Abundance and density estimation of the American black bear population in central Georgia

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Abstract: The Central Georgia Population (CGP) is the least abundant and most geographically isolated American black bear (Ursus americanus) population in Georgia, USA. We used DNA-based spatially explicit capture–recapture techniques to estimate density and abundance of bears in the CGP. We sampled bear hair over 2 8-week periods during the summers of 2012 and 2013 and recorded capture histories of individual bears identified via microsatellite genotyping. Population density for females was 0.123 bears/km² (SE = 0.018) and 0.152 bears/km² (SE = 0.024) in 2012 and 2013, respectively. Male bear density was 0.109 bears/km² (SE = 0.015) to 0.088 bears/km² (SE = 0.013) during the same years. Derived estimates of abundance of female bears was 125.4 (SE = 18.3) in 2012 and 154.9 (SE = 24.3) in 2013. Male bear abundance was 111.3 (SE = 15.2) and 89.8 (SE = 12.9) for 2012 and 2013, respectively. Based on these estimates and the isolated nature of the CGP, we recommend continued monitoring of demographic parameters and a conservative approach to determining annual harvest rates.

Key words: abundance, American black bear, density, DNA, secr, spatially explicit capture–recapture, Ursus americanus

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The American black bear (Ursus americanus; hereafter, bear) is the most common and widely distributed North American member of the family Ursidae (Pelton 2003). Within the United States, however, the current range of the black bear represents only approximately 45–62% of its historical range (Scheick and McCown 2014). Much of this range reduction has occurred in the southeastern United States (hereafter, Southeast). Maehr (1984) estimated that black bears inhabit only 10% of their historical range in the Southeast as a result of habitat loss and historical overexploitation. Furthermore, fragmentation of habitat has divided a once contiguous bear population into many, sometimes small and isolated, populations. Wooding et al. (1994) reported ≥13 separate populations of black bear within the Coastal Plain geophysical region of the Southeast.

Within the state of Georgia there are 3 bear populations—the North Georgia Population (NGP), the South Georgia Population (SGP), and the Central Georgia Population (CGP; Carlock et al. 1999). The least abundant and most geographically isolated of these populations is the CGP. Grahl (1985) reported a population estimate of 64 black bears for the CGP; but more recently, Sanderlin (2009) used web-design, noninvasive capture–mark–recapture (CMR) to derive annual, seasonal estimates ranging from 106 to 213 bears. However, several changes with potential to influence demography of the CGP have occurred since the work of Sanderlin (2009). One, the amount of land managed by Georgia Department of Natural Resources (DNR) in central Georgia (the geographic core of the CGP) has declined. In 2010, DNR had management authority over 16,588 ha of forested land within the range of the CGP. In 2011, the amount of forested land managed by DNR dropped to 12,275 ha, which was a 26% reduction. Also, prior to 2011, bear hunting was restricted to lands managed by DNR. These lands represented a small percentage of the available bear habitat in central Georgia. Consequently, harvest rates were low, averaging <1 bear/year. Beginning in autumn 2011, DNR changed bear-hunting regulations to allow bear hunting on private lands within 3 central Georgia counties (Bibb, Houston, and Twiggs) while prohibiting bear hunting on the DNR-managed lands.

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previously open to bear hunting. This increased the amount of bear habitat where bear hunting was permitted. Hunters harvested 34 (17 M: 17 F), 14 (6 M: 8 F), and 1 (1 M: 0 F) bear(s) during the 2011, 2012, and 2013 hunts, respectively (B. Bond, Georgia Department of Natural Resources, unpublished data).

To evaluate the effects these changes in land management and hunting regulations may have had on the CGP, the DNR requires contemporary estimates of population abundance and density for the CGP. Therefore, our objective was to estimate density and abundance of the CGP using non-invasively collected DNA and spatially explicit estimation methods.

