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# Estimating Black Bear Density in New Mexico Using Noninvasive Genetic Sampling Coupled with Spatially Explicit Capture- Recapture Methods

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Coupled with Spatially Explicit Capture-Recapture Methods**

**Federal Aid in Wildlife Restoration Project W93 R56 2.0**

**Final Report to The New Mexico Department of Game and Fish**

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## EXECUTIVE SUMMARY

During the 2004–2005 to 2015–2016 hunting seasons, the New Mexico Department of Game and Fish (NMDGF) estimated black bear abundance (*Ursus americanus*) across the state by coupling density estimates with the distribution of primary habitat generated by Costello et al. (2001). These estimates have been used to set harvest limits. For example, a density of 17 bears/100 km<sup>2</sup> for the Sangre de Cristo and Sacramento Mountains and 13.2 bears/100 km<sup>2</sup> for the Sandia Mountains were used to set harvest levels. The advancement and widespread acceptance of non-invasive sampling and mark-recapture methods, prompted the NMDGF to collaborate with the New Mexico Cooperative Fish and Wildlife Research Unit and New Mexico State University to update their density estimates for black bear populations in select mountain ranges across the state.

We established 5 study areas in 3 mountain ranges: the northern (NSC; sampled in 2012) and southern Sangre de Cristo Mountains (SSC; sampled in 2013), the Sandia Mountains (Sandias; sampled in 2014), and the northern (NSacs) and southern Sacramento Mountains (SSacs; both sampled in 2014). We collected hair samples from black bears using two concurrent non-invasive sampling methods, hair traps and bear rubs. We used a gender marker and a suite of microsatellite loci to determine the individual identification of hair samples that were suitable for genetic analysis. We used these data to generate mark-recapture encounter histories for each bear and estimated density in a spatially explicit capture-recapture framework (SECR). We constructed a suite of SECR candidate models using sex, elevation, land cover type, and time to model heterogeneity in detection probability and the spatial scale over which detection probability declines. We used Akaike's Information Criterion corrected for small sample size (AIC<sub>c</sub>) to rank and select the most supported model from which we estimated density.

We set 554 hair traps, 117 bear rubs and collected 4,083 hair samples. We identified 725 (367 M, 358 F) individuals; the sex ratio for each study area was approximately equal. Our density estimates varied within and among mountain ranges with an estimated density of 21.86 bears/100 km<sup>2</sup> (95% CI: 17.83 – 26.80) for the NSC, 19.74 bears/100 km<sup>2</sup> (95% CI: 13.77 – 28.30) in the SSC, 25.75 bears/100 km<sup>2</sup> (95% CI: 13.22 – 50.14) in the Sandias, 21.86 bears/100 km<sup>2</sup> (95% CI: 17.83 – 26.80) in the NSacs, and 16.55 bears/100 km<sup>2</sup> (95% CI: 11.64 – 23.53) in the SSacs. Overall detection probability for hair traps and bear rubs, combined, was low across all study areas and ranged from 0.00001 to 0.02. We speculate that detection probabilities were affected by failure of some hair samples to produce a complete genotype due to UV degradation of DNA, and our inability to set and check some sampling devices due to wildfires in the SSC. Ultraviolet radiation levels are particularly high in New Mexico compared to other states where NGS methods have been used because New Mexico receives substantial amounts of sunshine, is relatively high in elevation (1,200 m – 4,000 m), and is at a lower latitude. Despite these sampling difficulties, we were able to produce density estimates for New Mexico black bear populations with levels of precision comparable to estimated black bear densities made elsewhere in the U.S.

Our ability to generate reliable black bear density estimates for 3 New Mexico mountain ranges is attributable to our use of a statistically robust study design and analytical method.

There are multiple factors that need to be considered when developing future SECR-based density estimation projects. First, the spatial extent of the population of interest and the smallest average home range size must be determined; these will dictate size of the trapping array and spacing necessary between hair traps. The number of technicians needed and access to the study areas will also influence configuration of the trapping array. We believe shorter sampling occasions could be implemented to reduce degradation of DNA due to UV radiation; this might help increase amplification rates and thereby increase both the number of unique individuals identified and the number of recaptures, improving the precision of the density estimates. A pilot study may be useful to determine the length of time hair samples can remain in the field prior to collection. In addition, researchers may consider setting hair traps and bear rubs in more shaded areas (e.g., north facing slopes) to help reduce exposure to UV radiation. To reduce the sampling interval it will be necessary to either hire more field personnel or decrease the number of hair traps per sampling session. Both of these will enhance detection of long-range movement events by individual bears, increase initial capture and recapture rates, and improve precision of the parameter estimates. We recognize that all studies are constrained by limited resources, however, increasing field personnel would also allow a larger study area to be sampled or enable higher trap density.

In conclusion, we estimated the density of black bears in 5 study areas within 3 mountains ranges of New Mexico. Our estimates will aid the NMDGF in setting sustainable harvest limits. Along with estimates of density, information on additional demographic rates (e.g., survival rates and reproduction) and the potential effects that climate change and future land use may have on the demography of black bears may also help inform management of black bears in New Mexico, and may be considered as future areas for research.

## INTRODUCTION

Setting sustainable harvest limits for game species is one of the main duties of state wildlife management agencies. To this end, state agencies spend a large portion of their annual budget on population surveys to estimate abundance and population trends of game animals. Survey methodologies for large ungulates are well developed and can provide relatively robust estimates of common game species such as deer (*Odocoileus* spp.) and elk (*Cervus canadensis*). In contrast, estimating the abundance or density of large carnivores like American black bears (*Ursus americanus*), which are cryptic and occur at low densities is more difficult because their behavior makes the survey methods used for ungulates ineffective, e.g., assuming perfect detection probability (Miller 1990, Obbard et al. 2010). Historically, many state agencies set harvest limits for carnivores based on harvest data (Hristienko and McDonald 2007), including sex ratio and age structure of the harvested animals, which, along with other analytical approaches, can be used to infer harvest effects on a population (Garshelis 1990). Yet, hunter selectivity and sex-specific vulnerability may influence harvest composition (Miller 1990, Beston and Mace 2012). Thus, additional information provided by abundance and density estimates generated from robust statistical methods can aid in setting harvest limits for black bear populations.

New Mexico's most recent black bear density estimates were derived from a comprehensive, decade-long study on black bear ecology in the 1990s in which researchers estimated study area specific density using population reconstruction (Downing 1980), or backdating, to estimate the minimum population size during the study and then divided that estimate by the effective trapping area (ETA; Costello et al. 2001) to obtain a minimum density estimate. The ETA is an estimate of the actual area used by identified individuals to account for home ranges that straddle the study area boundary and may bias abundance estimates (Dice 1938, Wilson and Anderson 1985). Costello et al. (2001) estimated the ETA using the distribution of live-capture trap sites buffered by the mean activity radius of adult bears. Their minimum density estimate for the more northern, mesic, and presumably more productive Sangre de Cristo Mountains was 17.0 bears/100 km<sup>2</sup> (310 km<sup>2</sup> study area) while their estimate for the more southern, xeric, and presumably less productive Mogollon Mountains was 9.4 bears/100 km<sup>2</sup> (423 km<sup>2</sup> study area). It is important to note that backdating a population fails to account for undetected individuals or provide measures of uncertainty in estimates, thereby producing only a minimum population estimate. They extrapolated these minimum density estimates to similar black bear habitat throughout New Mexico assigning areas with habitat conditions in between the Sangre de Cristo Mountains and Mogollon Mountains a density equal to the mean of the two minimum density estimates (i.e., 13.2 bears/100 km<sup>2</sup>). Costello et al. (2001) estimated the statewide minimum population by multiplying minimum density by the area of statewide primary habitat identified through their habitat suitability analysis, which introduces another source of uncertainty that was not quantified. Along with the density estimates, Costello et al. (2001) provided the NMDGF with a population model that incorporated the new density estimates, harvest data, mast survey data, and the relationship between mast production and reproductive success to model abundance and trend of black bear abundance in each Bear Management Zone (BMZ). These model-based abundance estimates, coupled with yearly harvest and mast survey data, have been the basis for establishing black bear harvest limits in New Mexico (Rick Winslow, NMDGF, personal communication). Although live-capture provides a wealth of information on age, dispersal, fecundity, health, home range size, and mortality rates, it

is still inferentially limited due to small sample sizes. While Costello et al. (2001) was a progressive and highly informative study on New Mexico black bears, the capabilities of the technology at that time limited their ability to estimate abundance and density.

Capture-recapture (CR) is a common method for estimating abundance and density of animals and associated parameter uncertainty (Williams et al. 2002). Abundance estimates using CR are determined by comparing the ratio of uniquely marked individuals to unmarked individuals captured each sampling occasion in live capture studies (Pollock et al. 1990). Gould and Kendall (2013) summarize CR methodology and recent advances. Low capture probabilities and sample sizes inherent with species that typically reside at the low densities characteristic of carnivore populations hinders management agencies from utilizing traditional CR techniques for some species (Mills et al. 2000, Settlage et al. 2008). Noninvasive genetic sampling (NGS) revolutionized CR research by providing the ability to use remotely collected DNA samples to identify individuals (Waits and Paetkau 2005). Consequently, NGS enabled researchers to estimate population parameters for carnivores by increasing detection probability, increasing sample size of individuals detected, increasing the size of the study area, decreasing tag loss, and decreasing invasiveness compared to live capture studies (Woods et al. 1999, Mills et al. 2000). However, density estimators using traditional non-spatial CR methods are often less reliable because of the ad hoc and arbitrary estimate of the ETA, which introduces an unquantifiable error (Wilson and Anderson 1985, Parmenter et al. 2003).

Spatially explicit capture-recapture (SECR) models remedy this issue by estimating the number of home range centers within the study area, and subsequently density, directly, using a spatial point process (Efford 2004, Gopalaswamy 2013). By using SECR models, accounting for edge effects has been rooted in statistical theory and incorporated into the modeling process thereby eliminating the need to estimate ETA. Furthermore, integrating the distribution and location of sampling devices into the model eliminates individual heterogeneity related to unequal trap exposure (Borchers 2012). To date, SECR methods have shown improved parameter estimation compared to non-spatial methods with simulated datasets (Ivan et al. 2013, Whittington and Sawaya 2015) and similar or lower density estimates in empirical comparisons (Obbard et al. 2010, Stetz et al. 2014, Whittington and Sawaya 2015), particularly when distance to edge and sampling effort are not included in CR models. Although the accuracy of any density estimate is unknown, use of statistically robust estimation methods yields greater confidence in a management agency's ability to set defensible management objectives that will help ensure the long-term viability of harvested animal populations.

In light of advances in sampling (Woods et al. 1999) and statistical methods (Efford 2004), NMDGF began a collaborative project with the New Mexico Cooperative Fish and Wildlife Research Unit (NMCFWRU) and New Mexico State University (NMSU) to update their density estimates for New Mexico black bear populations. These estimates will then be used by NMDGF to set harvest limits in the respective study areas. Our (NMCFWRU and NMSU) objectives were to estimate the density of black bears  $\geq 1$  year of age in primary bear habitat within 7 of the 14 BMZs located within the Sangre de Cristo (BMZs 3, 4, and 5), Sandia (BMZ 8), and Sacramento Mountains (BMZs 11, 12, 13), New Mexico. We used non-invasive genetic samples from hair traps and bear rubs in combination with SECR models to estimate density for each study site.

