

Estimating density of American black bears (*Ursus americanus*) in New Mexico using noninvasive genetic sampling-based capture-recapture methods

M. J. Gould¹, J. W. Cain III², G. W. Roemer¹, W. R. Gould¹, S. G. Liley³

¹New Mexico State University, Las Cruces, N.M.; ²U.S. Geological Survey, New Mexico Cooperative Fish and Wildlife Research Unit, Las Cruces, N.M.; ³New Mexico Department of Game and Fish, Santa Fe, N.M.

INTRODUCTION

One of the main challenges a resource agency faces is estimating animal populations and setting harvest levels that ensure long-term existence of the species. This is especially true for animals that are cryptic and difficult to count through traditional methods such as aerial surveys. By using genetic material, wildlife managers can identify individuals within a population and use spatial mark-recapture analysis to determine population density. Objectives of this study were to estimate density of black bears older than 1 year in primary bear habitats in the Sangre de Cristo, Sandia, and Sacramento mountains (Figure 1). Results of this study will provide density estimates that will be used to establish harvest levels for responsible management and assured longevity of black bears in New Mexico.

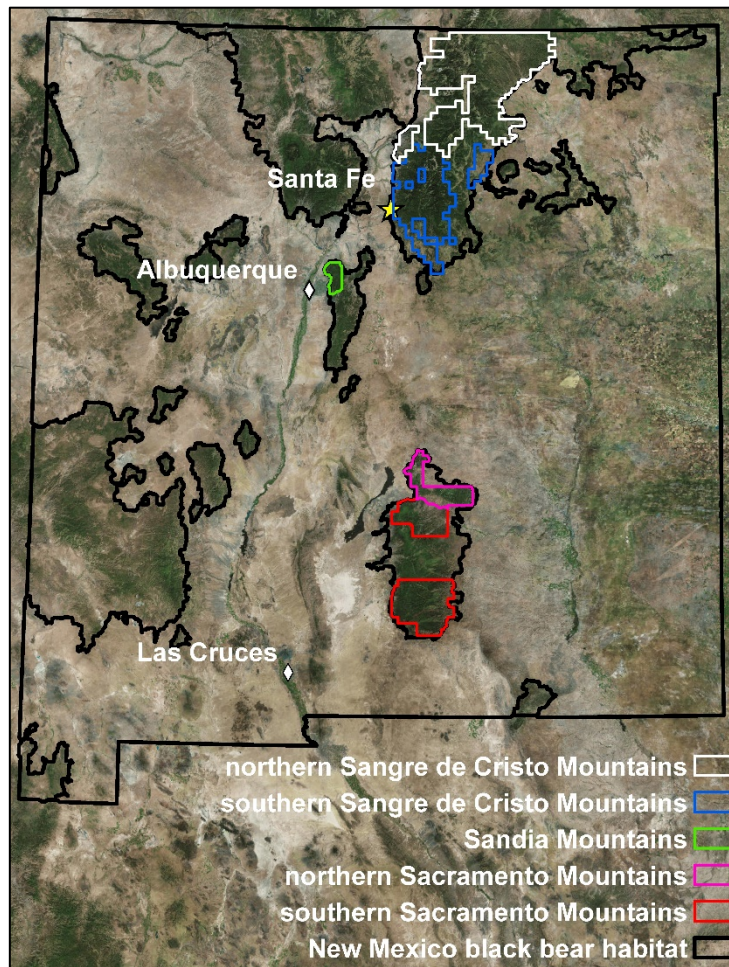


Figure 1. Aerial imagery of the Sangre de Cristo Mountains, Sandia Mountains, and Sacramento Mountains study areas.

METHODS

Field Sampling

We used two concurrent-noninvasive genetic sampling methods to collect samples for estimating black bear densities: hair traps, and bear rubs (Woods et al 1999, Kendall et al. 2008). We systematically distributed hair traps across primary habitat as identified by Costello et al. (2001), using a randomly distributed grid of 5 x 5-km cells, with 4 sampling occasions in the Sangre de Cristo Mountains and 6 sampling occasions in the Sandia and Sacramento Mountains throughout the summer months in 2012-2014 (Table 1).

Table 1. Number of grid cells and sampling dates in each of 5 black bear study areas in New Mexico, 2012-2014.

