Management and Conservation Note

Success of Grizzly Bear Population Augmentation in Northwest Montana

WAYNE F. KASWORM,[1] *United States Fish and Wildlife Service, 475 Fish Hatchery Road, Libby, MT 59923, USA*
MICHAEL F. PROCTOR,[2] *Department of Biological Sciences, University of Alberta, Edmonton, AB T6G 2E9, Canada*
CHRISTOPHER SERVHEEN, *United States Fish and Wildlife Service, College of Forestry and Conservation, 309 University Hall, University of Montana, Missoula, MT 59812, USA*
DAVID PAETKAU, *Wildlife Genetics International, Box 274, Nelson, BC V1L 5P9, Canada*

ABSTRACT Augmentation of large carnivore populations can be a valuable management and recovery tool, but success of many programs has not been well documented. The Cabinet–Yaak grizzly bear (*Ursus arctos*) population was located in northwestern Montana and northern Idaho, USA, and was estimated at 30–40 individuals. The Cabinet Mountains portion of this area may be isolated from the remainder of the zone and was the site of a test of grizzly bear population augmentation. Experimental objectives included evaluating site fidelity, reproduction, and long-term survival of the translocated bears. Four subadult females (2–6 yr old) were translocated from southeastern British Columbia, Canada, from 1990 to 1994. Three of 4 transplanted bears remained in the target area for ≥1 year and satisfied the short-term goal for site fidelity. Recent genetic evidence gathered through hair-snagging efforts has determined that at least one of the original transplanted animals has reproduced, thereby providing evidence of success for the long-term goals of survival and reproduction. (JOURNAL OF WILDLIFE MANAGEMENT 71(4):1261–1266; 2007)

DOI: 10.2193/2006-266

KEY WORDS brown bear, Cabinet Mountains, genetics, grizzly bear, Montana, population augmentation, reproductive success, *Ursus arctos.*

Population size is one of the most powerful predictors of the likelihood of population persistence (Berger 1990, Shaffer et al. 2000, Reed et al. 2003) evidenced by the World Conservation Union (IUCN) category of "high risk of extinction" for species with ≤50–100 adults (IUCN 2003). The continental range contraction of grizzly bears (*Ursus arctos*) in North America over the last 2 centuries (Mattson and Merrill 2002) left behind a set of island populations south of the main continental distribution (Fig. 1). With the exception of the Yellowstone island population, these isolates are small and at great risk. Because these populations are small, do not occupy a large protected area, and because grizzly bears have low reproductive rates (Bunnell and Tait 1981), one potential management tool is population augmentation through translocating wild bears from healthy populations elsewhere (Servheen et al. 1987, Maguire and Servheen 1992, Austin 2004).

Although achieving augmentation success is challenging, it has helped reestablish self-sustaining populations of a variety of species (Wolf et al. 1996). Projects wherein wild omnivores are released into the core of their historical range using prolonged efforts up to 10 years have had the most success (75–80%; reviewed in Wolf et al. 1996). Grizzly bears, however, are wide ranging and can be dangerous, making augmentation efforts both challenging and controversial (Maguire and Servheen 1992, Austin 2004).

One likely isolated grizzly population exists in the Cabinet Mountains of western Montana and northern Idaho, USA, which is part of the Cabinet–Yaak Recovery Zone (CYRZ; Fig. 1; United States Fish and Wildlife Service [USFWS] 1993, Kasworm et al. 2005). The Cabinet Mountain population has been estimated to be <15 individuals for the past 2 decades (Kasworm and Manley 1988, Kasworm et al. 2005). Because this population is likely too small for natural recovery, the USFWS carried out an experimental augmentation program in the Cabinet Mountains (USFWS 1990). Between 1990 and 1994, 4 subadult females (2–6 yr old) were translocated from the Canadian Rocky Mountains of southeastern British Columbia into the Cabinet Mountains (Servheen et al. 1995, Kasworm et al. 1998). The objectives of that experiment were to evaluate site fidelity, reproduction, and long-term survival of the translocated bears. Bears remaining in the target area for ≥1 year satisfied the short-term goal for site fidelity, as detailed in Servheen et al. (1995) and Kasworm et al. (1998). This article reports the results of long-term monitoring of that experiment. We also report on our use of DNA hair-grab sampling to track survival and reproductive fate of one translocated female.