Study area

The study area was located in central Georgia, approximately 160 km southeast of the city of Atlanta, and contained 1,020 km² of forested land within 5 counties—Bibb, Bleckley, Houston, Pulaski, and Twiggs (Fig. 1). Those counties are situated along the fall line between the Piedmont and Upper Coastal Plain physiographic regions and contain faunal and floral species common to each. Forest types included planted pine, natural pine, mixed upland hardwood, and bottomland hardwood. Common overstory tree species included loblolly pine (*Pinus taeda*), red and white oaks (*Quercus* spp.), sweetgum (*Liquidambar styraciflua*), red maple (*Acer rubrum*), American beech (*Fagus grandifolia*), yellow poplar (*Liriodendron tulipifera*), water tupelo (*Nyssa aquatica*), and bald cypress (*Taxodium distichum*). Clearcutting, tree thinning, and prescribed burning of the understory were common forestry practices in the study area.

Most forest land in the area was managed for timber harvest and seasonal, recreational hunting. Common large and medium-sized mammals found in the study area included white-tailed deer (*Odocoileus virginianus*), feral pigs (*Sus scrofa*), coyote (*Canis latrans*), grey fox (*Urocyon cinereoargenteus*), bobcat...
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(Lynx rufus), raccoon (Procyon lotor), opossum (Didelphis virginianus), and armadillo (Dasypus novemcinctus).

The Ocmulgee River flowed through the study area from north to south and was a defining geographical feature. Nearby human population centers included Macon (pop. 91,234), Warner Robins (pop. 70,712), Bonaire (13,999), Cochran (pop. 4,853), and Hawkinsville (pop. 4,589; U.S. Census Bureau 2010). Much of the land immediately to the west of the study area was dominated by urban development, whereas land to the south and east of the study area was primarily agricultural land. Predominant crops included cotton, corn, peanut, sorghum, and other grain crops. Commercial peach and pecan orchards were also common.

Central Georgia had a humid subtropical climate with hot, humid summers and generally mild winters. Average high temperatures ranged from 33.3°C in the summer to 14.4°C during winter (NOAA 2013). Lows of ≤0°C could be expected on 40–50 days annually. Measurable precipitation occurred on about 120 days annually, producing average annual amounts between 114 and 127 cm.

Methods

During summer (Jun–Aug) of 2012 and 2013, we collected bear hair from barbed-wire hair snares similar to those first described by Woods et al. (1999). We constructed our hair snares using 2 strands of 15.5-gauge, high-tensile barbed wire with 4 prongs/barb and barb spacing of 12.7 cm (Gauchos; Bekaert Corporation, Marietta, Georgia, USA). We stretched the wire strands at 30 cm and 65 cm above the ground around a group of 3–4 trees, forming a closed polygon with side lengths of 2–3 m. Within each enclosure, we suspended approximately 500 g of soured corn and a piece of cloth soaked in artificial raspberry flavor concentrate (Mother Murphy’s, Greensboro, North Carolina, USA).

We maintained 126 and 129 hair snares within the study area in 2012 and 2013, respectively. We placed hair snares at a density of approximately 1/2.6 km², which equated to a density of 3–4 snares in an area the size of the average female bear’s summer home-range in central Georgia (7.1 km²; Cook 2007). This approximates the trap density suggested by Otis et al. (1978) to allow all animals in the sampled population an adequate chance of being encountered.

We monitored each hair snare for 8 consecutive weeks beginning the second week of June and ending the first week of August. We visited each hair snare at 7-day intervals to ensure sample quality and prevent degradation of DNA. We collected samples from individual barbs and stored them separately in coin envelopes in a cool, dry environment. We labeled envelopes with a collection date and unique week–site–sample code that differentiated between samples collected from the top or bottom wires. We used a lighter or propane torch to burn off remaining hair and prevent contamination of future samples. Our methods were approved by the University of Georgia Institutional Animal Care and Use Committee (Protocol no. A2011 10-004-A1).

We used a subsampling protocol to select a subset of 400 samples for genetic analysis in 2011 and 2012 because analyzing all samples was cost-prohibitive. We chose 400 as our sample size with the goal of achieving adequate detection probabilities while reducing the likelihood of redundant detections of a bear at the same site in a given week. We assigned random numbers to each hair site–week combination that produced ≥1 sample. We then assigned hair samples within those site–week combinations a second series of random numbers. We did this to avoid consistently selecting samples collected from the top wire because samples typically were first collected, and numbered in order, from the top wire before the bottom wire. Without randomizing our sample selection process, our data set would have been biased toward older, larger bears more likely to encounter the top wire. We searched each site–week combination once in assigned order and selected a single optimal sample (i.e., ≥5 guard-hair roots, ≥20 underfur roots, or combination of both) from each until 400 samples were selected. In the event that the number of site–week combinations with ≥1 optimal sample was <400, we performed a second search through those that did not have optimal samples and selected a sample using a lower quality threshold, defined as ≥1 guard-hair root or ≥5 underfur roots. If necessary, we performed a third search through those combinations that had optimal samples remaining after the first 2 searches. Our subsampling protocol allowed variation in the number of samples collected each week to be reflected in the subsampled data set.

