ESTIMATING DENSITY AND ABUNDANCE OF THE CENTRAL GEORGIA BLACK BEAR POPULATION USING SPATIALLY EXPLICIT CAPTURE-MARK-RECAPTURE

by

ANNALIESE K. ASHLEY

(Under the Direction of Michael J. Chamberlain)

ABSTRACT

Of the 3 bear populations in Georgia, the population in the central portion of the state is the smallest, and is presumably geographically isolated from other Georgia populations. We used DNA capture-recapture hair-snare techniques to estimate density and derive abundance for the central Georgia black bear population. We analyzed 4 years of data (2012-2015) collected over 4, 8-week sampling periods, to determine bear density across a 1,126.97 km^2 region. Using spatially explicit methods (SECR), we estimated female densities to be 0.194 bears/km^2 in upland areas and 0.066 bears/km^2 in bottomland areas. We found male densities to be 0.117 bears/km^2 in upland areas and 0.040 bears/km^2 in bottomland areas. We derived overall abundance of the bear population to be 428.20, 412.49, 439.84, and 458.23 bears for 2012-2015, respectively. The estimates of female detection probability from 2012-2015 were: 0.017 (SE=0.002), 0.018 (SE=0.002), 0.013 (SE=0.001), and 0.014 (SE=0.002). The estimates of male detection probability from 2012-2015 were: 0.012 (SE=0.00), 0.018 (SE=0.002), 0.013 (SE=0.001), and 0.014 (SE=0.001). We recommend continued population and harvest monitoring, with particular attention to female recruitment and mortality, as females drive reproductive rates and population numbers.

INDEX WORDS: Black bear, *Ursus americanus*, capture-recapture, secr, population estimation, hair-snare sampling, Georgia, spatially explicit-capture-recapture

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DEDICATION

I dedicate this thesis to those who worked tirelessly out of the spotlight to ensure I had what I needed to succeed. With all my heart, I thank you for your patience, your willingness to teach, your humility, your humor, and your support. Without you, I would not have known what it was I was doing, nor would I have succeeded in doing it.

"Lying out at night under those giant sequoias was lying in a temple built by no hand of man, a temple grander than any human architect could by any possibility build, and I hope for the preservation of the groves of giant trees simply because it would be a shame to our civilization to let them disappear. They are monuments in themselves...We are not building this country of ours for a day. It is to last through the ages."

-Teddy Roosevelt

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To the landowners, without whom this study would have been much weaker: thank you. Thank you for trusting your keys and combinations, your roads and your land to someone only met with over the phone. I will never forget your generosity.

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CHAPTER 1

INTRODUCTION AND LITERATURE REVIEW

Across the United States, large carnivores have been removed from much of their historical range due to many factors, including overharvest and changing land uses. This is particularly true for the American black bear (*Ursus americanus*; hereafter, black bear) in the eastern United States, whose populations have been severely reduced since the 1700's (Maehr 1984, Pelton and van Manen 1994, Pelton 2003). Although the black bear is the most common and widely distributed North American member of the family Ursidae (Pelton 2003), its current range only represents 45-62% of its historical range (Scheick and McCown 2014). Maehr (1984) estimated that in the Southeastern United States black bears only inhabit 10% of their historical range, and Scheink and McCown (2014) noted that the Southeastern United States shows the largest loss of range from historic ranges. Pelton (1990) estimated that there are currently 30 distinct, disjunct populations of black bears in the Southeastern United States. Likewise, Wooding et al. (1994) reported approximately 13 separate black bear populations in the Coastal Plain of the Southeast. Population isolation in this region is primarily associated with anthropogenic influences on the landscape, including forest conversion to agriculture or timber production, residential and urban development, and the associated infrastructure to support these developments (Pelton 1990, Hellgren and Vaughan 1994). In particular, roads are considered the leading cause of habitat fragmentation and a primary barrier to bear movement in the Southeast, further contributing to smaller, often isolated black bear populations (Hellgren and Maehr 1992, Brody and Pelton 1989, Beringer et al 1998, Thompson et al 2005).

There are 3 distinct black bear populations in Georgia: a northern population associated with the Blue Ridge geophysical region and the Smoky Mountain black bear population (NGP), a southern population associated with the Okefenokee Swamp and the Osceola black bear population in northern Florida (SGP), and an isolated population in central Georgia associated with the Ocmulgee River watershed (CGP, Figure 1.1). The CGP is confined to habitats surrounded by human development, including the cities of Macon and the Warner Robins Air Force Base. Areas of primary bear habitat fall within the Ocmulgee and Oaky Woods Wildlife Management Areas (WMAs), which provide approximately 12,376 ha of undeveloped habitat on the east and west banks of the Ocmulgee River within Bibb, Bleckley, Houston, Pulaski, and Twiggs counties. However, consistent anecdotal sightings of black bears are reported annually to the Georgia Department of Natural Resources (GA DNR) in counties north and west of the aforementioned range of the CGP, including Jones, Laurens, and Wilkinson counties (B. Bond, GA DNR, personal communication). Fragmentation and loss of habitat resulting from urban sprawl continue to negatively affect the CGP by prohibiting habitat connectivity and dispersal between the NGP and SGP. Similar to other isolated black bear populations in the Southeast (Troxler 2013), the CGP is now geographically and potentially genetically isolated from the other Georgia populations. Due to its small size and isolation, the CGP is at a greater risk of reduced genetic diversity and extirpation than other black bear populations (Frankham et al. 2004).

Black bears are long-lived and exist at relatively low densities. These life history traits influence space use, colonization rates, and population persistence over broad geographic extents (Brown and Nicoletto 1991). Habitat fragmentation negatively influences black bears by ultimately reducing gene flow (Vos et al. 2001) and genetic variability (Sherwin and Moritz

2000). Black bears are particularly susceptible to losses in genetic variability due to the inherently low levels of genetic variation resulting from low density populations (Paetkau and Strombeck 1994). As black bear habitat becomes more fragmented and populations lack suitable movement corridors for dispersal and gene flow, subpopulations often become genetically distinct from other isolated populations (Larkin et al. 2004). Small, isolated populations are vulnerable to local extinction due to stochastic events such as environmental, demographic, and genetic effects (Shaffer 1981). Of particular concern within the CGP is the loss of genetic variation through inbreeding. Inbreeding occurs in small, isolated populations where related individuals mate. This may result in reduction of genetic variability and a risk of allele fixation, resulting in loss of genetic adaptability (Keller and Waller 2002). Such fixation can lead to a depression in reproduction, fitness, adaptability, and overall viability of populations (Lacy 1997).

Previous studies have focused on estimating population size of the CGP. Grahl (1985) reported a population estimate of 64 black bears in the CGP, and Sanderlin (2009) reported annual, seasonal estimates ranging from 106-213 individuals. More recently, Sylvest (2014) yearly, sex specific abundance estimates in 2012 of N = 98 (SE = 62) for males and N = 70 (SE = 16) for females, and in 2013 of N = 70 (SE=18) for males and N = 69 (SE = 18) for females. Hooker et al. (2015) used spatially explicit models to revise estimates found in Sylvest (2014), reporting that derived estimates of abundance of female bears were 125.4 (SE 5 18.3) in 2012 and 154.9 (SE 5 24.3) in 2013. Male bear abundance was 111.3 (SE 5 15.2) and 89.8 (SE 5 12.9) for 2012 and 2013, respectively. Previous works (Sanderlin 2009, Sylvest 2014) were either restricted to state owned lands or were conducted within the geographic extent that only includes the 5 counties (Bibb, Bleckley, Houston, Twiggs, and Pulaski) thought to comprise the CGP.

The increasing observations and reports of bears outside of these areas mandates research to estimate abundance of the CGP at a broader spatial extent.

