

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

Report on 2013 data collection and analysis for the southern Sangre de Cristo Mountains and an updated analysis for the northern Sangre de Cristo Mountains

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ABSTRACT

We estimated the density of American black bears (*Ursus americanus*) in the Sangre de Cristo Mountains, New Mexico. We used two non-invasive genetic sampling (NGS) methods: hair traps and bear rubs, to sample the population. Eight microsatellite and one gender marker were amplified to generate individual genotypes and associated capture histories. We estimated density using a spatially explicit capture-recapture (SECR) framework. Our density estimates were 18.6 bears/100 km² (95% CI = 13.0 - 26.8) for the southern Sangre de Cristo Mountains (SSC) and 23.7 bears/100 km² (95% CI = 19.4 - 29.0) for the northern Sangre de Cristo Mountains (NSC). Detection probability was influenced by vegetation type and time, suggesting that aspects of black bear denning and foraging ecology influenced our ability to detect them. The Jaroso and Tres Lagunas fires may have also negatively affected our ability to estimate detection probability because they prevented us from checking hair traps located in high quality bear habitat thereby reducing sample size. The success of identifying individuals through genetic typing was also hampered by high levels of DNA degradation, which we suspect may be a consequence of heightened exposure to UV radiation. Despite these issues, our density estimates and their precision are comparable to similar SECR-based NGS black bear studies conducted in other parts of North America. Our density estimates for the Sangre de Cristo Mountain's black bear population are higher than the previous density estimate (17.0 bears/100 km²) used by the New Mexico Department of Game and Fish to set harvest limits.

INTRODUCTION

Setting sustainable harvest limits for game species is one of the main duties of state wildlife management agencies. 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 provide relatively robust estimates of common game species such as deer and elk. In contrast, estimating the abundance or density of large carnivores that are cryptic and occur at low densities is more difficult because carnivore behavior makes the survey methods used for ungulates ineffective (Obbard et al. 2010). 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 the effects of harvest on a population (Garshelis 1990). Yet, harvest data may be influenced by hunter selectivity and sex-specific vulnerability (Kohlmann et al. 1999, Beston and Mace 2012) and consequently, these data are often not representative of the true population and may be inappropriate to use for setting harvest limits (Beston and Mace 2012). Recent innovations in non-invasive genetic sampling techniques (NGS, Woods et al. 1999) and robust statistical analyses such as spatially explicit capture-recapture (SECR; Efford 2004) have enabled researchers to better sample and estimate density and abundance for carnivore populations from which harvest limits can be established.

Our objective was to estimate the density of American black bears (*Ursus americanus*) >1 year of age in primary bear habitat within 6 of the 14 bear management zones (BMZs) located in the Sacramento and Sangre de Cristo Mountains, New Mexico. We began by estimating density of bears for the northern Sangre de Cristo Mountains (NSC; Figure 1), extended our sampling to the southern Sangre de Cristo Mountains (SSC; Figure 1) in 2013, and then we conducted a tandem analysis to compare estimates from the two study areas. We incorporated land cover into our density modeling and provide updated estimates for the NSC. Our results provide a baseline density estimate for black bear populations in the Sangre de Cristo Mountains.

METHODS

Field Sampling

We sampled the NSC in 2012 (Figure 2), and subsequently sampled the SSC in 2013 (Figure 3). For details regarding sampling the NSC see Gould et al. (2014).

We set hair traps from 29 April - 9 September 2013 across 4 sampling occasions in the SSC (Figure 3). Each sampling occasion lasted 4 weeks. We randomly distributed 141 5-km x 5-km cells (3,525 km²) across the landscape, and then systematically set hair traps within primary bear habitat as identified by Costello et al. (2001).

We used two concurrent NGS methods to collect hair samples: hair traps and bear rubs (Woods et al 1999, Kendall et al. 2008). A hair trap consisted of a single strand of barbed wire wrapped around 3-5 trees with a lure pile at the center (Woods et al. 1999). During each sampling occasion, 1 of 2 non-consumable lures (blood/fish emulsion or skunk/lanolin) was randomly selected to attract bears. When a bear passed over or under the wire 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 hung at 45 cm. A sample consisted of all hair caught in one barb and we included hair samples from the lure pile. We deposited each hair sample in a separate paper coin envelope. We removed any remaining hair from the barbed wire with a propane torch to prevent false recaptures during the next sampling occasion (Kendall et al. 2009). Hair traps were moved 100 m to 2.5 km between each occasion to help increase the novelty of a trap location in an attempt to increase recapture rates.

Bears rub on trees, power poles, barbed-wire fences, wooden signs, and road signposts (Burst and Pelton 1983; Green and Mattson 2003). We opportunistically collected hair from bear rubs along trails that were used to navigate to hair traps. We identified bear rubs by evidence of rubbing behavior such as a smoothed surface and presence of snagged hair (Kendall et al. 2008, 2009). We attached 3 short strands of barbed wire vertically to the rub structure to facilitate the collection of hair samples (Kendall et al. 2008, 2009, Stetz et al. 2014). Once located and modified, rubs were checked concurrently with nearby hair traps. We collected hair samples only from the barbed wire to ensure the samples were deposited during the current sampling occasion and we removed any remaining hair with a torch to prevent false recaptures. All hair samples were stored in an airtight container on a silica desiccant at room temperature.

Genetic Analysis

Individuals were identified by comparing multilocus genotypes generated from each tissue or hair sample using 8 nuclear, polymorphic microsatellite loci (G1D, G10B, G10L, G10M [Paetkau et al. 1995]; G10H, G10J, G10U [Paetkau et al. 1998]; MU59 [Taberlet et al. 1997]) and an amelogenin or ZFX/ZFY sex marker (Paetkau 2003, 2004; Yamamoto et al. 2002; Durin et al. 2007). We selected these specific markers because they had relatively high mean, expected heterozygosities (0.7 to 0.8; Paetkau 2003, 2004). These markers were chosen from a battery of markers that were amplified from samples collected from the northern Sangre de Cristo Mountains in 2012. Genotyping errors may occur owing to small quantities of DNA or because of poor quality DNA and can either create novel genotypes or result in allelic dropout, which may result in misidentifying previously identified individuals and which could bias density estimates (Mills et al. 2000, Lukacs and Burnham 2005). Such errors can overestimate the number of individuals identified or negatively influence recapture rate. We used previously developed analytical approaches to reduce genotyping errors (Paetkau 2003, Kendall et al. 2009). Dr. David Paetkau, President of Wildlife Genetics International in Nelson, British Columbia, Canada, directed the collection of the genetic data and provided a report for each analysis.