Wildlife Genetics International (Nelson, British Columbia, Canada) conducted the microsatellite analysis and used QIAGEN DNeasy® Tissue kits (Qiagen Inc., Mississauga, Ontario, Canada) to purify and
extract DNA from hair samples using standard protocols (Paetkau 2003). Roots from individual guard hairs were clipped for extraction, whereas entire clumps of underfur were used. We used 10 microsatellite markers (G1A, G10L, G10M, CXX20, MU59, G10X, CXX110, D1A, G10U, and D123) and a ZFX/ZFY sex marker to produce reliable individual identifications. Because genetic variability was low in our study area, standard protocols for re-analysis of mismatching markers in pairs of similar genotypes (Paetkau 2003, Kendall et al. 2009) were combined with extending genotypes in question with 2 additional markers (REN145P07 and G10H) to resolve potential genotyping errors.

To assess the power of the marker set to reliably identify individual bears, we estimated the probability that 2 full siblings would have the same multilocus genotype \(PI_{sibs}\) (Taberlet and Luikart 1999), which represented a conservative upper limit of the probability of observing identical genotypes among individuals within a population (Taberlet and Luikart 1999, Waits et al. 2001). We also assessed power by extrapolating the observed frequency distribution of pairs of individuals with genotypes mismatching at 1–10 markers (i.e., 1-MM-pair to 10-MM-pair) to estimate the likelihood that \(\geq 1\) individuals share the same genotype (Paetkau 2003). We used GenAlEx 6.5 (Peakall and Smouse 2012) to estimate multilocus \(PI_{sibs}\) which takes the product of all loci-specific \(PI_{ilbs}\), assuming independence of alleles among loci. We determined whether assumptions of independence and random sampling of alleles were met by testing for linkage disequilibrium using GENEPOP 4.2 (Raymond and Rousset 1995) and conformity to Hardy–Weinberg equilibrium using GenAlEx 6.5. We used a sequential Bonferroni correction to ensure an experiment-wise error rate of \(\alpha = 0.05\) for multiple tests (Rice 1989).

We used the secr v. 2.9.3 package (Efford 2015) and R v. 3.1.1 (R Core Team 2014) to maximize the full likelihood of a spatially explicit CMR model that treated the detection process as a binomial process (i.e., proximity detector type in secr), assumed a half-normal detection function, and assumed that home-range centers were Poisson distributed. This model consisted of 3 structural parameters: (1) population density \(D\), (2) the probability of detection when an animal’s home-range center coincided with a trap location \(g_0\), and (3) a scale parameter \(\sigma\) that governed the relationship between detection probability and distance between an animal’s home-range center and a trap location. We combined the DNA-based CMR data from 2012 and 2013 into a single data set that allowed fitting models with structural model parameters shared across years and sexes. In secr, we specified years as sessions and sex as a group factor. We fit 4 candidate models that differed only in how we modeled \(g_0\). For all models, modeled year- and sex-specific \(D\) by specifying a generalized linear model for \(D\) on the log scale that included an additive effect for year and sex and an interaction between year and sex, and modeled sex-specific \(\sigma\) on the log scale by only including sex as an additive effect. For \(g_0\), we specified logit-linear models that included only year (Model 1) or sex (Model 2) as additive effects, year and sex as additive effects (Model 3), and year and sex as additive effects plus an interaction between year and sex (Model 4).