Historically, the CGP has been hunted only on the WMAs, which resulted in an average of approximately 1 bear harvested every 1 to 2 years (B. Bond, GA DNR. personal comm.). Beginning in 2011, a one-day hunt was allowed on private lands in Bibb, Houston, and Twiggs counties. Although hunters were only allowed a one bear limit, there was no quota placed on harvest. The 2011 harvest yielded 34 (17M: 17F) black bears, approximately 10% of the population estimate at that time (Sanderlin 2009). The 2012 harvest yielded 14 (6M: 8F) black bears, whereas 1 male was harvested in 2013. During 2014, 5 bears (1M: 4F) were harvested, whereas 12 (3M: 9F) were harvested in 2015 (B. Bond, GA DNR, personal comm.). Hunting can have a significant effect on small black bear populations, primarily because loss of parturient females disproportionately affects the population, due to their role in reproduction and population growth (Miller 1990). Because the number of females in a population drives population productivity (Beecham 1980), it is especially important to monitor harvest effects on population numbers, as overharvest could cause the CGP population to decline.

OBJECTIVES

My objective was to provide a robust estimate of abundance and density for the geographic extent of the CGP using spatially explicit population modeling. This information will better inform management decisions regarding harvest limits, range delineation, and more specific management techniques for the CGP. This study was conducted in synchrony with a denning ecology and cub survival project (Gray 2015), and a larger-scale project seeking to determine effects of a highway-widening project occurring in the core area occupied by the CGP.

THESIS FORMAT

Chapter 1 is an introduction and literature review of research relevant to the framing and justification of my work. Chapter 2 focuses on specific population parameters (abundance and density) of black bears (*Ursus americanus*) in central Georgia, and will be submitted to a peer-reviewed journal for publication. Chapter 3 provides conclusions and management implications.

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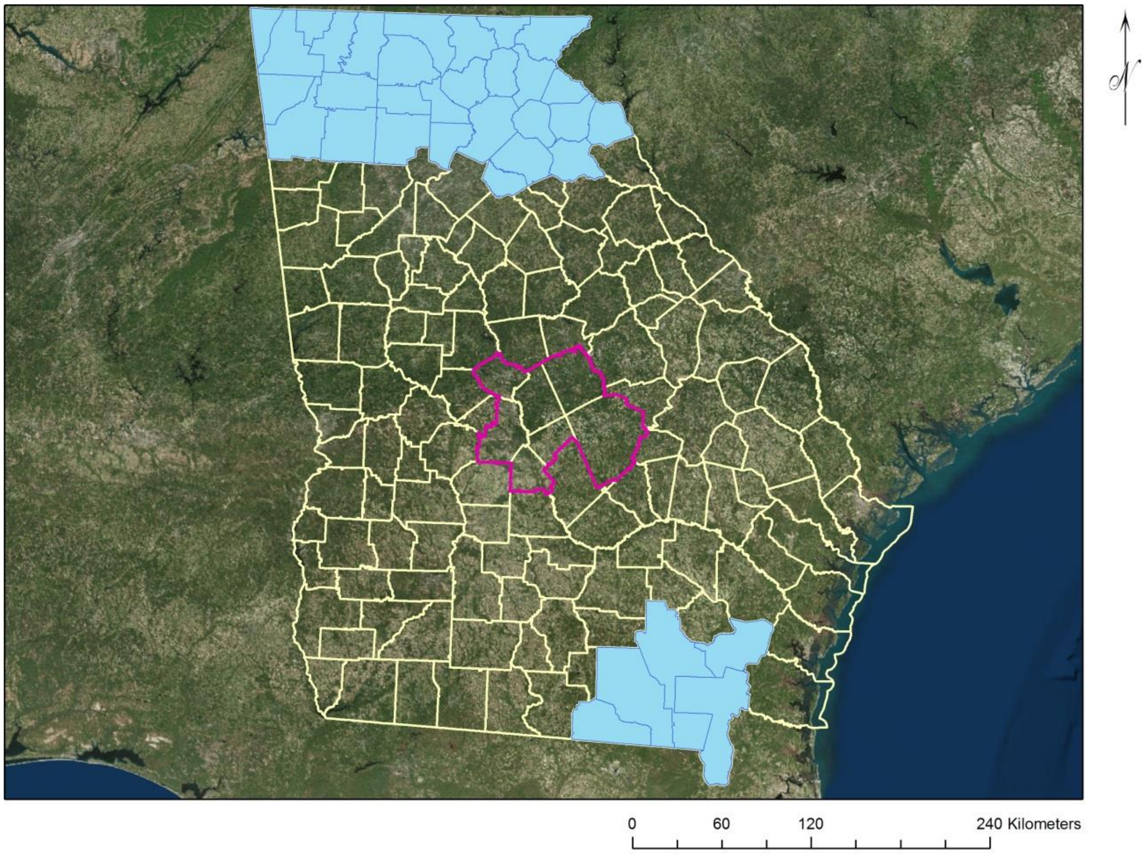

Figure 1.1. Ranges of the 3 black bear populations in Georgia: including the NGP associated with the Blue Ridge and Smoky Mountains, the SGP, associated with the Okefenokee Swamp and the Osceola (FL) black bear population, in the southeastern portion of the state, and the CGP, associated with the Ocmulgee River watershed (outlined in pink), 2012-2015 overlaid on a true color composite of the southeastern US.

CHAPTER 2

ESTIMATING DENSITY AND ABUNDANCE OF THE CENTRAL GEORGIA BLACK BEAR POPULATION USING SPATIALLY EXPLICIT CAPTURE-MARK-RECAPTURE[1]

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[1] Ashley, A. A., R. B. Chandler, J. S. Laufenberg, M. J. Chamberlain. To be submitted to *Journal of Wildlife Management*.

ABSTRACT

Of the 3 bear populations in Georgia, the population in the central portion of the state is the smallest, and is presumably geographically isolated from other Georgia populations. We used DNA capture-recapture hair-snare techniques to estimate density and derive abundance for the central Georgia black bear population. We analyzed 4 years of data (2012-2015) collected over 4, 8-week sampling periods, to determine bear density across a 1,126.97 km^2 region. Using spatially explicit methods (SECR), we estimated female densities to be 0.194 bears/km^2 in upland areas and 0.066 bears/km^2 in bottomland areas. We found male densities to be 0.117 bears/km^2 in upland areas and 0.040 bears/km^2 in bottomland areas. We derived overall abundance of the bear population to be 428.20, 412.49, 439.84, and 458.23 bears for 2012-2015, respectively. The estimates of female detection probability from 2012-2015 were: 0.017 (SE=0.002), 0.018 (SE=0.002), 0.013 (SE=0.001), and 0.014 (SE=0.002). The estimates of male detection probability from 2012-2015 were: 0.012 (SE=0.00), 0.018 (SE=0.002), 0.013 (SE=0.001), and 0.014 (SE=0.001). We recommend continued population and harvest monitoring, with particular attention to female recruitment and mortality, as females drive reproductive rates and population numbers.

INDEX WORDS: Black bear, *Ursus americanus*, capture-recapture, secr, population estimation, hair-snare sampling, Georgia, spatially explicit-capture-recapture

INTRODUCTION

The American black bear (*Ursus americanus*; hereafter black bear) is the most common and widely distributed North American member of the family Ursidae (Pelton 2003), although its current range only represents 45-62% of its historical range (Scheick and McCown 2014). Maehr (1984) estimated that in the Southeastern United States (hereafter Southeast) black bears only inhabit 10% of their historical range, and Scheink and McCown (2014) noted that the Southeast shows the greatest range loss of all populations. Wooding et al. (1994) reported approximately 13 separate black bear populations in the Coastal Plain of the Southeast. Population isolation in this region is primarily associated with anthropogenic influences on the landscape, including forest conversion to agriculture or timber production, residential and urban development, and the associated infrastructure to support these developments (Pelton 1990, Hellgren and Vaughan 1994). In particular, roads are considered the leading cause of habitat fragmentation and a primary barrier to bear movement in the Southeast, further contributing to smaller, often isolated black bear populations (Hellgren and Maehr 1992, Brody and Pelton 1989, Beringer et al 1998, Thompson et al 2005).

There are 3 distinct black bear populations in Georgia: a northern population (NGP), a southern population (SGP), and an isolated population in central Georgia associated with the Ocmulgee River watershed (CGP, Figure 2.1). The CGP is confined to habitats surrounded by human development, including the cities of Macon and the Warner Robins Air Force Base. Previous studies have reported overall abundance estimates of the CGP of 65 bears (Grahl 1985); annual, seasonal estimates from 106-213 (Sanderlin 2009); and yearly, sex specific abundance estimates in 2012 of N = 98 (SE = 62) for males and N = 70 (SE = 16) for females, and in 2013 of N = 70 (SE=18) for males and N = 69 (SE = 18) for females (Sylvest 2014). Hooker et al.