## STUDY AREA

We conducted our research in the Sangre de Cristo, Sandia, and Sacramento Mountains, New Mexico constituting 5 study areas: northern (NSC; 6,400 km<sup>2</sup>) and southern Sangre de Cristo Mountains (SSC; 3,525 km<sup>2</sup>), Sandia Mountains (300 km<sup>2</sup>), and northern (NSacs; 925 km<sup>2</sup>) and southern Sacramento Mountains (SSacs; 2,775 km<sup>2</sup>). Interstate 25 and Interstate 40 separated the 3-mountain ranges. The sampling area for each study area was limited to primary habitat identified by Costello et al. (2001; Figure 1). Costello et al. (2001) used the New Mexico Gap Analysis land cover map (NMGAP, Thompson et al. 1996) to classify primary habitat as all closed-canopy forest and woodland types. All 5 study areas were managed as multiple-use forests encompassing portions of 4 National Forests (Carson, Cibola, Lincoln, and Santa Fe), 6 wilderness areas (Columbine-Hondo, Latir Peak, Pecos, Sandia Mountain, Wheeler Peak, and White Mountain), and 25 private landowners. Maximum elevation was 4,011 m, 3,254 m, and 3,649 m for the Sangre de Cristo, Sandia, and Sacramento Mountains and minimum elevations were approximately 1,900 m, 1,700 m, and 1,500 m, respectively. The Southern Rocky Mountains floristic district characterizes the Sangre de Cristo Mountains while the Sandia and Sacramento Mountains are characterized by the Mogollon floristic district (McLaughlin 1992). Dominant vegetation types in the study areas include: oak–mountain mahogany (*Quercus* spp. – *Cercocarpus* spp.) scrublands; piñon pine (*Pinus edulis*) - juniper (*Juniperus* spp.) woodlands; ponderosa pine (*P. ponderosa*), white pine (*P. monticola*), Douglas fir (*Pseudotsuga menziesii*), aspen (*Populus tremuloides*), Engleman spruce (*Picea engelmannii*) and subalpine fir (*Abies lasiocarpa*) mixed-forest, and bristlecone (*P. aristata*) and limber (*P. flexilis*) pine forests (Costello et al. 2001). Important mast-producing species include oak, piñon pine, juniper, algerita (*Berberis haematocarpa*), chokecherry (*Prunus virginiana*), gooseberry (*Ribes* spp.), bear corn/squawroot (*Conopholus alpina*), cactus fruits (*Opuntia* spp.) and sumac (*Rhus* spp.; Kaufmann et al. 1998, Costello et al. 2001).

## METHODS

### Field Sampling

We used hair traps (Woods et al. 1999) and bear rubs (Kendall et al. 2008) concurrently to sample black bear populations (Sawaya et al. 2012, Stetz et al. 2014). We sampled the black bear populations by systematically distributing a grid of 5-km x 5-km cells, with a randomly determined origin, across the landscape. A 5-km x 5-km cell size allowed us to place 4 hair traps within the average fixed kernel female home range in the Sangre de Cristo Mountains (27.6 km<sup>2</sup>; Costello et al. 2001). We then set hair traps across primary habitat in areas most likely to encounter bears (Figure 2, 3, 4; Costello et al. 2001). We chose trap site locations based on suspected travel routes, occurrence of seasonal forage (e.g., green grass and ripe soft and hard mast), and presence of bear sign. We set hair traps and bear rubs across 4 sampling occasions in the NSC (22 April – 5 September 2012) and SSC (29 April - 9 September 2013) and across 6 sampling occasions in the Sandias, NSacs, and SSacs (5 May – 6 August 2014). Due to logistical constraints, a sampling occasion in the NSC and SSC lasted 4 weeks whereas the sampling occasion for the Sandias, NSacs, and SSacs was 2 weeks.

A hair trap consisted of a single strand of barbed wire wrapped around  $\geq 3$  trees with a lure pile constructed from woody debris, rocks, pine needles, and leaves at the center (Woods et al. 1999). During each sampling occasion in the NSC and SSC, 1 of 4 non-consumable lures (cow blood/fish emulsion mixture, anise oil, fatty acid scent tablet, or skunk tincture/lanolin



mixture) was randomly selected and applied to the lure pile to attract bears into the enclosure and increase the novelty of hair traps to increase recapture rates. In the Sandias, NSacs, and SSacs we randomly selected and applied 1 of 2 non-consumable lures (cow blood/fish emulsion mixture or skunk tincture/lanolin mixture) each occasion. Based on our judgement in the field, we eliminated anise oil and fatty acid scent tablets because their scent duration and dispersal distance was inferior compared to the other two lures. Therefore, we believe the cow blood/ fish emulsion and skunk tincture/lanolin mixtures provided a better opportunity to attract bears over a longer period of time and greater distance. When a bear passed over or under the wire to investigate the lure pile, a barb snagged a tuft of hair from the individual. We assumed that cubs of the year were too small to be sampled by the barbed wire based on the size of cubs photographed at hair traps by trail cameras. Thus, sub-adults and adults were our sampled population. A sample consisted of all hair caught in one barb, and we used our best judgement to define hair samples collected from the lure pile. We deposited each hair sample in a separate paper coin envelope. We sterilized the barbed wire with a propane torch to ensure we removed any remaining hair to prevent false recaptures during the next sampling occasion. Hair traps were moved (100 m – 2.5 km) each occasion to help increase novelty and recapture rates (Boulanger and McLellan 2001, Boulanger et al. 2004, Boulanger et al. 2008).

Bears rub on trees, power poles, barbed-wire fences, wooden signs, and road signposts (Burst and Pelton 1983, Green and Mattson 2003). We opportunistically identified and collected hair from bear rubs along trails used to navigate to hair traps. We identified bear rubs by evidence of rubbing behavior such as a smoothed surface and snagged hair on the surface (Kendall et al. 2008, 2009). We attached 3-short strands of barbed wire vertically to the rub structure in order to collect discrete, higher quality hair samples (Kendall et al. 2008, 2009, Stetz et al. 2014). Rubs were identified at varying time intervals across sampling occasions, however, once established they were checked concurrently with nearby hair traps. We collected hair samples only from the barbed wire to ensure that the samples collected were from individuals that visited the rub during the sampling occasion and we sterilized the barbed wire to prevent false recaptures (Kendall et al. 2009). All hair samples were stored in an airtight container on silica desiccant at room temperature.

## **Genetic Analysis**

We identified individuals by comparing multilocus genotypes generated for hair samples using 8 polymorphic microsatellite loci (G1D, G10B, G10L, G10M [Paetkau et al. 1995]; G10H, G10J, G10U [Paetkau et al. 1998]; MU59 [Taberlet et al. 1997]). We used the amelogenin or ZFX/ZFY markers to identify the sex of the individual (Paetkau 2003, 2004; Yamamoto et al. 2002; Durin et al. 2007). We selected specific markers for individual identification by ensuring that the mean expected heterozygosity for each marker was between 0.70 and 0.80 (Paetkau 2003, 2004). These markers were determined from an initial subsample from the NSC population in 2012. Because NGS-collected samples may contain low quantity and quality DNA (e.g., hair vs. tissue), genotyping errors may create or delete individuals, which may bias estimates (Mills et al 2000, Lukacs and Burnham 2005). Paetkau (2003) suggested that the largest source of genotyping error resulted from human error when identifying alleles at a locus, which only training and experience could reduce. Therefore, we sent our genetic samples to Wildlife Genetics International (WGI), which is a genetics laboratory that specializes in strict laboratory and error-checking methods that reduce genotyping errors that may arise from poor quality or small quantities of DNA (Paetkau 2003, Kendall et al. 2009). The laboratory has conducted over

2,000 projects including successfully identifying 653 samples without error during a blind sample test (Kendall et al. 2009). Thus, WGI has established a reputation for integrity and high quality work.

First, we eliminated samples that contained insufficient genetic material for analysis (no root,  $\leq 1$  guard hair, or  $< 5$  underfur hairs) or appeared to be from heterospecifics. Next, we used either the G10J or ZFX/ZFY marker as a prescreen to remove low quality hair samples that were likely to fail during the multilocus genotyping phase. After the prescreen, we amplified the 9 candidate markers for each sample. We eliminated samples that failed to amplify at  $\geq 3$  loci or that amplified  $\geq 3$  alleles at 1 marker because they indicated a mixed sample from 2 individuals. We reanalyzed the samples that failed at  $< 3$  loci resulting in either a full 9-locus genotype or a discarded sample. We examined pairs of samples that were mismatched at 1 or 2 markers (1MM pairs or 2MM pairs) for evidence of amplification or human error. We then reamplified and resequenced the mismatched pair for these samples under the assumption that genotyping error may have created the similarity between the two samples (Paetkau 2003). If a 1MM or 2MM pair remained between samples, then we considered the two samples to be from separate individuals, otherwise, we identified and corrected the genotyping error and we concluded that the two samples were from the same individual. We assigned individual ID to each sample with a unique multilocus genotype based upon the first sample to identify the individual's genotype. We calculated the expected and observed heterozygosity for the Sangre de Cristo, Sandia, and Sacramento Mountains using program GENEPOP (Genepop on the Web, Raymond and Rousset, 1995). Detailed laboratory methods may be found in Paetkau (2003, 2004).

## Density Estimation

We used genotypes of individual samples to generate capture-recapture encounter histories for each uniquely identified black bear. We then used these capture histories to estimate density using spatially explicit capture-recapture (SECR) models (Efford 2004, Efford et al. 2009a, Efford et al. 2013) with the R package “secr” (Efford 2013). We used SECR to estimate 3 parameters: density (D), detection probability ( $g_0$ ), and the spatial scale over which the detection probability declines ( $\sigma$ ; Efford et al. 2004). We used a half-normal detection function for our observation model, which represents the probability of detecting an individual as a function of the individual's home range location relative to the detection device (Efford et al. 2009a). We then specified a homogeneous Poisson distribution as our state model to represent the spatial distribution of animals across the sampling grid. We only included primary habitat as identified by Costello et al. (2001) for black bears in New Mexico for our habitat mask. The habitat mask identifies the area of habitat/non-habitat within and buffered around the trapping grid. We estimated the state space (i.e., the trapping grid and all individuals potentially exposed to capture outside the trapping grid) using the secr function suggest.buffer for each study area. However, this buffer is not to be confused with the ad hoc method of identifying a buffer using the ETA. Instead, the suggested buffer is the area of integration and includes all animals with a non-zero probability of detection (Ivan et al. 2013). Habitat may extend beyond the mask but individuals outside the buffer have a negligible probability of encounter (Borchers and Efford 2008, Royle et al. 2014). Derived from the capture data using suggest.buffer, we set the habitat mask buffer for the NSC, SSC, Sandias, NSacs, and SSacs as 18.75 km, 25.40 km, 13.23 km, 14.84 km, and 11.03 km, respectively. Variability in sampling effort may negatively bias density estimates and reduce the ability to explain variation in detection probability (Efford et al. 2013). We accounted

for variable sampling effort by using the number of days each hair trap and bear rub was active (Kendall et al 2009, Sawaya et al 2012, Efford et al. 2013).

We tested for variation due to time (t), sex, elevation (elev), detector type (type; hair trap versus bear rub), and land cover classification (veg) as predictors of  $g_0$ , and  $\sigma$ . Elevation was standardized prior to analyses by subtracting the mean and dividing by the standard deviation (Gelman and Hill 2007). We did not consider behavioral models because we did not provide a food reward. We modeled D only using sex because we did not expect bear density to vary by time, land cover type, or elevation. We entered sex into our models as a session covariate. We modeled  $g_0$  and  $\sigma$  concurrently by fitting 4 models that varied by time, sex, land cover type, and elevation. We also included models that varied by temporal variation for  $g_0$  and land cover for  $\sigma$ , temporal variation for  $g_0$  and elevation for  $\sigma$ , land cover for  $g_0$  and temporal variation for  $\sigma$ , and elevation for  $g_0$  and temporal variation for  $\sigma$ . We chose temporal variation and sex as covariates because multiple studies have reported that detection probability and movement patterns fluctuate over the course of the sampling period and differ between males and females (Kendall et al. 2009, Sawaya et al. 2012, Stetz et al. 2014, Ciucci et al. 2015). We selected elevation and land cover to represent the spatial heterogeneity of food resources exploited by black bears. We hypothesized that this heterogeneity could influence  $g_0$  and  $\sigma$  depending on the presence or absence and distribution of food on the landscape. However, we did not include both land cover type and elevation in the same model due to concerns of multicollinearity. We also constructed models with temporal variation for  $g_0$  and  $\sigma$  in addition to additive variation with either elevation or land cover. We included additive effects because we hypothesized that  $g_0$  and  $\sigma$  are likely to vary because of the black bear mating season, hyperphagic foraging behavior during late summer and early fall, and the temporally variable distribution of food resources on the landscape.

We extracted the elevation for each detector using the National Elevation Dataset 30 m resolution digital elevation model. We extracted land cover using the Interagency Landfire Project ([www.landfire.gov](http://www.landfire.gov); Rollins 2009) land cover classification at 30 m spatial resolution. We combined 6 Landfire land cover classifications into 5 categories: aspen – conifer, mixed conifer (combination of Douglas fir and white pine), piñon pine – juniper, ponderosa pine, and spruce – fir. Variability in abundance and distribution of each land cover classification across study areas resulted in a different number of categories and, consequently, number of parameters in each model among study areas. Aspen-conifer and spruce-fir were only included in the NSC and SSC. Mixed-conifer was included in all study areas except the Sandia Mountains. Piñon-juniper and ponderosa pine were included in all study areas. We extracted elevation and assigned the dominant land cover classification surrounding the location of each detector using ArcGIS 10.2.1 (Environmental Systems Research Institute, Inc. [ESRI], Redlands, California, USA). Each model serves as a hypothesis modeling the heterogeneity in the data for each estimable parameter. We used Akaike's Information Criterion corrected for small sample size ( $AIC_c$ ) to rank our final model set (Akaike 1973, Hurvich and Tsai 1989). We used the difference in  $AIC_c$  score ( $\Delta AIC_c$ ) between the top-ranked model and competing models to compare relative support, and we provide the  $AIC_c$  weights ( $w_i$ ) to show the proportional support for each model (Burnham and Anderson 2002). We used model averaging to account for model selection uncertainty when the top ranked model in the final model set garnered less than 0.90 of the model weight (Burnham and Anderson 2002).