STUDY AREA

The CYRZ encompassed approximately 6,800 km^2 in northern Idaho and northwestern Montana (48°N, 116°W) and was adjacent to grizzly bear populations in the southern Purcell Mountains of British Columbia. The CYRZ was fragmented into 2 populations, with the Cabinet population lying south of the Kootenai River and accounting for 60% of the area of the CYRZ (Fig. 1). The study area has been further described in Kasworm et al. (1998) and Wakkinen and Kasworm (2004).

---

[1] *E-mail: wayne_kasworm@fws.gov*

[2] *Present address: 331 Front Street, Kaslo, BC V0G 1M0, Canada*

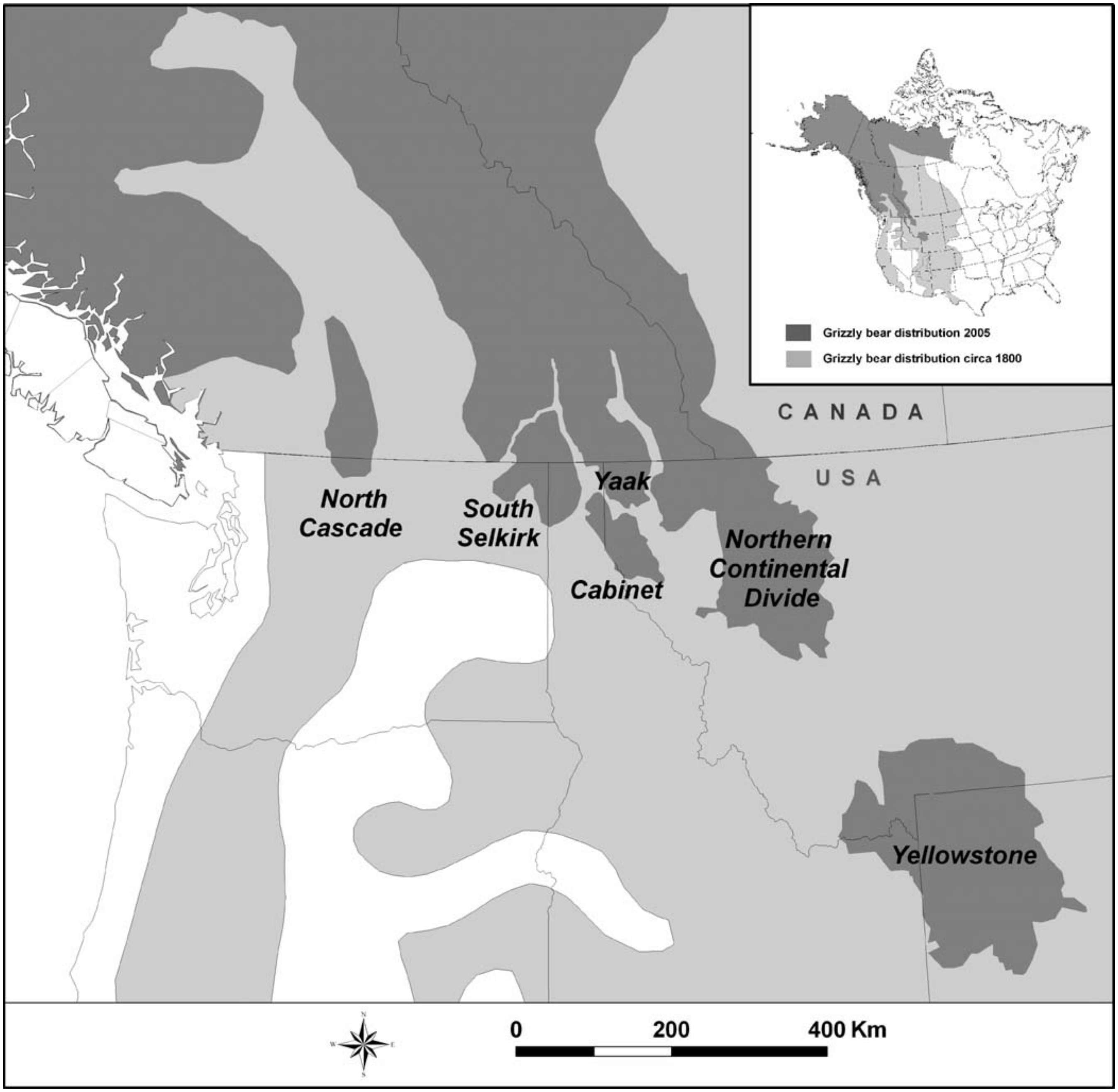

Figure 1. North American distribution of grizzly bears circa 1800 (light shading) and close-up of United States and trans-boundary island populations (dark shading) along the southern fringe of grizzly bear distribution, 2005.