(2015) revised estimates from Sylvest (2014), reporting that derived estimates of abundance of female bears were 125.4 (SE 5 18.3) in 2012 and 154.9 (SE 5 24.3) in 2013. Male bear abundance was 111.3 (SE 5 15.2) and 89.8 (SE 5 12.9) for 2012 and 2013, respectively. Previous works (Sanderlin 2009, Sylvest 2014) were either restricted to state owned lands or were conducted within the geographic extent that only includes the 5 counties (Bibb, Bleckley, Houston, Twiggs, and Pulaski) thought to comprise the CGP. Additionally, the amount of land managed by Georgia Department of Natural Resources (GA DNR) in central Georgia (the geographic core of the CGP), has declined. In 2010, GA DNR had management authority of 16,588 ha of forested land within the range of the CGP, but in 2011 the acreage declined to 12,275 ha, a 26% reduction. Moreover, beginning in 2011, a one-day bear hunt was instituted on private lands in Bibb, Houston, and Twiggs counties, resulting in a substantive increase in bear harvest within the CGP. Specifically, hunters harvested 34 (17M: 17F), 14 (6M: 8F), 1 (1M: 0F), 5 (1M: 4F), and 12 (3M: 9F) bear(s) during the 2011-2015 hunts, respectively. Prior to 2011, bear hunting was restricted to only lands managed by GA DNR, with harvest rates averaging <1 bear/year (B. Bond, GA DNR, unpublished data).

While the CGP has been impacted by hunting since 2011, it is unclear whether harvest rates have translated to a decline in bear abundance. Concomitant with increased bear harvest, there have been increasing anecdotal citizen reports of bears, and presence of bears observed by ongoing surveys conducted by GA DNR outside of the previously estimated areas that comprised the CGP (B. Bond, GA DNR, personal comm.). Additionally, continued advancements in statistical estimation using spatially explicit methods to estimate density and abundance have provided refined tools to strengthen these estimates. Spatially explicit models take into consideration spatial variation in density, location and size of home ranges (activity centers), and an understanding of how capture probability changes with distance between the trap and activity center of animals (Efford 2004, Royle et al. 2014). My objectives were to provide a robust estimate of abundance and density for the entire geographic extent of the CGP using spatially explicit population modeling. This information will better inform management decisions regarding harvest limits, range delineation, and more specific management techniques for the CGP.

STUDY AREA

We conducted research from 2012-2015 on the central Georgia black bear population, one of 3 in the state (Figure 2.1). Our study area was located within 7 counties (Bibb, Bleckley, Laurens, Pulaski, Twiggs, and Wilkinson; Figure 2.2), on Balls Ferry, Beaverdam, Ocmulgee, and Oaky Woods Wildlife Management Areas (WMAs) owned by the Georgia Department of Natural Resources (GADNR), and private lands, primarily owned by Plum Creek Timber Company. Comprising approximately 150,000 ha, the study area was located in the Upper Coastal Plain geophysical region and included the Ocmulgee River and Lower Oconee River drainage systems. Adjacent human developments included Macon (pop. 91,351), Warner Robins (pop. 66,588), Bonaire (pop. unavailable), Cochran (pop. 5,150), and Hawkinsville (pop. 4,589; U.S. Census Bureau 2010). Pine (*Pinus* spp.) plantations, upland and bottomland hardwood forests, black belt prairies, and cypress (*Taxodium* spp.)-gum (*Nyssa sylvatica*) swamps were primary habitats. The WMAs were mostly (90%) forested and private lands were primarily pine plantations, but also included agricultural fields and human development.

Dominant overstory species varied by forest type but included oaks (*Quercus* spp.), maples (*Acer* spp.), hickories (*Carya* spp.), pines, elms (*Ulmus* spp.), cherries (*Prunus* spp.), dogwoods (*Cornus* spp.), magnolias (*Magnolia* spp.), cypress, sweetgum (*Liquidambar* *styraciflua*), American beech (*Fagus grandifolia*), American sycamore (*Platanus occidentalis*), and persimmon (*Diospyros virginiana*). Common mid- and understory flora included grapes (*Vitis* spp.), blueberries (*Vaccinium* spp.), hollies (*Ilex* spp.), privet (*Ligustrum sinense*), hawthorn (*Crataegus* spp.), American beautyberry (*Callicarpa americana*), blackberries (*Rubus* spp.), honeysuckle (*Lonicera spp.*), wild plum (*Prunus americana*), wax myrtle (*Morella cerifera*), dwarf palmetto (*Sabal minor*), and needle palm (*Rhapidophyllum hystrix*). Common fauna in the area included white-tailed deer (*Odocoileus virginianus*), raccoon (*Procyon lotor*), Virginia opossum (*Didelphis virginiana*), nine-banded armadillo (*Dasypus novemcinctus*), gray fox (*Urocyon cinereoargentus*), red fox (*Vulpes vulpes*), coyote (*Canis latrans*), feral hog (*Sus scrofa*), bobcat (*Lynx rufus*), wild turkey (*Meleagris gallopavo*), eastern gray squirrel (*Sciurus carolinensis*), fox squirrel (*Sciurus niger*), and a variety of songbirds and birds of prey. Agricultural fields were planted in corn (*Zea* spp.), cotton (*Gossypium* spp.), soybeans (*Glycine max*), peanuts (*Arachis hypogaea*), wheat (*Triticum* spp.), and sorghum (*Sorghum* spp.).

Intensive management of pine plantations for timber production was a dominant land use in the study area, particularly on timber company tracts (e.g. Plum Creek) and various stands throughout the WMAs. Timber management practices included broadcast herbicide and pesticide treatments, prescribed burning, thinning, and clearcutting. Both timber management and habitat management for common game species occurred on WMAs and private lands. Common habitat management practices were to maintain food plots and openings to provide food sources for popular game species, namely wild turkey and white-tailed deer. Wildlife Management Areas were also open for fishing, camping, and other outdoor recreational activities (Sylvest 2014).