We conducted our study with authorization under Convention on International Trade in Endangered Species Export Permits 12US86417A/9, 13US19950B/9, and 14US43944B/9, and New Mexico Department of Game and Fish Authorization for Taking Protected Wildlife for Scientific and/or Education Purposes Permit 3504. All procedures were approved by the New Mexico State University Institutional Animal Care and Use Committee (Protocol number 2011-027).

## **RESULTS**

### **Field Sampling**

We set 557 hair traps that were open for 57,010 trap days and we collected 3,825 hair samples. In addition, we identified and sampled 112 bear rubs, which yielded 258 hair samples over 7,007 trap days (Figure 2, 3, and 4; Tables 1 and 2). Sampling effort varied across study areas and was dependent on the number of hair traps and bear rubs set, the length of a sampling occasion for each study area (4 weeks vs. 2 weeks), and the accessibility of areas due to stochastic weather events and wildfire. The number of hair traps that collected  $\geq 1$  hair sample ranged from 28% to 42% with most traps collecting a hair sample in 1 – 2 sampling occasions. The number of hair samples collected during a particular occasion increased over the course of the summer and decreased towards the conclusion of sampling with peak collection during June and July (Table 2).

### **Genetic Analysis**

The mean observed heterozygosity for our suite of genetic markers was 0.73 (Table 3). The number of individuals that were mismatched at 1 or 2 markers was extremely low with 3, 0, 0, and 0 observed 1MM-pairs and 0, 4, 0, and 4 observed 2MM-pairs and 3, 0, 0, and 0 for the NSC, SSC, Sandias, and Sacramento Mountains, respectively. Excluding the NSC, the observed mismatched pairs fell within the expected mismatch distribution for each population (Paetkau 2003). The deviation from expectation observed in the NSC was likely due to chance (D. Paetkau, WGI, personal communication). From the 4,083 total hair samples collected, we eliminated 27.7% from the genotyping process. Reasons for excluding hair samples included: the sample contained insufficient genetic material for analysis (26.1%), was not of black bear origin (1.49%), or contained DNA from more than one individual (0.17%). We attempted to genotype 2,950 (72.3%) hair samples but were only able to generate a full 9-loci genotype for 49.6% of the eligible samples and identified 726 (368 M: 358 F) individuals (Table 4). The observed sex ratio for each study area was approximately equal. Genotyping success varied across study areas (43% - 60%), but overall, our success rates were lower than the 75% success rate observed in similar studies (D. Paetkau, WGI, personal communication). Contrary to our prediction, when we shortened the length of the sampling occasion from 4 weeks (NSC and SSC) to 2 weeks (Sandias, NSacs, and SSacs), we increased the percentage of successful genotypes by 4%.

### **Density Estimation**

We detected the majority (61% – 85%) of individuals in each study area only once with similar average number of detections of males (1.19 – 1.67) and females (1.14 – 1.56; Table 5). The number of unique individuals detected during each occasion for the NSC, NSacs, and SSacs increased over the course of sampling, peaking mid-summer, and subsequently decreasing towards the end of the season (Figure 5); this pattern was similar to the total number of hair

samples collected per sampling occasion (Table 3). However, the number of unique individuals detected continued to increase over the course of the summer reaching its highest point during the last sampling occasion for both the SSC and the Sandias. Mean maximum recapture distance for males ranged from 4.23 to 12.46 km with a maximum distance of 52 km by one individual in the NSC ( $n = 3 - 33$ ). Mean maximum recapture distance for females ranged from 0.38 to 4.59 km with a maximum distance of 47 km by one individual, also in the NSC ( $n = 4 - 23$ ; Table 5). Three individuals were detected in two study areas. The first two detections were males we detected in the NSC in 2012 and then again in the SSC in 2013, and the third was a female we detected in the SSC in 2013 and then again 90 km away in the Sandias in 2014.

The most supported model for the NSC received all model weight and suggested that time and land cover type were important covariates explaining both  $g_0$  and  $\sigma$  (Table 6). The top model ( $w_i = 0.87$ ) for the SSC included time and elevation, whereas the second highest-ranking model ( $w_i = 0.13$ ) included time and land cover type (Table 7). The top model ( $w_i = 0.96$ ) for the Sandias indicated that both  $g_0$  and  $\sigma$  varied by sex (Table 8). The highest-ranking model ( $w_i = 0.96$ ) for the NSacs included time and land cover type for both  $g_0$  and  $\sigma$  (Table 9). There was higher model selection uncertainty for the SSacs than any other site, but the most supported model ( $w_i = 0.50$ ) included land cover type for both  $g_0$  and  $\sigma$  (Table 10). The second and third ranked models included time and land cover, and time and elevation, respectively; these three top-ranked models contained all of the model weight (Table 15). For the NSC, we were able to fit all models except when  $g_0$  and  $\sigma$  were modeled concurrently with elevation (i.e.,  $g_0 \sim \text{elev}$ ,  $\sigma \sim \text{elev}$ ), concurrently with time and elevation (i.e.,  $g_0 \sim t + \text{elev}$ ,  $\sigma \sim t + \text{elev}$ ), independently with elevation (i.e., either  $g_0 \sim \text{elev}$ ,  $\sigma \sim \text{constant}$ ; or  $g_0 \sim \text{constant}$ ,  $\sigma \sim \text{elev}$ ), independently with time and elevation (i.e., either  $g_0 \sim t + \text{elev}$ ,  $\sigma \sim \text{constant}$ ; or  $g_0 \sim \text{constant}$ ,  $\sigma \sim t + \text{elev}$ ), and with time and elevation for different parameters (i.e., either  $g_0 \sim t$ ,  $\sigma \sim \text{elev}$ ; or  $g_0 \sim \text{elev}$ ,  $\sigma \sim t$ ) because of computational limitations. For the NSacs, we did not fit a model using detector type to predict  $g_0$  and  $\sigma$  concurrently because only one bear rub was set.

Detection probability ( $g_0$ ) was highest for the Sandias ( $g_0 = 0.02$ ), but overall,  $g_0$  was low across all study areas (Table 11). The final model for all study areas, except the Sandias, did not support a sex effect. Despite having the highest  $g_0$  relative to the other study areas, the precision of the Sandias density estimate was the lowest; whereas, the NSC density estimate was the most precise despite a low  $g_0$  (Table 11). Mean density estimates varied within and between mountain ranges (range 16.55 to 21.86 bears/100 km<sup>2</sup>) and were model averaged for the SSC and SSacs (Table 11).

## DISCUSSION

Our study provided the most current density estimates for multiple New Mexico black bear populations in over a decade (Costello et al. 2001). Our results suggest that densities are similar (SSacs) to or higher (NSC, SSC, Sandia, and NSacs) than the previous estimates used by NMDGF (17 bears/100 km<sup>2</sup> and 13.2 bears/100 km<sup>2</sup>) to manage New Mexico black bear populations. The differences in estimated density could be a result of an increasing black bear population, simple variation in population density due to time, a difference in the state of environmental conditions, or different sampling and analytical methods. For example, Costello et al. (2001) did not account for uncollared individuals in their density estimation approach and thus likely underestimated the density of the population by not accounting for imperfect detection. Furthermore, their abundance and density estimates provided no measure of

uncertainty because their estimation technique was not statistically based and did not provide a measure of uncertainty. As a result, Costello et al. (2001) used minimum abundance to derive their density estimates, which may explain at least some of the difference in our density estimates given we estimated mean density. Regardless, unless populations are extremely stable, we would expect density of a population to vary across space and with time.

The relative importance of the covariates we selected for modeling parameters was similar across study areas. The top model for all study areas held density constant suggesting an equal sex ratio in each population. Time of the detection event and the land cover type or elevation at which the detector was deployed were helpful covariates in modeling heterogeneity in both  $g_0$  and  $\sigma$  for all study areas except the Sandia Mountains, which included sex of the individual detected as an important explanatory variable. The importance of temporal variability is likely a result of seasonal reproductive and foraging behaviors (Alt et al. 1980, Garshelis and Pelton 1981, Costello et al. 2003). Black bear mating season begins with den emergence, which can be as early as late March, peaks in June, and typically ends by July (Costello et al. 2001). During this period, males move more as they traverse their home range searching for receptive females (Young and Ruff 1982, Costello 2008, Lewis and Rachlow 2011). Mast season begins in July, with peak masting occurring during late summer and early fall (Costello 2008). At this time, bears begin to enter a hyperphagic state when they increase daily caloric intake from 8,000 kcal to 15,000 – 20,000 kcal to build up fat stores for hibernation and reproduction in females (Nelson et al. 1980). Bear home range size and distance between sequentially recorded movements increases as bears travel outside their core area to exploit the spatially and temporally variable mast (Ostfeld et al. 1996, Costello 2008), which is an important food source and highly correlated with black bear reproductive output in New Mexico (Costello et al. 2003). Increased movement rates and enlarged home range size during mating and hyperphagia would likely affect trap exposure rates on the landscape, thus affecting  $g_0$  and  $\sigma$ .

The influence of land cover and elevation is likely a function of black bears responding to spatio-temporal changes in food abundance (Costello and Sage 1994, Costello et al. 2001, Mazur et al. 2013, McCall et al. 2013). Using scat surveys, Costello et al. (2001) reported that grasses, forbs, and ants tend to dominate bear diets during the pre-mast season (den emergence – 20 July). As the summer progresses, early mast season (21 July – 15 September) diets included soft mast species including chokecherry, squawroot (*Conopholis alpina*), and gooseberry as well as acorns (56% of scat volume). Diets during the late mast season (15 September – den entrance) are dominated by acorns (87% of scat volume) and supplemented with juniper berries (Costello et al. 2001). Mid-elevation land cover types (i.e., mixed conifer) are likely to contain a higher abundance of pre-mast species (grass and forbs) due to earlier snowmelt (compared to higher elevations) and moist conditions near riparian areas compared to dry, lower elevations. As snow melts, grasses and forbs will increase in abundance and distribution. With the arrival of monsoonal rains, soft mast will begin to ripen at lower elevations. Once oak acorns ripen in late summer/early fall, black bears begin to shift their attention towards vegetation types containing abundant acorns.

The main challenge we faced was genetic samples failing to produce a reliable genotype (i.e., not generating an individual ID for a particular hair sample). The inability to assign a reliable genotype to half of our genetic samples (44% - 61%) reduced the number of unique individuals and spatial recaptures (i.e., recapture of individuals at different traps) available for analysis. Consequently, this led to low detection probability and likely affected estimation of  $\sigma$

inducing larger standard errors and less precise density estimates (Efford et al. 2004, Sollmann et al. 2012, Sun et al. 2014). The relatively more precise NSC density estimate, despite a low  $g_0$ , may be a result of a greater number of unique individuals and recaptures, which provided sufficient data for the model to predict unobserved movement distances (Table 5; Sollmann et al. 2012, Sun et al. 2014). Interestingly, despite having the highest estimated  $g_0$  among all study areas, the density estimate for the Sandias was the least precise, which may have been influenced by a low number of recaptures for both sexes, a low  $g_0$  for males, a large individual heterogeneity in male movement patterns, and/or an over-partitioning in data due to estimating sex specific detection parameters (i.e.,  $g_0$  and  $\sigma$ ). However, we believe the greatest factor affecting the density estimate is the number of individuals detected. Detecting fewer individuals results in less data to estimate the model parameters. Consequently, small sample size coupled with few recaptures can result in wider confidence intervals (Sun et al. 2014), which is likely the case for the Sandia density estimate. Our second highest-ranking model for the Sandias estimated density as 18.4 bears/100 km<sup>2</sup>, which is still higher than the current density estimate used to manage the population (13.2 bears/100 km<sup>2</sup>). Replicative sampling may help provide more information on the density of the Sandias.

