

American black bear population size and genetic diversity at Apostle Islands National Lakeshore

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Abstract: Effective management of American black bears (*Ursus americanus*) requires an understanding of population demographics. In 2002, we obtained DNA from hair collected at barbed-wire traps to estimate black bear population size and study population genetics on Stockton (4,069 ha) and Sand (1,193 ha) islands at Apostle Islands National Lakeshore (AINL), Wisconsin. Hair samples also were collected from 2 nuisance bears on Oak Island. We analyzed 372 hair samples from Stockton and Sand islands collected on 4 occasions at about 14-day intervals. Genetic analysis of 6 microsatellite DNA markers resulted in 71 captures of 26 individuals on Stockton Island and 13 captures of 6 individuals on Sand Island. The estimated bear populations on Stockton and Sand islands were 26 (SE = 0.54, 95% CI [confidence interval] = 26–26) and 6 (SE = 0.60, 95% CI = 6–7) individuals, respectively. The estimated density on Stockton Island was 0.64 bears/km² and on Sand Island was 0.50 bears/km². Genetic variation within both island populations was higher (mean $H_E \geq 0.77$) than could be maintained by populations of this size in isolation, suggesting substantial immigration from the mainland population occurred. Genetic assignment testing using log genotype likelihoods demonstrated sufficient variation between bear populations on Stockton and Sand islands to permit identification of natal origins. The 2 bears from Oak Island were genetically intermediate between Stockton and Sand islands. Islands within AINL contain small black bear populations of high density that are genetically distinct and apparently influenced by immigration from the mainland population.

Key words: American black bear, Apostle Islands National Lakeshore, genetic diversity, mark–recapture, population estimates, *Ursus americanus*, Wisconsin

Ursus 16(1):85–92 (2005)

Knowledge of animal population sizes and connectivity, and how they vary temporally, is necessary for effective species management. The National Park Service (NPS) is mandated to “. . . maintain as parts of the natural ecosystems of parks all native plants and animals” (National Park Service 2000). The NPS is also required to monitor important resources that are necessary to accomplish management objectives as required by law or planning documents (National Park Service 2000). Black bears (*Ursus americanus*) are an important component of many units in the National Park system, including Wisconsin’s Apostle Islands National Lakeshore (AINL). At AINL, understanding black bear abundance and ecology is critical because: (1) they have

an inherent role in maintaining ecological integrity, (2) harvest of black bears is legal in AINL, and (3) of potential interactions with tourists.

Techniques to estimate bear populations that could be used for long-term monitoring are impractical in heavily-forested areas like AINL or are cost prohibitive. However, use of genetic markers to identify individual animals has increased considerably in recent years (Parker et al. 1998). Small amounts of tissue, including hair, are now used frequently in genetic studies to identify individuals, as well as determine sex, species, and genealogy (Taberlet et al. 1993; Paetkau and Strobeck 1994, 1998; Foran et al. 1997; Haig 1998). Advances in genotyping using non-invasive collection of tissue samples (Woods et al. 1996, 1999) and mark–recapture modeling (White et al. 1982) have provided an additional means to estimate animal populations, including estimates of precision. Mark–recapture modeling employing

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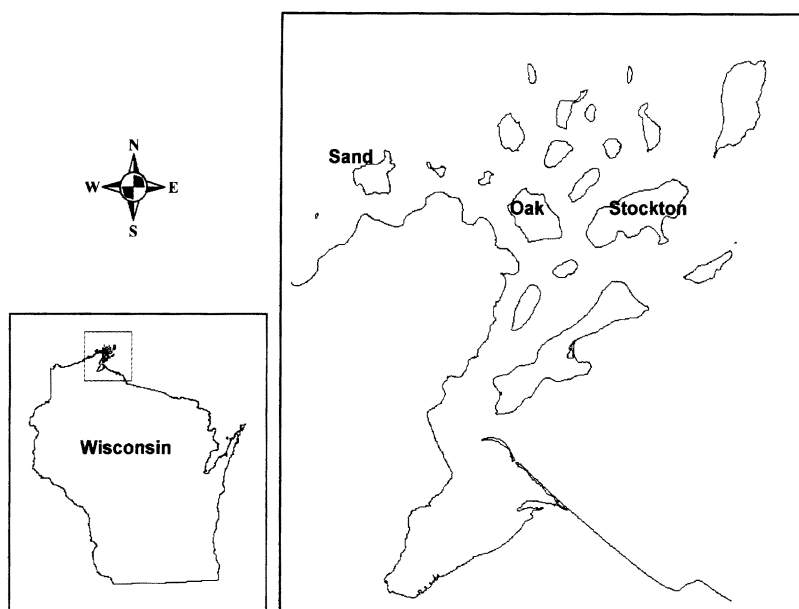