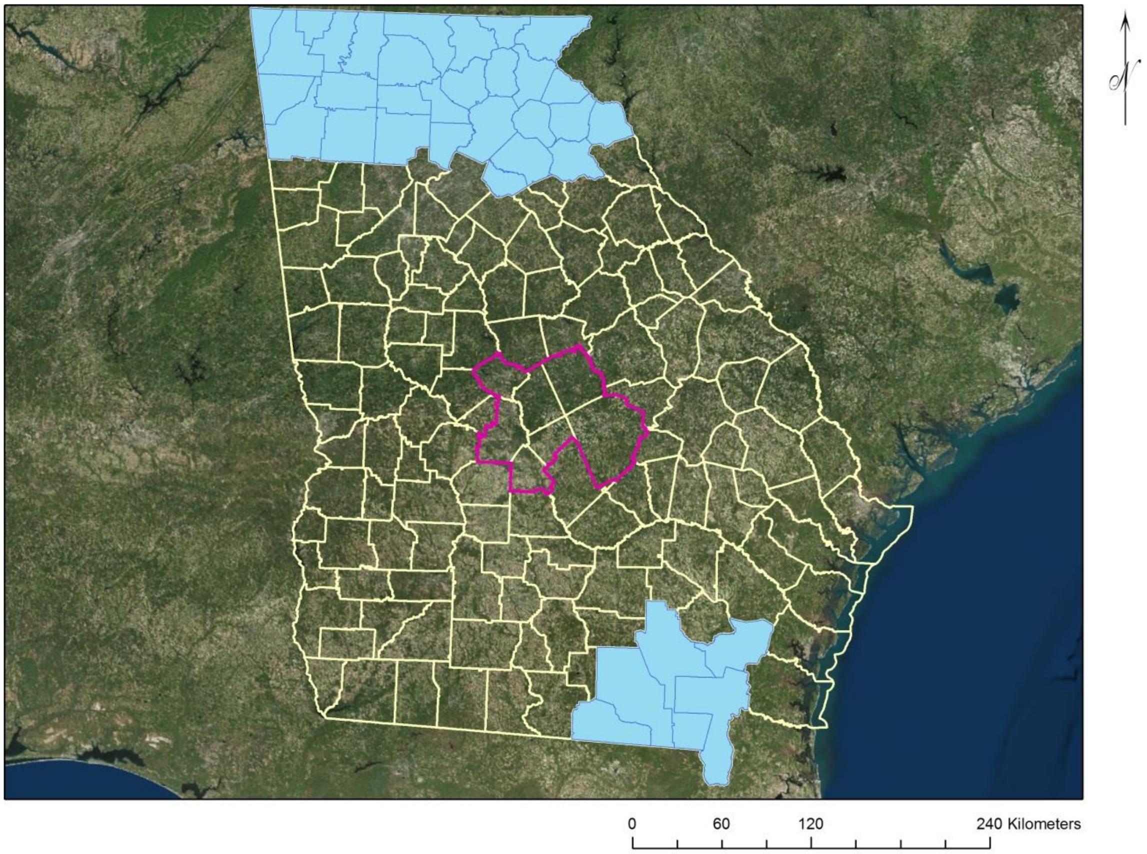


Figure 2.1. Ranges of the 3 black bear populations in Georgia, including the North Georgia population in the northern portion of the state, the South Georgia population in the southeastern portion of the state, and the central population (outlined in pink), 2012-2015.

Figure 2.2. Geographic extent of the study area used to estimate population size and density of the central Georgia black bear population during 2012-2015. Counties are outlined in pink and overlaid over a true color composite showing forest (green) interspersed with fields and human development (tan).

METHODS

During summer (June–August) of 2012-2015, we marked and recaptured black bears by collecting hair samples and identifying individuals by genotyping DNA from roots of sampled hair. Hair snares are widely used in genetic capture-recapture studies because they are safer, less intrusive, and less expensive than live-capture studies (Woods et al. 1999, Poole et al. 2001, Boulanger et al. 2002). We constructed snares using 2 strands of 15.5-gauge, high-tensile barbed wire with 4 prongs per barb and barb spacing of 12.7 cm (Gaucho®, Bekaert Corporation, Marietta, GA, USA). We stretched 2 wire strands at 30 cm and 65 cm above the ground around a group of 3–5 trees forming a closed polygon with side lengths of 2–3 m (Figure 2.3; Hooker 2010). Within each enclosure, we suspended approximately 500 g of soured corn in a plastic grocery bag and a piece of cloth soaked in artificial raspberry flavor oil (Mother Murphy's Laboratories, Greensboro, NC, USA). Where topographic features prevented the bottom wire from maintaining a consistent height, we used brush and debris to encourage bears to enter at another point.

Mean summer home-range size for adult females in central Georgia was 14.97 km^2, which represented the smallest average home range between sexes and among seasons in the area (Cook 2007). By placing 4 sites within an area equivalent to the smallest possible home range in the area, we increased the likelihood of 4 snares being present within a reasonable home range for any of the adult black bears in the central Georgia population, thus increasing our capture probability (Otis et al. 1978). We constructed hair snares at least 1.2 km from one another across the study area, where land access and feasibility would allow (Otis et al. 1978, Williams et al. 2002). We created a 1.2 × 1.2 km grid using ArcGIS 10.2 and overlaid it on a digitized map of the study area to extract Universal Transverse Mercator (UTM) coordinates for the center of each grid (Sylvest 2014). We constructed snares as close as possible to the center of each grid. From 2012-2013, Sylvest collected data in a southern grid (Figure 2.4), whereas from 2014-2015 we collected data in both the southern and an expanded northern grid (Figure 2.5).

We monitored snares approximately once weekly from June to August, and preferentially collected bear hair using visual identification. We removed hair from individual barbs using tweezers and placed it into coin envelopes. We considered each barb as a unique sample. After all hair samples were collected and labeled, we burnt the wires using propane torches to remove any unnoticed hair, preventing contamination of samples across secondary sampling periods (weeks). 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 from the southern grid (Figure 2.4) for each primary sampling period (2012–2015). Analyzing all samples was cost-prohibitive, therefore we chose 400 (50 samples per week) as the sample size to achieve adequate detection probabilities while reducing likelihood of redundant detections of a bear at the same site in a given week (Laufenberg et al. 2013, Sylvest 2014, Hooker et al. 2015). We assigned random numbers to each hair site-week combination that produced ≥ 1 sample. We assigned each hair sample within those site-week combinations a second series of random numbers. We did this to avoid oversampling from the top wire, as those samples were typically recorded before the samples from the bottom wire. Randomizing sampling locations from wires at each site prevented biased sampling of 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. This subsampling protocol allowed variation in number of samples collected each week to be reflected in the subsampled data set. All samples obtained from the northern study area above I-16 (Figure 2.5) during 2014-2015 were selected for microsatellite analysis, due to the low number of total samples collected from that study area. area.

DNA Extraction, Marker Selection, and Microsatellite Analysis

Wildlife Genetics International (WGI, Nelson, British Columbia, Canada) conducted the microsatellite analysis using 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.

The 2012 samples were originally analyzed for 9 microsatellite markers (*G1A, G10H, G10L, G10M*, *CXX20*, *MU59*, *G10X*, *CXX110*, and *D1A*), and the *ZFX/ZFY* sex marker. However, during the error-checking process many errors discovered, so an additional 3 markers (*REN145P07*, *D123,* and *G10U*) were analyzed to ensure accurate individual identification (Paetkau, WGI, personal comm.). Because genetic variability was low in the study area, standard protocols for re-analysis of mismatching (MM) 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 (Paetkau, WGI, personal comm.). Hence, we used *D123* and *G10U* instead of *G10H* to minimize the number of 1MM-pairs found, and to increase marker power (Paetkau 2003). Therefore, we analyzed 2013-2015 samples at 10 microsatellite markers (*G1A, G10L*, *G10M, CXX20, MU59, G10X*, *CXX110, D1A*, *G10U,* and *D123*) and the *ZFX/ZFY* sex marker.

Probability of Individual Identification and Hardy-Weinberg Equilibrium

In populations where genetic variability is low, misidentification may occur due to individuals sharing identical genotypes at examined loci. This phenomenon is called the shadow effect, and can positively bias capture probabilities and negatively bias abundance estimates (Mills et al. 2000). Therefore, 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 ≥1 individual share the same genotype (Paetkau 2003, Hooker et al. 2015). We used GenAlEx 6.5 (Peakall and Smouse 2012) to estimate multilocus PI_{sibs}, which takes the product of all loci-specific PI_{sibs}, assuming independence of alleles among loci.

The Hardy-Weinberg equilibrium principle assumes that allele and genotype frequencies are expected to reach and remain at equilibrium over time in populations that exhibit random mating and no selection, mutation, immigration, or emigration. We tested genetic samples for conformation to this principle by comparing the statistical difference after sequential Bonferroni correction between observed heterozygosity (H_o) and expected heterozygosity (H_e) in GenAlEx 6.5 (Peakall and Smouse 2012). We used a sequential Bonferroni correction to ensure an experiment-wide error rate of $\alpha = 0.05$ for multiple tests (Rice 1989). Finally, 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).

Capture-mark-Recapture Assumptions

Capture-mark-recapture (CMR) techniques estimate population abundance by capturing, marking, and releasing a portion of a population and comparing the proportion of marked to unmarked individuals at a subsequent capture occasion. Recent advancements in genetic analysis have allowed non-invasive, DNA-based survey methods to be integrated into CMR analyses (Boersen et al 2003, Boulanger et al 2008, Woods et al 1999). Genetic CMR techniques offer several benefits compared to traditional CMR techniques, including higher capture probabilities; decreased bias, invasiveness, and cost; and no loss of marks (Woods et al 1999). Baited hair-snares are widely used for systematic DNA collection in the field and are commonly used in population surveys for bears (Boulanger et al. 2004, Mowat and Strobek 2000, Mowat et al. 2005). These genetic CMR techniques are effective tools for modeling CMR data when the following assumptions of CMR studies are met:

1. animals do not lose their marks
2. animals are correctly identified
3. the population is demographically and geographically closed
4. all animals have an equal chance of being captured

Unique genetic markers ensured that we did not violate assumptions 1 and 2. Assumption 3 was satisfied through an 8-week sampling period during summer when the study population experienced no recruitment and high survival. While assumption 4 is valid in basic CMR studies, spatial models assume an inconsistent distribution of animals across a landscape. Spatial models allow for variation in capture probability among individuals due to varying distances between traps and activity centers. Furthermore, we included 2 wires per hair-snare to increase the chance of capture for bears of varying sizes and systematically sampled the entire study area.