Spatially explicit CMR models require explicitly defining an area, commonly referred to as the area of integration or state space, in which the population of interest occurs. This area must be large enough to include the home-range centers of all individuals exposed to capture in the trap array. In secr, that can be accomplished by specifying a distance from the trap array beyond which animals have a zero probability of being captured. However, specifying such an area by simply buffering the trap array may inadvertently include non-habitat where animal home-range centers are not likely to occur. Alternatively, the buffered area can be modified to mask non-habitat and only include habitat where animals are likely to occur. Because our study area was located within a heterogeneous landscape that included non-habitat such as urban and agricultural areas close to the trap array (Fig. 1), we used a habitat mask to restrict the area of integration to habitat where black bear home-range centers were likely to occur.

We used 30-m-resolution 2012 cropland data from U.S. Department of Agriculture National Agricultural Statistics Service (2012) to identify habitat and non-habitat located within our study area. We reclassified forest, shrubland, wetlands, deciduous forest, evergreen forest, mixed forest, and shrubland cover types as natural land cover and all other cover types as non-natural land cover. We then smoothed the re-classified raster by calculating the percent natural land cover within a moving circular window with a 1.5-km radius that is equivalent to the average female summer home-range (Cook 2007). Finally, we reclassified raster pixels that were \(\geq 70\%\) natural land...
Table 1. Model selection results for candidate models used to estimate sex- and year-specific abundance and density of the black bear population in central Georgia, USA, in 2012 and 2013. Population density (D), baseline detection probability (g₀), and spatial scale parameter (σ) were modeled as functions of sex (SEX) and year (YEAR).

<table>
<thead>
<tr>
<th>Model</th>
<th>AIC_c</th>
<th>ΔAIC_c</th>
<th>w_i</th>
<th>K_d</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model 4: D ~ YEAR × SEX, g₀ ~ YEAR × SEX, σ ~ SEX</td>
<td>5,617.94</td>
<td>0.00</td>
<td>1</td>
<td>10</td>
</tr>
<tr>
<td>Model 2: D ~ YEAR × SEX, g₀ ~ SEX, σ ~ SEX</td>
<td>5,644.05</td>
<td>26.11</td>
<td>0</td>
<td>8</td>
</tr>
<tr>
<td>Model 3: D ~ YEAR × SEX, g₀ ~ YEAR + SEX, σ ~ SEX</td>
<td>5,646.04</td>
<td>28.11</td>
<td>0</td>
<td>9</td>
</tr>
<tr>
<td>Model 1: D ~ YEAR × SEX, g₀ ~ YEAR, σ ~ SEX</td>
<td>5,670.73</td>
<td>52.79</td>
<td>0</td>
<td>8</td>
</tr>
</tbody>
</table>

a Akaike’s Information Criterion with a second-order correction for small sample sizes
b Relative difference between AIC_c of model and the top model with the lowest AIC_c
c Model wt.
d No. of model parameters.

cover as habitat and <70% natural land cover as non-habitat based on the lower range of percent natural land cover within bear home ranges observed by Murrow et al. (2013). We then converted the reclassified raster to a polygon shapefile to define our habitat mask used in secr. Smoothing of the original raster and subsequent conversion to a polygon resulted in several small isolated patches of habitat smaller than the average female summer home-range (i.e., <6 km²). These were unlikely to contain home-range centers and we removed them from the habitat mask. Our final habitat mask encompassed an area of 1,020 km² of habitat (Fig. 1).

We ranked models using Akaike’s Information Criterion with a second-order correction for small sample sizes (AIC_c; Burnham and Anderson 2002). We considered the model with the lowest AIC_c value to be the best fit for the data and most parsimonious. We derived estimates of abundance and associated standard errors by multiplying the density estimates by the area of integration defined by our habitat mask.

Results

We collected 3,570 hair samples from 126 hair snares in 2012. The number of sites producing ≥1 sample within a given week ranged from 37 (29%) during the initial weeks of sampling in 2012 to 68 (54%) during the eighth week. The mean number of samples collected from sites that produced ≥1 sample was 36 (SD = 30, range = 1–144). We collected 2,659 hair samples from 129 hair snares in 2013. The number of sites producing ≥1 sample within a given week in 2013 ranged from 41 (32%) during the initial week to 78 (60%) during the eighth week. The mean number of samples collected from sites that produced ≥1 sample in 2013 was 23 (SD = 16, range = 1–53). The mean number of samples collected per week in 2012 and 2013 was 446 (SD = 151) and 332 (SD = 113), respectively.

