 187	151 153	214 214	163 163	137 139	122 122	239 239
E38	196 200	160 164	215 217	176 178	241 253	187 187	149 149	210 210	159 159	139 139	122 122	239 239
E39	196 196	160 160	215 215	176 186	241 247	187 187	149 153	214 214	163 163	137 139	122 122	239 239
E40	196 200	152 164	209 217	178 178	241 247	187 187	149 153	210 218	159 163	137 137	122 122	239 239

Table 5. Continued

Highlands/Glades						*Loci*						
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
H1	190 198	152 156	215 215	184 184	241 255	203 203	139 139	210 212	159 163	141 141	122 122	243 243
H2	190 198	152 156	215 215	176 176	253 253	203 203	139 139	210 212	159 163	141 141	122 134	243 243
H3	190 190	156 156	215 215	176 176	253 255	199 203	139 139	212 212	163 163	141 141	122 122	243 243
H4	198 198	152 156	215 215	176 184	241 255	203 203	139 139	210 210	163 163	141 149	122 122	239 243
H5	190 198	156 156	215 215	184 184	255 255	199 203	139 139	212 212	147 163	141 141	122 122	243 243
H6	190 190	156 156	215 215	184 184	255 255	199 203	139 139	212 212	163 163	141 141	122 134	239 243
H7	190 190	156 156	215 219	176 176	241 253	199 199	139 139	210 210	147 163	141 141	122 122	243 243
H8	190 198	156 156	207 219	184 184	241 255	203 203	139 139	212 212	163 163	141 149	122 122	239 239
H9	190 198	152 152	215 215	176 176	255 255	199 199	139 139	212 212	163 163	141 141	122 122	243 243
H10	190 190	152 156	207 215	178 184	255 255	203 203	139 139	210 212	161 163	141 141	122 122	243 243
H11	190 198	156 156	207 215	176 176	241 241	203 203	139 139	210 212	163 163	149 149	122 122	241 243
H12	190 198	152 156	207 215	176 176	255 255	203 203	139 139	212 212	147 159	141 149	122 122	243 243
H13	190 198	152 156	215 215	176 178	241 241	203 203	139 139	210 212	163 163	141 149	122 122	243 243
H14	190 198	154 156	215 215	176 188	253 253	199 203	139 139	212 214	163 163	141 141	134 134	241 243
H15	190 190	152 156	207 207	176 176	253 255	199 203	139 139	210 210	163 163	141 149	122 122	243 243
H16	190 198	152 156	215 215	176 184	255 255	203 203	139 139	212 212	163 163	141 149	122 122	243 243
H17	198 198	152 156	215 215	176 184	255 255	203 203	139 139	212 212	163 163	141 149	122 122	243 243
H18	190 198	152 152	207 215	176 176	255 255	199 203	139 139	212 212	147 159	141 141	122 122	243 243
H19	190 190	152 156	215 215	176 176	255 255	199 203	139 139	212 212	159 163	141 141	122 122	243 243
H20	190 190	152 156	215 215	184 184	241 253	199 203	139 139	210 212	163 163	141 141	122 122	243 243
H21	190 190	156 156	215 215	176 184	255 255	203 203	139 139	210 212	147 163	141 141	122 122	243 243
H22	198 198	152 156	215 215	176 184	255 255	185 203	139 139	210 210	147 161	141 141	122 122	239 243

Table 5. Continued

Highlands/Glades *Loci*

Bear #	G1A	G10B	G10C	G1D	G10H	G10J	G10L	G10M	G10P	G10X	MU50	MU59
H23	190 198	152 156	207 215	176 184	253 255	203 203	139 139	210 212	163 163	141 141	122 122	243 243
H24	190 198	156 156	215 215	176 176	241 241	199 203	139 139	210 210	147 163	141 141	122 122	243 243
H25	190 198	156 156	207 215	184 184	241 253	203 203	139 139	210 212	163 163	141 141	122 122	243 243
H26	190 198	156 156	207 215	176 176	241 241	203 203	139 139	212 212	163 163	149 149	122 122	243 243
H27	198 198	152 156	207 215	176 176	241 255	203 203	139 139	210 210	161 163	141 149	122 122	243 243
H28	190 198	156 156	215 215	184 184	241 255	199 203	139 139	210 210	163 163	141 141	122 122	239 243