Fig. 1. Location of Sand, Oak, and Stockton islands and the Apostle Island Archipelago, Wisconsin, USA.

data from systematically obtained hair samples is now likely the most common method to estimate bear population size (Mowat and Strobeck 2000, Poole et al. 2001, Boersen et al. 2003).

As for connectivity, aquatic and other geographic or human created barriers such as roads can greatly inhibit animal movement and dispersal (Schmiegelow and Nudds 1987, Proctor et al. 2002), increasing the risk of population extinction (Lande 1994). The NPS is obligated to "... protect the full range of genetic types (genotypes) of native plant and animal populations in the parks by perpetuating natural evolutionary processes and minimizing human interference with evolving genetic diversity" (National Park Service 2000). Understanding the demographic and genetic connectivity of potentially isolated bear populations at AINL will help ensure appropriate management of metapopulations.

Our initial study goal was to estimate the population size of bears on Stockton and Sand islands. Specific objectives were to: (1) estimate bear density on Stockton and Sand islands and compare bear density on Stockton Island to previous estimates, (2) estimate the sex ratio of these island populations and compare it to previous estimates, and (3) conduct preliminary assessment of genetic variation within and between these island populations.

Study area

The Apostle Islands Archipelago is located in southwest Lake Superior (46°42'–47°05'N; 90°24'–91°03'W), Wisconsin, USA (Fig. 1). Twenty-one of the 22 islands are within AINL. Islands range from 1.2–4,069 ha. Mean maximum and minimum daily temperatures are 25.5°C and 12°C in July and –4.5°C and –14°C in January, respectively. Annual precipitation is about 75 cm, including 200 cm of snow. Before European settlement, about 90% of the Apostle Islands contained mixed conifer–hardwood forests (Frederick and Rakestraw 1976).

Black bear occurrence has been documented on 8 islands within AINL (Belant and Van Stappen 2002). Although timing and duration of presence is generally unknown for the islands, black bears apparently most recently colonized Stockton Island in the early

1970s or later, and the island had an estimated population of 3 bears in 1984 (Fleming 1997; R.K. Anderson and D. Trauba, 1989, Black bear density on Stockton Island and mainland Wisconsin, University of Wisconsin, Stevens Point, Wisconsin, USA). Bear hunting has been allowed within AINL except for 1983–94, during a black bear research project when hunting was closed on Stockton Island (Fleming 1997). Only 1 bear has been recorded as harvested since inception of AINL in 1970 (AINL, Bayfield, Wisconsin, USA, unpublished data).

Number of bear–human interactions was roughly stable from 1990 through 2002, with most interactions occurring in mid-August. Until 2002, bear–human interactions at AINL resulted in 1 bear translocation every 2–4 years. As a result of increased bear–human interactions, more aggressive management was needed in 2002–03, resulting in the removal of 11 bears.

We conducted this study on Stockton and Sand islands. These islands were selected based on previous studies (Trauba 1996, Fleming 1997) and observations that suggested viable populations were present. Stockton Island (4,069 ha) is the largest island within AINL and is 7.7 km from the mainland; elevations range from 183–242 m. Logging began during the late 1800s and continued through 1955, with extensive fires occurring during the 1950s (Rakestraw 1976). Currently, deciduous

forests cover 87% of this island and are dominated by red (*Acer rubrum*) and sugar (*A. saccharum*) maple, with trembling aspen (*Populus tremuloides*), white birch (*Betula papyrifera*), and red oak (*Quercus rubra*) (Trauba 1996). Forested wetlands comprise 6% of the island with overstory dominated by black spruce (*Picea mariana*) and white cedar (*Thuja occidentalis*). Ponds resulting from beaver (*Castor canadensis*) activities (flowages) comprised 3% of the island area. Forests dominated by red (*Pinus resinosa*) and white (*P. strobus*) pine occurred on 2% of the island.