In the SSC, we likely lost hair samples due to two forest fires, the Tres Lagunas and Jaroso Fires (Figure 6). The Tres Lagunas Fire started 30 May 2013 and burned 4,135 ha just below the southern boundary of the Pecos Wilderness. The Jaroso Fire started 10 June 2013 and burned 4,511 ha in the northwest corner of the Pecos Wilderness. We suspect these fires contributed to a less precise density estimate for the SSC. These fires affected 450 km<sup>2</sup> (12.7%) of the trapping grid and prevented us from checking hair traps located in close proximity to the fire primarily during the second and third sampling occasions (3–13% of total hair traps). Moreover, many of the fire-affected traps were in relatively high quality bear habitat where we would expect higher bear abundance. Anecdotally, post-fire these hair traps consistently yielded more hair samples than hair traps located in some areas that were unaffected by the fires. The inability to collect samples in this area may have reduced the number of new individuals detected, and, more importantly, most likely reduced the number of recaptures necessary for more precise parameter estimates. The limited access also prevented us from identifying more bear rubs across the SSC, restricting our ability to utilize multiple sampling methods and hindering our ability to minimize the impacts of capture heterogeneity (e.g., age, sex, reproductive status) caused by any one survey method (Boulanger et al. 2008). The use of hair traps and bears rubs concurrently has also been shown to increase the precision of parameter estimates compared to those generated by hair traps alone (Sawaya et al. 2012, Stetz et al. 2014), and likely aided our ability to generate more precise density estimates given our low amplification rates. We also hypothesize that the presence of fire on the landscape increased movements of individuals (Cunningham and Ballard 2004) as seen by our estimate of  $\sigma$  for the SSC, which is 3x – 24x larger than the other study areas.

Overall, a net loss in sampling occasions and hair samples reduced the amount of data available for the SSC analysis. The few individuals we recaptured in each occasion and the large number of unique bears identified in the last occasion, after the fires were extinguished or contained, support our argument that the fires in the SSC affected our model parameter estimates. Ideally, as a population is sampled the number of unique individuals captured declines

over time (i.e., fewer unmarked individuals are encountered). Yet, in the SSC we captured 34% of all unique individuals during the last sampling occasion. While the number of individuals detected the last occasion in the NSC is still high (20%), it seems that the fires in the SSC influenced our ability to detect bears in this area as compared to the NSacs and SSacs (both 10%; Figure 5). Limited access to these hair traps during the fires led to longer sampling occasions and greater exposure to environmental conditions (i.e., exposure increased from 4 weeks to  $\geq 8$  weeks), subjecting hair samples to longer periods of environmental exposure, particularly to ultraviolet radiation (UV).

We suspect that for all study areas UV radiation is the main factor explaining failure of hair samples to produce a complete genotype (Stetz et al. 2015). Ultraviolet radiation causes DNA degradation by the formation of chemical compounds known as dimers. Dimers form by the binding of two adjacent, pyrimidine-nucleotide bases (cytosine and thymine) on a single strand of the double helix instead of binding between cross-strand partners (Jagger 1985). This fusion forms a bulge in the chemical structure of the DNA preventing DNA polymerase from progressing past the dimer and correctly duplicating the sequence, which prevents further amplification of the DNA molecule resulting in an incomplete genotype. Consequently, we suspect that the inability to assign an identity to a large portion of the genetic samples may have reduced the number of unique individuals and recaptures across all study areas. Multiple factors influence UV levels and, subsequently, its effects on DNA degradation including cloud cover, elevation, latitude, time of day, time of year, length of exposure, season, ozone depletion, and atmospheric turbidity (Piazena 1996, Stetz et al. 2015). For example, UV radiation increases with decreasing cloud cover, increases with elevation (9.0% – 11.0% per 1,000 m), and increases with lower latitude (Blumthaler et al. 1997). New Mexico receives substantial amounts of sunshine (Albuquerque 76% vs. U.S 58% average annual possible sunshine; NOAA 2004), is relatively high in elevation (1,200 m – 4,000 m), and is at a lower latitude than other geographic areas where NGS methods have been used to estimate bear abundance and density. Collectively, these factors result in UV radiation levels across much of New Mexico being higher than across most of the U.S. Further, we would expect UV radiation levels to be 1% – 26% higher in our study areas compared to those for Albuquerque, NM (Figure 7; NOAA 2015) because our study areas were typically located at higher elevations. Reducing sampling interval length should increase genotyping success, however, when we reduced our sampling interval from 4 to 2 weeks (which is a common time frame used by similar NGS studies), in the Sandias, NSacs, and SSacs we observed only a marginal improvement in genotyping success (4%). Surprisingly, the lowest genotyping success rate was in the SSacs (44%) given sampling occasions in the SSacs were 2 weeks shorter than the NSC and SSC. Thus, we suggest researchers consider conducting a pilot study to determine the optimal sampling interval for reducing UV degradation of DNA within hair samples particularly for study areas in the southwestern U.S.

Despite these sampling difficulties, we were able to produce density estimates with comparable levels of precision as those obtained in black bear studies conducted elsewhere in the U.S. (Table 12). We believe these estimates were possible due to the large extent of our study areas, which allowed us to detect a larger proportion of the population within each mountain range, increased the potential number of recaptures, and buffered the data from the low



amplification success rates. In addition, we believe because there was no observable spatial pattern in the collection locations of samples that failed to amplify we were still able to gather an adequate representation of movement of individuals on the landscape due to our sampling intensity and use of multiple survey methods. This allowed us to model unobserved movement distances (Sollmann et al. 2012). However, a small data set affected the Sandias estimate resulting in larger confidence intervals than the other study areas, particularly the NSC. It is likely that precision for these two study areas was influenced by the number of individuals detected (NSC:  $n = 379$  vs. Sandias:  $n = 18$ ).

Black bears are naturally difficult to sample due to their cryptic behavior and large home ranges. Furthermore, spatially and temporally stochastic environmental (e.g., mast oak and wildfire; Cunningham et al. 2003, Mazur et al. 2013) and anthropogenic (e.g., recreation and roads; Boyle and Samson 1985, Kasworm and Manley 1988) factors confound black bear detection by influencing the distribution of individuals across the landscape. In New Mexico, the abundance and distribution of mast oak heavily influences black bear fitness and movement patterns as they accrue adequate fat reserves for hibernation and reproduction for females (Costello et al. 2001, Costello et al. 2003, Inman et al. 2007). Under the assumption of a count index, multiple years of low black bear harvest may indicate a declining population while multiple years of high black bear harvest may indicate an increasing population. While observed harvest numbers may be a function of a changing population, the observed changes in harvest could be a product of various factors unrelated to the number of animals harvested. In years with average or above average precipitation levels, acorn and soft mast abundance increases. During these times, black bear movement rates are smaller due to the high availability of food on the landscape. Smaller movement rates reduce black bear exposure to hunters resulting in hunters observing, and subsequently, harvesting fewer individuals (Costello et al. 2001, Fieberg et al. 2010). However, when food crops fail, particularly acorn crops, black bear home range size increases, along with hunter harvest rates, due to the increased movements of black bears searching for food (Costello et al. 2001, Fieberg et al. 2010).

In developing sampling designs for future SECR-based black bear density estimation projects, there are multiple considerations. First, the spatial extent of the population must be determined (Sun et al. 2014). Sollmann et al. (2012) suggested that trapping arrays could be smaller than an average male home range but 1.5x larger than the average female home range. Yet, they cautioned that a small trapping array might not provide an accurate representation of movement patterns necessary to inform  $\sigma$ . A larger trapping array may buffer against stochastic environmental events (e.g., mast crop failure) which may cause individuals to move larger distances (McCall et al. 2013). If trapping arrays are large, there is a reduced chance that individuals will move off of the study area and thus not be detected. Selecting study area boundaries is an important aspect to consider when trying to avoid violating geographic closure of the study area. The spacing between hair traps will also influence the spatial extent of the trapping array. Non-spatial CR literature has suggested a trapping density of 4 traps per individual home range, which we adhered to, however, recent simulation work has suggested only 2 hair traps per individual home range may be required when using SECR models (Sollmann et al. 2012, Sun et al. 2014). We stress that an accurate representation of the smallest average home range size is necessary to prevent traps from being spaced too far apart. When traps are spaced too widely, the number of unique individuals and recaptures declines causing a decrease in the precision of the parameter estimates (Sun et al. 2014). If hair traps can be spaced

closer together, then a regular trapping array configuration may be used, however, if they cannot, then a cluster configuration may be preferred with clusters wider than the spacing between hair traps (Sun et al. 2014). Use of fewer traps has the benefit of decreasing the trapping array size, reducing the sampling occasion length reducing environmental exposure, or reducing the number of technicians required for the study potentially saving both time and money. However, depending on the extent of the population, the size of the study area, and available resources it may not be possible to sample all available black bear habitat. In that case, it may be more appropriate to distribute multiple, smaller trapping arrays randomly across the available sampling area instead of one large array (Wilton et al. 2014).

We suggest that future efforts to estimate the density of black bear populations in New Mexico may need to shorten the length of the sampling occasion to reduce DNA degradation via UV radiation, which will increase microsatellite amplification success helping to reduce genotyping errors and increase the number of individual genotypes identified (Stetz et al. 2015). When we decreased sampling occasion length from 4 weeks to 2 weeks the genotype success rate increased by only 4% (Sandia and Sacramento Mountains: 52% vs. SSC: 48%). Thus, a pilot study may be useful to determine the length of time hair samples can remain in the field prior to collection. In addition, researchers may consider setting hair traps and bear rubs in more shaded areas (e.g., north facing slopes) to help reduce exposure to UV radiation. This may help increase the amplification success for hair samples. Increasing the number of personnel would be preferable over fewer hair traps because it would allow for a larger study area or a denser trapping array to be sampled, which should increase detection of long-range movements helping to inform  $\sigma$ , increase recapture rates, and increase the precision of parameter estimates (Sollmann et al. 2012). A larger study area will also place density estimates at the spatial scale at which state agencies make management decisions (Dreher et al. 2007). Personnel should be able to check and reset, on average, 3 – 5 hair traps per day depending on road density. For example, we were able to check more traps in the Sacramento Mountains ( $n = 148$ ) than the SSC ( $n = 141$ ) in half the time (2 weeks vs. 4 weeks, respectively) due to the higher road density in the Sacramento Mountains. Increased seasonal personnel will certainly increase cost, but this cost will be offset by a reduction in total sampling time per season. The other option is to reduce the number of hair traps resulting in a smaller study area or an increased distance between hair traps. A small study area, relative to home range size, will increase the probability that individuals travel off the sampling grid and are unavailable for capture. Individuals will also be unavailable for capture when traps are widely spaced relative to home range size causing some home ranges to fall in between hair traps. Both scenarios will reduce the number of unique individuals identified, the number of recaptures, and ultimately the precision of the parameter estimates (Sollmann et al. 2012, Sun et al. 2014). Careful consideration of these factors must be taken into account when reducing the number of hair traps to ensure a reasonable tradeoff between study area size and the distance between hair traps.

To estimate density, we used SECR models. The SECR analysis may be performed using inverse prediction (Efford 2004), maximum likelihood (ML; Borchers and Efford 2008), or Bayesian based methods (Royle et al. 2009). Inverse prediction was the original constitution of SECR models, but it is applied only to single catch traps (e.g. Sherman-live traps), due to the lack of a ML based single-catch model. Inverse prediction is limited in regards to model selection and the inclusion of parameter covariates (Borchers and Efford 2008). The two prominent statistical paradigms in SECR-based analyses are ML and Bayesian with both

methods providing similar density estimates (Borchers and Efford 2008, Royle et al. 2009). The ML framework is advantageous because these models require less computation time compared to Bayesian methods (Noss et al. 2012). Although, we note that larger study areas and finer discretization increases the necessary computation time for a model. Maximum likelihood methods may require less user knowledge compared to the Bayesian because the latter requires a prior distribution be specified and “model warnings” are often prompted if an error has occurred during model fitting (Noss et al. 2012, Efford 2013). However, users should evaluate model output carefully regardless of statistical paradigm chosen. Bayesian models may be preferred in cases where data sets with small sample size are expected (Noss et al. 2012) because ML models rely on asymptotic theory, which requires larger sample sizes in order to approach normality (Gerber and Parmenter 2015). Model output generated by a Bayesian approach may be difficult to decipher due to the mechanisms of the analysis. To interpret model output, a researcher must be able to understand the influence of model priors, the distribution of the MCMC chains, the posterior model output, and other results generated by the model (Noss et al. 2012). Inverse prediction and ML based SECR models may be fitted in either program DENSITY, which offers a Graphical User Interface (GUI), or the R package “secr” (Efford et al. 2004, Efford 2013). The secr package allows a wider range of analyses including modeling density surfaces and telemetry-integrated capture-recapture, and it provides the user greater flexibility in model optimization and processing. Bayesian estimation may be conducted in either program SPACECAP (Gopalaswamy et al. 2012), which offers a GUI, or in Program R using JAGS (Just Another Gibbs Sampler) in the BUGS (Bayesian inference Using Gibbs Sampling) language (Royle et al. 2014). For our study, we chose to estimate density using the ML based approach because the statistical knowledge and expertise of our research laboratory is rooted in ML theory.