Defining the region of interest

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 hair-snare array. This can be accomplished by specifying a distance from the hair-snare array beyond which animals have a zero probability of being captured. However, specifying such an area by simply buffering the hair-snare 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. Although a previous assessment of the study population created a uniform mask that included suitable habitat (Hooker et al. 2015), we chose to create a state-space with which to model spatial variation in density. We created this state space by placing a 10km buffer around the southern hair snare grid from 2015, which represented the largest area sampled in the southern grid (Figure 2.6). We chose the 10km buffer to minimize the chance of excluding an activity center, based on home range information from Cook (2007) and current GPS location data being collected on bears in the CGP (M. Hooker, UGA, personal comm.).

We created a single raster layer representing 2 land cover types to allow us to model spatial variation in density as a function of habitat. We used 30m resolution 2014 cropland data from U.S. Department of Agriculture National Agricultural Statistics Service (2014). We re-classified all land cover types into 2 discrete categories: upland and bottomland. We excluded anthropogenic habitat that consisted of developed areas and cropland. Bottomland habitat consisted of undeveloped wetland. Upland habitat consisted of all other natural, undeveloped land cover types, including planted pine. We chose these habitat categorizations based on GPS data from a concurrent study tracking movements and habitat use of bears in the CGP, which has shown bears to use upland and bottomland natural habitats differently, while largely ignoring anthropogenic habitat (M. Hooker, UGA, unpublished data). We then smoothed the re-classified raster using a 300m radius focal statistic. We chose this radius to smooth the raster to a 600m resolution without losing areas of a category large enough to be biologically significant to bear use. This yielded a total area of 1,126.97 km^2. The 2 habitat covariates we created using cropland data and a 300 m radius focal statistic yielded the following areas: 881.00 km^2 of upland cover, and 245.97 km^2 of bottomland cover (Figure 2.7).

Density Estimation and Abundance Derivation

We analyzed data using the secr package version 2.10.3 (Efford 2016) in Program R version 3.3.0 (R Core Team 2016) to estimate density and abundance. We analyzed capture histories using a full-likelihood, 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 followed a Poisson point process. These models consisted of 3 structural parameters, including population density (D), the probability of detection when an animal's home-range center coincided with a trap location (g_0), and a scale parameter (σ) that governed the relationship between detection probability and distance between an animal's home-range center and a trap location. We formatted the DNA-based CMR data from 2012-2015 to only include capture histories of animals captured in the southern grid. We developed a suite of multi-session models to estimate male and female density in the 2 habitat types in the southern grid. These models differed in how we modeled all parameters (D, g_0 and σ). For all models, we modeled habitat-, session-, and sex-specific (called "g") D. We also modeled sex (g) as an interactive effect on the habitat and session covariates of D. We modeled g_0 as a function of sex (g), session, general behavioral responses to traps (b), and trap-specific behavioral response (bk) in our models, and we modeled σ as a function of sex (Table 2.1).

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 density estimates by the area of integration defined by the habitat mask, specific to each habitat covariate.

Figure 2.3. Schematic showing design of a double-stranded hair snare used to collect bear hair in the central Georgia black bear population during 2012-2015.

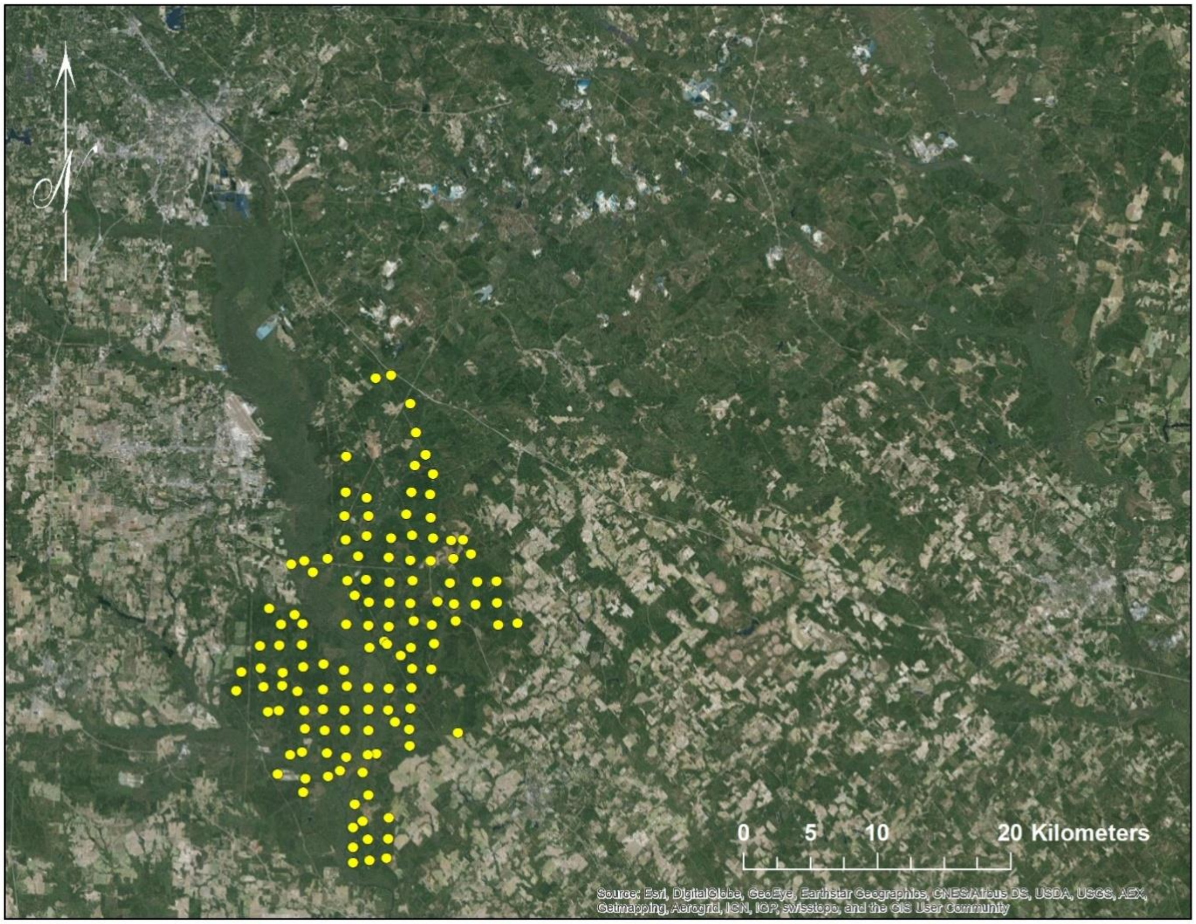
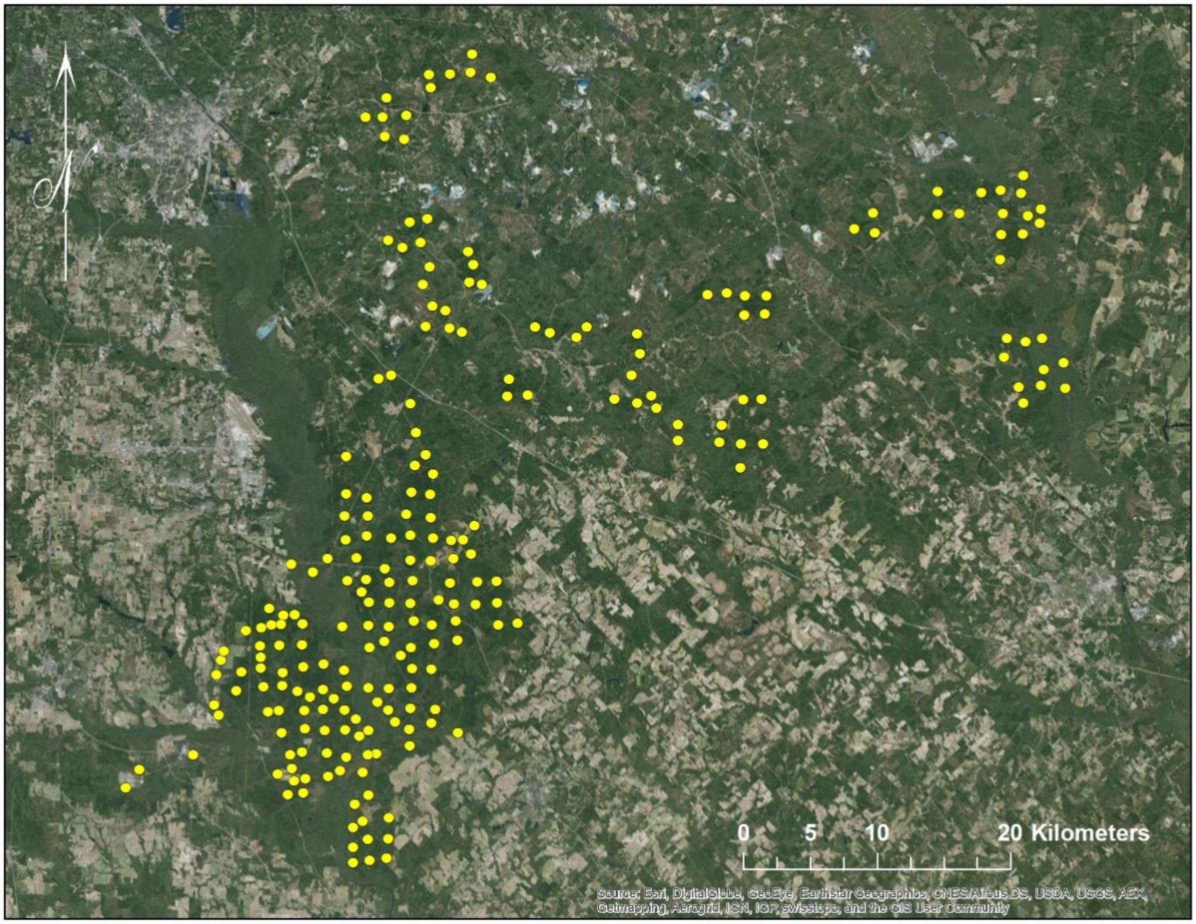