In 2012, we identified 105 individuals (56 M: 49 F) from 334 capture events. The average number of captures for males and females was 3.3 (SD = 3.4) and 3.1 (SD = 2.2), respectively. Percentage of males and females that were captured only once in 2012 was 45% and 22%, respectively. In 2013, we identified 99 individuals (50 M: 49 F) from 335 capture events, 62 of which were also detected in 2012. The average number of captures for males and females in 2013 was 4.8 (SD = 6.0) and 1.9 (SD = 1.3), respectively. Percentage of males and females captured only once was 38% and 51%, respectively.

The set of 10 markers used for individual identification averaged 3.3 alleles/loci, with an overall mean observed and expected heterozygosity of 0.56 and 0.57, respectively. The PI_uses was 1.7 × 10⁻³, which represented a 1 in approximately 560 probability of 2 related individuals sharing the same genotype at the same 10 markers. Additionally, we observed 1 1-MM-pairs and 8 2-MM-pairs, which indicated the likelihood that ≥1 bear had identical genotypes was acceptable. Chi-square results comparing observed and expected heterozygosity at the individual loci were not significant after sequential Bonferroni correction, indicating the loci used for identification did not deviate from Hardy–Weinberg equilibrium and that the calculated PI_uses statistics were reliable.

Model 4, which included an interaction between sex and year for g₀, was the only model supported by the data (Table 1). Population density estimates for females based on that model increased from 0.123 bears/km² (SE = 0.018) in 2012 to 0.152 bears/km² (SE = 0.024) in 2013, whereas male density estimates decreased from 0.109 bears/km² (SE = 0.015) to 0.088 bears/km² (SE = 0.013) across those
years. The estimate of \( g_0 \) for females in 2012 (0.24, SE = 0.03) was greater compared with 2013 (0.12, SE = 0.02) and lower for males in 2012 (0.07, SE = 0.01) than in 2013 (0.11, SE = 0.01). Estimated \( \sigma \) was greater for males (1,973.9 m, SE = 66.4) compared with females (889.5 m, SE = 36.8). Derived estimates of abundance for the area defined by the habitat mask increased for females from 125.4 (SE = 18.3) in 2012 to 154.9 (SE = 24.3) in 2013, but decreased for males from 111.3 (SE = 15.2) to 89.8 (SE = 12.9) across those years (Fig. 2).

Discussion

Our overall (i.e., male and female combined) estimate of density for the CGP was 0.232 and 0.240 bears/km² for 2012 and 2013, respectively. Although there is a wide range among reported estimates of density for bear populations in the Southeast, direct comparisons between our estimates and many of the reported density estimates in the literature are difficult because of different estimation methods used and various methods by which study areas were delineated. Of studies using spatially explicit estimation methods, our estimates were lower than those reported for coastal North Carolina, USA (0.46–0.77 bears/km²; Tredick and Vaughan 2009), and Lewis Ocean Bay, North Carolina (0.339 bears/km²; Drewry et al. 2013), but higher than an estimate for Carvers Bay, North Carolina (0.046 bears/km²; Drewry et al. 2013). Our estimates are most similar to those of Clark et al. (2010), who documented a 4-year decline in density of a bear population at White River National Wildlife Refuge, Arkansas, USA, from a high of 0.262 bears/km² in 2004 to a low of 0.136 bears/km² in 2007.

Sanderlin (2009) estimated population abundance to be 192 (95% BCI = 143–280) in 2006 for a 184-km² study area encompassing the Ocmulgee and Oaky Woods Wildlife Management Areas in Georgia, which resulted in an estimated population density of 1.04 bears/km² (CI = 0.78–1.52). A combination of factors likely caused our pooled density estimate for both sexes to be lower than that estimated by Sanderlin (2009). First, our study area was considerably larger (i.e., 1,020 km² vs. 184 km²) and likely encompassed a wider range of habitat conditions and population densities compared with Sanderlin (2009), who focused her work on high-quality habitat located on state Wildlife Management Areas. Because both studies assumed homogeneous density, differences in composition of bear habitat and, thus, estimated bear densities between study areas would be expected. Additionally, the net loss of forested habitat under DNR management between the time of Sanderlin (2009) and our study may have exacerbated differences in the distribution and availability of quality bear habitat in the CGP. Second, the altering of bear hunting regulations in 2011 by Georgia DNR that continued through 2013 resulted in an increased source of mortality that may have had additive demographic effects, thus reducing overall density across the CGP immediately before and during our study.