METHODS

We translocated four subadult female grizzly bears (2–6 yr old) from southeastern British Columbia into the Cabinet Mountains in the summers of 1990 to 1994 (Servheen et al. 1995, Kasworm et al. 1998). We fit these bears with very-high frequency radiocollars that provided location data for 1–2 years. The University of Montana Institutional Animal Care and Use Committee (Project 006-03CSFWB-040103) reviewed and approved bear handling protocols.

Ten years later, we carried out systematic hair-snag DNA surveys (Woods et al. 1999) in the Cabinet Mountains to assess population status and look for evidence of translocated bears. We only had DNA material for one of the 4 translocated bears (samples from 3 bears were shipped to a research lab in 1990 but were inadvertently discarded). During 2002, 2004, and 2005, sampling sites ($n = 27$, 14, and 16, respectively) were established based on previous sightings, sign, and radiotelemetry locations of research bears. In 2003, we placed one site in each of 187 5×5-km cells on a grid across 4,300 km^2. We baited sites with 2 L of a blood-and-fish mixture to attract bears across a barbed wire perimeter placed to snag hair. Sites were in place for 2 weeks prior to hair collection. We sampled one-third of the sites during each of the months of June, July, and August, and we stratified sites by elevation to coincide with seasonal

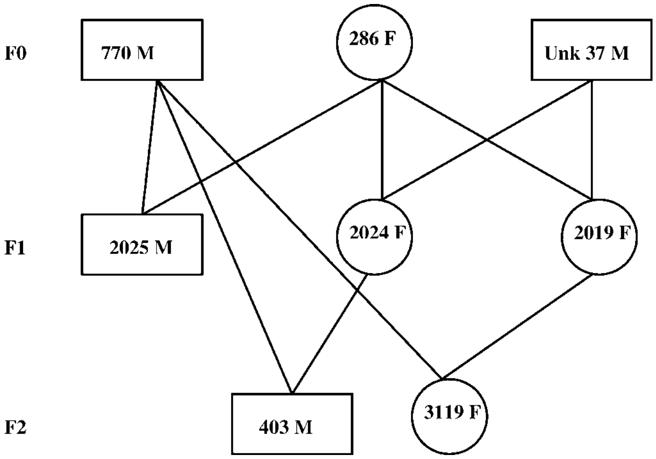

Figure 2. Most likely pedigree resulting from translocated grizzly bear 286 F into the Cabinet Mountains, USA, 1993–2005. Pedigree contains family groups where both parents complementarily share one allele at all loci with the offspring and match as parents (see Table 1). Squares indicate males and circles represent females. Lines indicate a parent–offspring relationship. Pedigree shown includes all the family group triads found in our sample. Alternative pedigrees (not shown) must ignore one or more of these family groups, and are therefore less likely. F0 is the initial generation, F1 is the first generation of offspring for translocated female 286, and F2 is the second generation.

shifts in grizzly bear habitat use. We also used remote cameras at some sites during all years.

Between 1983 and 2005, we collected genetic samples from wild grizzly bears from the Cabinet ecosystem through research captures, mortalities, or hairs from the environment (rub trees, etc).

Wildlife Genetics International (Nelson, BC, Canada) performed genetic analyses. The lab used total cell DNA from 1–10 hair follicles or a tissue biopsy to generate 7-locus microsatellite genotypes to identify individual grizzly bears (Paetkau et al. 1998). Because multiple samples were often assigned to the same individual, we selected one sample from each individual to be sexed (Ennis and Gallagher 1994) and genotyped at an additional 8 microsatellite markers (for a total of 15 loci; Paetkau et al. 1998, Proctor et al. 2002). To minimize genotyping errors during analysis of individual identity (using 7 loci), we followed protocols detailed in Woods et al. (1999) and Paetkau (2003). When using one sample per individual to run the additional 8 loci necessary for pedigree analysis, these protocols do not apply. Therefore, analysis of gender and additional markers made use of the best sample from each individual, as judged by signal strength during analysis of individual identity; better samples presumably have higher concentrations of DNA and are less prone to errors during genotyping (Taberlet et al. 1996).