Ocala

Bear #	G1A	G10B	G10C	G1D	G10H	G10J	G10L	G10M	G10P	G10X	MU50	MU59
OC1	192 192	156 156	207 215	184 184	241 241	187 205	139 139	212 214	159 159	137 149	128 134	239 239
OC2	194 198	152 156	217 217	184 184	241 253	187 203	139 139	206 212	159 159	141 149	122 134	245 245
OC3	194 194	160 164	215 217	176 184	241 241	187 187	139 139	206 212	159 163	149 149	122 138	231 245
OC4	192 194	160 164	217 217	176 188	241 249	187 187	139 139	212 214	163 163	149 149	134 138	245 245
OC5	190 198	152 160	215 215	184 190	249 249	203 203	139 139	212 214	161 161	141 149	122 134	231 239
OC6	192 194	152 156	215 215	184 184	241 253	203 203	139 139	212 214	159 163	139 149	134 134	231 245
OC7	190 194	156 156	215 215	172 186	241 243	187 205	139 139	206 214	159 159	149 149	122 134	239 245
OC8	192 194	156 156	215 215	184 184	241 241	187 187	139 139	212 212	159 163	149 149	134 144	239 239
OC9	194 194	156 164	215 217	176 184	241 241	187 205	139 155	212 212	159 163	149 149	122 122	231 245
OC10	192 198	154 160	215 215	172 188	243 249	187 187	139 139	206 212	161 163	149 149	128 134	231 235
OC11	192 198	160 160	215 217	190 190	243 249	187 203	139 139	206 212	159 161	141 147	122 134	235 243
OC12	192 198	156 156	215 215	184 184	241 241	187 205	139 139	206 214	159 163	147 149	122 134	231 239
OC13	192 192	152 160	215 215	172 176	241 249	187 187	139 149	212 214	159 159	149 149	122 138	231 245
OC14	192 198	154 156	215 215	184 190	249 253	187 187	149 155	212 214	159 163	137 149	134 134	231 239

Table 5. Continued

Ocala						*Loci*						
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
OC15	192 194	154 156	215 215	172 176	241 249	187 187	139 139	212 212	159 161	147 147	134 134	239 245
OC16	192 200	156 156	215 215	184 184	253 259	187 187	139 139	212 214	159 163	141 141	122 134	231 243
OC17	190 192	154 156	215 215	184 190	249 253	187 187	139 155	206 212	159 159	149 149	128 134	239 239
OC18	190 198	156 156	215 215	172 176	253 259	187 187	139 139	212 212	159 159	141 149	122 134	239 243
OC19	192 192	156 164	215 217	176 186	241 249	187 187	139 139	214 214	159 163	141 149	122 138	231 245
OC20	190 194	152 160	215 215	176 176	253 259	187 187	139 149	206 206	159 159	149 149	134 134	231 241
OC21	192 192	156 156	215 215	172 188	241 249	187 205	139 139	212 212	159 163	149 149	128 134	239 239
OC22	194 198	152 156	215 215	172 190	249 249	205 205	139 139	212 218	159 161	137 149	122 128	239 245
OC23	192 194	154 156	215 215	176 188	241 259	187 187	139 155	206 212	163 163	141 149	128 134	239 243
OC24	190 198	152 156	213 215	184 184	241 249	187 203	139 155	212 212	159 163	137 141	122 128	239 241
OC25	194 194	156 156	215 217	172 176	241 241	187 203	139 139	206 206	159 159	149 149	122 134	239 243
OC26	190 198	156 160	215 217	184 190	249 249	187 187	139 139	206 212	157 159	137 147	122 134	231 237
OC27	194 198	154 154	215 215	172 184	259 259	187 187	139 149	212 214	159 163	141 149	122 134	239 243
OC28	192 194	154 156	213 215	176 190	241 253	187 187	139 139	212 218	161 163	149 149	122 134	231 239
OC29	192 194	152 156	215 215	176 188	241 241	187 203	139 149	212 212	159 159	137 137	122 122	237 239
OC24	190 198	152 156	213 215	184 184	241 249	187 203	139 155	212 212	159 163	137 141	122 128	239 241
OC25	194 194	156 156	215 217	172 176	241 241	187 203	139 139	206 206	159 159	149 149	122 134	239 243
OC26	190 198	156 160	215 217	184 190	249 249	187 187	139 139	206 212	157 159	137 147	122 134	231 237
OC27	194 198	154 154	215 215	172 184	259 259	187 187	139 149	212 214	159 163	141 149	122 134	239 243
OC28	192 194	154 156	213 215	176 190	241 253	187 187	139 139	212 218	161 163	149 149	122 134	231 239
OC29	192 194	152 156	215 215	176 188	241 241	187 203	139 149	212 212	159 159	137 137	122 122	237 239