Figure 2.4. Locations used by Sylvest (2014) to collect bear hair samples during 2012-2013; these locations were also maintained and sampled during 2014-2015 to estimate abundance and density of bears in the central Georgia black bear population.



Source: Esri, DigitalGlobe, GeoEye, Earthstar Geographics, CNES/Airbus DS, USDA, USGS, AEX, Getmapping, Aerogrid, IGN, IGP, swisstopo, and the GIS User Community

Figure 2.5. Locations used to collect bear hair samples and estimate density and abundance of bears in the central Georgia black bear population during 2012-2015.

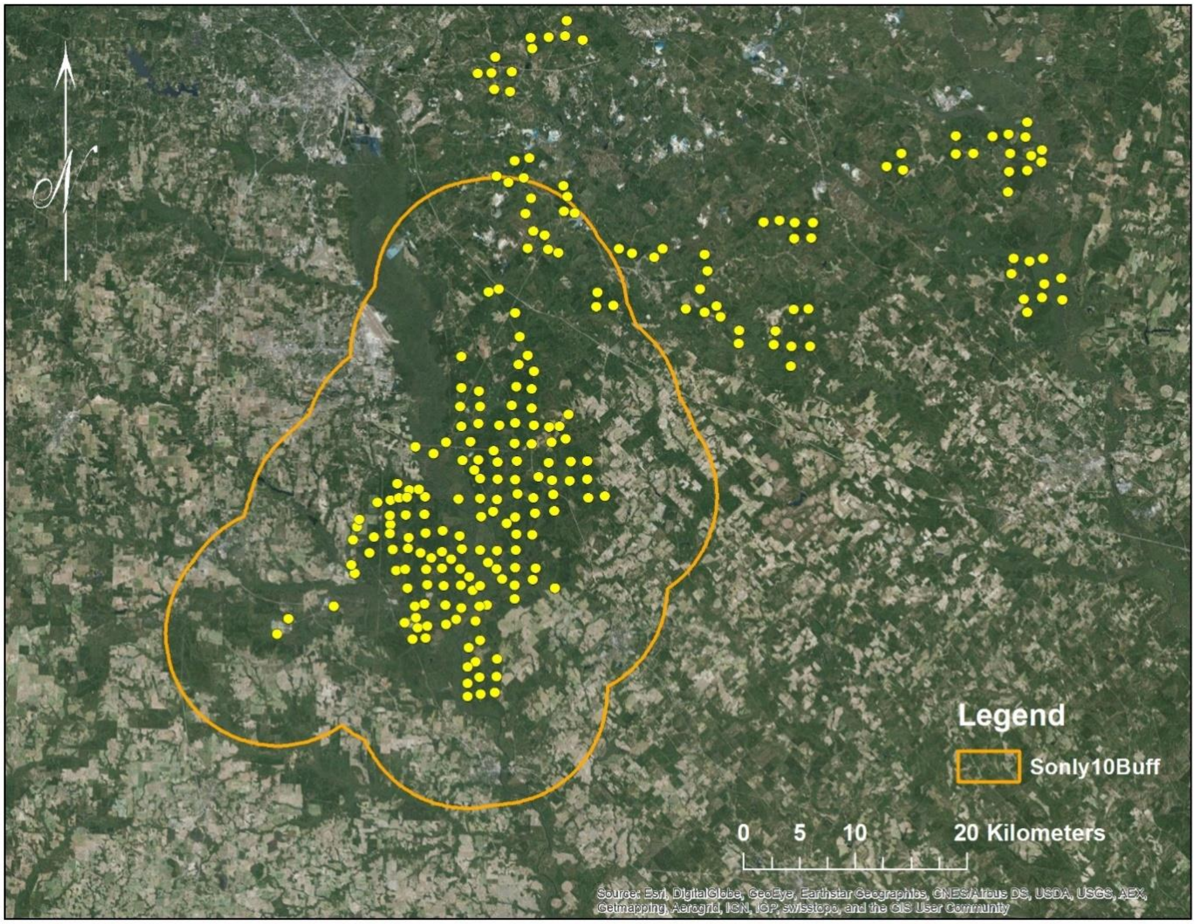
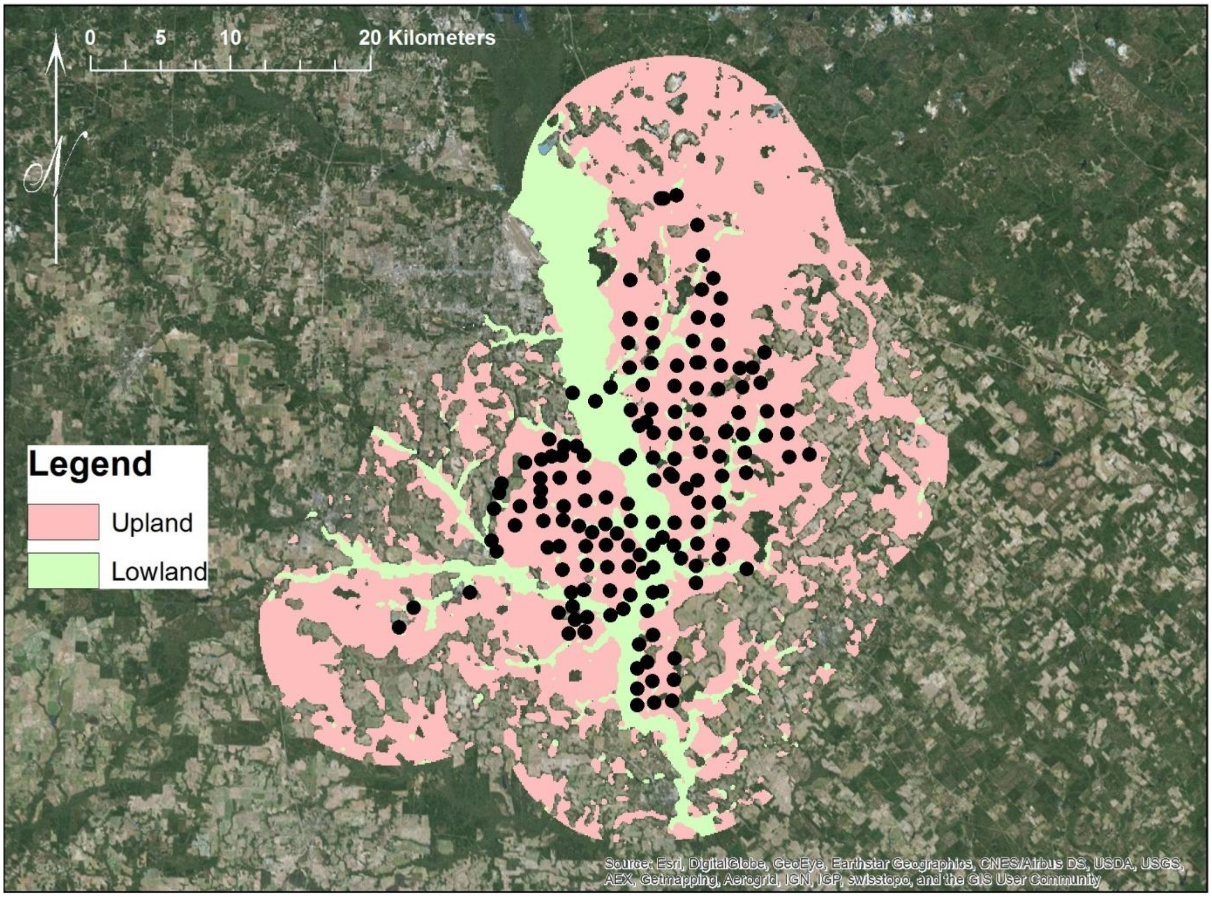


