Research Summary 2019–2021

Estimating Black Bear Abundance Using Spatial Capture-Recapture in Bear Management Zones 1 and 10

Introduction:

Management of black bear hunting in New Mexico is predicated on regulation through a Bear Management Zone (BMZ) system, wherein a BMZ is a collection of Game Management Units (GMUs) across which there are similar habitat, landscape connectivity, and high likelihood of strong, local population dynamics occurring. These BMZs are not isolated populations, as ear-tag and GPS collar data over the years have shown bears moving large distances across the state and beyond. However, the sky-island effect that creates large stretches of non-preferred habitat between core areas of bear habitat in New Mexico (Atwood et al. 2011), as well as social considerations that drive hunting pressure and human-bear interactions, necessitate management at this local-population level, while recognizing the existence of metapopulation dynamics across the state.

Bear hunting is managed through this BMZ system by setting zone-specific harvest limits that restrict the number of bears that can be taken in a given zone. Currently, setting bear harvest limits relies on density estimates from two study areas and traditional capture-recapture methods using live capture and radio-telemetry tracking (Costello et al. 2001) and three mountain ranges where modern non-invasive genetic sampling (NGS) was used (Gould et al. 2018). Those density estimates were then applied across the amount of primary bear habitat in a zone as defined by a habitat suitability model developed in 2015. Although bears use secondary and edge habitat, these habitats were not included in density estimation resulting in conservative estimates. Population estimation through this extrapolation of density estimates to bear habitat is used for the zones where these studies occurred, as well as for other zones according to similarities in habitat and geography.

From that zone-specific population estimate, hunting is managed for a sustainable harvest by allocating only 8–12% of the population estimate as the total allowable harvest for that zone (Miller 1990). To further ensure sustainable populations, only 30% of that 8–12% total harvest limit can be female bears without cubs. A zone closes when the harvest reaches either the total harvest limit or the female sub-limit, or if neither limit is reached then zones close at the end date of the season. Hunters are required by law to have their harvested bear pelt-tagged with a Department employee or law enforcement officer within five days of harvest, allowing the Department to how many bears have been harvested and close the zone accordingly.

The study by Gould et al. (2018) was the first implementation of modern NGS (via 'hair snares') to monitor black bear populations in New Mexico. The use of hair snares (barbed wire corrals that pull hair from bears as they pass across the wires to access bait) allows for large geographic areas to be sampled and a high volume of captures with compared with traditional capture-recapture methods (Woods et al. 1999). Used in conjunction with spatial-recapture (SCR) models, which can accommodate large sampling areas and explicitly link estimation to the space in which animals occurred, we can generate estimates of population size at a scale meaningful to management with no need for extrapolation. Of those zones not covered by Gould et al. (2018) we chose BMZs 1 and 10 for implementation of this NGS and SCR modelling approach.

Bear Management Zones 1 and 10 consistently have had high harvest over the past 12 years, reaching the total or female harvest limit most years. Both zones have also had recent landscape altering wildfires (2011's Las Conchas fire and preceding fires in BMZ1; 2012's Whitewater-Baldy fire in BMZ 10), which may have had both negative effects (short-term displacement during fires) and positive effects (eg. beneficial seral stage of vegetation communities with abundant mast and forage). Obtaining contemporary estimates in these zones, using updated analytical techniques, will provide the best available information for sustainable management of black bear populations in those zones.

Methods:

Study Area

The BMZ 1 study area (14,043 km^2) included GMUs 4, 5A/B, 6A/B/C, 51A/B, and 52. These GMUs are a contiguous area of similar bear habitats in the Jemez Mountains and southern San Juan mountains, as well as surrounding foothill and lowland habitats, that are representative of various habitat types under the 'Southern Rockies' Ecoregion III level habitat classification (Griffith et al. 2006). This study area did not include GMU 7, which is also part of BMZ 1 and has contiguous, suitable bear habitat with the study area. However, habitat in GMU 7 transitions into San Juan/Chaco tablelands habitats that becomes more arid and sparsely forested as you head west from the study area. Given the difference in habitat type and logistical constraints for sampling that additional area, we did not include GMU 7 in the study area.