Table 5. Continued

Ocala	*Loci*											
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
OC30	194 194	156 156	215 215	172 172	241 253	187 187	139 139	214 218	159 159	147 149	122 134	239 239
OC31	190 198	152 160	215 217	172 176	241 249	187 187	139 139	206 212	159 163	147 149	122 134	239 245
OC32	190 200	156 160	215 217	176 176	241 259	187 205	149 155	206 212	159 159	137 147	122 122	243 243
OC33	190 190	156 164	215 215	172 184	241 241	187 187	139 139	206 212	159 159	141 149	134 134	235 239
OC34	192 192	152 156	215 215	172 172	259 259	187 187	139 139	206 214	159 159	137 137	122 122	231 239
OC35	190 190	156 156	213 215	184 186	249 259	187 187	139 149	206 206	159 163	137 149	134 134	231 239
OC36	192 192	154 156	215 217	172 176	241 241	187 205	139 139	206 212	159 163	137 141	134 134	235 243
OC37	194 194	156 164	215 215	172 176	241 241	187 187	139 139	212 212	161 163	149 149	122 122	231 243
OC38	190 192	152 156	213 215	184 186	241 259	187 187	139 155	206 214	159 159	137 149	122 134	231 239
OC39	192 192	154 156	215 217	172 184	241 249	187 187	139 155	206 206	159 159	147 149	122 134	231 239
OC40	192 194	152 156	215 215	186 188	243 253	187 187	149 157	206 212	159 163	137 141	134 134	231 231

Osceola

Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
OS1	196 200	154 158	215 217	176 184	235 243	187 187	151 153	212 214	155 159	141 149	124 134	239 239
OS2	198 198	160 160	217 217	176 186	241 243	187 187	149 155	218 218	159 159	141 149	124 124	239 239
OS3	190 200	160 164	213 217	184 186	241 243	191 203	143 151	206 206	157 159	141 147	126 134	239 239
OS4	198 198	154 160	207 217	176 186	243 243	187 187	139 143	214 214	159 159	141 149	124 134	239 243
OS5	194 198	152 154	215 217	186 188	243 253	187 199	151 153	212 218	159 159	141 149	122 134	239 241
OS6	196 198	152 152	215 217	176 188	245 251	187 187	149 157	210 216	147 159	141 149	122 134	231 239
OS7	194 198	166 166	217 217	176 188	243 243	187 189	151 151	212 212	159 159	141 149	134 134	239 239
OS8	194 200	158 160	217 217	176 188	243 243	187 187	139 153	210 214	147 159	141 141	122 134	231 231

Table 5. Continued

Osceola						*Loci*						
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
OS9	194 194	156 156	217 219	176 184	241 243	187 189	151 153	210 218	147 159	149 155	122 134	231 241
OS10	190 198	156 160	215 217	178 188	235 243	187 199	135 139	214 218	159 159	141 149	144 144	239 239
OS11	194 200	160 160	217 217	184 188	249 255	187 189	139 151	212 212	159 163	147 151	134 134	239 243
OS12	194 194	154 166	207 217	176 180	241 241	187 189	151 155	210 214	159 159	149 149	124 134	231 243
OS13	200 200	156 158	215 217	176 184	235 243	189 203	139 149	210 214	157 159	141 149	134 134	231 243
OS14	192 196	156 156	215 215	176 186	241 255	187 187	139 149	206 214	157 159	141 149	122 144	231 243
OS15	194 198	160 164	217 217	176 186	243 243	185 187	135 153	214 214	159 159	149 149	134 144	239 243
OS16	190 194	160 164	213 219	176 176	235 241	187 187	143 151	206 214	147 159	149 149	122 126	239 239
OS17	194 198	156 160	207 217	178 184	243 245	187 199	139 155	214 218	159 159	149 151	124 144	231 239
OS18	194 198	156 164	213 219	176 184	243 245	187 189	143 151	206 210	159 163	149 149	122 126	231 239
OS19	196 196	152 156	215 215	188 190	241 241	187 189	135 139	206 214	159 159	141 149	126 144	239 249
OS20	192 198	152 160	215 215	186 188	241 243	187 199	139 153	206 210	159 161	139 149	124 134	231 241
OS21	194 198	160 164	217 217	176 186	243 243	187 199	153 155	216 218	159 159	149 149	124 134	239 239
OS22	196 200	156 160	211 217	176 176	245 255	187 187	135 151	212 212	159 163	141 149	140 144	239 239
OS23	194 200	154 160	217 217	176 184	241 243	187 189	151 153	210 214	159 159	141 147	122 134	239 241
OS24	196 200	156 160	217 219	176 188	241 255	187 189	139 157	206 212	159 163	141 147	124 134	239 243
OS25	194 198	160 160	215 217	176 188	235 253	187 205	153 153	212 212	157 159	141 141	122 122	231 239
OS26	194 200	160 164	217 217	176 186	243 255	187 199	139 155	206 218	159 161	141 149	134 144	239 239
OS27	194 196	164 166	217 217	176 184	241 241	191 199	143 151	206 214	159 159	141 149	122 134	239 241
OS28	194 198	160 160	217 217	176 176	241 243	187 199	153 153	214 214	157 163	141 147	126 134	239 243
OS29	194 194	156 160	217 217	188 188	235 251	187 205	153 153	212 214	157 159	141 141	122 122	231 231
OS30	194 200	156 160	217 217	184 184	241 241	199 205	151 153	206 212	157 159	141 141	122 126	239 243