Sand Island (1,193 ha) is located 2 km from the mainland; elevations range from 183–203 m. Sand Island was repeatedly logged, with 7 large timber harvests occurring from the late 1800s until 1975. Presently, mixed hardwood–conifer forests including yellow birch (*Betula alleghaniensis*), balsam fir (*Abies balsamea*), white birch, white cedar, and red maple cover 83% of the island. Canada yew (*Taxus canadensis*) and mountain maple (*Acer spicatum*) are prevalent in the understory. Remaining habitat includes about 7% black spruce–tamarack (*Larix laricina*) swamp, 6% semi-open bog, and 3% white pine–hemlock (*Tsuga canadensis*) forest.

Methods

Hair trapping

We used a systematic grid (1.6 × 1.6 km) overlaid on each island to distribute trapping effort. Grid cells that contained <50% land were included with adjacent cells. We constructed hair traps as described by Woods et al. (1999), using 4-barbed, 2-strand wire to create an enclosure around ≥3 trees with wire about 50 cm above ground. We placed hair traps in areas we believed would maximize black bear captures. Enclosures were baited with 0.5 L fish oil poured on a decaying log positioned in the center of the enclosure. Anise oil was applied to vegetation about 2 m above ground at or near the perimeter of the enclosure. Traps were rebaited and relured during each session. We established 15 hair traps on Stockton (1 trap/2.7 km²) and 5 hair traps on Sand Island (1 trap/2.4 km²) and monitored them for 4 sessions between 26 June and 13 August 2002. We attempted to remove hair from traps at 2-week intervals. During each trap check, all hair from each barb was placed in a separate paper envelope, labeled, and air dried before processing. Because of the comparatively high density of hair traps (e.g., Mowat and Strobeck 2000, Poole et al. 2001, Boersen et al. 2003), we did not move the traps between sessions.

Home ranges of adult female and male black bears on Stockton Island were 7.2- and 32.9 km², respectively (Trauba 1996). With a hair-trap density of 1 trap/2.7 km², about 3 hair traps were available to each adult female and 12 traps were available to each adult male. Home range data were unavailable for Sand Island. Otis et al. (1978) recommended ≥4 traps/individual home range for mark–recapture studies.

Population parameters

The study areas were islands separated from the nearest land by ≥2 km. Although bears have been observed swimming between islands and between islands and the mainland (Trauba 1996; AINL, unpublished data), we assumed immigration and emigration were low. During a 12-year (1984–95) radiotelemetry study of black bears on Stockton Island, only 4 occurrences of natural emigration and 1 instance of immigration were observed (Trauba 1996, Fleming 1997). All of these movements were temporary; only 2 occurred during summer when our study was conducted. Finally, mean annual subadult and adult mortality on Stockton Island was <10% (Fleming 1997). Because of these factors and the short duration of our study, we considered our study areas to be geographically and demographically closed. Therefore, we used closed mark–recapture models available in program CAPTURE (Otis et al. 1978, White et al. 1982, Rexstad and Burnham 1991) to estimate population size for each island. Model selection was based on statistical tests conducted in CAPTURE and our knowledge of bear biology. We further verified population closure using the program CloseTest (Stanley and Richards 2003), which uses the Stanley and Burnham closure test (Stanley and Burnham 1999), a chi-square statistic developed under a null model allowing for time-specific variation in capture probabilities under closure. This closure test is most sensitive to permanent emigration, intermediately sensitive to permanent or temporary immigration, and least sensitive to temporary emigration (Stanley and Burnham 1999). We also estimated if the sex ratio of identified bears differed from 1:1 using a chi-square test for equal proportions. All tests were considered significant at alpha = 0.05.

DNA analyses

In addition to hair samples collected from traps, we conducted DNA analyses on hair samples collected from 2 black bears captured in nuisance situations on Oak Island (Fig. 1). For all samples we used 10 guard hairs for extraction when possible to reduce the probability of genotyping errors (Gossens et al. 1998).