Density Estimation

Previously, we estimated density with two different approaches: by dividing an estimate of abundance by the “effective trapping area” (ETA; Dice 1938, Huggins 1989) and comparing this estimate to that derived from SECR models (Gould et al. 2014). Herein we report only the estimates derived from SECR models because: 1) abundance estimates derived from the former

approach have been shown to be positively biased because “edge effects” can negatively bias capture probabilities (Wilson and Anderson 1985, Parmenter et al. 2003), 2) there is considerable uncertainty in estimating the ETA and the approach is necessarily ad hoc (Wilson and Anderson 1985), and 3) simulations have shown that SECR–based density estimates typically outperform ETA–based approaches especially when capture probabilities are low (Ivan et al. 2013).

We generated capture histories for each uniquely identified black bear and used these to estimate density directly using SECR models (Efford et al. 2004, Borchers and Efford 2008, Efford et al. 2013) with the R package “secr” (Efford 2013). We estimated 3 parameters: density (D), a detection probability (g_0), and the spatial scale over which the detection probability declines (σ ; 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 location of the individual’s home range and the trap (Efford et al. 2009a). We then used a 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, and we estimated the habitat-mask buffer (*secr* command suggest.buffer) for each study area (NSC = 18.2 km; SSC = 19.5 km). However, this buffer is not to be confused with the aforementioned ad hoc method of identifying a buffer to estimate the ETA. Instead the *secr* suggested buffer, is the area that is *sufficiently large* to include all animals with a negligible probability of encounter (Royle et al. 2014). It is not the finite area from which the density estimate is based upon. We accounted for variable sampling effort by using the number of days each hair trap and bear rub was active because variability in sampling effort may negatively bias density estimates and reduce the ability to explain variation in detection probability (Efford et al. 2013).

Detection probability and its decay function can be modeled with predictor variables. The variables we examined as predictors of g_0 and σ included detector type (i.e., hair trap or bear rub), temporal variation (t), and land cover (veg). We included both additive (+) and interactive (*) effects between predictor variables for each parameter. We chose the former two covariates because multiple studies have shown that detection probability may be dependent on both hair sampling method and time (Kendall et al. 2009, Sawaya et al. 2012, Stetz et al. 2014, Ciucci et al. 2015). Because we used a lure to attract bears to our sets, the probability of detecting a bear may differ from opportunistically sampled bear rubs, which did not incorporate a lure. Rubs may also target a portion of the population not susceptible to detection by hair traps (Boulanger et al. 2008, Kendall et al. 2009). Time may also affect detection probability as the physiological state and behavior of bears changes over the active season. For example, upon den emergence black bears enter the mating season and consequently they may wander more widely. Following this period, the seasonal availability of foods, such as masting of acorns or pine nuts (hard mast) and of soft mast species (e.g., three-leaf sumac, *Rhus trilobata*) or the calving of elk may cause changes in landscape use that may influence our ability to detect a bear. We also evaluated the influence of land cover as the spatial heterogeneity of food resources exploited by black bears could influence our ability to detect them. We hypothesized that this heterogeneity could

influence g_0 and σ depending on the presence or absence of food and its distribution within each land cover type. We used the Interagency Landfire Project (www.landfire.gov; Rollins 2009), which contains land cover data at 30-m spatial resolution for developing our land cover classes. We assigned land cover type for the location of each detector. We used 8-dominant land cover types: aspen (*Populus tremuloides*) –conifer, Douglas fir (*Pseudotsuga menziesii*), cottonwood (*Populus* spp.) – willow (*Chilopsis* spp.), oak (*Quercus* spp.), piñon pine (*Pinus edulis*) – juniper (*Juniperus* spp.), ponderosa pine (*Pinus ponderosa*), Engelmann spruce (*Picea engelmannii*) – subalpine fir (*Abies lasiocarpa*), and white pine (*Pinus strobus*). However, oak was not included in our NSC analysis because hair traps and bear rubs were not set in that category. We included additive effects because we hypothesized that g_0 and σ are likely to vary due to variation in temporally-dependent shifts in physiological state and behavior of black bears. We included interactive effects to represent changes in spatio-temporal distribution of food resources across the land cover types.

We used a sequential approach to determine the best structure for the two modeled parameters, g_0 and σ . While holding D and σ constant, we first ran all *a priori* candidate models for g_0 , this enabled us to assess which covariates influenced g_0 the most. We then ran all *a priori* candidate models for σ while holding g_0 and D constant to evaluate the influence of covariates on the decay function, σ . We then combined the modeling results for both g_0 and σ to estimate density and used the most supported model to make our final density estimate. We used Akaike's Information Criterion corrected for small sample size (AIC_c) to rank models for each of these model sets (Akaike 1973, Hurvich and Tsai 1989). The top model is the model with the lowest AIC_c score and represents the model, in the model set, that best balances the number of parameters used and the model's explanatory power (Burnham and Anderson 2002, Boulanger et al. 2008). We used the difference in AIC_c score (ΔAIC_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).