Mountain Range	# of Grid Cells	Sampling Dates
Northern Sangre de Cristo Mountains	265	April 22 - Sept 5, 2012
Southern Sangre de Cristo Mountains	141	April 29 - Sept 9, 2013
Sandia Mountains	12	May 6 – Aug 7, 2014
Northern Sacramento Mountains	37	May 5 – Aug 5, 2014
Southern Sacramento Mountains	109	May 5 – Aug 5, 2014

A hair trap consisted of a single strand of barbed wire placed around 3-6 trees with a non-consumable lure placed at the center. During each sampling occasion, hair traps were moved and 1 of 4 lures (blood/fish emulsion, skunk/lanolin, anise oil, and fatty acid scent tablet) was randomly selected to increase novelty of hair traps and consequently increase recapture rates. When a bear passed over or under the wire a barb snagged a tuft of hair from the individual. We deposited each hair sample in a separate paper coin envelope, and sterilized barbed wire using a propane torch to ensure any remaining hair was removed to prevent false recaptures the next sampling occasion.

Bear rubbing is a natural behavior in which bears rub on structures including trees, power poles, barbed-wire fences, wooden signs, and road sign posts. We opportunistically collected hair on bear rubs and power poles along trails and roads used to deploy hair traps. We attached 3 short strands of barbed wire to the structure in order to collect higher quality samples (Kendall et al. 2008, 2009). All hair samples were stored in an air-tight container on a silica desiccant at room temperature (Kendall et al 2009).

Genetic Analysis

Individuals were identified by comparing multilocus genotypes generated from genetic samples using eight nuclear, polymorphic microsatellite loci: G1D, G10B, G10L, G10M, G10H, G10J, G10U, MU59, and an amelogenin sex marker. Specific markers were selected by ensuring that mean expected heterozygosity for each marker was between 0.70 and 0.80. Dr. David Paetkau, President of Wildlife Genetics International in Nelson, British Columbia, directed collection of genetic data.

Density Estimation

We estimated black bear density in the following study areas: the northern Sangre de Cristos including Vermejo Park, northern Sangre de Cristos excluding Vermejo Park, southern Sangre de Cristos, Sandias, northern Sacramentos, and southern Sacramentos. The northern Sangres was analyzed with and without Vermejo Park because it is a large privately owned area whose natural resource management activities differ from surrounding areas. We used genotypes of individual samples to generate a capture history for each uniquely identified black bear. We used this capture history to estimate density using spatially explicit capture-recapture models (SECR; Borchers and Efford 2008, Efford et al. 2013) using the R package “secr” (Efford 2013). The advantage of SECR is that it provides direct density estimates without having to estimate an effective trapping area, which introduces an unknown but potentially substantial source of error. We used model covariates to help explain differences in detection and heterogeneity, which can bias density estimates. Candidate model covariates included detection type (hair trap or bear rub), temporal variation, land cover, and both additive and interactive effects. We also modeled sampling effort by using the number of days each hair trap and bear rub was active.

RESULTS

Field Sampling and Genetic Analyses

Number of hair samples collected and number of hair samples which were assigned an individual identity are presented in Table 2. These values represent samples collected during all 4 (Sangre de Cristo Mountains) and 6 (Sandia and Sacramento mountains) sampling occasions.

Table 2. Number of hair samples collected and number of hair samples which were assigned an individual identity in New Mexico, 2012-2014

Mountain Range	# of Hair Samples Collected	# of Hair Samples Assigned an Individual Identity (%)
Northern Sangre de Cristo Including Vermejo	1,895	699 (37%)
Northern Sangre de Cristo Excluding Vermejo	1,284	577 (45%)
Southern Sangre de Cristo	746	267 (36%)
Sandia	177	61 (35%)
Northern Sacramento	374	185 (50%)
Southern Sacramento	888	272 (31%)

Density Estimation

Black bear density estimates and associated 95% confidence intervals produced by using SECR statistical methods are presented in Table 3.

Table 3. Density estimates and 95% confidence intervals for black bears in study areas in New Mexico, 2012-2014.

Mountain Range	Mean Density Estimate (bears/100 km²)	95% Confidence Interval
Northern Sangre de Cristo Including Vermejo	21.5	17.5 - 26.3
Northern Sangre de Cristo Excluding Vermejo	25.2	20.1 - 31.6
Southern Sangre de Cristo	18.6	13.0 - 26.8
Sandia	18.4	10.1 - 33.7
Northern Sacramento	19.9	14.3 - 27.6
Southern Sacramento	13.4	10.1 - 17.9

SUMMARY

Recent advances in molecular tools and error checking protocols (Paetkau 2003), sampling techniques (Woods et al. 1999), and statistical analyses (Efford 2004) have enabled researchers to better sample and estimate black bear density. The genotyping success for bear hairs was notably low (1,484/4,080 = 36%) which reduced sample size and the number of individuals that were recaptured. We suspect increased UV radiation at high elevations was the primary factor in degrading DNA samples.