In conclusion, we estimated the density of black bears in 5 study areas within 3 mountains ranges of New Mexico. Our estimates will aid the NMDGF in setting sustainable harvest limits. In addition to density estimates, information on demographic rates (e.g., survival rates and reproduction) and the potential effects that climate change and future land use may have on the demography of black bears may also help inform management of black bears in New Mexico, and may be considered as future areas for research.

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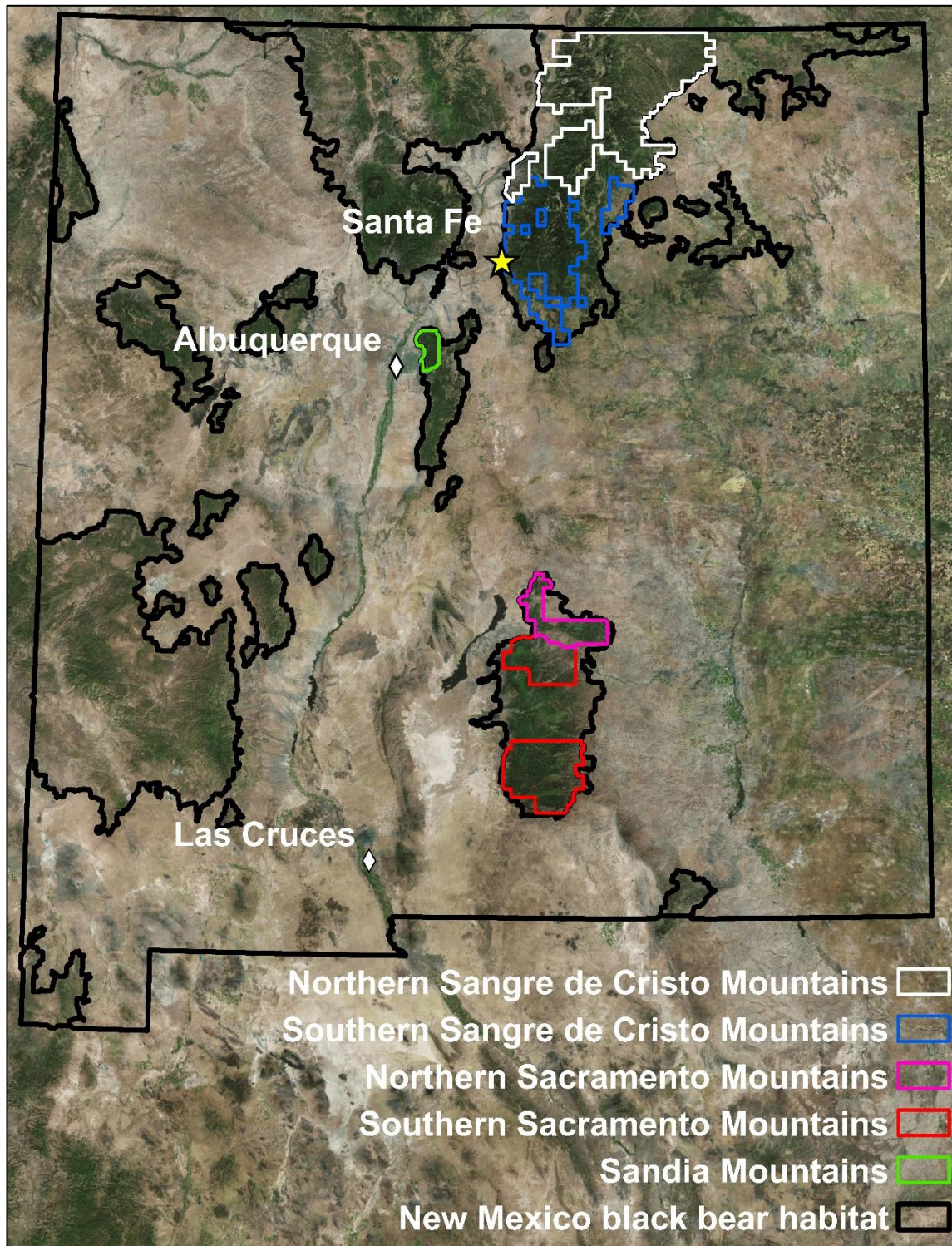
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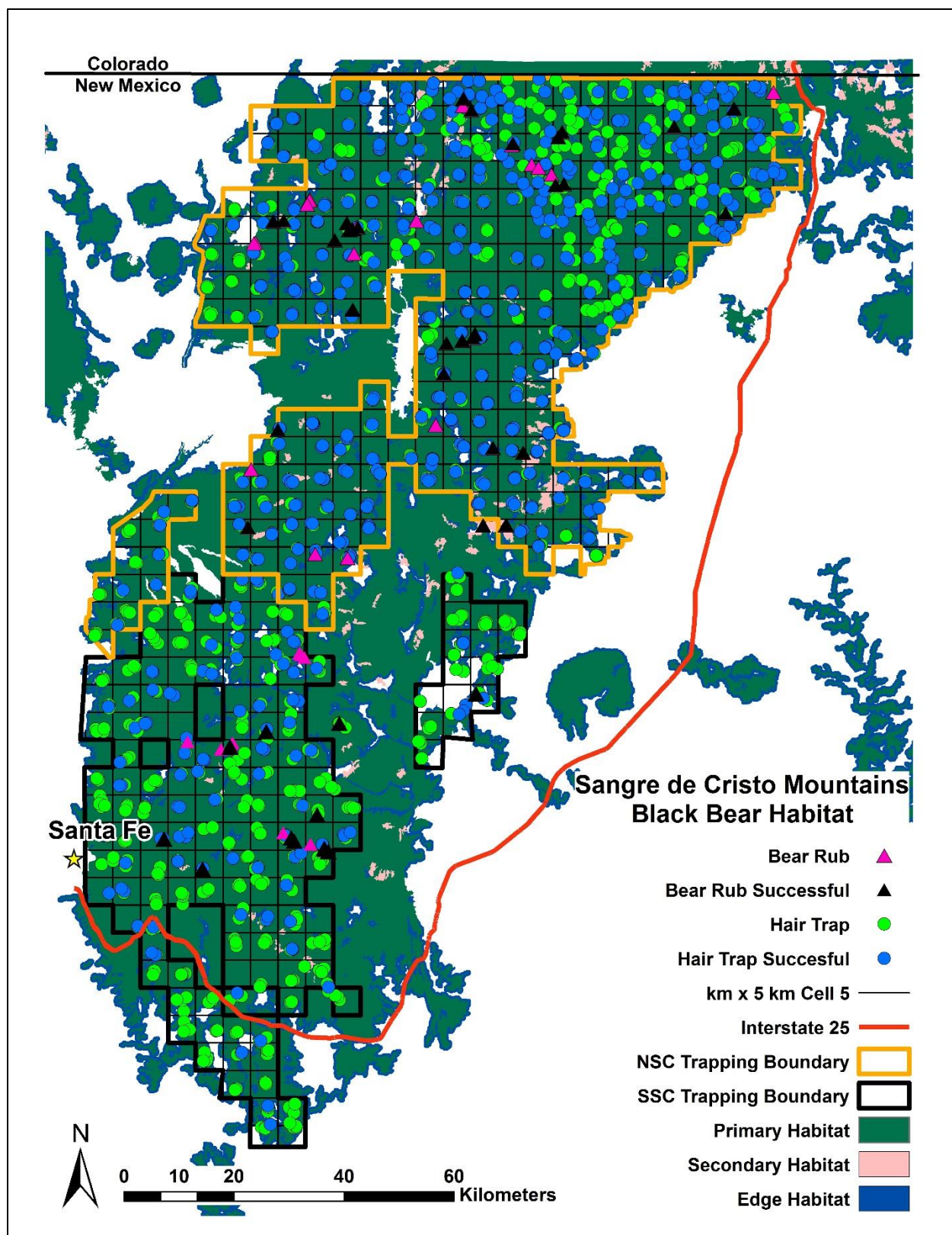
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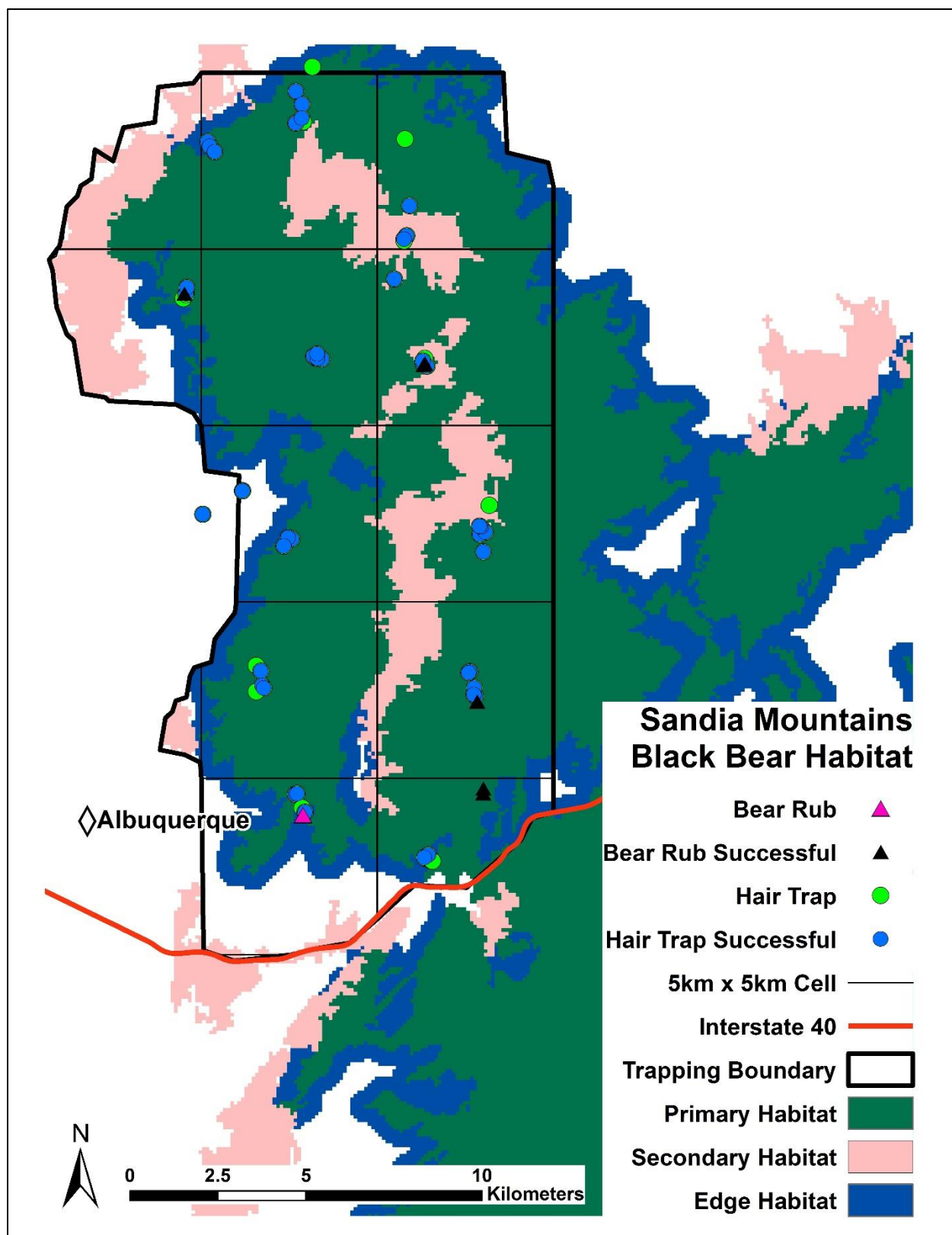


**Figure 1.** Aerial imagery of black bear habitat in New Mexico highlighting the study areas located within the Sangre de Cristo Mountains, Sandia Mountains, and Sacramento Mountains.