RESULTS

Field Sampling and Genetic Analyses

From 29 April – 9 September, we sampled 141 hair traps and 30 bear rubs from the southern Sangre de Cristo Mountains (Figure 3). We acquired 694 hair samples from hair traps (Table 1) and 52 hair samples from bear rubs for a total of 746 hair samples. Of this total, 251 samples (33.65%) were assigned an individual genotype, 281 (37.67%) samples contained enough genetic material for DNA extraction but failed to amplify an entire genotype, 202 (27.08%) lacked enough genetic material for DNA extraction and analysis, 10 (1.34%) were identified as non-target captures, and 2 (0.26%) produced mixed results which indicated multiple bears where captured in one sample. Only 48% of the samples that produced a sufficient quantity of DNA yielded individual genotypes.

We identified 130 individual bears (66 M, 64 F). Of these 130 individuals, hair traps detected 126 individuals and bear rubs detected 9 individuals. The sum of individuals detected

does not total 130 individuals because both sampling methods detected some of the same individuals. We detected 21 individuals, or only 16%, more than once (Table 1).

Density Estimation

The top ranked model for g_0 and σ for the SSC included an additive effect with covariates time and land cover (Table 2). This model configuration was the most highly supported model, receiving all of the model weight (Table 3). Similarly, the updated analysis for the NSC showed both g_0 and σ were influenced by time and land cover, but in this case, the highest ranked model revealed an interactive influence whereas the second highest ranked model revealed an additive effect on g_0 (Table 4). However, when combined to estimate density, this model configuration produced unrealistic parameter estimates, e.g., infinite standard error for σ . Consequently, we removed the interactive models from the model set and the resulting model that received the greatest support only included land cover and not time (Table 5).

The mean g_0 for the SSC was low compared to the NSC and had a larger coefficient of variation, 18% compared to 10% for the NSC (Table 6). The mean estimated σ for the SSC was 18.1 km (SE = 5.5) whereas the mean estimated σ for the NSC was much lower 1.2 km (SE = 4.4). Our density estimate from the top ranked model for the SSC was 18.6 bears/100 km² (SE = 3.47) whereas our density estimate for the NSC was higher, 23.7 bears/100 km² (SE = 2.45; Table 6).

DISCUSSION

Estimates of population parameters needed by wildlife management agencies to set sustainable harvest limits are often difficult to obtain due to logistical and methodological constraints (Settlage et al. 2008). These constraints are exacerbated for elusive species that may also reside at low population densities necessitating greater reliance on non-invasive survey techniques (Long et al. 2008). Furthermore, density estimators using traditional non-spatial capture-recapture methods are often less reliable because of the ad hoc and often arbitrary estimate of the ETA that is used to correct for edge effects (Wilson and Anderson 1985, Parmenter et al. 2003). With the introduction of SECR models, accounting for edge effects has been rooted in statistical theory and incorporated into the modeling process because the spatial location of traps and an estimate of detection probability can be used to estimate the number of individual activity centers and subsequently density, directly. To date, SECR methods continue to garner support by outperforming non-spatial methods with simulated datasets (Whittington and Sawaya 2015). Although the accuracy of any density estimate is unknown, use of improved methods for estimation yields greater confidence in a management agency's ability to set defensible management objectives that will help ensure the long-term viability of animal populations.

Our estimate of density for the SSC (18.6 bears/100 km²) is similar to previous estimates used by NMDGF (17.0 bears/100 km²) to set harvest limits. However, our density estimate for the NSC (23.7 bears/100 km²) is higher than the previously used estimate. Our analysis

suggested time of the detection event is a helpful covariate in modeling heterogeneity in g_0 and σ for the SSC but not the NSC (Tables 3 and 6). The temporal variability of g_0 and σ is likely a result of variable reproductive and foraging behaviors (Alt et al. 1980, Garshelis and Pelton 1981, Costello et al. 2003). Mating season spans from den emergence, which occurs in late March through mid-May, until July with peak mating in June. During this period, males move more and traverse their home range repeatedly while actively searching for receptive females (Young and Ruff 1982, Costello 2008, Lewis and Rachlow 2011). Mast season begins in July and ends at den entry with peak masting during the late summer and early fall (Costello 2008). At this time, bears begin to enter a hyperphagic state to increase daily-caloric intake from 8,000 kcal to 15,000 – 20,000 kcal to build up fat stores for hibernation (Nelson et al. 1980). Bear home range size and distance between sequentially recorded movements tends to increase as bears travel outside their core area to utilize the spatially and temporally variable mast (Ostfeld et al. 1996, Costello 2008), which is an important food source and highly predictive of black bear reproductive output in the Sangre de Cristo Mountains (Costello et al. 2003). Increased movement rates and home range size during mating and hyperphagia would likely expose individuals to more traps on the landscape, thus affecting g_0 and σ . The irrelevance of time in our NSC modeling is surprising, however, we are unable to determine if this result is representative of the state of the system during sampling or if our sampling was simply unable to detect the trend.

Land cover was influential in explaining variability in g_0 and σ in both the SSC and NSC. The influence of land cover is likely a function of black bears responding to spatio-temporal changes in food abundance (Costello and Sage 1994). 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 more soft mast species including chokecherry (*Prunus virginiana*), squawroot (*Conopholis alpina*), and gooseberry (*Ribes* spp.) as well as acorns (56%). Diets during the late mast season (15 September – den entrance) are dominated by acorns (87%) and supplemented with juniper berries (Costello et al. 2001). The abundance of food resources varies spatially and temporally across the landscape. Mid-elevation land cover types (e.g., 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 moister conditions near riparian areas (compared to lower elevations). Food resources will become more available and occur in a larger area as snow melts, and once monsoonal rains occur soft mast ripens. Once oaks begin to drop their acorns in late summer/early fall, black bears begin to shift their attention towards vegetation types with abundant oak.