To determine if the translocated individual for which we had DNA was present in the Cabinet Mountains 10 years after augmentation, we looked for an exact 15-loci match with any new bear identified from the 2002 to 2004 surveys. To determine whether this bear had contributed offspring to the population we looked for genotypes that shared ≥ 1 of their 2 alleles with the translocated bear at each of the 15 markers. Bears meeting these criteria became our pool of potential mother–offspring pairs. Then, we looked for males whose genotypes could account for all of the alleles in these potential offspring that were not accounted for by the translocated female and thereby qualified as potential fathers. After identifying all of the putative father–mother–offspring triads that matched perfectly at 15 loci, we built pedigrees posed as hypotheses with all matching family group options.

The probability of a complementary 15-locus match between a potential mother, father, and offspring being due to chance is many times smaller than a 15-locus match between an offspring and one parent. However, we did not have a sufficient sample of unrelated individuals that originated from the Cabinet Mountains to estimate biologically realistic allele frequencies that could be used to calculate family dyad and triad probabilities.

For further confirmation that our results were not due to chance matching of genotypes, we tested to see how common it would be for a random female from the Rocky Mountains to match an offspring and a father in the Cabinet Mountains. In other words, we examined how easy it was to obtain our family triad results by chance alone. To do this we tested 172 female grizzly bears from the Rockies (the source population of the augmented bears) that we had in a 15-locus genetic database to see how many (if any) fit in a complementary allele–sharing family group.

RESULTS

Three of the 4 originally translocated bears remained in the Cabinets for ≥ 1 year, and one died of unknown causes after 1 year (Kasworm et al. 1998). There were no reports of conflict with humans for any of these translocated bears.

We opportunistically collected 34 hair or blood samples from capture and mortalities or hair located at rub sites, such as signs or bridges, during 1983 to 2005. The DNA surveys from 2002 to 2005 yielded 1,194 bear hair samples ($n = 153$, 908, 61, and 72, respectively), 33 of which were from grizzly bears. The grizzly bear samples yielded 15 different genotypes. One of these genotypes matched the translocated female (bear 286), indicating she was still alive in the Cabinet Mountains 12 years after release. This bear shared ≥ 1 allele at all 15 loci with 3 other bears, consistent with the possibility of parent–offspring relationships. Furthermore, we found males with genotypes that contained alleles with a perfect complementary match for each of these putative offspring. These allele-sharing patterns strongly suggest that translocated female 286 had 2 litters with 2 separate fathers, producing ≥ 3 offspring (Fig. 2). An example of evidence used for these family group inferences is displayed in Table 1. This type of complementary allele sharing exists for the entire pedigree displayed in Fig. 2. Female 286 was 2 years old in 1993 when she was released in the Cabinet Mountains. The likely earliest age for her first litter would be in 1996 at 5 years of age. If that litter consisted of bears 2019 and 2024, they would have been 5–6 years old, capable of reproducing in 2001 or 2002. During the Cabinet

Table 1. Allele sharing pattern of maternal and paternal grizzly bear contributions to offspring produced in the Cabinet Mountains, USA, 1990–2005.

		Locus[a]							
Relationship	**Bear**	**A**	**B**	**C**	**D**	**H**	**J**	**L**	**M**
Mother[b]	286	**194** 198	**162** 158	**205** 207	**175** 180	**223** 223	**190** 190	**157** 157	**210** 206
Cub	2019	**194** *194*	**162** *162*	***205*** *203*	**175** *184*	**223** *231*	**190** *202*	**157** *155*	**210** *206*
Father[c]	Unk39	198 *194*	158 *162*	211 *203*	183 *184*	223 *231*	186 *202*	157 *155*	212 *206*

		Locus[a]						
Relationship	**Bear**	**P**	**U**	**X**	**20**	**110**	**50**	**59**
Mother[b]	286	**151** 159	**163** 163	**139** 141	**131** 127	**151** 151	**130** 130	**223** 223
Cub	2019	**151** *159*	**163** *165*	**139** *141*	**131** *131*	**151** *155*	**130** *138*	**223** *223*
Father[c]	Unk39	151 *159*	163 *165*	141 *141*	127 *131*	153 *155*	132 *138*	223 *223*

[a] Genotypes consist of 15 locus microsatellite markers. There are 2 alleles at each locus within each individual. In this case, alleles are the number of base pairs in the DNA sequence at any particular locus. Note the complementary sharing of alleles within the offspring. The pedigree in Fig. 2 is supported by complete complimentary matching within each family triad.