In addition to harvest, 16 bears were documented to have died of vehicle strikes (14, 10 M: 3F: 1 unknown) or unknown causes (2 F) immediately prior to and during our study (B. Bond, unpublished data). Finally, the modeling approach taken by Sanderlin (2009) did not account for bears moving among trapping webs within sampling occasions. Based on our estimates of \( \sigma \), especially for males, the distances between many pairs of trapping webs from Sanderlin’s (2009) study were well within the movement capabilities of bears in the CGP, likely resulting in bears being captured in >1 web during a sampling season. Not accounting for such movements and treating web-specific estimates as

Fig. 2. Abundance estimates from 2012 (open symbols) and 2013 (closed symbols) for male (triangles) and female (circles) black bears in the central Georgia black bear population, USA. Whiskers represent 95% confidence intervals.
Our model set contained models that only differed in how we modeled \( g_0 \), and our data clearly supported the most complex model that incorporated an interaction between year and sex effects. A variety of factors can drive differences in detectability of bears at hair snares across years. Annual fluctuation in distribution and abundance of natural foods can influence distribution of bear activity centers during sample collection, thus affecting site visitation and frequency. Variation in the distribution of conspecifics across years can also affect detection probability. For example, baseline detection probability for females may decrease in years during a synchronized breeding event, because females with cubs may be more reluctant to visit a hair snare given the elevated risk of encountering adult males. Although we did not explicitly model such factors, we were able to account for them by modeling the interacting effects of sex and year on \( g_0 \). The same factors that cause annual variation in detection probability may also affect space use by bears from year to year, which can be modeled with year and sex–year interaction effects on \( \sigma \). We chose not to include models with those effects because of potential difficulties associated with estimating additional parameters with a relatively small data set. For the same reason, we did not attempt to model latent heterogeneity in \( g_0 \) or \( \sigma \) with finite mixture models available in secr.

Behavioral response to capture at baited traps or hair snares has been documented in black bear studies (Tredick et al. 2007, Gardner et al. 2010, Drewry et al. 2013) and likely occurred in our study given that food (i.e., corn) was available at our sites. Although closed-population CMR models can account for behavioral responses by conditioning on initial capture, abundance estimates based on those models can be biased when data are missing, as is the case when the full set of hair samples is thinned by subsampling or when genotyping failures occur (Laufenberg et al. 2013, Augustine et al. 2014). Augustine et al. (2014) developed a modeling approach that explicitly accounted for processes that cause missing data, which resulted in a substantial decrease in estimator bias. However, that approach was based on a complete random subsampling design (i.e., randomly selecting a specified number of samples from the entire pool of samples), which differed from the subsampling approach we used, thus negating the possibility of applying their model to our data. Given that the response to bait in our study was likely positive and that abundance estimates from non-behavior models typically are negatively biased in the presence of positive behavioral effects (Otis et al. 1978), our estimates of black bear abundance should be considered conservative. We also note that we consider our estimates of abundance only valid for the population of bears \( \geq 1 \) year old, because bears \(< 1 \) year old are unlikely to be detected by the sampling methods we used (Drewry et al. 2013, Laufenberg and Clark 2014).

Management implications

Our results showed a substantial decrease in population density in the CGP that was likely caused, in part, by changes in harvest regulations and decrease in the amount of state-managed forests. We suggest monitoring of population density and abundance continue so that managers can assess the effects that future management decisions have on the CGP bear population. In addition to abundance and density, we also recommend managers consider monitoring demographic parameters such as recruitment, survival, and population growth rate, which would provide a mechanistic understanding of factors driving population dynamics. With sufficient data, a population viability analysis could be conducted to determine the long-term viability of the CGP and to guide management decisions regarding bear hunting and conservation in central Georgia. Harvest, though not inconsistent with population conservation, should be closely monitored because of the relatively small size of the CGP. Further consideration should be given to the low genetic diversity of the CGP (Miller 1995, Sanderlin et al. 2009). Future research also should quantify the level of demographic and genetic isolation between the CGP and other bear populations.

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