We suspect that the Tres Lagunas and Jaroso Fires contributed to a decrease in precision in our density estimates for the SSC (Figure 4). The Tres Lagunas Fire started 30 May, burned 10,219 acres, and traveled east from Tres Lagunas, New Mexico to the Pecos Wilderness. The Jaroso Fire started 10 June, burned 11,149 acres, and was located in the northwest corner of the Pecos Wilderness. These fires affected 450 km² (12.7%) of the trapping grid and prevented us

from checking hair traps located in close proximity to the fires primarily during the second and third sampling occasions (3-13% of total hair traps). Furthermore, 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 produced more and more consistent hair samples than hair traps located in areas of lower quality habitat that were unaffected by the fires. The limited access also prevented us from checking more bear rubs across the SSC, limiting 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). Overall, a net loss in sampling occasions and a reduction in hair samples ultimately affected the number of new captures, the number of recaptured individuals, and the amount of data for analysis. This is supported by the few number of individuals we recaptured in each occasion and the large number of ‘new’ bears that were identified in each occasion (Table 1). Ideally, as you sample a population the number of new individuals captured declines over time (i.e., we should encounter fewer and fewer unmarked individuals and more marked individuals). Yet, in the SSC we captured 33% of all individuals identified during the last sampling occasion. While the number of individuals detected the last occasion in the NSC is still high (18%), it seems that the fires in the SSC impacted our ability to detect bears in this area. Our inability to check these hair traps during the fires led to longer sampling occasions and greater exposure to environmental conditions (i.e., exposure increased potentially from 4 weeks to ≥ 8 weeks), thus subjecting hair samples to longer periods of environmental exposure, particularly to ultraviolet radiation (UV).

We suspect that UV is the main factor explaining the failure of hair samples to produce a complete genotype (Stetz et al. 2015). Ultraviolet radiation causes DNA degradation by binding adjacent nucleotide bases in the double helix to each other instead of their cross-strand partner (Jagger 1985). These bonds form a bulge in the chemical structure of the DNA and thus prevent the DNA polymerase from correctly duplicating the sequence, which then prevents further amplification resulting in incomplete genotypes. Consequently, the inability to assign an identity to a large portion of the genetic samples reduced both the number of new captures and the number of recaptured individuals. 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 (76% annual possible sunshine; NOAA 2004), is relatively high in elevation (1,200 m – 4,000 m), and is at a lower latitude than other states. 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 our sampling of the Sacramento Mountains in 2014 we had only a marginal improvement in genotyping success for samples collected from hair traps (2013: 48% versus 2014: 52%).

Despite these sampling difficulties, we were able to produce a relatively precise density estimate for the NSC and SSC black bear populations with comparable levels of precision as those obtained in other efforts to estimate black bear densities conducted elsewhere in the U.S (Table 7). As a result, this study provides the most up to date density estimates for the NSC and SSC in a decade (Costello et al. 2001). In conclusion, our results suggest that the density of the SSC black bear population is slightly higher than the previous density estimate used by the NMDGF (17.0 bears/100 km²) whereas our density estimate for the NSC black bear population appears to be higher.

UPDATE

We sampled the Sacramento Mountains, NM, from 5 May – 5 August 2014 with 149 hair traps and 39 bear rubs. We collected 1,262 total hair samples. Citizen volunteers sampled the Sandia Mountains, NM, from 6 May – 7 August 2014 with 12 hair traps and 7 bear rubs, collecting 177 hair samples. We submitted 1,339 samples to Wildlife Genetics International for analysis.

We received the genetic data back from WGI in mid-June and conducted a preliminary analysis. Preliminary SECR based density estimates are 23.1 bears/100 km² (95% CI = 17.5 – 30.6) for the northern Sacramento Mountains (GMU 37), 17.1 bears/100 km² (95% CI = 12.1 – 24.2) for the southern Sacramento Mountains (GMUs 34 and 36), and 18.4 bears/100 km² (95% CI = 10.1 – 33.7) for the Sandia Mountains.

We anticipate producing a full report detailing density estimates for the Sangre de Cristo Mountains, the Sacramento Mountains, and the Sandia Mountains during the winter-spring of 2016.

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Table 1. Hair trap sampling results for the northern Sangre de Cristo Mountains, NM, USA (NSC) in 2012 and the southern Sangre de Cristo Mountains, NM, USA (SSC) in 2013. We conducted 4, 28-day sampling occasions from 22 April – 5 September 2012 in the NSC and from 29 April – 9 September 2013 in the SSC. The total number of new bears identified is less than the minimum detected, which includes bears sampled by rub trees.

Location	Occasion	Hair Traps Set	Hair Traps Hit	Hair Trap Success (%)	Samples Collected	Samples Analyzed ^a	Sample Success ^b	Sample Success (%)	Bears Identified	New Bears Identified
NSC	A	251	109	43	334	216	87	40	60	60
	B	256	122	48	600	433	209	48	128	120
	C	256	133	52	510	411	226	55	133	107
	D	256	113	44	347	257	129	50	93	67
	Total	1019	477	47	1791	1317	651	49	414	354
SSC	A	141	40	28	141	98	42	43	29	29
	B	123	33	27	124	99	40	40	27	26
	C	137	48	35	183	131	66	50	36	30
	D	140	55	39	246	168	92	55	54	41
	Total	541	176	33	694	496	240	48	147	126

^aSamples analyzed is the number of samples that contained enough genetic material for genetic analysis.

^bSample success is the number of samples that produced a full-individual genotype.

^cNumber of bears identified in the *i*th occasion not identified in a previous occasion.

Table 2. Model selection results for the spatially explicit capture-recapture models where both detection probability (g_0) and spatial scale (σ) were modeled separately for the southern Sangre de Cristo Mountains, NM, in 2013. We modeled each parameter as a function of time (t), detector type (type), and land cover type (veg) with both additive (+) and interactive (*) effects. Models identified with a period (.) indicate the parameter was constant over all occasions. We combined the top model from each parameter into a final model (see Table 3).