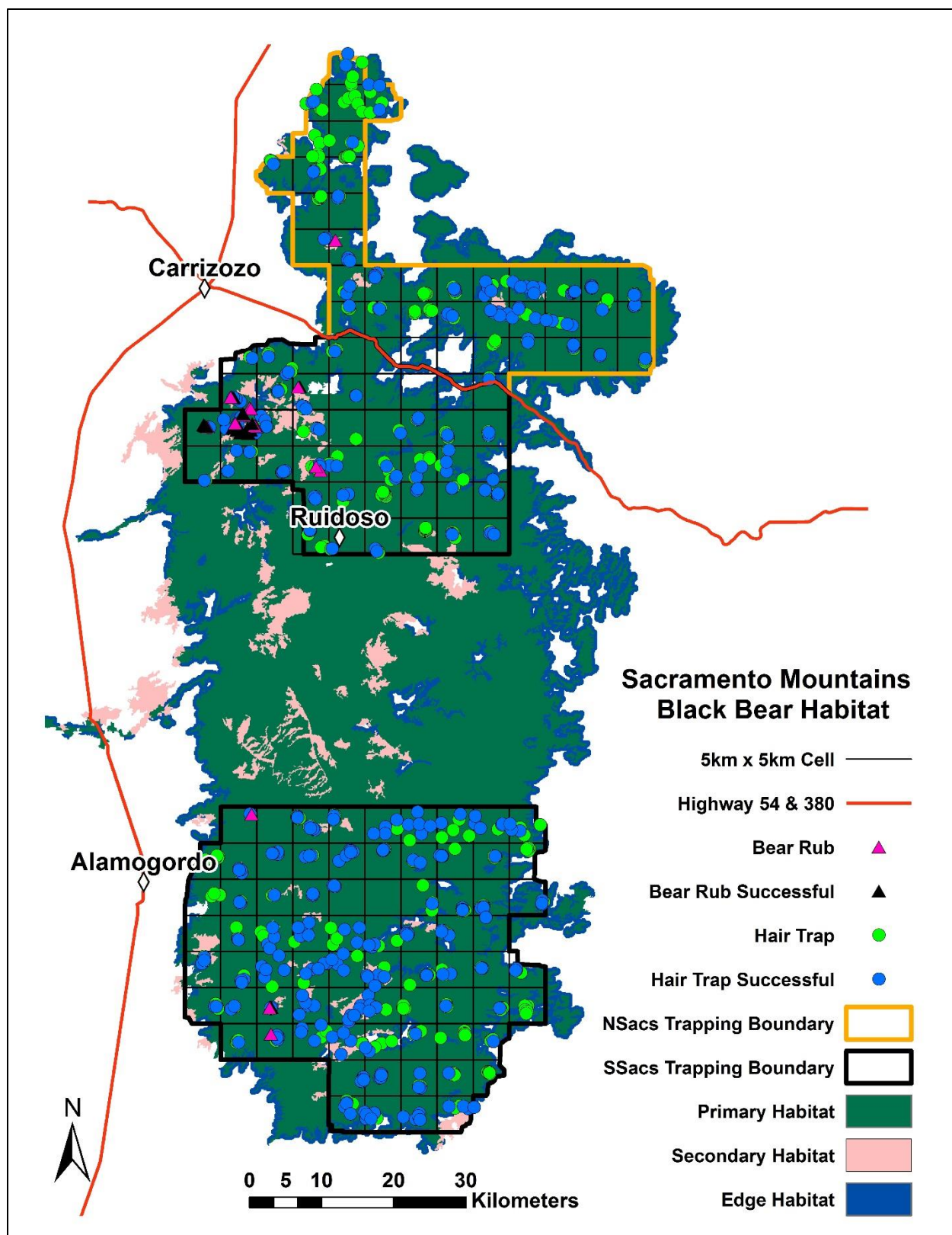


**Figure 2.** Black bear habitat identified by Costello et al. (2001) overlaid with hair traps and bear rubs set for the northern Sangre de Cristo Mountains, NM in 2012 and 2013.

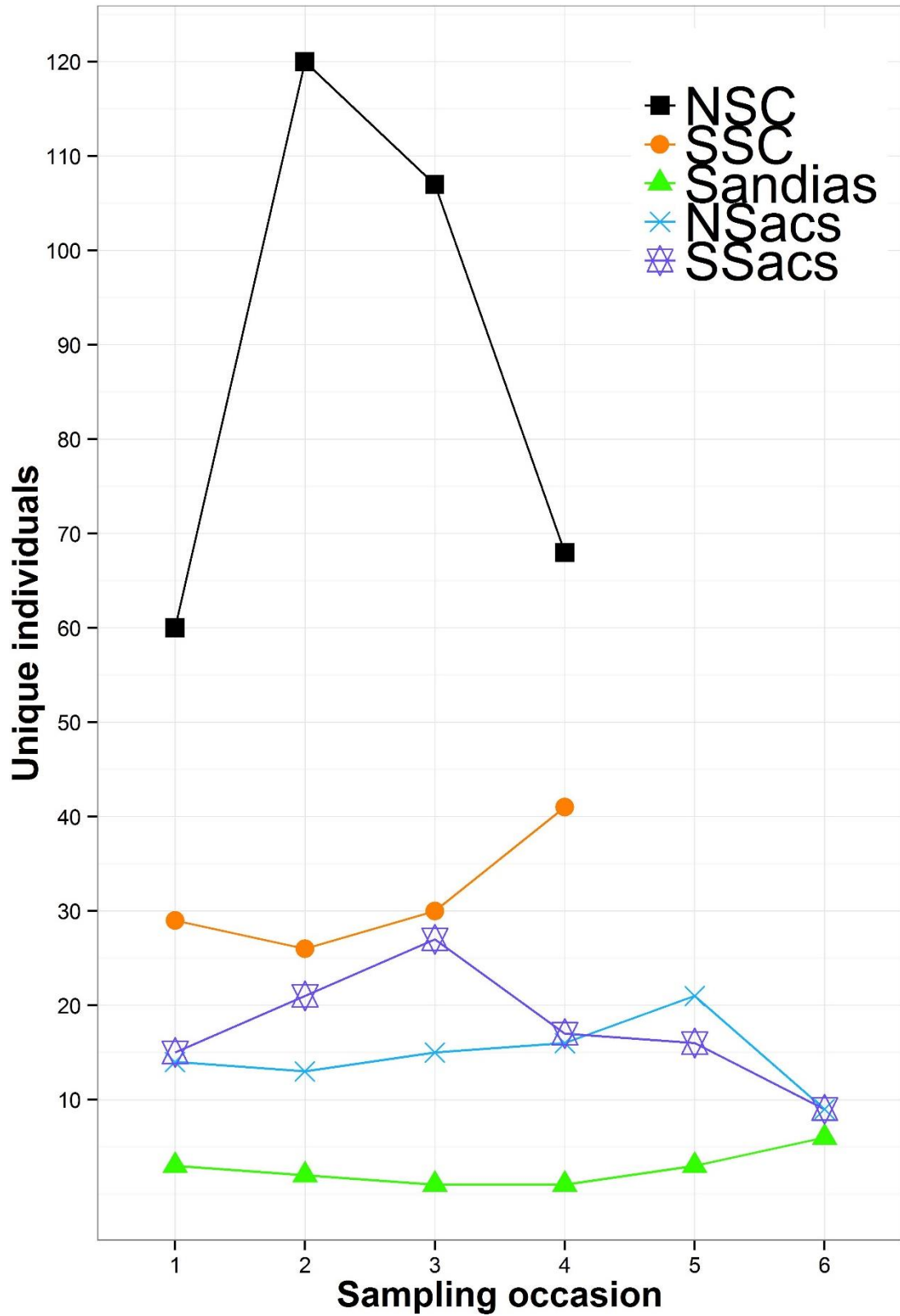


**Figure 3.** Black bear habitat identified by Costello et al. (2001) overlaid with hair traps and bear rubs set for the Sandia Mountains, NM in 2014.



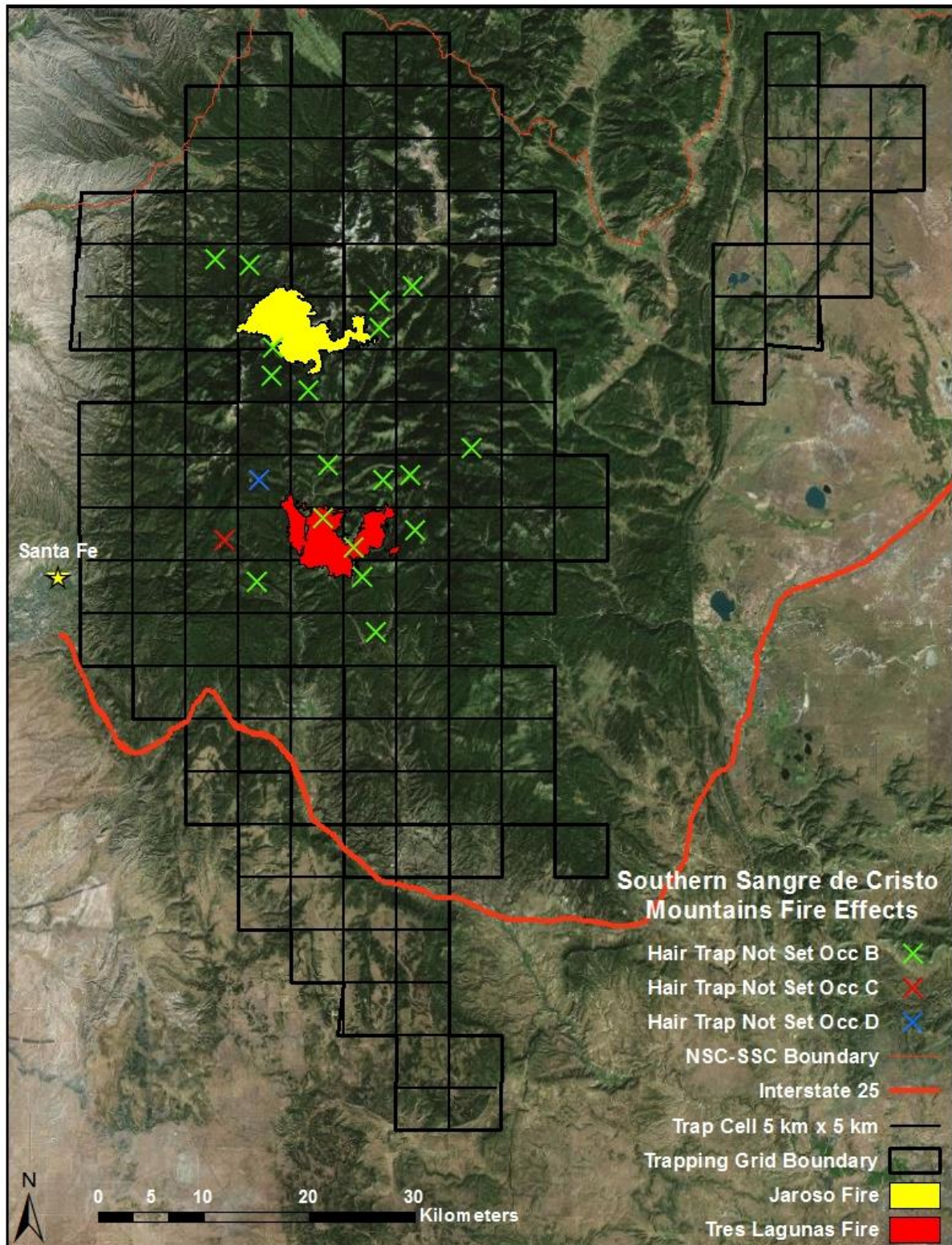


**Figure 4.** Black bear habitat identified by Costello et al. (2001) overlaid with hair traps and bear rubs set for the Sacramento Mountains, NM in 2014.