Figure 2.6. The orange outline is a smoothed 10km buffer around the complete southern trapping grid, whereas yellow points are a combined layer of all traps across all years of the study. Georgia, 2012-2015.



Source: Esri, DigitalGlobe, GeoEye, Earthstar Geographics, CNES/Airbus DS, USDA, USGS, AEX, Getmapping, Aerogrid, IGN, IGP, swisstopo, and the GIS User Community

Figure 2.7. Schematic of the landcover classes created for estimation of a density surface of the state space of the central Georgia black bear population. This data was gathered from the most recent cropland data (2014) available from the USDA Agricultural Statistics Services.

Table 2.1. Truncated model statements used to estimate density and derive a density surface and abundance estimate for the state space within the central Georgia bear population, 2012-2015.

	Model	*npar*
M23.2.noAnthro	D~(g + habitat) g_0~(g + bk + session) σ~g	11
M25.noAnthro	D~(session + g + habitat) g_0~(g + bk + session) σ~g	14
noAnthro2	D~(g+habitat) g_0~(g + b + session) σ~g	11
M25.noAnthro.B	D ~ (session + g + habitat) g_0~(g + b + session) σ~g	14

RESULTS

We used data from 126 and 129 hair-snares sampled during 2012 and 2013, respectively. Specifically, we used 3,570 hair samples collected from 126 hair snares in 2012; 100 hair snares produced at least 1 sample (79% success rate). Mean number of samples collected from sites that produced at least 1 sample during 2012 was 36 (SD=30, range= 1-144). We added 4 hair snares during 2013 and lost 1 from 2012 due to flooding, so we collected 2,659 hair samples from 129 hair snares in 2013 (81% success rate). Mean number of samples collected from sites that produced at least one sample in 2013 was 23 (SD=16, range = 1-53). Mean number of samples collected per week in 2012 and 2013 was 446 (SD=151) and 332 (SD=113), respectively.

During 2014 and 2015, we maintained 216 hair-snares. We collected 1,790 hair samples in 2014: 55 samples from the northern grid and 1,735 samples from the southern grid. 115 hair snares produced at least 1 sample (53% success rate), 12 of which were from the northern grid (13% success rate). Mean number of samples collected from sites that produced at least 1 sample was 15 (SD=12, range=1-63). We collected 2,026 hair samples (63 from northern grid, 1963 from southern grid) in 2015 and 116 hair snares produced at least 1 sample (53% success rate), 11 of which were from the northern grid (12% success rate). Mean number of samples collected from sites that produced at least 1 sample was 17 (SD=12, range=1-59). Mean number of samples collected per week in 2014 and 2015 was 224 (SD=43) and 253 (SD=55), respectively.

DNA Extraction, Marker Selection, and Microsatellite Analysis

In 2012, microsatellite analysis identified 103 individuals (54 M: 49 F) from 419 capture events. Average number of captures for males and females was 3.7 (SD=3.7) and 3.3 (SD=2.3), respectively. Two females and 5 males were captured 10 or more times. The percentage of males and females that were captured only once in 2012 was 42% and 20%, respectively. In 2013, there were 99 individuals (50 M: 49 F) identified from 482 capture events, 62 of which were also detected in 2012. Average number of captures for males and females in 2013 was 8.0 (SD=8.8) and 4.1 (SD=3.6), respectively. Six females and 16 males were captured 10 or more times and percentage of males and females captured only once was 20% and 24%, respectively.

In 2014, microsatellite analysis identified 108 individuals (64M: 44F) from 402 capture events; 68 were previously detected in 2012-2013. Average number of captures for males and females was 5 (SD=12) and 2 (SD=4), respectively. Six males were captured 10 or more times. The percentage of males and females that were captured only once in 2014 was 6.2% and 6.8%, respectively. In 2015, microsatellite analysis identified 122 individuals (70M: 52F) from 390 capture events; 83 were previously detected in 2012-2014. Average number of captures for males and females was 7 (SD=10) and 4 (SD=3), respectively. One female and 5 males were captured 10 or more times. Percentage of males and females that were captured only once in 2015 was 4% and 7%, respectively. Across the 4 years, 237 individuals (121M: 116F) were identified through at least one sample from hair snares.

Probability of Individual Identification and Hardy-Weinberg Equilibrium

PI values for the 10 non-sex loci in the 11- marker suite used for identification of all samples ranged from 0.14 to 0.37 (Table 2.2**)**. Overall probability of identity for the 10-marker suite was 1.4 x10^{-6}, or a 1 in ~71,428 chance of capturing 2 individuals with the same genotype at the 10 markers used for individual identification. The PI for siblings was 1.8 x 10^{-3}, which represented a 1 in ~555 probability of 2 related individuals sharing the same genotype at the same 10 markers. Observed versus expected heterozygosity at the individual loci were significant for the G10L and G10X loci, but not for the remainder of loci, indicating that 8 of the

10 loci used for identification did not deviate from Hardy-Weinberg Equilibrium, and that the calculated PI statistics were reliable (Table 2.3).

Density Estimation and Abundance Derivation

We found model M23.2.noAnthro to be the best fit model (Table 2.4). This model indicated that density (D) differed between sexes and habitat types. Female densities were higher in upland areas (0.194 bears/km^2), than bottomland areas (0.066 bears/km^2), and overall higher than male densities, which showed the same trend in habitat variation at 0.117 bears/km^2 in upland areas, and 0.040 bears/km^2 in bottomland areas (Figures 2.8 and 2.9, Table 2.5). The estimates of female g_0 from 2012-2015 were: 0.017 (SE=0.002), 0.018 (SE=0.002), 0.013 (SE=0.001), and 0.014 (SE=0.002). The estimates of male g_0 from 2012-2015 were: 0.012 (SE=0.00), 0.018 (SE=0.002), 0.013 (SE=0.001), and 0.014 (SE=0.001). We found that trap-specific behavioral responses had a significant positive effect on g_0 for both sexes. Estimated σ for females across all 4 years was 2,306.40m (SE=109.02), whereas estimated σ for males across all 4 years was 4,315.32m (SE=158.05).