Model	No. Parameters	AIC _c ^a	Δ AIC _c ^b	w_i ^c	Deviance ^d
Parameter Modeled: g_0					
$g_0(t + \text{veg})$	14	980.28	0.00	0.99	948.62
$g_0(t)$	6	989.93	9.66	0.01	977.26
$g_0(t + \text{type})$	7	990.83	10.55	0.00	975.92
$g_0(\text{veg})$	11	998.62	18.35	0.00	974.38
$g_0(.)$	3	1003.94	23.66	0.00	997.76
$g_0(\text{type})$	4	1005.20	24.92	0.00	996.88
$g_0(t * \text{veg})$	39	1027.72	47.45	0.00	915.06
Parameter Modeled: σ					
$\sigma(t + \text{veg})$	14	984.09	0.00	0.94	952.44
$\sigma(t)$	6	989.77	5.68	0.06	977.08
$\sigma(\text{veg})$	11	1003.16	19.07	0.00	978.92
$\sigma(.)$	3	1003.94	19.85	0.00	997.76
$\sigma(t * \text{veg})$	39	1027.20	43.11	0.00	914.54

^aAkaike's Information Criteria for small sample sizes.

^bThe difference between the top ranked model and the i th ranked model.

^cAIC_c model weight.

^dDeviance was calculated by multiplying the log likelihood of each model by -2.

Table 3. The final set of *a priori* spatially explicit capture-recapture models for the southern Sangre de Cristo Mountains, NM, in 2013. We modeled detection probability (g_0) and spatial scale (σ) as a function of time (t), detector type (type), and land cover type (veg) with both additive (+) and interactive (*) effects. Models identified with a period (.) indicate the parameter was constant over all occasions.

Model	No. Parameters	AIC _c ^a	Δ AIC _c ^b	w_i ^c	Deviance ^d
g0(t + veg), σ (t + veg), D(.)	25	964.16	0.00	1.00	901.66
g0(t), σ (t), D(.)	9	977.99	13.83	0.00	958.48
g0(t + veg), σ (.), D(.)	14	980.27	16.11	0.00	948.62
g0(.), σ (t + veg), D(.)	14	984.09	19.92	0.00	952.42
g0(.), σ (t), D(.)	6	989.77	25.60	0.00	977.08
g0(t), σ (.), D(.)	6	989.93	25.76	0.00	977.24
g0(t + type), σ (.), D(.)	7	990.82	26.66	0.00	975.9
g0(veg), σ (.), D(.)	11	998.62	34.45	0.00	974.38
g0(veg), σ (veg), D(.)	19	998.87	34.70	0.00	953.96
g0(.), σ (veg), D(.)	11	1003.15	38.99	0.00	978.92
g0(.), σ (.), D(.)	3	1003.94	39.77	0.00	997.74
g0(type), σ (.), D(.)	4	1005.19	41.03	0.00	996.86
g0(.), σ (t * veg), D(.)	39	1027.20	63.03	0.00	914.52
g0(t * veg), σ (.), D(.)	39	1027.72	63.55	0.00	915.04

^aAkaike's Information Criteria corrected for small sample sizes.

^bThe difference between the top ranked model and the *i*th ranked model.

^cAIC_c model weight.

^dDeviance was calculated by multiplying the log likelihood of each model by -2.

Table 4. Model selection results for the spatially explicit capture-recapture models where both detection probability (g_0) and spatial scale (σ) were modeled separately for the northern Sangre de Cristo Mountains, NM, in 2012. We modeled each parameter as a function of time (t), detector type (type), and land cover type (veg) with both additive (+) and interactive (*) effects. Models identified with a period (.) indicate the parameter was constant over all occasions. We combined the top model from each parameter into a final model (see Table 5).

Model	No. Parameters	AIC _c ^a	Δ AIC _c ^b	w_i^c	Deviance ^d
<u>Parameter Modeled: g_0</u>					
$g_0(t * \text{veg})$	35	2703.79	0.00	0.89	2626.44
$g_0(t + \text{veg})$	13	2707.89	4.102	0.11	2680.90
$g_0(\text{veg})$	10	2727.49	23.70	0.00	2706.88
$g_0(t + \text{type})$	7	2754.43	50.64	0.00	2740.12
$g_0(t)$	6	2785.93	72.14	0.00	2763.70
$g_0(\text{type})$	4	2784.81	81.02	0.00	2776.70
$g_0(.)$	3	2802.95	99.17	0.00	2796.88
<u>Parameter Modeled: σ</u>					
$\sigma(t * \text{veg})$	35	2696.99	0.00	1.00	2619.64
$\sigma(t + \text{veg})$	13	2723.88	26.89	0.00	2696.88
$\sigma(\text{veg})$	10	2733.89	36.90	0.00	2713.30
$\sigma(t)$	6	2786.58	89.59	0.00	2774.36
$\sigma(.)$	3	2802.95	105.96	0.00	2796.88

^aAkaike's Information Criteria for small sample sizes.

^bThe difference between the top ranked model and the i th ranked model.

^cAIC_c model weight.

^dDeviance was calculated by multiplying the log likelihood of each model by -2.

Table 5. The final set of *a priori* spatially explicit capture-recapture models for the northern Sangre de Cristo Mountains, NM, in 2012. We modeled detection probability (g_0) and spatial scale (σ) as a function of time (t), detector type (type), and land cover type (veg) with both additive (+) and interactive (*) effects. Models identified with a period (.) indicate the parameter was constant over all occasions. We did not include the stepwise-developed model from Table 5 in our AICc selection due to unrealistic parameter estimates.

Model	No. Parameters	AIC _c ^a	Δ AIC _c ^b	w_i ^c	Deviance ^d
g0(veg), σ (veg), D(.)	17	2629.36	0.00	1.00	2593.66
g0(.), σ (t * veg), D(.)	35	2696.99	67.62	0.00	2619.64
g0(t * veg), σ (.), D(.)	35	2703.78	74.42	0.00	2626.44
g0(t + veg), σ (.), D(.)	13	2707.88	78.52	0.00	2680.88
g0(.), σ (t + veg), D(.)	13	2723.88	94.51	0.00	2696.88
g0(veg), σ (.), D(.)	10	2727.48	98.12	0.00	2706.88
g0(t), σ (t), D(.)	9	2731.65	102.28	0.00	2713.16
g0(.), σ (veg), D(.)	10	2733.89	102.28	0.00	2713.30
g0(t + type), σ (.), D(.)	7	2754.42	104.53	0.00	2740.12
g0(t), σ (.), D(.)	6	2775.92	125.05	0.00	2763.70
g0(type), σ (.), D(.)	4	2784.81	155.44	0.00	2776.70
g0(.), σ (t), D(.)	6	2786.58	157.21	0.00	2774.34
g0(.), σ (.), D(.)	3	2802.95	173.58	0.00	2796.88

^aAkaike's Information Criteria for small sample sizes.