[b] The set of alleles from the mother are in boldface.

[c] The set of alleles from the father are in italics.

Mountains DNA survey, bears 2019 and 3119 (Fig. 2) were both sampled at the same DNA sampling station at the same time. Sample 2019 was taken off the barbed wire (50 cm off the ground) and sample 3119 was taken off the bait pile in the center of the wire enclosure, as might be expected from a cub traveling with its mother and that was small enough to pass under the wire without leaving a hair sample. Bear 3119 was struck and killed by a train in 2005. Samples from bears 2024 and 403 (Fig. 2) were also caught at the same station at the same time. Furthermore, a remote camera documented a mother and cub visiting the site together during the period they were sampled. All ancillary evidence we collected surrounding these samples is consistent with our hypothesized pedigree (Fig. 2).

In our search for south Rocky Mountain females that would match family groups in the Cabinet Mountains by chance, we found no females out of 172 that fit within a family group with complementary allele matching at 15 loci.

DISCUSSION

Our results suggested that experimental augmentation affected the persistence, size, and genetic diversity of the Cabinet Mountains grizzly bear population between 1990 and 2005. Five of 15 sampled individuals from this population, and possibly more if the other translocated females reproduced, appeared to trace some of their genetic ancestry to translocated female 286. Our method for establishing pedigrees was limited for several reasons. First, the Cabinet Mountains population is very small and subsequently so was our sample size (n = 15). More importantly, we believe that many of the individuals in our sample were immediate relatives, so they did not constitute independent samples for the purposes of estimating allele frequencies. It also appears that many of the individuals in our sample have genes imported from the Canadian Rocky Mountains source population. In essence, our genetic sample for the Cabinet Mountains is a mixture of 2 populations and is heavily skewed by closely related individuals. Therefore, developing traditional probabilities for population-specific allele frequencies would not be biologically meaningful (Hartl and Clark 1997). The fact that none of the 172 females from the southern Rocky Mountains source population matched within a family triad with any of the Cabinet Mountains grizzly bears supported the family group relationships portrayed in Fig. 2.

This effort demonstrated the utility of hair-grab genetic sampling as a monitoring tool for rare and elusive organisms. While we recommend that all future translocated bears be fitted with radiocollars, we also recommend that periodic genetic sampling should complement augmentation efforts. It has been difficult to capture grizzly bears in the Cabinet Mountains during a prolonged effort over several years (7 bears captured over 6,144 trap-nights). Although radiotelemetry would provide needed information, genetic sampling enabled us to detect the presence of grizzly bears in a small, low-density population. Genetic sampling can also provide a mechanism to estimate population size through time (Boulanger et al. 2004), particularly if the population grows enough to allow sufficient sample sizes for statistical rigor. Because augmentation is artificially moving genes between populations, it will be difficult to use individual-based population genetics to monitor any natural migration and assess the efficacy of management that improves interpopulation linkages (Proctor et al. 2005).

This technique detected ≥ 1 of the 3 possible augmentation bears placed in the Cabinet Mountains during 1990 to 1994 that could have survived to reproduce. We could not detect the other 2 bears because we lacked reference genetic material, but they may have survived and produced young.

Beyond the family groups detected in the pedigree in Fig. 2, we found the remaining 7 bears appear to belong to 2 family groups. One triad contained a mother–father–offspring (bears 678, 14, and 680, respectively, captured 1983 to 1985) with perfect complementary matching alleles. In this case, the mother is thought to have been 37 years old when she died and may be one of the oldest recorded wild grizzly bears. Her death was documented by discovery of a claw and bones by a hunter. We were able to extract DNA from the claw and match it to the DNA obtained when she was previously captured. The other family group was a mother and 3 yearlings, sampled when the mother was killed by a train in 2001. This female appeared to have left 3 surviving offspring that were captured near the kill site and shared alleles with the putative mother in a pattern consistent with family group status. The frequency of closely related individuals among our sample from the Cabinet Mountains grizzly bears is unusual relative to samples from larger populations and suggests a small population with limited breeding opportunities from unrelated individuals.