Table 5. Continued

Osceola

	Loci											
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
OS31	190 192	156 156	215 215	184 186	243 249	187 203	139 157	212 214	161 163	149 149	128 134	243 243
OS32	194 194	154 156	217 217	184 184	243 253	187 191	151 153	214 216	157 159	141 149	126 134	231 231
OS33	194 198	160 160	215 217	176 188	251 253	187 199	135 149	212 212	159 159	141 149	122 122	239 249
OS34	190 194	156 160	211 217	184 188	235 241	189 205	149 153	212 214	147 159	149 151	122 134	239 239
OS35	194 196	160 160	215 217	176 186	241 251	187 199	149 151	206 206	157 159	141 149	126 134	231 239
OS36	194 194	160 160	217 217	176 188	235 253	187 189	135 143	212 212	159 163	141 141	122 140	239 249
OS37	194 194	160 160	217 217	176 186	241 243	185 187	153 153	214 214	159 159	149 149	122 124	239 249
OS38	194 196	156 164	215 217	178 186	241 243	187 199	139 143	212 218	159 161	141 141	134 144	239 239
OS39	194 200	160 164	217 217	176 184	245 253	187 205	135 139	212 214	157 163	147 149	126 134	239 243
OS40	194 194	160 160	217 217	186 186	243 251	187 199	151 153	206 214	159 159	141 149	134 144	231 249
OS41	192 192	156 156	207 215	184 188	243 253	187 187	139 139	212 212	159 163	147 149	134 134	241 245

St. Johns

Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
S1	190 194	152 156	215 215	184 186	249 255	187 205	139 139	206 212	159 163	141 149	122 134	231 239
S2	190 194	154 156	207 215	176 184	241 253	187 203	139 139	212 214	159 163	147 149	122 122	239 245
S3	190 194	152 160	213 217	176 184	241 253	187 203	139 155	212 218	159 163	141 141	122 138	239 243
S4	194 198	156 156	215 215	172 184	241 249	187 205	139 139	206 206	159 159	137 141	122 144	245 245
S5	190 194	156 156	215 217	176 190	241 241	187 205	139 139	212 218	159 163	141 149	134 138	239 239
S6	194 200	152 156	211 213	172 188	241 249	185 187	139 139	214 216	159 159	147 147	122 134	241 243
S7	192 194	154 156	215 217	172 186	249 259	187 205	139 155	212 212	161 161	141 149	122 134	237 239
S8	192 200	152 156	211 215	184 188	241 241	187 205	139 139	212 214	159 159	137 147	122 128	241 243

Table 5. Continued

St. Johns	*Loci*											
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
S9	194 200	152 156	211 215	172 184	249 249	187 187	139 139	214 214	159 159	147 147	122 134	241 247
S10	192 192	156 156	215 215	172 184	241 249	203 205	139 149	212 212	159 161	137 149	122 134	241 245
S11	192 192	156 156	215 217	172 184	241 241	187 203	139 155	206 206	159 159	137 141	122 128	231 239
S12	186 198	152 152	207 215	176 180	241 241	187 187	139 139	212 214	163 163	137 141	134 134	239 239
S13	186 194	152 160	215 215	176 188	241 259	187 189	139 139	214 214	159 159	141 141	122 134	243 243
S14	194 198	152 156	213 215	176 184	241 249	187 187	139 139	206 218	159 163	147 149	122 122	231 239
S15	190 192	154 156	215 215	172 176	253 259	187 187	139 139	212 212	159 159	149 149	122 128	231 231
S16	194 194	154 156	211 215	184 184	249 259	187 203	149 155	212 212	159 159	141 147	122 122	237 245
S17	192 194	152 156	207 215	176 184	249 249	187 203	139 149	212 212	159 163	137 137	134 134	231 243
S18	190 198	152 152	215 215	176 184	249 249	185 203	139 139	212 214	163 163	137 137	134 140	231 243
S19	194 194	152 156	207 215	172 172	249 259	187 187	139 139	212 218	159 159	141 141	122 134	231 239
S20	194 194	156 156	217 217	172 176	241 253	187 187	139 139	212 218	159 159	141 149	122 134	239 239
S21	194 198	152 156	207 207	180 184	249 259	187 187	139 139	214 214	161 161	137 147	138 138	243 247
S22	192 192	156 156	211 215	172 184	249 259	187 187	139 139	206 214	159 159	141 149	122 122	235 243
S23	194 198	152 156	215 215	172 176	235 241	185 187	139 139	212 214	159 163	137 155	122 138	231 239
S24	190 194	152 156	215 215	176 190	241 253	185 203	139 139	212 214	157 163	147 149	122 134	245 245
S25	194 198	154 160	215 215	184 190	259 259	187 205	139 139	206 214	159 163	149 149	128 134	231 239
S26	186 192	156 160	207 215	172 184	241 249	187 189	139 139	206 214	159 159	147 149	122 138	239 243
S27	190 194	152 152	215 215	176 186	241 255	187 191	139 143	206 212	159 163	149 149	138 140	239 239
S28	190 192	152 156	211 215	172 186	241 249	187 191	139 143	206 212	159 159	149 149	122 140	239 243
S29	190 192	152 156	211 215	176 184	255 259	187 187	139 139	206 206	159 159	141 149	122 138	235 239
S30	186 194	152 154	207 213	184 184	241 259	187 189	139 155	206 214	161 163	137 147	122 126	231 239