^bThe difference between the top ranked model and the *i*th ranked model.

^cAIC_c model weight.

^dDeviance was calculated by multiplying the log likelihood of each model by -2.

Table 6. Density (D ; bears/ 100 km²), detection probability at the activity center (g_0), and spatial scale over which detection probability declines (σ), and their 95% confidence intervals estimated using spatially explicit capture-recapture models for the southern Sangre de Cristo Mountains, NM, (SSC) in 2013 and the northern Sangre de Cristo Mountains, NM, (NSC) in 2012.

Study Area	\hat{D}^a	\hat{g}_0	$\hat{\sigma}$ (km)
SSC	18.6 (13.0 - 26.8)	0.000027 (0.0000086 - 0.000087)	18.1 (10 - 32.7)
NSC	23.7 (19.4 - 29.0)	0.01 (0.002 - 0.04)	1.2 (0.58 - 2.41)

^a95% confidence intervals are in parentheses for all three parameters.

Table 7. Spatially explicit capture-recapture based density estimates (bears/100 km²) in ascending order for noninvasive genetic sampling based black bear studies in the United States.

State	\hat{D}^b	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
Glacier National Park, Montana ^a	12.0 (10.0 – 14.4)	Stetz et al. 2014 ^a
Southern Sangre de Cristo Mountains, New Mexico	18.6 (13.0 – 26.8)	This study
Fort Drum Military Installation, New York	20.0 (16.8 – 23.1)	Gardner et al. 2010
Northern Sangre de Cristo Mountains, New Mexico	23.7 (19.4 – 29.0)	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

^aBlack bear population sympatric with grizzly bears (*Ursus arctos*).

^b95% confidence intervals are in parentheses.

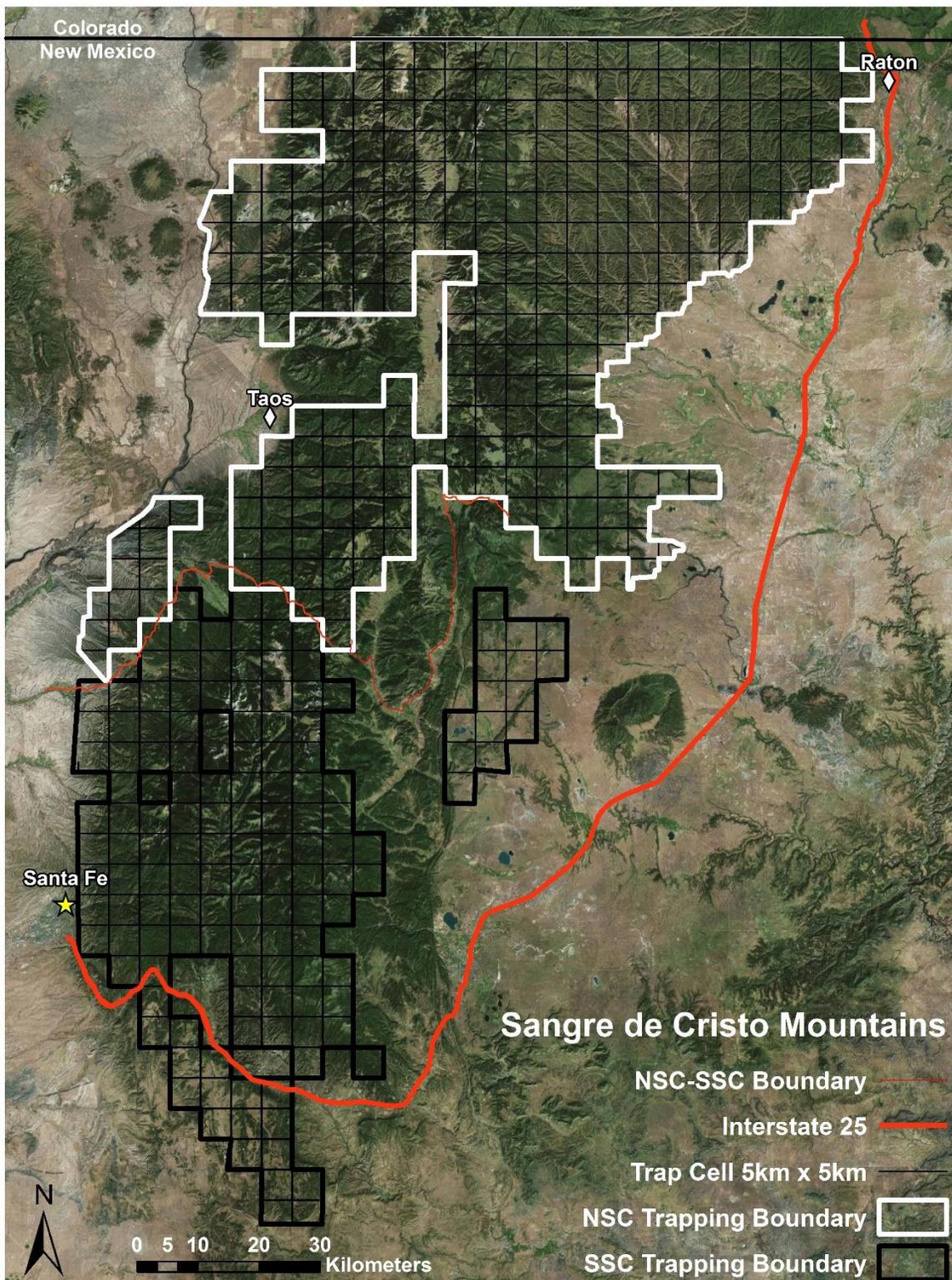


Figure 1. Map of the northern Sangre de Cristo Mountains (NSC) and the southern Sangre de Cristo Mountains (SSC), NM overlaid with their respective trapping grids.