The BMZ 10 study area included GMUs 15, 16A/B/C/D/E, 17, 21A/B, 22, 23, and 24. These GMUs are a contiguous area of similar bear habitats in the Greater Gila region that are representative of various habitat types under the Arizona/New Mexico Mountains Ecoregion level III habitat classification (Griffith et al. 2006). This study area did not include GMUs 12 and 13, which have contiguous suitable bear habitat with the study area; nor did the study area include GMUs 18, 20, 26, or 27, which have sky-islands of suitable bear habitat separated from the study area by large expanses of non-preferred lowland habitat. These GMUs were not included because of the logistical constraints of sampling such a large area.

We established hair snare sites within all habitat types as identified in the Department's 2015 habitat model for black bear (Figures 1 and 2). This allows for area-wide estimation of population size, in recognition that bears utilize multiple habitat types, movement occurs between patches of primary habitat, habitat may change year to year, and to model the population with as direct an estimate as possible of the management area and minimize or eliminate the need to extrapolate to a habitat model.

Field Sampling

Simulations indicated that clusters of detectors with 1.6–km spacing between detectors, 11.2-km spacing between clusters, and sampling for 8 occasions would produce precise and unbiased density and abundance estimates from spatial capture-recapture models. We deployed hair snares in grids of 6–12 sites, with spacing of 1.2–2.4 km (2019 avg. = 1.63 km; 2020 and 2021 av. = 1.48 km) between sites to adjust for access and the effect of topography and landscape ruggedness. Grids were spaced roughly 11.2 km apart. We revisited sites every 7–10 days for a total of 8 occasions spanning early June to mid-August. Hair snares were set with two strands of barbed wire wrapped around ≥3 trees, with one strand at 35 cm high and another at 65 cm high (Woods et al. 1999). Bait (pastries) were placed at the center of the hair snare, and a scent lure (cherry and anise oil) was applied to the site and surrounding area.

Samples were collected from the barbed wire strands, off of trees which the barbed wire was attached to, and off the ground if the bear rubbed against objects on the ground within the hair snare. A sample consisted of all the hair at a single barb, or hair from up to three adjacent barbs (along the same wire or vertically adjacent on each strand) if the hair was consistent in appearance. Hair was deposited in a paper coin envelope, and the barbs from which the hair was collected were sterilized with a lighter.

Genetic Analysis

We did not analyze samples if they contained zero guard hair roots and <5 underfur hairs, or if they were visually recognized as nontarget species. Following the initial screening, we purified DNA from the remaining samples using QIAGEN DNeasy Blood and Tissue kits, ran samples through a single-locus prescreening to identify samples that were degraded, unsuitable, or from nontarget species. Samples that passed the prescreen were analyzed at 9 microsatellite loci (including the ZFX/ZFY marker used for the pre-screen) used previously for black bear in New Mexico (G1D, G10B, G10H, G10J, G10L, G10M, G10U, MU59; Gould et al. 2018). For any sample with mismatch pairs at one or two loci, we amplified those samples at another three loci (CXX20, CXX110, and G10X) to determine whether the mismatches were due to genotyping error or if the samples were from different individuals (Kendall et al. 2009). We then assigned an individual identifier for each unique 9-locus genotype (or 12 locus genotypes for those that had one or two loci with mismatches between replications). Genotyping of all hair and tissue samples, error-checking, and PCA analysis of genotypes was conducted by Wildlife Genetics International in Nelson, British Columbia, Canada (WGI; Paetkau 2003).

Density Estimation

We used spatial capture recapture (SCR) models (Efford 2004, Borchers and Efford 2008) from the secr package (v. 4.5.3, Efford 2022) in program R to estimate population size ($\hat{N}$), baseline detection probability at an individual's activity center ($g0$), and the movement coefficient for decay in detection as distance from an activity center increases (σ). We modeled density as uniform across space with a homogenous Poisson point process, and an observation model using the half normal detection function. We defined the 'state space' (a mathematical representation of the effective sampling area across which animals can be detected) by creating a polygon from the 2015 bear habitat model using primary, secondary and edge habitats for BMZ 1, and only primary and secondary habitats for BMZ 10. We then buffered those polygons (5 km for BMZ 1, and 4 km for BMZ 10) by distances suggested by the suggest.buffer function in the secr package, which allows for the models to account for bears that could occur at the edge of the state space (Royle et al. 2014).

