Effectiveness of DNA Sampling to Monitor Black Bear Abundance in the Southern Appalachians

KATIE E. SETTLAGE, Department of Forestry, Wildlife and Fisheries, University of Tennessee 274 Ellington Plant Sciences Building, Knoxville, TN 37996; ksettlag@utk.edu
FRANK T. VAN MANEN, JOSEPH D. CLARK, and TIM KING, U.S. Geological Survey, Leetown Science Center; DAVID GREGORY, Georgia Department of Natural Resources; MARK JONES, North Carolina Wildlife Resources Commission; SKIP STILL, South Carolina Department of Natural Resources; BILL STIVER, National Park Service; and GARY PETERS, U.S. Forest Service.

INTRODUCTION

In 1976, state and federal biologists from Georgia, North Carolina, South Carolina, and Tennessee formed what is formally known as the Southern Appalachian Black Bear Study Group (SABBSG) to share data and develop consistent techniques for monitoring the regional black bear population (*Ursus americanus*). Over the years, participating agencies have consistently identified the need for an accurate population estimate for the region and the ability to track population trends over time. Conventional mark-recapture techniques based on capture and release have been used to estimate bear populations in smaller study areas but are costly, labor intensive, logistically difficult to conduct, and often provide population estimates with relatively low precision and accuracy. A relatively new technique is to "mark" and recapture animals based on DNA collected from hair samples. This technique has advantages over live trapping, including increased capture probability, tag permanency, reduced bias, and decreased intrusiveness (Woods et al. 1999, Mills et al. 2000). However, as with any population estimation technique, DNA sampling requires an investment of time and resources, and its feasibility and optimal sampling regimes should be established before a full-scale monitoring program can be put into place. Therefore, we conducted a pilot study to determine the feasibility of DNA sampling for black bear population estimation in the southern Appalachians.

METHODS

We conducted our study in two study areas: the northwest portion of Great Smoky Mountains National Park in Tennessee (≈ 16,000 ha), and a southern study area on national forest lands where Georgia, South Carolina and North Carolina meet (≈ 32,900 ha). Locations for hair-capture sites were established by generating locations within 500 m from roads or trails with ArcView® GIS (ESRI, Redlands, California, USA). The total number of hair-capture sites was determined by examining the effective sampling area of each site, which we defined by a radius around each sample site based on the size of an average female home range. Our goal was to have a density of 4 hair capture sites per average female home range (Otis et al. 1978). We established 64 sample sites in the northern study area and 57 sites in the southern study area (Fig. 1).

Each hair-capture site consisted of a barbed-wire enclosure with bait. Barbed wire was stretched 40–50 cm above ground around 4 corner trees to form a square of approximately 5 x 5 m. Bait, consisting of bakery products, was hung on a wire stretched diagonally between 2 corner trees in such a way that a bear could not reach it without entering the enclosure. All sites were checked for hair samples and rebaited once every 7 days for 10 weeks during summer 2003.

We randomly chose up to 25 samples per weekly sampling period for DNA analysis in each study area. Microsatellite DNA sequencing was performed at Leetown Science Center, a U.S. Geological Survey facility. It is important to quantify the power of the microsatellites to identify different individuals. Therefore, we calculated the probability of identity (PI), a commonly used statistic that estimates the probability of obtaining identical genotypes given certain allele frequency distributions.

We used multiple mark-recapture models (closed models) to estimate population size (Seber 1982, Otis et al. 1978). These models allow for the relaxation of certain sampling assumptions because they are able to incorporate the effects of behavioral responses to trapping (model *Mb*), temporal biases (model *Mt*), heterogeneity (model *Mh*), or a combination of the three. We also considered 3 additional models described by Chao (1987, 1988, 1989) and Chao et al. (1992). Those models are modified calculations of *Mh* and *Mt* described by Otis et al. (1978) and are specifically designed to provide reliable population estimates when capture probabilities are relatively low. Population estimates were generated with Program CAPTURE (Rexstad and Burnham 1992).

We will use the DNA data to determine the feasibility of this sampling technique for estimating bear abundance in the southern Appalachians. Various scenarios of trap density, sampling duration, and subsamples per period will be analyzed to determine how these factors influence population estimation.

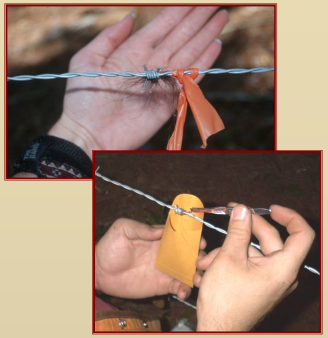
ACKNOWLEDGMENTS

Funding and logistical support for this study was provided by The University of Tennessee, U.S. Geological Survey, U.S. Forest Service, Friends of the Smokies, North Carolina Wildlife Resources Commission, South Carolina Department of Natural Resources, Georgia Department of Natural Resources, The National Park Service, and U.S. Geological Survey. Many thanks to the field technicians: C. Hill, D. Gammons, A. Brown, H. Millsaps, C. Lowe, M. Penrod, M. Smith, and M. Garner.

PRELIMINARY RESULTS

We collected 1,372 hair samples in Great Smoky Mountains National Park from 64 sites. The number of sites visited by week was highest during the middle of the 10-week sampling period (Fig. 2). A total of 205 DNA samples could be analyzed for Great Smoky Mountains National Park, representing 129 different bears. There were 117 sample matches representing 41 bears. As such, 88 bears were not recaptured. Using Program CAPTURE, we generated a preliminary population estimate (model *Mh* jackknife) of 291 bears (95% CI = 251-345) for the study area in Great Smoky Mountains National Park.