Table 5. Continued

St. Johns

	Loci											
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
S31	190 192	156 160	217 217	176 184	241 241	187 203	155 155	214 218	159 163	141 149	122 122	241 243
S32	194 198	154 156	215 217	172 184	241 249	187 205	139 139	206 214	159 159	149 149	134 134	239 241
S33	190 194	152 156	213 217	176 176	241 253	187 187	139 155	218 218	159 163	141 149	122 138	239 243
S34	190 198	152 154	215 215	184 190	241 259	203 203	139 139	212 214	157 159	149 149	122 122	237 245
S35	192 198	152 160	213 217	184 184	241 249	205 205	139 139	212 212	159 163	137 141	134 134	239 245
S36	190 194	156 156	207 215	172 184	253 259	187 187	139 139	206 212	159 159	141 147	134 134	231 239
S37	198 198	156 156	215 217	172 184	241 249	187 203	139 139	212 212	159 163	149 149	122 134	239 241
S38	194 198	156 156	215 215	176 184	241 259	189 205	139 139	206 214	159 159	137 147	134 144	231 245
S39	198 198	152 156	207 215	176 184	259 259	187 189	139 139	206 214	159 159	137 147	122 134	231 239
S40	198 198	156 156	215 217	176 184	249 259	187 187	139 139	212 212	159 163	149 149	122 138	231 239

Osceola/Ocala Corridor

Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
OO1	192 194	154 156	215 215	172 184	241 241	187 203	149 155	212 214	159 159	149 149	122 134	239 243
OO2	190 198	152 156	215 215	172 184	241 259	187 205	139 149	214 214	159 159	137 141	122 134	231 231
OO3	192 194	156 156	215 215	172 188	241 243	187 187	139 139	206 212	159 163	137 139	122 134	231 245
OO4	192 194	156 156	215 215	184 186	249 259	187 205	139 157	214 218	159 159	141 149	122 122	239 243
OO5	192 194	156 156	213 215	176 188	243 249	187 187	139 149	212 214	161 163	141 149	122 124	231 239
OO6	192 192	154 156	215 215	176 184	241 249	187 187	139 139	212 214	161 163	149 149	134 134	241 241
OO7	192 192	154 160	215 215	172 176	241 249	187 187	139 139	206 212	159 163	137 149	122 122	231 239
OO8	192 200	154 160	215 217	172 190	241 259	187 205	139 139	212 212	159 161	139 149	122 122	231 231
OO9	192 198	152 158	215 217	172 184	241 253	187 187	139 155	212 214	159 159	141 149	134 134	231 239