We evaluated a set of models that included a trap-specific behavioral response (bk) on g0 because the sites were baited, and evaluated for sex-specific predictors for estimates of g0 and σ. Estimates were made for each study area separately. We pooled data for BMZ 10 across 2020 and 2021 to get a single population estimate because geographically distinct portions of the study area were sampled each year. We evaluated models using Akaike's Information Criterion corrected for small sample size (AIC_c), and used model averaging if AIC_c weight was less than 0.90 for the top model.

Results

Field Sampling and Genetic Analysis

In BMZ 1 during 2019, we collected 1,097 samples from 179 sites over eight 7–10 day sessions. Of those samples, 714 (65%) were visually identified as bear hair or had enough material for DNA analysis, and of those samples 482 (68%) were genotyped to an individual identification for a total of 94 bears (49F:45M) Those 482 successfully identified samples represented 191 unique detections of individuals across sites and occasions (Table 1).

In BMZ 10, we collected a total of 1,706 samples (1,012 in 2020; 694 in 2021) from 349 sites (249 in 2020; 110 in 2021) over eight 7–10 day sessions. Of the 1,012 samples from 2020, 895 (88%) were visually identified as bear hair or had enough material for DNA analysis, and of those samples 725 (81%) were genotyped to an individual identification for a total of 152 bears (74F:78M). Those 725 successfully identified samples represented 311 unique detections of individuals across sites and occasions (Table 1). Of the 694 samples from 2021, 657 (94%) were visually identified as bear hair or had enough material for DNA analysis, and of those samples 493 (75%) were genotyped to an individual identification for a total of 118 bears (63F:55M). Those 493 successfully identified samples represented 244 unique detections of individuals across sites and occasions (Table 1). One male bear was detected both years, once in 2020 and three times in 2021 approximately 16 and 35 km away.

Through our error-checking process that compared samples with mismatches, we found two samples in 2019 with a mismatch at two markers, and those were amplified at the additional three loci to distinguish that these samples came from different individuals. Mismatches at two loci were found for 30 samples in 2020, and amplification at the additional three loci revealed that these were not due to genotyping error and were due to the samples coming from different bears. In 2021, mismatches at two loci were found for 29 genotypes, and amplification at the three additional loci revealed differences at those loci as well confirming that the genotypes were from different bears. A genotype-based PCA analysis to assess potential outliers revealed slight overlap between BMZ 1 and BMZ 10, but a stronger pattern of genetic differentiation between the zones (Figure 3).

Density Estimation

The number of re-detections of individuals at a single site across different occasions, or at multiple sites, represented a significant portion of the detections at each study area (Table 1). The average distance moved between sites was 2,402 m in BMZ 1 and 2,964 in BMZ 10, with a maximum distance moved of 7,725 m in BMZ 1 and 21,904 in BMZ 10.

The top two models (>0.9 AIC_c weight) for BMZ 1 included both behavioral and sex effect on g0, and differed in including a sex effect on sigma (Table 2). Similarly, the top model for BMZ 10 (AIC_c weight = 1) included behavioral and sex effects on g0, and a sex effect on sigma (Table 2). Model estimates of population size ($\widehat{N}$) for the given study area were 1,574 (95% CI = 1,050 – 2,358) in the BMZ 1 study area, and 2,192 (95% CI = 1,791 – 2,698) in the BMZ 10 study area (Table 3). Estimates of g0 and sigma were similar across both study areas (Table 3).

Discussion

Our estimates of population size are similar to previous estimates for BMZ 1 (17 bears per 100 km^2 of primary habitat), and higher than previous estimates for BMZ 10 (9 bears per 100 km^2 of primary habitat, Costello et al. 2001). In BMZ 10, converting the population estimate to a density per 100km^2 of primary habitat to compare to the method previously used to estimate population size, returns a density of 15.9 bears per 100km^2 of primary habitat. That estimate is similar to densities found for other New Mexico mountain ranges (Gould et al 2018) and to a similar conversion of our results for BMZ 1 (16.9 bears/100 km^2 of primary habitat). This observed higher density is more reasonable given the understanding that the Gila region contains highly productive bear habitat, comparable to other mountain ranges in New Mexico. The previous estimate is much lower than densities that have been found in more contemporary studies conducted in similar New Mexico habitat using NGS and SCR.