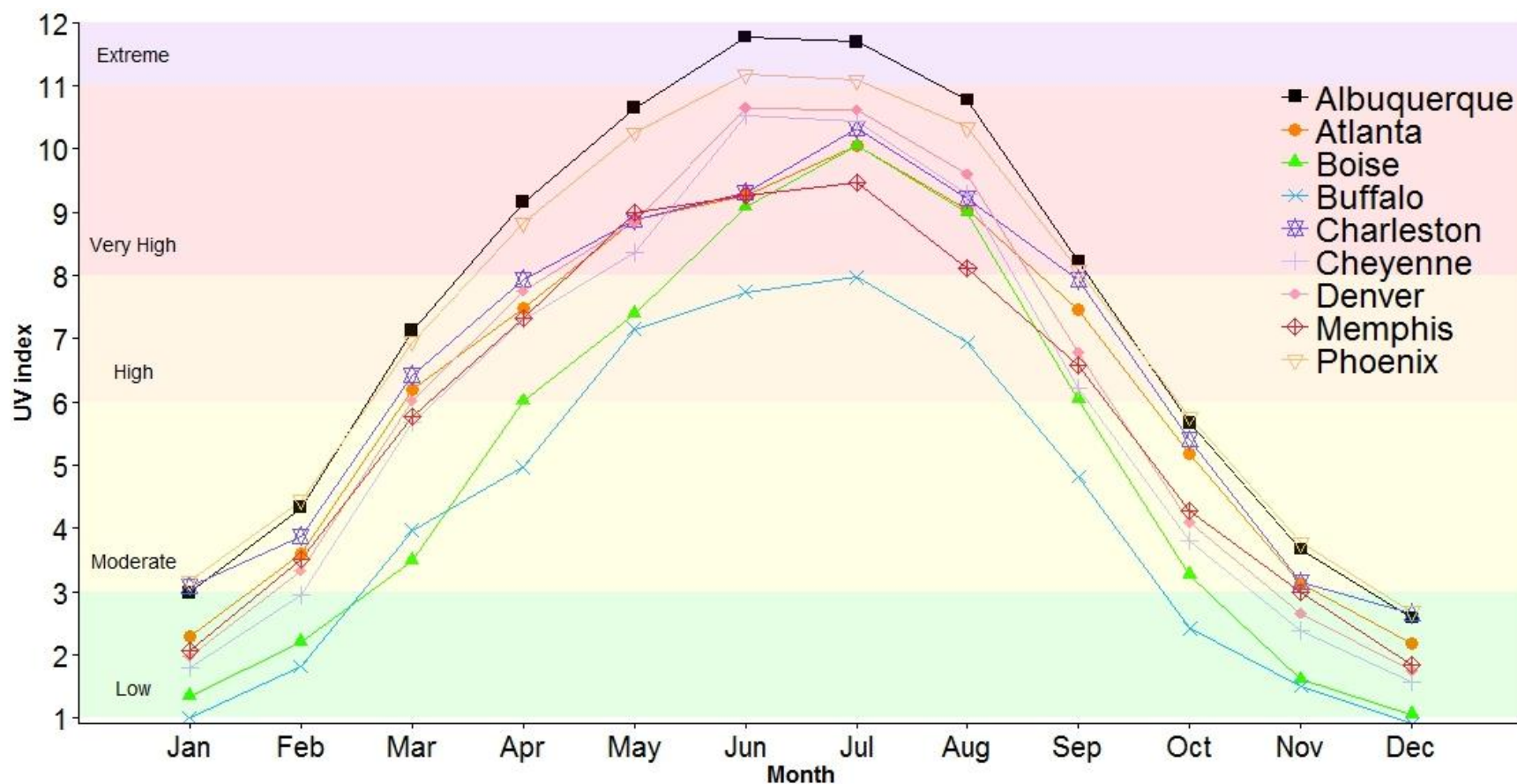
**Figure 5.** Number of unique individuals detected by hair traps and bear rubs combined for each sampling occasion in the Northern (NSC) and Southern (SSC) Sangre de Cristo, Sandia, and Northern (NSacs) and Southern (SSacs) Sacramento Mountains, NM.





**Figure 6.** Map of hair traps not deployed due to the Jaroso and Tres Lagunas fires in the southern Sangre de Cristo Mountains, NM in 2013.





**Figure 7.** Mean montly ultraviolet index (UVI) generated by the National Oceanic and Atmospheric Administration showing estimated noontime intensity of ultraviolet radiation coupled with the World Health Organization human health hazard UVI classification for Albuquerque, NM, Atlanta, GA, Boise, ID, Buffalo, NY, Charleston, SC, Cheyenne, WY, Denver, CO, Memphis, TN, and Phoenix, AZ, USA in 2012.

**Table 1.** Field sampling summary statistics allocated by number of detector types set (hair traps = HR & bear rub = BR), for the Northern (NSC) and Southern (SSC) Sangre de Cristo, Sandia, and Northern (NSacs) and Southern (SSacs) Sacramento Mountains, NM.

Study Area	HT <sup>a</sup>	HT Sites <sup>b</sup>	HT Hit <sup>c</sup>	HT Effort <sup>d</sup>	BR <sup>a</sup>	BR Effort <sup>d</sup>
NSC	256	1018	0.36	28,183	46	3,730
SSC	141	537	0.29	15,768	25	1,816
Sandias	12	69	0.42	979	7	293
NSacs	37	217	0.41	2,990	1	56
SSacs	111	656	0.29	9,090	33	1,112
Total	557	2497	0.33	57,010	112	7,007

<sup>a</sup> Number of sampling detectors set.

<sup>b</sup> Number of sampling detectors cumulatively summed across all sampling occasions.

<sup>c</sup> Number of traps which collected  $\geq 1$  hair sample over the all sampling occasions.

<sup>d</sup> Sampling effort represented by the number of days a sampling detector (hair trap & bear rub) was set summed across all detectors and all sampling occasions.

**Table 2.** The total number of hair samples collected across sampling occasions (1-6) and detector type (hair trap:bear rub) , and the overall total for the Northern (NSC) and Southern

Study Area	1	2	3	4	5	6	Total
NSC	312 (299:13)	634 (582:52)	597 (571:26)	374 (339:35)	-	-	1917 (1791:126)
SSC	145 (141:4)	125 (124:1)	184 (183:1)	273 (246:27)	-	-	727 (694:33)
Sandias	8 (8:0)	30 (30:0)	23 (19:4)	28 (19:9)	51 (35:16)	37 (31:6)	177 (142:35)
NSacs	49 (49:0)	58 (58:0)	77 (73:4)	75 (73:2)	123 (118:5)	82 (79:3)	464 (450:14)
SSacs	93 (93:0)	143 (143:0)	183 (179:4)	135 (118:17)	129 (118:11)	115 (97:18)	798 (748:50)
Total	607 (590:17)	990 (937:53)	1064 (1025:39)	885 (795:90)	303 (271:32)	234 (207:27)	4083 (3825:258)

(SSC) Sangre de Cristo, Sandia, and Northern (NSacs) and Southern (SSacs) Sacramento Mountains, NM.

**Table 3.** Number of alleles, expected heterozygosity ( $H_E$ ), and observed heterozygosity ( $H_O$ ) for eight microsatellite markers used for individual identification of American black bears in the Sangre de Cristo Mountains, Sandia Mountains, and Sacramento Mountains, NM.

Marker	<u>No. Alleles</u>			<u><math>H_E</math></u>			<u><math>H_O</math></u>		
	Sangres	Sandias	Sacramentos	Sangres	Sandias	Sacramentos	Sangres	Sandias	Sacramentos
G10L	8.00	6.00	6.00	0.80	0.81	0.74	0.80	0.78	0.73
G1D	7.00	4.00	5.00	0.76	0.76	0.61	0.76	0.56	0.60
G10H	12.00	6.00	8.00	0.76	0.77	0.63	0.76	0.61	0.60
G10M	6.00	4.00	6.00	0.72	0.73	0.71	0.70	0.72	0.72
G10B	7.00	4.00	4.00	0.72	0.72	0.68	0.72	0.83	0.65
G10J	9.00	6.00	7.00	0.71	0.78	0.73	0.72	0.67	0.72
MU59	10.00	4.00	5.00	0.70	0.49	0.50	0.71	0.50	0.50
G10U	9.00	6.00	6.00	0.65	0.78	0.69	0.66	0.78	0.70
Mean	8.50	5.00	5.88	0.73	0.73	0.66	0.73	0.68	0.65

**Table 4.** Number of samples collected, number of samples that contained enough genetic material for analysis (samples analyzed), the proportion of samples that produced a successful genotype (Sample Success) and the number of unique individuals identified by each detector type (hair trap only = HT; bear rub only = BR; hair trap and bear rub = HTBR) for the Northern (NSC) and Southern (SSC) Sangre de Cristo, Sandia, and Northern (NSacs) and Southern (SSacs) Sacramento Mountains, NM.

Study Area	Samples Collected	Samples Analyzed	Sample Success	Unique Individuals		
				M (HT:BR:HTBR)	F (HT:BR:HTBR)	Total (HT:BR:HTBR)
NSC	1917	1416	0.49	190 (171:18:1)	189 (179:10:0)	379 (350:28:1)
SSC	727	517	0.48	67 (63:2:2)	64 (61:2:1)	131 (124:4:3)
Sandias	177	115	0.53	9 (5:1:3)	9 (8:1:0)	18 (13:2:3)
NSacs	464	360	0.61	49 (46:0:3)	39 (38:0:1)	88 (54:0:4)
SSacs	798	542	0.44	53 (50:2:1)	57 (53:3:1)	110 (103:5:2)
Total	4083	2950	0.50	368 (335:23:10)	358 (339:16:3)	726 (674:39:13)

**Table 5.** A summary of the capture history data for both male and female black bears identified by samples collected across the Northern (NSC) and Southern (SSC) Sangre de Cristo, Sandias, and Northern (NSacs) and Southern (SSacs) Sacramento Mountains,

	Males								Females							
	N <sup>a</sup>	Det <sup>b</sup>	Avg <sup>c</sup>	SD <sup>d</sup>	Max <sup>e</sup>	R <sup>f</sup>	MMR (km) <sup>g</sup>	MaxD (km) <sup>h</sup>	N <sup>a</sup>	Det <sup>b</sup>	Avg <sup>c</sup>	SD <sup>d</sup>	Max <sup>e</sup>	R <sup>f</sup>	MMR (km) <sup>g</sup>	MaxD (km) <sup>h</sup>
NSC	190	239	1.26	0.43	3	33	7.57	52.03	189	216	1.14	0.35	3	23	3.98	47.41
SSC	67	80	1.19	0.38	3	8	12.46	29.33	64	77	1.20	0.39	2	12	2.53	20.33
Sandias	9	15	1.67	0.46	2	3	8.27	9.84	9	14	1.56	0.73	3	4	0.38	0.69
Nsacs	49	74	1.51	0.74	5	14	9.22	36.18	39	58	1.49	0.72	3	12	2.47	7.05
Ssacs	53	69	1.30	0.41	3	10	4.23	8.02	57	73	1.28	0.54	3	11	4.59	14.88
Total	368	477	1.39	0.48	5	68	8.35	27.08	358	438	1.33	0.55	3	62	2.79	18.07

NM.

<sup>a</sup> Number of animals detected.

<sup>b</sup> Total number of detections across all sampling occasions.

<sup>c</sup> Average number of detections per individual detected across all sampling occasions.

<sup>d</sup> Standard deviation for the average number of detections.

<sup>e</sup> Maximum number of detections of a single individual across all sampling occasions.

<sup>f</sup> Number of recaptured individuals across all sampling occasions.

<sup>g</sup> Mean maximum recapture distance.

<sup>h</sup> Maximum distance moved by an individual.

**Table 6.** The final set of *a priori* spatially explicit capture-recapture models for the Northern Sangre de Cristo Mountains, NM in 2012.

<b>D<sup>a</sup></b>	<b>g0<sup>a</sup></b>	<b>σ<sup>a</sup></b>	<b>K<sup>b</sup></b>	<b>AIC<sub>c</sub><sup>c</sup></b>	<b>ΔAIC<sub>c</sub><sup>d</sup></b>	<b>w<sub>i</sub><sup>e</sup></b>	<b>Dev<sup>f</sup></b>
constant	t + veg	t + veg	17	3149.15	0.00	1.00	3113.46
constant	t	t	9	3201.03	51.88	0.00	3182.54
constant	veg	veg	11	3216.43	67.28	0.00	3193.71
constant	t	veg	10	3221.75	72.59	0.00	3201.15
constant	veg	t	10	3236.73	87.58	0.00	3216.14
constant	type	type	5	3251.32	102.17	0.00	3241.16
constant	sex	sex	5	3271.17	122.02	0.00	3261.01
constant	constant	constant	3	3271.37	122.22	0.00	3265.31
sex	constant	constant	4	3273.42	124.26	0.00	3265.31

<sup>a</sup> Model parameters a function of: sex; t = time variation; type = detector type, veg = land cover type; + = additive effect; constant = no variation.

<sup>b</sup> Number of model parameters.

<sup>c</sup> Akaike's Information Criterion adjusted for small sample size.