Due to low genotyping success, this study had lower capture probabilities than are typically reported in black bear studies, which may have affected density estimates and increased their associated confidence intervals. These problems were exacerbated in the northern Sangre de Cristos when Vermejo Park was excluded from the analysis because the reduced study area further reduced capture probabilities and recapture events such that statistical model stability was questionable and estimated density was inflated. Including Vermejo Park with the remainder of the northern Sangre de Cristos produces more precise and likely more accurate results.

Our results show that black bear density is substantially higher than estimates currently used by NMDGF in the northern Sangre de Cristo (21.5 bears/100 km² vs. 17 bears/100 km²) and Sandia (18.4 bears/100 km² vs. 13.2 bears/100 km²) mountains, and slightly higher than estimates currently used in the southern Sangre de Cristo (18.6 bears/100 km² vs. 17 bears/100 km²) and northern Sacramento (19.9 bears/100 km² vs. 17 bears/100 km²) mountains. Black bear density is lower than estimates currently used by NMDGF in the southern Sacramento Mountains (13.4 bears/100 km² vs. 17 bears/100 km²). Using the new density estimates for management decisions will more accurately reflect current black bear population size in these study areas.

LITERATURE CITED

- Borchers, D. L., and M. G. Efford. 2008. Spatially Explicit Maximum Likelihood Methods for Capture–Recapture Studies. *Biometrics* 64:377-385
- Costello, C.M., D.E. Jones, K.A. Green-Hammond, R.M. Inman, K.H. Inman, B.C. Thompson, R.A. Deitner, and H.B. Quigley. 2001. A study of black bear ecology in New Mexico with models for population dynamics and habitat suitability. Final Report, Federal Aid in Wildlife Restoration Project W-131-R, New Mexico Department of Game and Fish, Santa Fe, New Mexico, USA.
- Costello, C. M. 2008. The spatial ecology and mating system of black bears (*Ursus americanus*) in New Mexico. *Ph.D. dissertation*, Montana State University, Bozeman.
- Efford, M.G. 2013. secr: Spatially explicit capture-recapture in R. 2.6.1. <http://CRAN.R-project.org/package=secr>
- Efford, M.G., D.L. Borchers, and G. Mowat. 2013. Varying effort in capture-recapture studies. *Methods in Ecology and Evolution* 4:629-636.
- Efford, M.G., D.K. Dawson, and C.S. Robbins. 2004. DENSITY: software for analyzing capture-recapture data from passive detector arrays. *Animal Biodiversity and Conservation* 27: 217-228.
- Inman, R.M., C.M. Costello, D.E. Jones, K.H. Inman, B.C. Thompson, and H.B. Quigley. 2007. Denning chronology and design of effective bear management units. *Journal of Wildlife Management* 71:1476-1483.
- Kendall, K.C., J.B. Stetz, J. Boulanger, A.C. Macleod, D. Paetkau, and G.C. White. 2009. Demography and genetic structure of a recovering grizzly bear population. *Journal of Wildlife Management* 73:3-17.
- Kendall, K.C., J.B. Stetz, D.A. Roon, L.P. Waits, J.B. Boulanger, and D. Paetkau. 2008. Grizzly Bear Density in Glacier National Park, Montana. *Journal of Wildlife Management* 72:1693-1705.
- Paetkau, D. 2003. An empirical exploration of data quality in DNA-based population inventories. *Molecular Ecology* 12:1375-1387.
- Proctor, M. B. McLellan, J. Boulanger, C. Apps, G. Stenhouse, D. Paetkau, and G. Mowat. 2010. Ecological investigations of grizzly bears in Canada using DNA from hair, 1995-2005: a review of methods and progress. *Ursus* 21:169-188.
- Woods, J.G., D. Paetkau, D. Lewis, B.N. McLellan, M. Proctor, and C. Strobeck. 1999. Genetic tagging of free-ranging black and brown bears. *Wildlife Society Bulletin* 27:616–627