Table 1. American black bear hair capture results from Stockton ($n = 15$ trap sites) and Sand ($n = 5$ trap sites) islands, Apostle Islands National Lakeshore, Wisconsin, USA, 2002.

Island	Session	Trap duration (days)		Traps with hair samples	Hair samples/trap		No. hair samples	No. bears	No. new bears
		\bar{x}	SD		\bar{x}	SD			
Stockton	1	14.2	2.4	14	7.8	2.9	109	17	17
	2	13.6	1.3	15	7.6	4.1	114	22	7
	3	13.6	1.7	13	4.3	2.5	56	17	2
	4	14.6	1.4	14	3.2	1.7	45	15	0
Grand mean		14.0	0.5		5.7	2.3			
Total				56			324	71	26
Sand	1	12.4	0.5	3	3.3	1.5	10	4	4
	2	15	0	4	3.8	2.8	15	4	2
	3	14	0	3	1.7	0.6	5	2	0
	4	18	0	4	4.5	3.9	18	3	0
Grand mean		14.9	2.4		3.3	1.2			
Total				12			48	13	6

We used 6 microsatellite loci for analyses of individual identity: G10C, G10M, G10X, G1D, G10H, and MU59 (Paetkau et al. 1998a and references therein). Ten additional loci (CXX20, CXX110, G1A, G10B, G10J, G10L, G10P, G10U, MU50, and gender) from a sample of each identified bear were analyzed to improve population genetics analyses. Gender was determined using size polymorphism in the amelogenin gene (Ennis and Gallagher 1994). We conducted DNA extractions using QIAGEN DNeasy Tissue kits (Qiagen, Mississauga, Ontario, Canada), following the manufacturer's instructions.

We examined distribution of genotype similarity to estimate the probability of 2 or more sampled individuals having identical genotypes at the 6 loci that we examined. The observed numbers of pairs of similar genotypes were used to estimate the expected number of pairs of identical genotypes (0 mismatching marker [MM] pairs; Paetkau 2003). The typical pattern reflects an order of magnitude decline with each successive decrease in number of mismatching markers. Thus, one would expect a single error for every 10 1MM pairs (Paetkau 2003). We used the genetic assignment test (Paetkau et al. 1995, Waser and Strobeck 1998), which calculates the probability of observing specific individual genotypes in a series of reference populations, based on observed allele frequencies in those populations. Log-likelihood estimates of the cumulative probability of occurrence of individual alleles were used to determine genetic similarity. We describe genetic diversity using the observed number of alleles (A) and expected heterozygosity (H_E) because they are metrics commonly used to describe genetic variability

(Paetkau and Strobeck 1998). We present probability of identity (P_{ID}) values to demonstrate the power markers have to identify individuals (Paetkau and Strobeck 1998).

Results

Hair trapping

We collected 635 hair samples from both islands during the study, 372 of which we considered had adequate amounts of DNA for analyses. We obtained 324 usable hair samples from 56 trap visits on Stockton Island and 48 usable samples from 14 trap visits on Sand Island (Table 1). The number of traps with hair samples remained relatively constant throughout the study. The mean number of hair samples/trap declined during successive sessions on Stockton Island. In contrast, although samples sizes were low, the mean number of hair samples/trap was greatest on Sand Island during session 4. Mean interval between trap sessions typically was within 1 day of desired duration except between sessions 3 and 4 when inclement weather delayed access to hair traps on Sand Island.

DNA analyses

Of 372 samples processed, 256 (69%) were suitable for assignment to individual black bears. Of the remaining samples, 22% were extracted but we were unable to generate a reasonable genotype, 7% were likely a mixture of DNA from 2 bears, and 2% lacked suitable material for extraction. We found only 2 pairs of genotypes that matched at 4 of 6 markers (2MM pairs) and 1 pair that matched at all but 1 marker (1MM pair). This suggests it

is highly unlikely that we sampled even a single pair of individuals with identical 6-locus genotypes.