The goal of this study was to estimate population size across the entire area of a BMZ, but even with the easing of logistical constraints when using NGS this broad coverage was still not entirely possible for these studies. These population estimates for the given study areas are for a significant portion of each zone, however there were still GMUs with bear habitat that were not covered and for which extrapolation will be necessary to get a zone-wide population estimate. The contemporary estimates from our studies will provide a robust baseline from which to make those extrapolations to these neighboring GMUs, which are contiguous with habitat in our study areas and in close proximity to them. The Department will make these extrapolations at the most conservative levels informed by the confidence intervals we observed.

These studies were conducted in years of unique environmental conditions, including an ongoing, historic drought. Both of these study areas share a similar post-fire dynamic (similar large burns in the early 2010s), and moderate wildfires burned in BMZ 10 while we conducted sampling (the Cub, Good, and Tadpole fires in 2020; the Johnson fire in 2021). The role of fire on landscapes in the Southwest is complex and changing, however it should be noted that low to moderate intensity fires are a natural stochastic event for these ecosystems and the species that live here have adapted to persist in the face of that change. The population estimates we found through these studies are encouraging in illustrating the ability for these black bear populations to persist through the immediate dangers of a wildfire, and thrive on the post-fire landscape.

We achieved higher success rates for genotyping than previous efforts in New Mexico (Gould et al. 2018), which we attribute to the decreased time between sampling occasions (7–10 in our study; 14–28 days in previous study) which subsequently decreased exposure time to environmental conditions. The higher genotyping success rates we observed resulted in a greater number of observations, and in combination with sampling across multiple habitat classifications we had a robust data set for modeling over such a large area.

The Department plans to continue implementing this methodology in BMZs throughout the state to provide contemporary estimates in zones not previously studied and in zones where significant habitat changes may occur. Future work will focus on evaluating models for the effect of habitat variation on density, analyzing data from trail cameras at hair snare sites to compare camera detections to NGS captures, looking at metapopulation dynamics and population genetics to investigate further geneflow between zones, and genotyping harvested bears from zones where we've conducted our studies to compare with animals detected through our research efforts. In conjunction with these point estimates of population size generated by these studies, the Department is also developing an Integrated Population Model (IPM) approach for monitoring population dynamics in each zone. These IPMs will incorporate data from a variety of sources, including: over 20 years of age, sex, and hunter effort harvest data, population estimates from our SCR studies, and survival and other population demographic information collected through the Department's or our collaborator's research efforts. All of these data sources will go into these IPMs to monitor abundance and other demographics annually.

Citations

Atwood, T.C., J.K. Young, J.P. Beckman, S.W. Breck, J. Fike, O.E. Rhodes, and K.D. Bristow. 2011. Modelling connectivity of black bears in a desert sky island archipelago. Biological Conservation 144: 2851–2862.

Borchers, D.L., and M.G. Efford. 2008. Spatially explicit maximum likelihood methods for capture-recapture studies. Biometrics 64:377–385.

Costello, C. M., D. E. Jones, K. A. Green-Hammond, R. M. Inman, K. H. Inman, B. C. Thompson, R. A. Deitner, and H. B. Quigley. 2001. A study of black bear ecology in New Mexico with models for population dynamics and habitat suitability. Final Report, Federal Aid in Wildlife Restoration Project W-131-R, New Mexico Department of Game and Fish, Santa Fe, New Mexico, USA.

Efford, M.G. 2004. Density estimation in live-trapping studies. Oikos 106:598–610.

Efford, M. G. 2022. secr: Spatially explicit capture-recapture models. R package version 4.5.3.

https://CRAN.R-project.org/package=secr.

Gould, M. J., J. W. Cain III, G. W. Roemer, W. R. Gould, and S. G. Liley. 2018. Density of American black bears in New Mexico. The Journal of Wildlife Management 82: 775–788.

Griffith, G.E., J.M. Omernik, M.M. McGraw, G.Z. Jacobi, C.M. Canavan, T.S. Schrader, D. Mercer, R. Hill, and B.C. Moran. 2006. Ecoregions of New Mexico (color poster with map, descriptive text, summary tables, and photographs): Reston, Virginia, U.S. Geological Survey (map scale 1:1,400,000).