In the southern study area, 57 sites yielded a total of 584 hair samples. Although the proportion of sites visited by week was lower compared with Great Smoky Mountains National Park, the temporal trends were similar (Fig. 3). A total of 181 DNA samples could be analyzed, representing 60 different bears. There were 150 sample matches representing 29 bears; 31 bears were not recaptured. The preliminary population estimate for the southern study area (model *Mh* jackknife) was 103 bears (95% CI = 85-136).



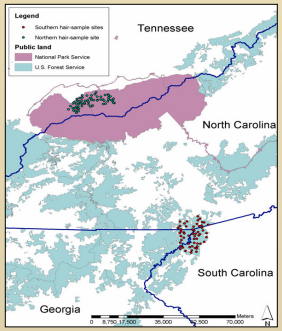


Fig. 1. Distribution of hair-snares in Great Smoky Mountains National Park and the southern study area, 2003.

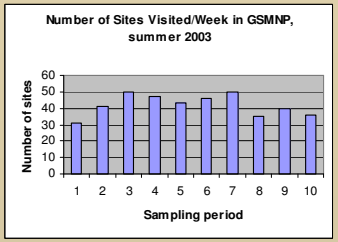


Fig. 2. Number of hair-capture sites visited by week in Great Smoky Mountains National Park, 2003.

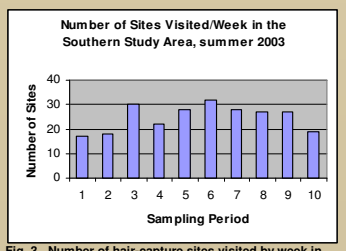


Fig. 3. Number of hair-capture sites visited by week in the southern study area, 2003.

DISCUSSION, MANAGEMENT IMPLICATIONS, AND FUTURE ANALYSES

Black bears in the southern Appalachian mountains inhabit relatively contiguous habitat and thus represent a shared resource for the state and federal agencies in charge of bear management. As such, regional estimates of black bear population abundance and techniques to monitor regional population trends are important information needs. For example, a better understanding of regional bear densities and population trends can be useful to set regional harvest levels and to develop effective measures to control bear nuisance activity. DNA sampling offers one of the first potentially useful techniques to establish regional population estimates for wide-ranging carnivores such as black bears. Our pilot study was designed to determine the feasibility of DNA sampling for regional population estimation and, if feasible, to establish optimal sampling regimes.

The preliminary findings of our study indicate that a sufficient number DNA samples can be collected in an efficient manner. Although the sample sizes for the southern study area were lower than those from the national park study area, samples sizes from both areas were relatively large. The number of sample sites visited per week typically represented 30 to 80% of the total sample sites, providing a good sampling intensity. Moreover, samples from both study areas had sufficient amounts of DNA for sequencing, as indicated by a 82% success rate for the national park and a 86% success rate for the southern study area. The precision of the DNA-based estimates was greater than those based on livecapture data. For example, using mark-recapture data for 1989-2004, the 2003 Jolly-Seber population estimate for the traditional national park study area (328-km^2) was 215 bears with a 95% confidence interval of 157–272.

Future analyses of the DNA data will focus on determining the effects of sampling site density, sampling duration, and subsampling intensity on capture probabilities and the precision of the population estimates. We will examine a variety of sampling scenarios to provide guidelines for proper sampling regimes. High or low bear densities or closely related bear populations may pose unique challenges to this sampling technique. For example, capture probabilities in the southern study area were greater than in the national park; the lower population densities in the southern study area likely provided more opportunities for bears to be recaptured, thus increasing the precision of the population estimates. Therefore, we will also examine how the different bear densities in the 2 study areas may influence the feasibility and effectiveness of population estimation based on DNA sampling.

LITERATURE CITED

Chao, A. 1987. Estimating population size for capture-recapture data with unequal catchability. Biometrics 43:783–791.
_____. 1988. Estimating animal abundance with capture frequency data. Journal of Wildlife Management 52:295–300.
_____. 1989. Estimating population size for sparse data in capture-recapture experiments. Biometrics 45:427–438.
_____, S.M. Lee, and S.L. Jeng. 1992. Estimating population size for capture-recapture data when capture probabilities vary by time and individual animal. Biometrics 48:201–216.
Mills, L.S., J.J. Citta, K.P. Lair, M.K. Schwartz, D.A. Tallmon. 2000. Estimating animal abundance using noninvasive DNA sampling: promise and pitfalls. Ecological Applications 10:283–294.
Otis, D.L., K.P. Burnham, G.C. White, and D.R. Anderson. 1978. Statistical inference from capture data on closed animal populations. Wildlife Monographs 62.
Rexstad, E., and K.P. Burnham. 1992. User's guide for interactive program CAPTURE. Colorado Cooperative Fish and Wildlife Research Unit, Colorado State University, Fort Collins, Colorado, USA.
Seber, G.A.F. 1982. The estimation of animal abundance and related parameters. Second edition. MacMillan, New York, New York, USA.
Woods, J.G., D. Paetkau, D. Lewis, B.L. McLellan, M. Proctor, and C. Strobeck. 1999. Genetic tagging free-ranging black and brown bears in mark-recapture experiments. Wildlife Society Bulletin 27:616–627.

A collaborative project of the State and Federal agencies of the Southern Appalachian Black Bear Study group (SABBSG)