We identified 32 individual bears from hair samples; 6 bears (1 male, 5 females) on Sand Island and 26 bears (14 males, 12 females) on Stockton Island. These individuals were captured 84 times; 71 captures on Stockton Island and 13 captures on Sand Island. For both islands combined, we captured 9 females during 2 sessions, 6 during 3 sessions, and 2 during 4 sessions. Combining males resulted in 4 captured during 1 session, 1 during 2 sessions, 6 during 3 sessions, and 4 during 4 sessions. The numbers of individuals captured during sessions 1–4 were 21, 26, 19, and 18, respectively. No new individuals were captured on Stockton Island after session 3 and on Sand Island after session 2.

Overall, 25 of 32 (78%) bears were captured at >1 hair trap. Females on Sand Island were captured on average at 2.5 (SD = 1) traps; the male was captured at 1 trap. Females on Stockton Island were captured on average at 2.9 (SD = 1.7) traps; males were captured at 4.6 (SD = 2.6) traps. During individual trap checks from which we obtained genetically identifiable hair from ≥ 1 individual ($n=57$), most (72%) contained hair from 1–3 bears; 25% contained hair from 4–6 bears, and 2% contained hair from 7 bears. No bears were captured at hair traps on both islands and no bears were removed from the islands during the study for management purposes.

Population estimates

We conducted population estimates for Stockton and Sand Island from 8 closed mark–recapture models used in CAPTURE. For Stockton Island, we used the null estimator (M_0) because we did not detect variation in capture due to heterogeneity among individuals ($\chi^2 = 0.15$, 1 df, $P = 0.70$), behavior response after initial capture ($\chi^2 = 0.09$, 1 df, $P = 0.76$), or among trapping sessions ($\chi^2 = 6.31$, 3 df, $P = 0.10$) using chi-square goodness-of-fit tests provided in CAPTURE. Additionally, the Stanley and Burnham closure test suggested the population was closed ($\chi^2 = 1.10$, 2 df, $P = 0.58$). The estimated population for Stockton Island was 26 (SE = 0.54) bears with 95% confidence interval (CI) range of 26–26. This represents a density of 0.64 bears/km². Population estimates for males ($n = 14$) and females ($n = 12$) also were identical to the known number of individuals obtained from DNA analyses. The mean capture probability among sessions was 0.68. The M:F sex ratio of 1.16:1 was similar to 1:1 ($\chi^2 = 0.15$, 1 df, $P = 0.70$).

For Sand Island, we also used the null estimator (M_0) because of lack of variation in capture due to behavior

Table 2. Variability of genetic markers used to identify individual American black bears, Stockton Island, Apostle Islands National Lakeshore, Wisconsin, USA, 2002. H_E = expected heterozygosity, H_O = observed heterozygosity, A = mean observed number of alleles, and P_{ID} = probability of identity.

Marker	H_E	H_O	A	P_{ID}
MU59	0.84	0.92	8	0.05
G1D	0.83	0.89	8	0.05
G10X	0.80	0.85	9	0.06
G10H	0.77	0.89	9	0.08
G10M	0.75	0.81	7	0.10
G10C	0.63	0.69	7	0.21
Mean	0.77	0.84	8	
Overall probability of identity				2E-07

response after initial capture ($\chi^2 = 2.28$, 1 df, $P = 0.13$) and among trapping sessions ($\chi^2 = 2.06$, 3 df, $P = 0.56$). Sample size was inadequate to test for heterogeneity of trapping probabilities among individuals in the population. Additionally, the Stanley and Burnham closure test suggested the population was closed ($\chi^2 = 0.99$, 2 df, $P = 0.61$). The estimated population for Sand Island was 6 (SE = 0.60) bears with 95% CI range of 6–7. This represents a density of 0.50 bears/km². Mean capture probability among sessions was 0.54. We also conducted an analysis using Chao's heterogeneity model (M_h) in the event heterogeneity of trapping probabilities occurred and we were unable to detect it. Model M_h performs well under strong trapping heterogeneity (Mowat and Strobeck 2000). Using M_h , we derived a similar estimate of 6 (SE = 0.54) bears (95% CI 6–9).