Kendall, K.C., J.B. Stetz, J. Boulanger, A.C. Macleod, D. Paetkau, and G.C. White. 2009. Demography and genetic structure of a recovering grizzly bear population. The Journal of Wildlife Management 73: 3–17.

Miller, S.D. 1990. Population management of bears in North America. International Conference on Bear Research and Management 8:357–373.

Royle, J.A., R.B. Chandler, R. Sollmann, and B. Gardner. 2014. Spatial capture-recapture. Academic Press, Waltham, Massachusetts, USA.

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

Figure 1. Map of the Bear Management Zone 1 study area, hair snare sites with the captures observed, and black bear habitat map.

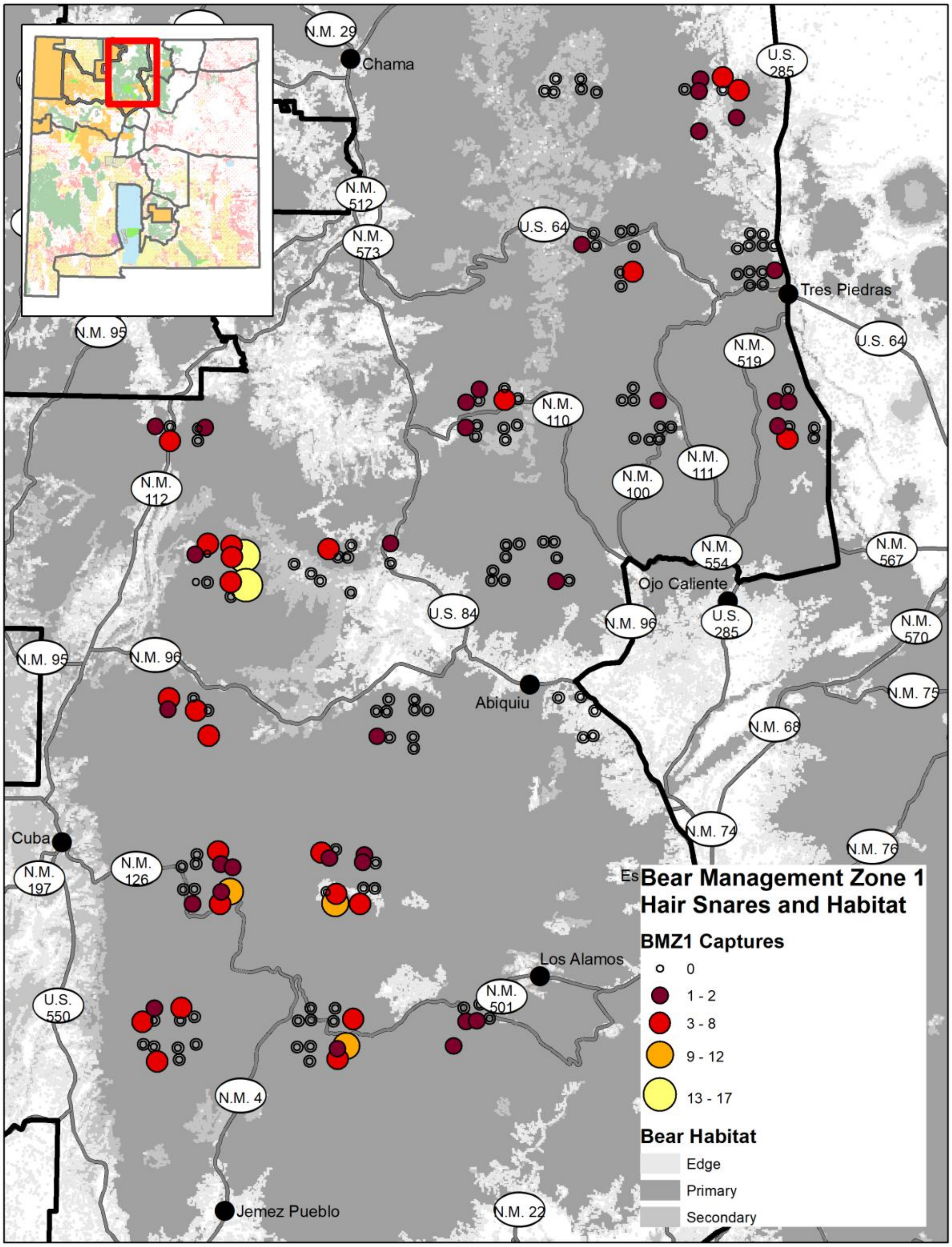

Figure 2. Map of the Bear Management Zone 10 study area, hair snare sites with the captures observed, and black bear habitat map.