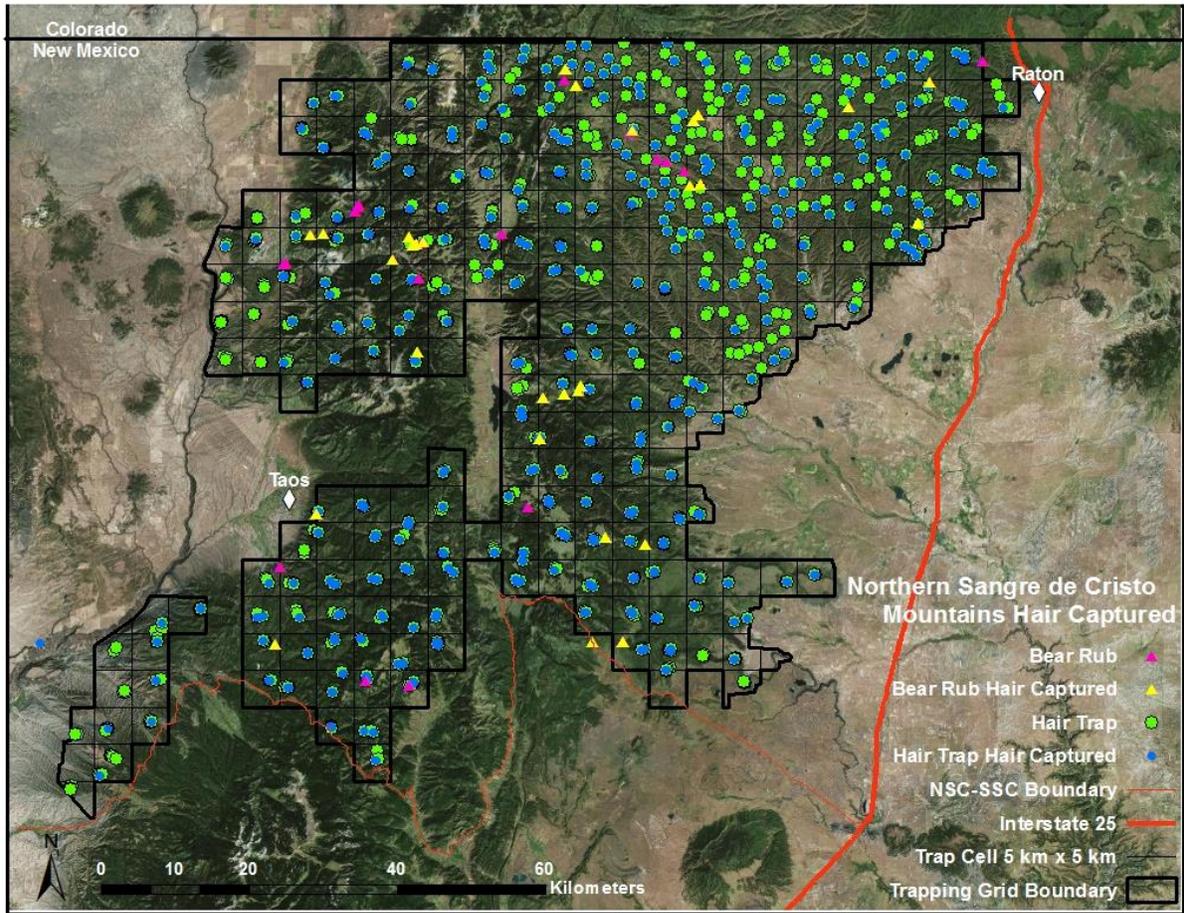


Figure 2. Map of hair traps and bear rubs set versus hair traps and bear rubs that captured hair samples from black bears in the northern Sangre de Cristo Mountains, NM in 2012.