Because self-sustaining status is a primary goal of recovery efforts in the Cabinet Mountains (USFWS 1993), augmentation should be considered a temporary action within a comprehensive conservation strategy that includes actions that improve conditions over current threatened status. Simulations demonstrate that augmentation alone will not recover a small grizzly bear population when mortality is high. Improved female survival in addition to augmentation and linking this small isolated population with adjacent grizzly populations are all essential (Proctor et al. 2004). Human-caused mortality dominates grizzly bear population dynamics in the region (McLellan et al. 1999, Wakkinen and Kasworm 2004) and its reduction can aid recovery of small bear populations. The USFWS is currently implementing strategies to minimize human-caused mortality, improve interpopulation linkage with adjacent areas, improve habitat quality and security, and enhance public support for coexistence with grizzly bears (Servheen et al. 1995, Proctor et al. 2004). Augmentation is a necessary additional component, and is key to increasing numbers of bears so that the comprehensive management program can be successful. Furthermore, because we do not know much about the number and ages of the current reproductive male cohort in the Cabinet Mountains, we recommend that, in addition to subadult females, several males be transplanted to ensure adequate genetic variation and reproductive opportunities for all adult females. Our results demonstrate that augmentation can have dramatic positive impacts on isolated grizzly bear populations and is an important tool in recovery efforts.

MANAGEMENT IMPLICATIONS

The Cabinet Mountains population may be isolated from any adjacent occupied grizzly bear area; therefore, augmentation combined with other conservation measures (Proctor et al. 2004) may be required to achieve recovery of this population. We recommend that augmentation be resumed in addition to increased efforts to reduce human-caused mortality and improve linkage to adjacent populations.

ACKNOWLEDGMENTS

We are indebted to C. Bechtold, J. Brown, M. Burcham, H. Carriles, A. Christensen, R. Demarchi, J. Frey, A. Fontana, B. Forbes, B. Giddings, S. Greer, R. Groom, D. Johnson, W. Johnson, K. Kinden, M. Madel, T. Manley, B. McLellan, G. Miller, C. Miller, J. Picton, R. Pisciotta, T. G. Radandt, D. Reiner, R. Shoemaker, B. Summerfield, S. Smith, T. Thier, T. Vecchiolli, C. Whitman, S. T. Wong, G. Woods, and C. Wultsch for assistance on this project. We thank E. C. Hellgren and L. G. Adams for reviews of the draft manuscript.

LITERATURE CITED

Austin, M. A. 2004. Grizzly bear recovery planning in the British Columbia portion of the north Cascades: lessons learned and re-learned. Ursus 15:123–128.

Berger, J. 1990. Persistence of different-sized populations: an empirical assessment of rapid extinctions in bighorn sheep. Conservation Biology 4: 91–98.

Boulanger, J., B. N. McLellan, J. G. Woods, M. F. Proctor, and C. Strobeck. 2004. Sampling design and bias in DNA-based capture–mark–recapture population and density estimates of grizzly bears. Journal of Wildlife Management 68:457–469.

Bunnell, F. L., and D. E. N. Tait. 1981. Population dynamics of bears—implications. Pages 75–98 *in* T. D. Smith and C. Fowler, editors. Dynamics of large mammal populations. John Wiley and Sons, New York, New York, USA.

Ennis, S., and T. F. Gallagher. 1994. A PCR-based sex determination assay in cattle based on the bovine Amelogenin locus. Animal Genetics 25: 425–427.

Hartl, D. L., and A. G. Clark. 1997. Principles of population genetics. Third edition. Sinauer, Sunderland, Massachusetts, USA.

IUCN. 2003. Guidelines for application of IUCN Red List criteria at regional levels. Version 3.0. IUCN Species Survival Commission, IUCN—The World Conservation Union, Gland, Switzerland, and Cambridge, United Kingdom.

Kasworm, W. F., H. Carriles, T. G. Radandt, and C. Servheen. 2005. Cabinet–Yaak grizzly bear recovery area 2004 research and monitoring progress report. U.S. Fish and Wildlife Service, Missoula, Montana, USA.

Kasworm, W. F., and T. L. Manley. 1988. Grizzly bear and black bear ecology in the Cabinet Mountains of Northwest Montana. Montana Department Fish, Wildlife, and Parks, Helena, USA.