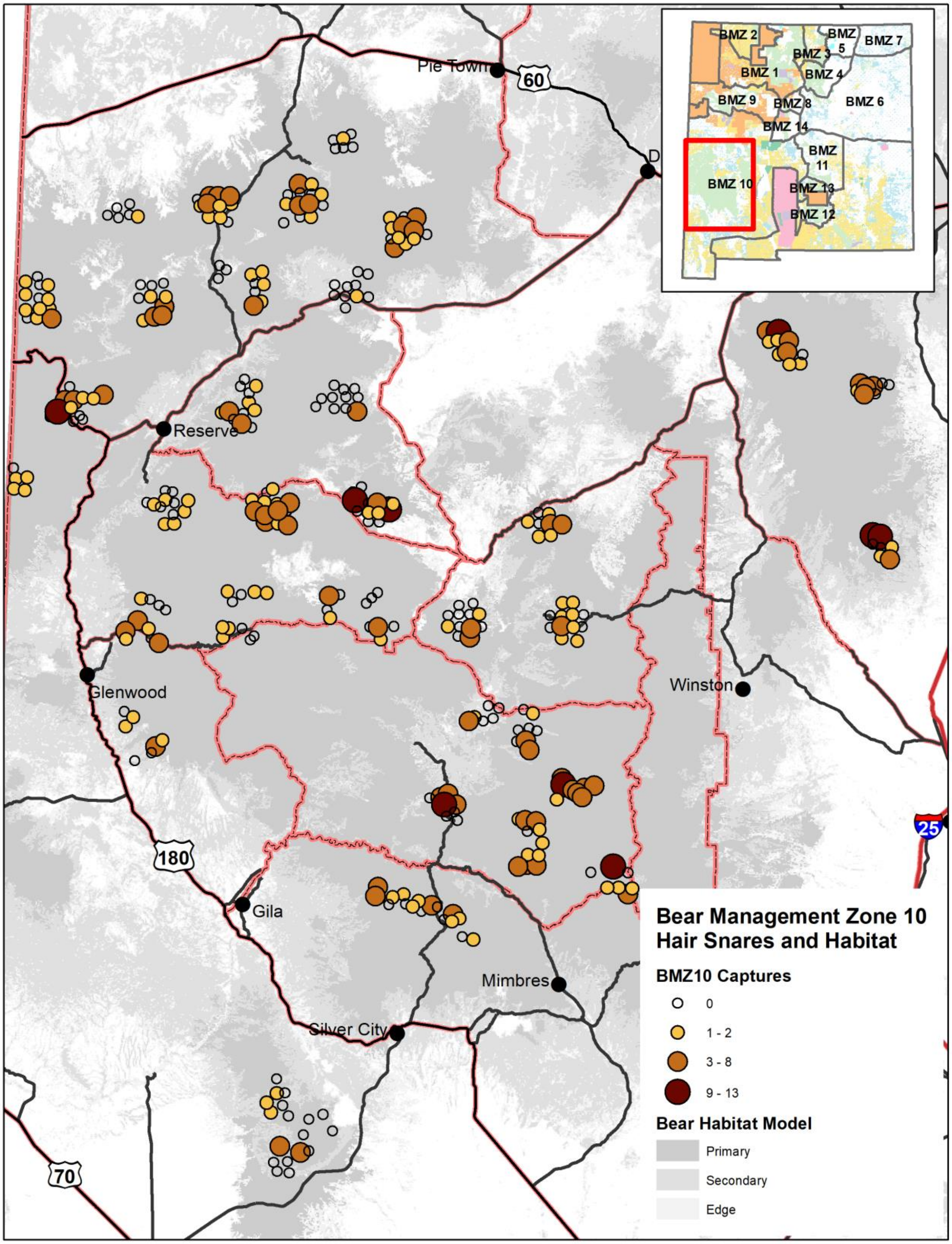

Figure 3. PCA based on 8-locus microsatellite genotypes from bears detected in BMZ 10 (blue) or BMZ 1 (yellow) showing substantial genetic differentiation between the zones.