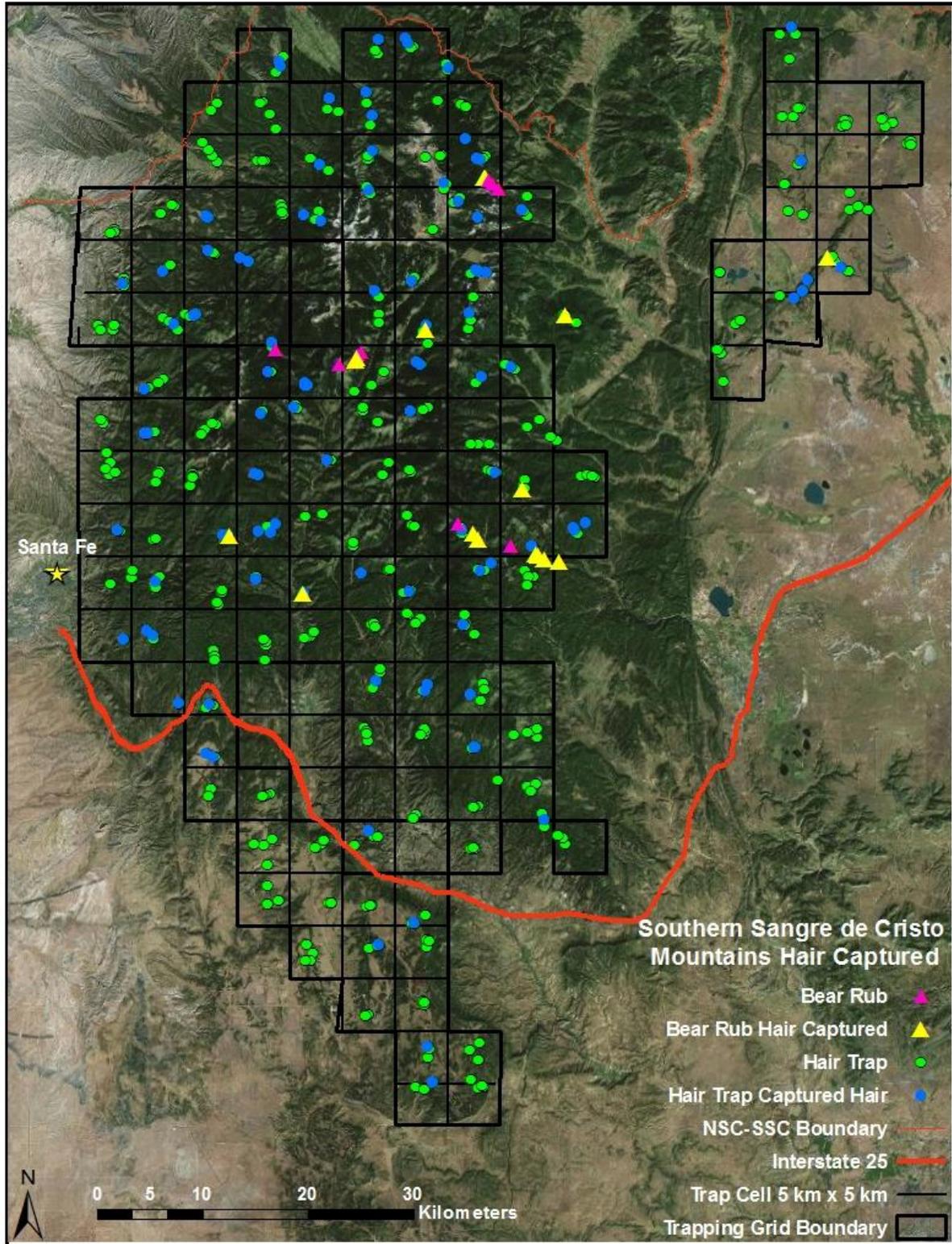


Figure 3. Map of hair traps and bear rubs set versus hair traps and bear rubs that captured hair samples from black bears in the southern Sangre de Cristo Mountains, NM in 2013.

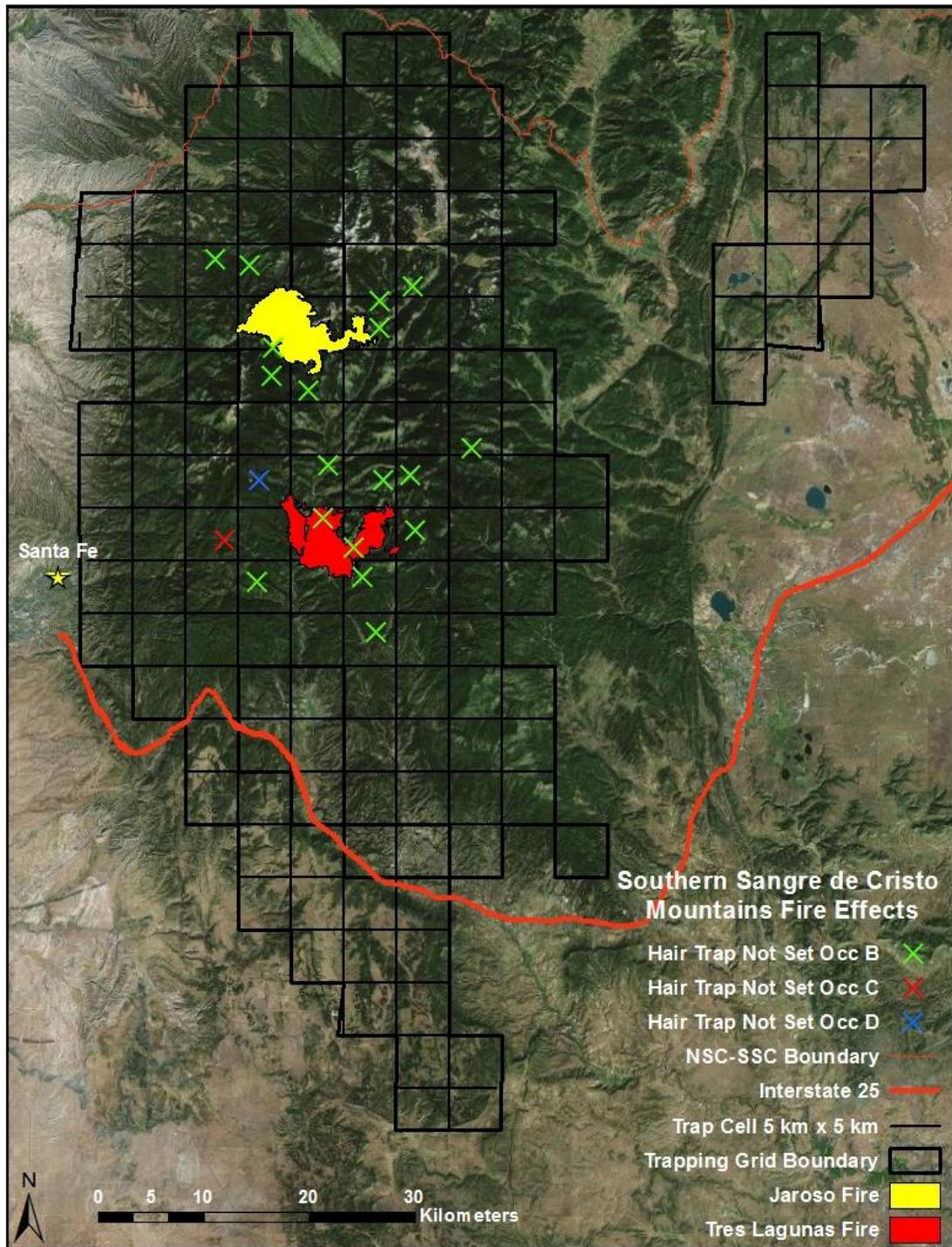


Figure 4. Map of hair traps not deployed due to the Jaroso and Tres Lagunas fires in the southern Sangre de Cristo Mountains, NM in 2013.