Genetic variation among islands

Considerable genetic variation was observed within and among islands at the 6 markers that were used to identify individuals. The mean H_O was 0.84 for Stockton Island with the probability of 2 randomly drawn, unrelated individuals with identical genotypes of 2×10^{-7} (Table 2). Although sample size was limited for Sand Island, mean H_O for markers used was 0.94, which suggests black bears on Sand Island possess higher genetic variability than black bears on Stockton Island. Using all 15 markers, 25 of 30 single-locus genotypes for the 2 Oak Island bears were heterozygous ($H_O = 0.83$).

Genetic assignment testing demonstrated considerable variation between Sand and Stockton Island bear populations (Fig. 2). A notable exception was a male captured on Stockton that had a probability of occurrence 9 orders of magnitude lower (10^{-35}) than that of the next lowest probability observed for an individual (10^{-26})

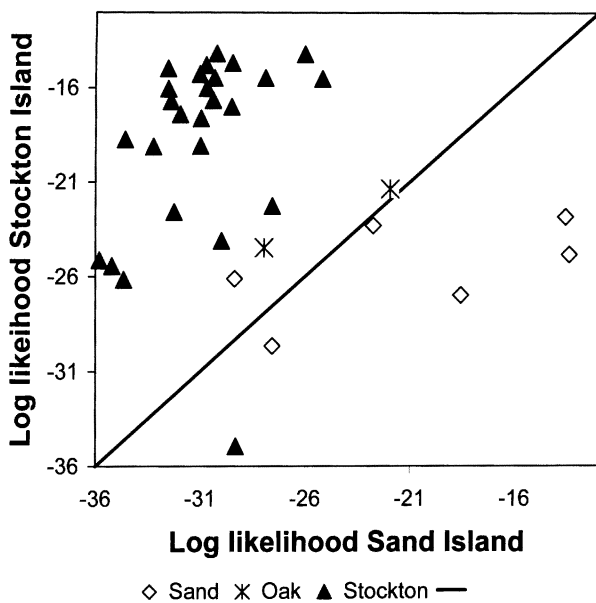


Fig. 2. Assignment testing based on log genotype likelihood probabilities for black bears on Stockton, Sand, and Oak islands, Apostle Islands National Lakeshore, Wisconsin, USA, 2002.

sampled on Stockton Island. The 2 individuals from Oak Island were intermediate to black bears on Stockton and Sand islands.

Discussion

We report the first bear population estimates in Wisconsin with data from nonharvested animals that included estimates of precision. The density of bears on Stockton Island (0.64 bears/km²) remains the highest reported in Wisconsin (Kohn 1982, Storlid 1995, Fleming 1997) and among the highest reported in North America (Garshelis 1994). The density of bears on Stockton Island was estimated previously at 0.07 bears/km² in 1984 and increased to 0.76 bears/km² in 1994 before declining to 0.61 bears/km² in 1996 (Fleming 1997). Methods between studies are not directly comparable; however, previous and current estimates suggest the population has remained approximately stable during 1990–2002. Similarly, the 1:1 sex ratio we observed for Stockton Island is comparable to those reported during earlier studies (Trauba 1996). Although population trends are unknown for Sand Island, the apparently stable population size, 1:1 sex ratio, and approximately stable age distribution during the early 1990s (Fleming 1997) on Stockton Island suggests that

the black bear population has reached the demographic effective population size (Caughley and Sinclair 1994).

We obtained a limited amount of data to develop a population estimate for Sand Island ($n = 13$ samples). However, because of geographic and demographic closure, high capture probability, and high mean number of trap sites individuals were captured at, we believe the population estimate for Sand Island is reasonable. Although the density on Sand Island was less than Stockton Island, the density of females (0.42 bears/km²) was greater than the female density on Stockton Island (0.29 bears/km²). Greater density of female bears on Sand Island could be because of greater food abundance, closer proximity to the mainland population, or a combination of these and other factors.