Table 5. Continued

Osceola/Ocala Corridor

	Loci											
Bear #	**G1A**	**G10B**	**G10C**	**G1D**	**G10H**	**G10J**	**G10L**	**G10M**	**G10P**	**G10X**	**MU50**	**MU59**
OO10	190 192	154 156	211 215	188 188	249 249	187 187	139 149	212 212	159 159	137 149	134 134	235 243
OO11	190 198	152 156	215 215	172 186	241 249	187 205	139 155	212 214	163 163	137 141	134 134	231 239
OO12	194 198	152 154	215 215	172 172	241 249	187 205	139 139	206 212	159 159	149 149	134 134	231 237
OO13	192 194	152 156	215 215	172 190	241 259	187 203	139 149	206 212	159 159	137 149	122 134	239 239
OO14	192 198	156 164	213 215	172 172	241 249	187 203	139 139	212 214	159 159	149 149	122 134	243 245
OO15	190 194	156 160	207 215	184 188	243 259	187 205	139 155	212 214	159 159	141 149	134 138	231 245
OO16	198 198	152 156	215 215	172 172	241 259	187 203	139 139	212 212	159 159	141 149	134 134	231 243
OO17	192 192	152 156	213 215	186 186	249 259	187 187	139 139	206 214	159 159	149 149	122 134	231 239
OO18	190 192	156 156	215 215	176 188	241 259	187 187	135 139	206 214	159 163	141 149	134 134	231 231
OO19	192 192	156 164	215 217	176 184	241 249	187 187	139 139	212 212	163 163	149 149	122 134	239 239
OO20	200 200	156 158	215 217	176 186	243 243	187 187	143 153	214 218	159 159	149 149	134 144	231 239
OO21	192 194	156 156	215 215	186 188	243 249	203 205	139 139	206 212	159 163	139 147	122 134	231 239
OO22	194 198	152 160	215 215	172 184	241 249	187 203	139 139	212 212	159 159	141 149	122 134	239 239
OO23	190 192	160 160	215 215	172 176	249 259	187 205	139 149	206 214	159 163	141 149	134 138	231 239
OO24	198 198	156 160	215 217	190 190	241 249	187 205	139 139	214 214	157 159	137 149	134 134	241 245
OO25	192 194	154 156	215 215	184 188	241 253	187 187	139 139	206 212	159 159	149 149	134 144	231 239
OO26	196 198	160 160	217 217	176 186	241 241	187 199	149 153	206 218	159 159	141 149	124 134	231 239
OO27	192 192	156 160	213 215	172 184	259 259	187 187	139 149	212 214	159 159	141 141	134 134	231 243
OO28	190 192	152 154	207 215	186 188	241 249	203 205	139 149	206 212	159 159	141 149	134 138	231 235
OO29	190 192	152 156	207 215	176 186	241 241	187 205	139 139	206 214	159 163	137 141	122 122	231 243
OO30	198 198	154 156	215 215	172 188	241 241	203 203	139 139	212 212	159 159	137 141	134 134	231 235
OO31	200 200	156 160	215 217	188 188	241 243	187 189	143 143	212 218	159 159	149 149	134 134	231 239

Table 6. Allele frequencies for 12 microsatellite loci in 10 populations of Florida black bears.

	Alleles at locus G1A							
Population	*186*	*190*	*192*	*194*	*196*	*198*	*200*	*202*
Apalachicola	0	0.2	0.038	0.125	0.075	0.188	0.275	0.1
Aucilla	0	0.167	0	0.056	0	0.444	0.333	0
Big Cypress	0	0.622	0.037	0.037	0.024	0.11	0.171	0
Chassahowitzka	0	0.086	0	0	0	0.914	0	0
Eglin	0	0.05	0	0.013	0.512	0.013	0.325	0.087
Highlands/Glades	0	0.571	0	0	0	0.429	0	0
Ocala	0	0.175	0.363	0.287	0	0.15	0.025	0
Osceola/Ocala Corridor	0	0.129	0.403	0.161	0.016	0.21	0.081	0
Osceola	0	0.061	0.061	0.415	0.122	0.195	0.146	0
St. Johns	0.05	0.175	0.188	0.338	0	0.213	0.038	0

	Alleles at locus G10B							
Population	*152*	*154*	*156*	*158*	*160*	*162*	*164*	*166*
Apalachicola	0	0.2	0.038	0.125	0.075	0.188	0.275	0.1
Aucilla	0	0.167	0	0.056	0	0.444	0.333	0
Big Cypress	0	0.622	0.037	0.037	0.024	0.11	0.171	0
Chassahowitzka	0	0.086	0	0	0	0.914	0	0
Eglin	0	0.05	0	0.013	0.512	0.013	0.325	0.087
Highlands/Glades	0	0.571	0	0	0	0.429	0	0
Ocala	0	0.175	0.363	0.287	0	0.15	0.025	0
Osceola/Ocala Corridor	0	0.129	0.403	0.161	0.016	0.21	0.081	0
Osceola	0	0.061	0.061	0.415	0.122	0.195	0.146	0
St. Johns	0.05	0.175	0.188	0.338	0	0.213	0.038	0

Table 6. Continued

	Alleles at locus G10C							
Population	*205*	*207*	*209*	*211*	*213*	*215*	*217*	*219*
Apalachicola	0.038	0.062	0.275	0.237	0	0.387	0	0
Aucilla	0.333	0.056	0	0.056	0	0.556	0	0
Big Cypress	0	0.585	0	0	0.061	0.354	0	0
Chassahowitzka	0	0.207	0	0.776	0.017	0	0	0
Eglin	0	0	0.05	0	0	0.625	0.325	0
Highlands/Glades	0	0.196	0	0	0	0.768	0	0.036
Ocala	0	0.013	0	0	0.05	0.762	0.175	0
Osceola/Ocala Corridor	0	0.048	0	0.016	0.065	0.742	0.129	0
Osceola	0	0.049	0	0.024	0.037	0.22	0.622	0.049
St. Johns	0	0.125	0	0.087	0.075	0.55	0.162	0