Kasworm, W. F., T. J. Their, and C. Servheen. 1998. Grizzly bear recovery efforts in the Cabinet–Yaak ecosystem. Ursus 10:147–153.

Maguire, L. A., and C. Servheen. 1992. Integrating biological and social concerns in endangered species management; augmentation of grizzly bear populations. Conservation Biology 6:426–434.

Mattson, D. J., and T. Merrill. 2002. Extirpations of grizzly bears in the contiguous United States, 1850–2000. Conservation Biology 16:1123–1136.

McLellan, B. N., F. W. Hovey, R. D. Mace, J. G. Woods, D. W. Carney, M. L. Gibeau, W. L. Wakkinen, and W. F. Kasworm. 1999. Rates and causes of grizzly bear mortality in the interior mountains of British Columbia, Alberta, Montana, Washington, and Idaho. Journal of Wildlife Management 63:911–920.

Paetkau, D. 2003. An empirical exploration of data quality in DNA-based population inventories. Molecular Ecology 12:1375–1387.

Paetkau, D., G. F. Shields, and C. Strobeck. 1998. Gene flow between insular, coastal, and interior populations of brown bears in Alaska. Molecular Ecology 7:1283–1292.

Proctor, M., B. N. McLellan, and C. Strobeck. 2002. Population fragmentation of grizzly bears in southeastern British Columbia, Canada. Ursus 13:153–160.

Proctor, M. F., B. N. McLellan, C. Strobeck, and R. M. R. Barclay. 2005. Genetic analysis reveals demographic fragmentation of grizzly bears yielding vulnerably small populations. Proceedings of the Royal Society of London, Series B 272:2409–2416.

Proctor, M. F., C. Servheen, S. D. Miller, W. F. Kasworm, and W. L. Wakkinen. 2004. A comparative analysis of management options for grizzly bear conservation in the U.S.–Canada trans-border area. Ursus 15: 145–160.

Reed, D. H., J. J. O'Grady, B. W. Brook, J. D. Ballou, and R. Frankham.

2003. Estimates of minimum viable population sizes for vertebrates and factors influencing those estimates. Biological Conservation 113:23–34.

Servheen, C., W. Kasworm, and A. Christensen. 1987. Approaches to augmenting grizzly bear populations in the Cabinet Mountains of Montana. International Conference on Bear Research and Management 7:363–367.

Servheen, C., W. F. Kasworm, and T. J. Thier. 1995. Transplanting grizzly bears *Ursus arctos horribilis* as a management tool—results from the Cabinet Mountains, Montana, USA. Biological Conservation 71:261–268.

Shaffer, M. L., L. Hood, W. J. I. Snape, and I. Latchis. 2000. Population viability analysis and conservation policy. Pages 123–142 *in* S. R. Bessinger and D. R. McCullough, editors. Population viability analysis. University of Chicago Press, Chicago, Illinois, USA.

Taberlet, P., S. Griffin, B. Goossens, S. Questiau, V. Manceau, N. Escaravage, L. P. Waits, and J. Bouvet. 1996. Reliable genotyping of samples with very low DNA quantities using PCR. Nucleic Acids Research 24:3189–3194.

United States Fish and Wildlife Service [USFWS]. 1990. Final environmental assessment, grizzly bear population augmentation test, Cabinet–Yaak ecosystem. U.S. Fish and Wildlife Service, Missoula, Montana, USA.

United States Fish and Wildlife Service [USFWS]. 1993. Grizzly bear recovery plan. U.S. Fish and Wildlife Service, Missoula, Montana, USA.

Wakkinen, W. L., and W. F. Kasworm. 2004. Demographics and population trends of grizzly bears in the Cabinet–Yaak and Selkirk ecosystems of British Columbia, Idaho, Montana, and Washington. Ursus 15:65–75.

Wolf, C. M., B. Griffith, C. Reed, and S. A. Temple. 1996. Avian and mammalian translocations: update and reanalysis of 1987 survey data. Conservation Biology 10:1142–1154.

Woods, J. G., D. Paetkau, D. Lewis, B. N. McLellan, M. Proctor, and C. Strobeck. 1999. Genetic tagging free-ranging black and brown bears. Wildlife Society Bulletin 27:616–627.

Associate Editor: McCorquodale.