There are at least 2 possible explanations for the low number of males ($n = 1$) detected on Sand Island. The first is that we were unable to capture hair from other males on the island. We believe this is unlikely because of our overall high mean capture probability. It is possible, however, that additional males immigrated to the island temporarily, particularly during the breeding season, and these nonresident individuals may not have been detected. It could also be that only one male bear was present. Because of its small size (<12 km²), resources (e.g., food, territory) on Sand Island may be too limited to support additional male bears. This male bear may have used Sand Island as only part of its home range, as has been reported in other island studies (Garshelis 1994), including Stockton Island (Trauba 1996, Fleming 1997). In a previous study of mammalian biogeography at AINL, we demonstrated a significant positive relationship between island size and body mass of mammals that could be supported (Belant and Van Stappen 2002).

Although the populations on Stockton and Sand islands were small, the high genetic variability of bears in this study was similar to other mainland bear populations (Paetkau et al. 1998b). These population characteristics are incompatible unless a high rate of immigration has occurred. For example, when population estimates are available for 2 populations, and an estimate of heterozygosity is available for 1 of those populations, the heterozygosity for the second population can be estimated assuming that both populations are at equilibrium for immigration, mutation, and genetic drift (Paetkau et al. 1998b). Using data from the isolated black bear population on the island of Newfoundland (approximate $N = 6,400$, $H_E = 0.41$) and the population estimate for Stockton Island, we expect heterozygosity to be 0.3% in the latter population, assuming that this population was isolated and at equilibrium. An indistinguishable estimate

is obtained when data from Kodiak brown bears (*U. arctos*) are used (Paetkau et al. 1998b). We know from historic data that the Stockton Island population was founded too recently to be at equilibrium. Additionally, the high levels of genetic variation are incompatible with any significant period of isolation.

Considering the inescapably low sample sizes, the genetic data were remarkably successful in clustering bears based on island of origin. The exceptional Stockton Island male was clearly not born on Stockton Island, providing direct evidence of population connectivity and one of the first examples of using genetic assignment of natal origins to directly study animal movements from a single capture location. This individual may have been born on the mainland and immigrated to Stockton Island.

The placement of the 2 individuals from Oak Island intermediate to Sand and Stockton Island populations corresponds with their respective distances from the mainland and further demonstrates that a high level of genetic differentiation across islands exists. A general trend in genetic similarity as a function of distance has also been demonstrated in mainland black bear populations (Miller et al. 1998). We conclude that AINL contains bear populations small enough to cause rapid genetic drift but possesses a level of intra-population variability that could only be maintained by gene flow from the mainland population. Also, based on genetic variability observed and apparent immigration, we suggest that inbreeding depression is unlikely to be a significant threat to these populations.

Future studies quantifying levels of genetic differentiation among bear populations on additional islands at AINL and mainland Wisconsin are warranted. Such research could aid in determining dispersal patterns among islands that resulted in the relatively high variability we observed. Also, because of the range of distances among islands and between islands and the mainland, we could gain insight into sex-specific rates of movement. Paetkau et al. (1998a) demonstrated for brown bears that oceanic water crossings of 3–4 km eliminated female-mediated gene flow, whereas male dispersal continued at this level but was eliminated by 8-km water crossings.

Obtaining population estimates from mark–recapture studies using DNA from hair samples is a method suitable for long-term monitoring at AINL. Other techniques, including mark–resight estimates (e.g., Miller et al. 1997), are not feasible because of their comparative high cost and forest cover which limits visibility. Population estimators involving captured animals, however, can provide additional information, such as age, reproduc-

tion, and survival, which are also critical demographic metrics that cannot be obtained using techniques we employed. High mean individual bear capture probabilities and the low 95% CI we observed suggests that the number of hair traps at Stockton Island could be reduced. Simulation modeling with existing data from Stockton Island could refine the experimental approach for future studies. We do not recommend reducing the density of hair traps on smaller islands such as Sand Island because of the low number of traps that would be deployed and the limited number of bears likely present. We recommend periodic monitoring of bear populations on these and other islands at AINL relative to bear nuisance activity, harvest management, and to population connectivity.

Acknowledgments

We thank U. Gafvert, S. Johnson, J. Kroll, and H. Quint for field assistance. S. Waterhouse was responsible for the genetic analyses. Primary funding was provided by the National Park Service's Natural Resource Preservation and Protection program.

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Received: 25 February 2004

Accepted: 3 December 2004

Associate Editor: G. Shields