	Alleles at locus G1D								
Population	*172*	*176*	*178*	*180*	*182*	*184*	*186*	*188*	*190*
Apalachicola	0.013	0.375	0	0	0.125	0.025	0.188	0.15	0.125
Aucilla	0.111	0.111	0	0.333	0	0	0	0.222	0.222
Big Cypress	0.037	0.402	0.037	0	0	0.22	0.256	0.037	0.012
Chassahowitzka	0.724	0	0	0	0	0.207	0.069	0	0
Eglin	0	0.213	0.275	0	0	0	0.213	0	0.3
Highlands/Glades	0	0.571	0.036	0	0	0.375	0	0.018	0
Ocala	0.225	0.225	0	0	0	0.312	0.062	0.075	0.1
Osceola/Ocala Corridor	0.29	0.145	0	0	0	0.161	0.145	0.194	0.065
Osceola	0	0.354	0.037	0.012	0	0.207	0.183	0.195	0.012
St. Johns	0.213	0.25	0	0.025	0	0.375	0.05	0.038	0.05

Table 6. Continued

	Alleles at locus G10H												
Population	*235*	*239*	*241*	*243*	*245*	*247*	*249*	*251*	*252*	*253*	*255*	*259*	*261*
Apalachicola	0	0.112	0.712	0	0	0.013	0.013	0.062	0.013	0.075	0	0	0
Aucilla	0.222	0	0.722	0	0	0	0	0.056	0	0	0	0	0
Big Cypress	0.098	0	0.256	0.012	0	0	0.049	0.012	0	0.524	0	0.012	0.037
Chassahowitzka	0	0	0.552	0	0	0.448	0	0	0	0	0	0	0
Eglin	0	0	0.738	0	0	0.225	0	0	0	0.025	0.013	0	0
Highlands/Glades	0	0	0.286	0	0	0	0	0	0	0.179	0.536	0	0
Ocala	0	0	0.45	0.05	0	0	0.237	0	0	0.125	0	0.138	0
Osceola/Ocala Corridor	0	0	0.419	0.113	0	0	0.258	0	0	0.032	0	0.177	0
Osceola	0.098	0	0.256	0.354	0.061	0	0.024	0.061	0	0.085	0.061	0	0
St. Johns	0.013	0	0.375	0	0	0	0.275	0	0	0.087	0.038	0.213	0

	Alleles at locus G10J						
Population	*185*	*187*	*189*	*191*	*199*	*203*	*205*
Apalachicola	0.062	0.475	0	0	0.138	0.325	0
Aucilla	0	0.556	0	0.167	0.278	0	0
Big Cypress	0.207	0.378	0	0	0.354	0.061	0
Chassahowitzka	0	0.052	0	0	0.948	0	0
Eglin	0	0.775	0	0	0.188	0	0.038
Highlands/Glades	0.018	0	0	0	0.25	0.732	0
Ocala	0	0.775	0	0	0	0.112	0.112
Osceola/Ocala Corridor	0	0.645	0.016	0	0.016	0.145	0.177
Osceola	0.024	0.549	0.134	0.037	0.159	0.037	0.061
St. Johns	0.05	0.575	0.062	0.025	0	0.15	0.138

Table 6. Continued

	Alleles at locus G10L										
Population	*135*	*137*	*139*	*141*	*143*	*149*	*151*	*153*	*155*	*157*	*161*
Apalachicola	0.162	0	0	0.038	0.112	0	0.013	0.225	0.112	0.338	0
Aucilla	0.056	0	0	0.111	0.222	0	0.5	0.056	0	0.056	0
Big Cypress	0.11	0	0.354	0.012	0	0	0	0.134	0.159	0.195	0.037
Chassahowitzka	0	0.155	0.19	0	0	0.655	0	0	0	0	0
Eglin	0.025	0	0	0	0	0.138	0.087	0.4	0.287	0.062	0
Highlands/Glades	0	0	1	0	0	0	0	0	0	0	0
Ocala	0	0	0.788	0	0	0.1	0	0	0.1	0.013	0
Osceola/Ocala Corridor	0.016	0	0.677	0	0.048	0.145	0	0.032	0.065	0.016	0
Osceola	0.085	0	0.195	0	0.085	0.085	0.207	0.244	0.061	0.037	0
St. Johns	0	0	0.837	0	0.025	0.038	0	0	0.1	0	0