<sup>d</sup> The difference between the top ranked model and the *i*th ranked model.

<sup>e</sup> Model weight.

<sup>f</sup> Model deviance = -2(log-likelihood).

**Table 7.** The final set of *a priori* spatially explicit capture-recapture models for the Southern Sangre de Cristo Mountains, NM in 2013.

<b>D<sup>a</sup></b>	<b>g0</b>	<b>σ</b>	<b>K<sup>b</sup></b>	<b>AIC<sub>c</sub><sup>c</sup></b>	<b>ΔAIC<sub>c</sub><sup>d</sup></b>	<b>w<sub>i</sub><sup>e</sup></b>	<b>Dev<sup>f</sup></b>
constant	t + elev	t + elev	11	1169.98	0.00	0.87	1145.76
constant	t + veg	t + veg	17	1173.85	3.87	0.13	1134.44
constant	veg	t	10	1195.99	26.01	0.00	1174.16
constant	elev	t	7	1197.67	27.69	0.00	1182.76
constant	t	veg	10	1199.07	29.09	0.00	1177.24
constant	t	elev	7	1199.91	29.93	0.00	1185.00
constant	veg	veg	11	1205.12	35.14	0.00	1180.90
constant	t	t	9	1210.10	40.12	0.00	1190.61
constant	elev	elev	5	1210.48	40.50	0.00	1200.00
constant	sex	sex	5	1214.90	44.92	0.00	1204.42
constant	type	type	5	1216.35	46.37	0.00	1205.87
constant	constant	constant	3	1223.86	53.88	0.00	1217.67
sex	constant	constant	4	1225.92	55.94	0.00	1217.60

<sup>a</sup> Model parameters a function of: elev = elevation; sex; t = time variation; type = detector type; veg = land cover type; + = additive effect; constant = no variation.

<sup>b</sup> Number of model parameters.

<sup>c</sup> Akaike's Information Criterion adjusted for small sample size.

<sup>d</sup> The difference between the top ranked model and the *i*th ranked model.

<sup>e</sup> Model weight.

<sup>f</sup> Model deviance = -2(log-likelihood).

**Table 8.** The final set of *a priori* spatially explicit capture-recapture models for the Sandia Mountains, NM in 2014.

<b>D<sup>a</sup></b>	<b>g0<sup>a</sup></b>	<b>σ<sup>a</sup></b>	<b>K<sup>b</sup></b>	<b>AIC<sub>c</sub><sup>c</sup></b>	<b>ΔAIC<sub>c</sub><sup>d</sup></b>	<b>w<sub>i</sub><sup>e</sup></b>	<b>Dev<sup>f</sup></b>
constant	sex	sex	5	209.23	0.00	0.96	194.23
constant	constant	constant	3	216.23	6.99	0.03	208.51
constant	elev	elev	5	219.20	9.97	0.01	204.20
sex	constant	constant	4	219.59	10.36	0.00	208.51
constant	type	type	5	219.84	10.60	0.00	204.84
constant	veg	veg	5	219.97	10.74	0.00	204.97
constant	t	elev	9	235.19	25.96	0.00	194.69
constant	t	veg	9	238.34	29.11	0.00	197.84
constant	elev	t	9	243.24	34.00	0.00	202.74
constant	veg	t	9	243.52	34.29	0.00	203.02
constant	t	t	13	311.75	102.52	0.00	194.75
constant	t + elev	t + elev	15	451.94	242.71	0.00	189.35
constant	t + veg	t + veg	15	461.61	252.38	0.00	191.61

<sup>a</sup> Model parameters a function of: elev = elevation; sex; t = time variation; type = detector type; veg = land cover type; + = additive effect; constant = no variation.

<sup>b</sup> Number of model parameters.

<sup>c</sup> Akaike's Information Criterion adjusted for small sample size.

<sup>d</sup> The difference between the top ranked model and the *i*th ranked model.

<sup>e</sup> Model weight.

<sup>f</sup> Model deviance = -2(log likelihood).

**Table 9.** The final set of *a priori* spatially explicit capture-recapture models for the Northern Sacramento Mountains, NM in 2014.

<b>D<sup>a</sup></b>	<b>g0<sup>a</sup></b>	<b>σ<sup>a</sup></b>	<b>K<sup>b</sup></b>	<b>AIC<sub>c</sub><sup>c</sup></b>	<b>ΔAIC<sub>c</sub><sup>d</sup></b>	<b>w<sub>i</sub><sup>e</sup></b>	<b>Dev<sup>f</sup></b>
constant	t + veg	t + veg	17	868.31	0.00	0.96	825.57
constant	veg	t	10	874.86	6.55	0.04	852.01
constant	t	veg	10	880.74	12.44	0.00	857.89
constant	veg	veg	7	883.07	14.76	0.00	867.67
constant	t + elev	t + elev	15	910.39	42.08	0.00	873.72
constant	sex	sex	5	910.45	42.14	0.00	899.71
constant	t	t	13	922.95	54.65	0.00	892.04
constant	elev	elev	5	923.70	55.39	0.00	912.97
constant	t	elev	9	925.73	57.42	0.00	905.42
constant	elev	t	9	928.60	60.30	0.00	908.30
constant	constant	constant	3	951.19	82.88	0.00	944.91
sex	constant	constant	4	952.25	83.94	0.00	943.77

<sup>a</sup> Model parameters a function of: elev = elevation; sex; t = time variation; veg = land cover type; + = additive effect; constant = no variation.

<sup>b</sup> Number of model parameters.

<sup>c</sup> Akaike's Information Criterion adjusted for small sample size.

<sup>d</sup> The difference between the top ranked model and the *i*th ranked model.

<sup>e</sup> Model weight.

<sup>f</sup> Model deviance = -2(log-likelihood).



**Table 10.** The final set of *a priori* spatially explicit capture-recapture models for the Southern Sacramento Mountains, NM in 2014.

<b>D<sup>a</sup></b>	<b>g0<sup>a</sup></b>	<b>σ<sup>a</sup></b>	<b>K<sup>b</sup></b>	<b>AIC<sub>c</sub><sup>c</sup></b>	<b>ΔAIC<sub>c</sub><sup>d</sup></b>	<b>w<sub>i</sub><sup>e</sup></b>	<b>Dev<sup>f</sup></b>
constant	veg	veg	7	1168.68	0.00	0.50	1153.58
constant	t + veg	t + veg	17	1169.62	0.94	0.31	1128.97
constant	t + elev	t+ elev	15	1170.58	1.90	0.19	1135.47
constant	veg	t	10	1180.23	11.54	0.00	1158.00
constant	type	type	5	1182.05	13.37	0.00	1171.48
constant	elev	elev	5	1182.51	13.83	0.00	1171.93
constant	elev	t	9	1184.24	15.56	0.00	1164.44
constant	t	t	13	1186.59	17.91	0.00	1156.80
constant	t	elev	9	1191.22	22.54	0.00	1171.42
constant	t	veg	10	1193.33	24.65	0.00	1171.10
constant	constant	constant	3	1196.53	27.85	0.00	1190.31
constant	sex	sex	5	1198.08	29.40	0.00	1187.50
sex	constant	constant	4	1198.54	29.86	0.00	1190.16

<sup>a</sup> Model parameters a function of: elev = elevation; sex; t = time variation; type = detector type; veg = land cover type; + = additive effect; constant = no variation.

<sup>b</sup> Number of model parameters.

<sup>c</sup> Akaike's Information Criterion adjusted for small sample size.

<sup>d</sup> The difference between the top ranked model and the *i*th ranked model.

<sup>e</sup> Model weight.

<sup>f</sup> Model deviance = -2(log-likelihood).

**Table 11.** Density and model parameter estimates, coefficient of variation of the density estimate (CV), detection probability at the activity center ( $g_0$ ), spatial scale over which detection probability declines ( $\sigma$ ; km), and their 95% confidence intervals for the Northern (NSC) and Southern (SSC) Sangre de Cristo, Sandia, and Northern (NSacs) and Southern (SSacs) Sacramento Mountains, NM. Competing models for the SSC and SSacs were model averaged. We performed all analyses within a spatially explicit capture-recapture framework.

Study Area	D <sup>a</sup>	$g_0^b$	$\sigma^c$	$\hat{D}^d$	CV( $\hat{D}$ )	$\hat{g}_0^e$	$\hat{\sigma}^f$
NSC	constant	t + veg	t + veg	21.86 (17.83 – 26.80)	0.10	0.00060 (0.000233 - 0.001528)	3.31 (2.09 – 5.25)
SSC	constant constant	t + elev t + veg	t + elev t + veg	19.74 (13.77 – 28.30)	0.18	0.00001 (0.000006 – 0.000052)	18.35 (12.73 – 26.46)
Sandias	constant	sex	sex	25.75 (13.22 – 50.14)	0.35	0.02941 <sup>g</sup> (0.010779 – 0.077689) 0.00163 <sup>h</sup> (0.000480 – 0.005488)	0.76 <sup>g</sup> (0.49 – 1.15) 4.99 <sup>h</sup> (2.46 – 10.09)
NSacs	constant	t + veg	t + veg	20.17 (15.35 – 26.52)	0.14	0.00266 (0.000580 – 0.012125)	5.42 (2.03 – 14.44)
SSacs	constant constant constant	veg t + veg t + elev	veg t + veg t + elev	16.55 (11.64 – 23.53)	0.18	0.00318 (0.001087 - 0.009279)	2.67 (1.69 – 4.21)

<sup>a</sup> Final model structure for the secr parameter, density (D).

<sup>b</sup> Final model structure for the secr parameter, detection probability ( $g_0$ ).

<sup>c</sup> Final model structure for the secr parameter,  $\sigma$ , the spatial scale over which detection probability declines.

<sup>d</sup> Black bear density estimate (bears/100 km<sup>2</sup>) with the 95% confidence intervals in parentheses.

<sup>e</sup> Detection probability ( $g_0$ ) parameter estimate with the 95% confidence intervals in parentheses.

<sup>f</sup>  $\sigma$  (km) parameter estimate with the 95% confidence intervals in parentheses.

<sup>g</sup> Parameter estimate for female black bears.

<sup>h</sup> Parameter estimate for male black bears.

**Table 12.** Mean density estimates for black bears (bears/100 km<sup>2</sup>) and 95% CIs in parentheses for noninvasive genetic sampling studies conducted in the United States that also used a spatially explicit capture-recapture framework.

State	$\hat{D}$	Reference
Ozark Highlands, Missouri	1.7 (1.1 – 2.4)	Wilton et al. 2014
Carver Bay, South Carolina	4.6 (2.4 – 6.7)	Drewry et al. 2013
Southern Black Bear Range, New York	9.1 (7.6 – 11.3)	Sun et al. 2014
Picture Rocks National Lakeshore, Michigan	10.5 (8.5 – 12.7)	Sollmann et al. 2012
Glacier National Park, Montana <sup>a</sup>	12.0 (10.0 – 14.4)	Stetz et al. 2014 <sup>a</sup>
Southern Sacramento Mountains, New Mexico	16.5 (11.6 – 23.5)	This Study
Southern Sangre de Cristo Mountains, New Mexico	19.7 (13.8 – 28.3)	This Study
Fort Drum Military Installation, New York	20.0 (15.0 – 26.0)	Gardner et al. 2010
Northern Sacramento Mountains, New Mexico	20.1 (15.3 – 26.5)	This Study
Northern Sangre de Cristo Mountains, New Mexico	21.8 (17.8 – 26.8)	This Study
Sandia Mountains, New Mexico	25.7 (13.2 – 50.1)	This Study
Spanish Peaks, Colorado	44.0 (32.1 – 55.8)	Apker et al. 2009
Lewis Ocean Bay, South Carolina	33.9 (22.9 – 44.8)	Drewry et al. 2013
Alligator River National Wildlife Refuge, North Carolina 2004	37.0 (30.7 – 43.2)	Tredick et al. 2009
Great Dismal Swamp National Wildlife Refuge, North Carolina and Virginia	46.0 (34.6 – 57.3)	Tredick et al. 2009
Alligator River National Wildlife Refuge, North Carolina 2003	57.0 (47.9 – 66.0)	Tredick et al. 2009
Pocosin Lakes National Wildlife Refuge, North Carolina 2002	58.0 (49.1 – 66.8)	Tredick et al. 2009
Pocosin Lakes National Wildlife Refuge, North Carolina 2003	77.0 (65.4 – 88.5)	Tredick et al. 2009

<sup>a</sup> Black bear population sympatric with grizzly bears (*Ursus arctos*).