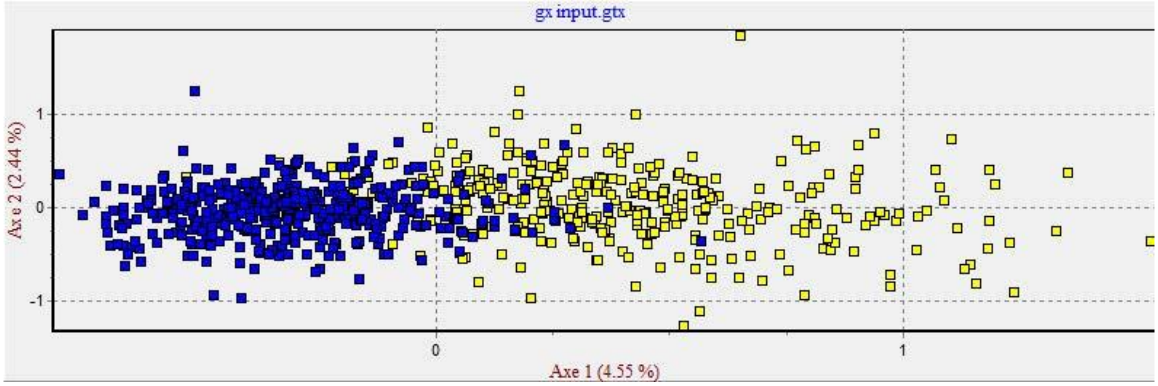

Table 1. Black bear capture summary via hair snares for Bear Management Zone 1 in 2019, and Bear Management Zone 10 in 2020 and 2021. Individuals is the total number of individuals detected at hair snares, detections is the total number of unique detections, N-once is the number of individuals caught only one time, N-multi is the number of individuals caught at multiple sites, D-mean is the average distance moved by individuals that were caught at multiple detectors, and D-max is the maximum distance an individual moved between two detectors.

	Individuals	**Detections**	**N-once**	**N-multi**	**D-mean (km)**	**D-max (m)**
BMZ 1	94	191	54	23	2.4	7.7
BMZ 10	270	554	155	69	2.9	21.9

Table 2. Model selection for estimating black bear population size in Bear Management Zones 1 and 10, New Mexico, 2019–2021, using Akaike's Information Criterion corrected for small sample size (AICc). We included models with a behavioral effect (bk) on probability of detection at an activity center (g0), and an effect of sex on g0 and the movement coefficient for decay in detection over space (σ).

Model	**K**	**Log-likelihood**	**AIC_c**	**ΔAIC_c**	**AIC_c Weight**
BMZ 1					
D(~1) g0(~bk + sex) sigma(~1)	4	-669.486	1347.427	0	0.711
D(~1) g0(~bk + sex) sigma(~sex)	5	-669.404	1349.499	2.072	0.252
D(~1) g0(~bk) sigma(~1)	3	-674.034	1354.338	6.911	0.022
D(~1) g0(~bk) sigma(~sex)	4	-673.484	1355.423	7.996	0.013
BMZ 10					
D(~1) g0(~bk + sex) sigma(~sex)	5	-1941.435	3893.102	0	1
D(~1) g0(~bk + sex) sigma(~1)	4	-1966.703	3941.561	48.459	0
D(~1) g0(~bk) sigma(~sex)	4	-1974.224	3956.601	63.499	0
D(~1) g0(~bk) sigma(~1)	3	-1981.744	3969.58	76.478	0

Table 3. Estimated abundance ($\hat{N}$) and 95% confidence interval, detection probability at an activity center (g0), and movement coefficient for decay in detection over space (σ [km]) for the top ranked model. Density ($\hat{D}$) is reported here as the number of bears per 100 km2 of primary habitat within the study area as identified in the Department's 2015 habitat model for comparison to previous estimation technique.

	$\hat{N}$ (95% CI)	**$g0$**	**σ**	**$\hat{D}$ (95% CI)**
BMZ 1	1,574 (1,050 – 2,358)	0.08	1.80	16.9 (11.2 – 25.3)
BMZ 10	2,192 (1,791 – 2,698)	0.07	1.95	15.9 (12.4 – 18.6)