	Alleles at locus G10M					
Population	*206*	*210*	*212*	*214*	*216*	*218*
Apalachicola	0.112	0	0.2	0.387	0.225	0.075
Aucilla	0.278	0	0.611	0.056	0.056	0
Big Cypress	0.012	0.122	0.451	0.402	0.012	0
Chassahowitzka	0	0.017	0.983	0	0	0
Eglin	0.1	0.213	0.05	0.438	0.05	0.15
Highlands/Glades	0	0.411	0.571	0.018	0	0
Ocala	0.3	0	0.475	0.188	0	0.038
Osceola/Ocala Corridor	0.194	0	0.452	0.29	0	0.065
Osceola	0.171	0.098	0.28	0.305	0.037	0.11
St. Johns	0.225	0	0.387	0.275	0.013	0.1

Table 6. Continued

	Alleles at locus G10P						
Population	*147*	*151*	*155*	*157*	*159*	*161*	*163*
Apalachicola	0	0.075	0.275	0.087	0.3	0.05	0.213
Aucilla	0	0	0	0.5	0.278	0	0.222
Big Cypress	0.232	0	0	0	0.28	0.037	0.451
Chassahowitzka	0	0	0	0.121	0.845	0	0.034
Eglin	0	0	0.1	0	0.2	0	0.7
Highlands/Glades	0.125	0	0	0	0.089	0.054	0.732
Ocala	0	0	0	0.013	0.613	0.1	0.275
Osceola/Ocala Corridor	0	0	0	0.016	0.742	0.048	0.194
Osceola	0.061	0	0.012	0.122	0.646	0.049	0.11
St. Johns	0	0	0	0.025	0.65	0.075	0.25

	Alleles at locus G10X								
Population	*137*	*139*	*141*	*143*	*147*	*149*	*151*	*155*	*157*
Apalachicola	0.087	0.013	0.175	0	0.287	0.25	0.013	0.175	0
Aucilla	0.056	0	0.389	0	0.167	0.167	0	0.222	0
Big Cypress	0	0	0.134	0.012	0.146	0.683	0.012	0	0.012
Chassahowitzka	0	0	0.293	0	0	0.707	0	0	0
Eglin	0.338	0.375	0.213	0	0	0.075	0	0	0
Highlands/Glades	0	0	0.786	0	0	0.214	0	0	0
Ocala	0.175	0.013	0.162	0	0.112	0.538	0	0	0
Osceola/Ocala Corridor	0.145	0.048	0.258	0	0.016	0.532	0	0	0
Osceola	0	0.012	0.402	0	0.085	0.451	0.037	0.012	0
St. Johns	0.188	0	0.25	0	0.188	0.363	0	0.013	0

Table 6. Continued

	Alleles at locus MU50									
Population	*122*	*124*	*126*	*128*	*134*	*136*	*138*	*140*	*142*	*144*
Apalachicola	0.087	0.45	0.15	0.062	0	0.013	0.213	0	0.025	0.087
Aucilla	0.611	0.278	0.111	0	0	0	0	0	0	0.611
Big Cypress	0.28	0	0.183	0.012	0.524	0	0	0	0	0.28
Chassahowitzka	0	0	0	0	0	0	0	1	0	0
Eglin	0.712	0.025	0.038	0	0	0	0	0	0.225	0.712
Highlands/Glades	0.929	0	0	0	0.071	0	0	0	0	0.929
Ocala	0.375	0	0	0.087	0.475	0	0.05	0	0	0.375
Osceola/Ocala Corridor	0.29	0.032	0	0	0.597	0	0.048	0	0	0.29
Osceola	0.232	0.122	0.11	0.012	0.378	0	0	0.024	0	0.232
St. Johns	0.438	0	0.013	0.05	0.312	0	0.125	0.038	0	0.438

	Alleles at locus MU59								
Population	*231*	*235*	*237*	*239*	*241*	*243*	*245*	*247*	*249*
Apalachicola	0.025	0	0	0.575	0.013	0.387	0	0	0
Aucilla	0	0	0	0.944	0	0.056	0	0	0
Big Cypress	0.049	0.037	0	0.488	0.037	0.378	0	0.012	0
Chassahowitzka	0.052	0	0	0.948	0	0	0	0	0
Eglin	0	0	0	0.988	0	0.013	0	0	0
Highlands/Glades	0	0	0	0.107	0.036	0.857	0	0	0
Ocala	0.25	0.05	0.025	0.363	0.025	0.125	0.162	0	0
Osceola/Ocala Corridor	0.403	0.048	0.016	0.306	0.048	0.113	0.065	0	0
Osceola	0.207	0	0	0.5	0.073	0.146	0.012	0	0.061
St. Johns	0.188	0.025	0.038	0.35	0.087	0.162	0.125	0.025	0

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BIOGRAPHICAL SKETCH

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