We estimated female abundance of 240.85 (SE=18.14) in 2012, 232.54 (SE=18.03) in 2013, 247.85 (SE=18.84) in 2014, and 256.60 (SE=18.58) in 2015 (Figure 2.10, Table 2.6). We estimated male abundance of 187.35 (SE=11.04) in 2012, 179.95 (SE=10.93) in 2013, 191.99 (SE=11.34) in 2014, and 201.63 (SE=11.23) in 2015 (Figure 2.10, Table 2.7). Overall estimates of abundance did not vary significantly across years, with estimates of 428.20 (SE=21.24), 412.49 (SE=21.08), 439.84(SE=21.99), and 458.23(SE=21.71) bears from 2012-2015, respectively (Figure 2.11).

Northern Sampling Grid Results

Due to the low number of samples from the northern grid, we were unable to model density or abundance and chose instead to simply report how many individuals were identified in 2014 and 2015. In 2014, from the 55 samples collected, we identified 3 individuals (3M: 0F), none of which had been previously detected. In 2015, from the 63 samples we collected, we identified 5 individuals (5M: 0F), one of which (GA153) was previously detected in 2012, and 2 others (GA3180 and GA3262) previously detected in 2014 (Figure 2.12). Bear GA153 was originally detected in the southeastern grid in 2012, and travelled approximately 31.79km (straight line) to be detected during 2015 in the northern grid. Bear GA3180 was detected at the northern most point in the southeastern grid in 2013, and travelled approximately 11.37km (straight line) to be detected during 2015 in the northern grid (Figure 2.12).

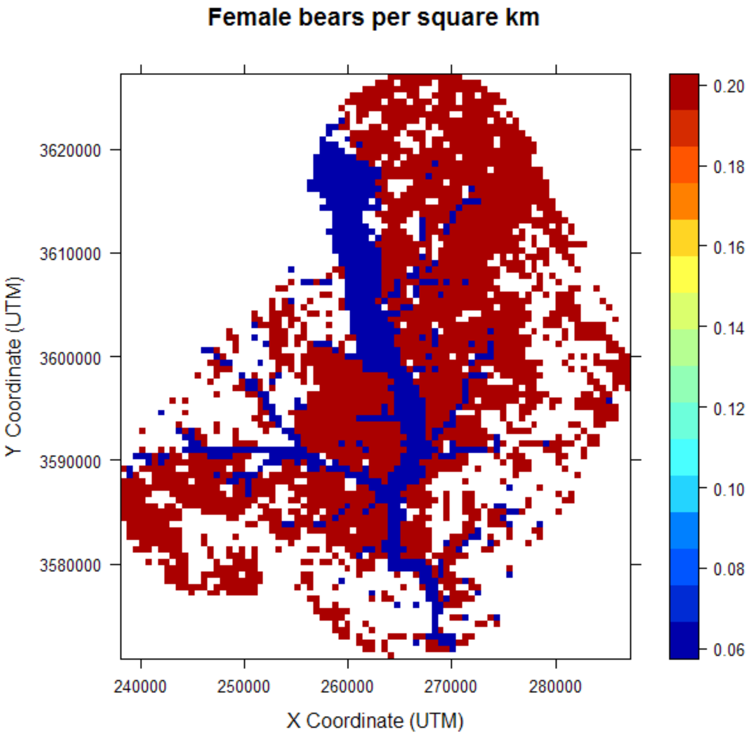


Figure 2.8. Density surface map for female black bears (bears/km^2) during 2012-2015 with the higher density in upland landcover and lower density in bottomland landcover.

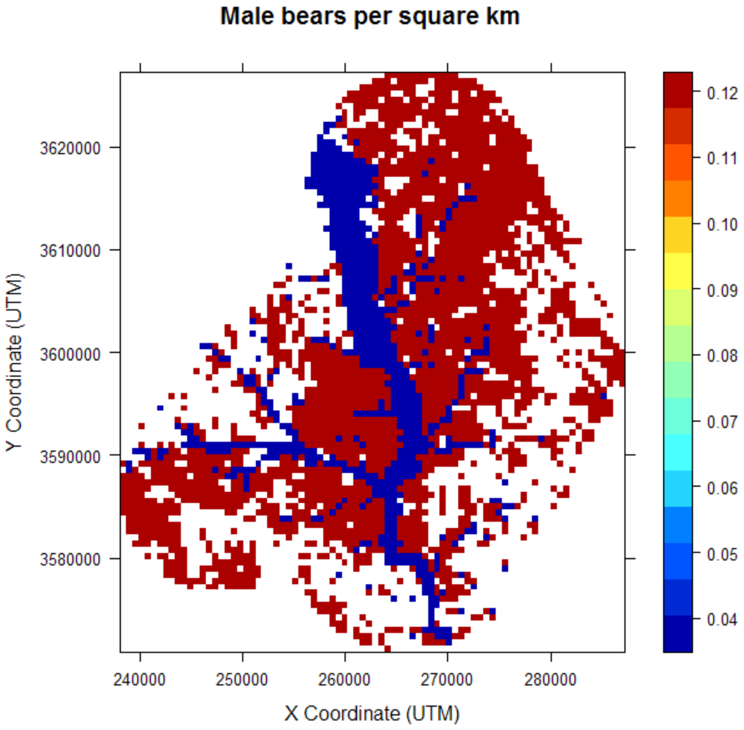


Figure 2.9. Density surface maps for male black bears (bears/km^2) during 2012-2015 with the higher density in upland landcover and lower density in bottomland landcover.

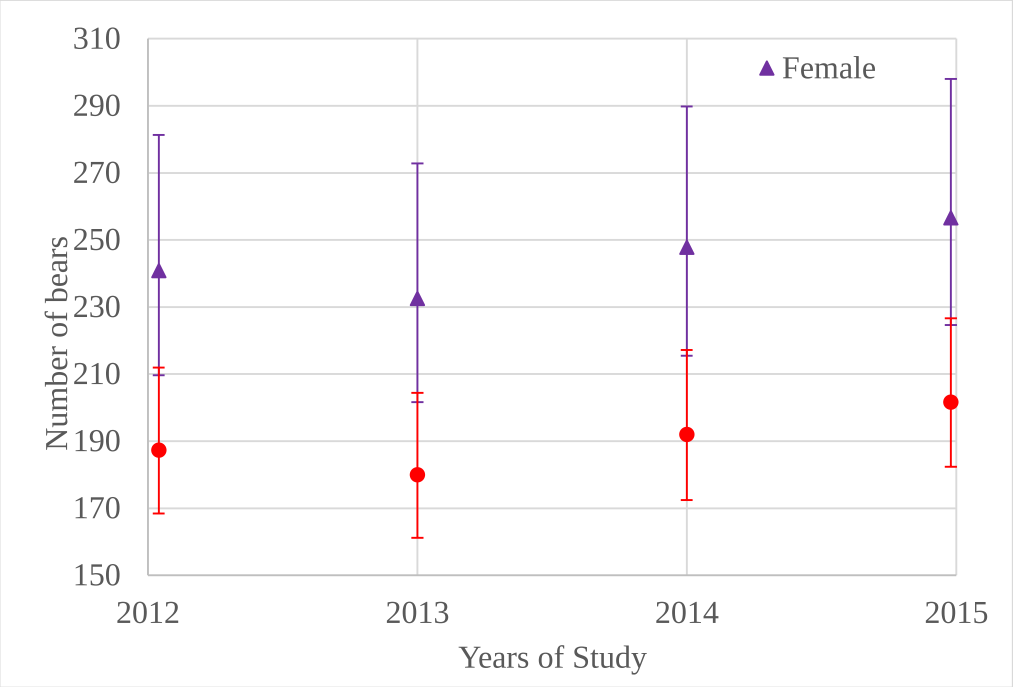


Figure 2.10. Annual sex-specific abundance estimates for black bears during 2012-2015 across the region of interest (1,126.97 km^2) for the central Georgia black bear population based on the best fit model and region.N calculations.

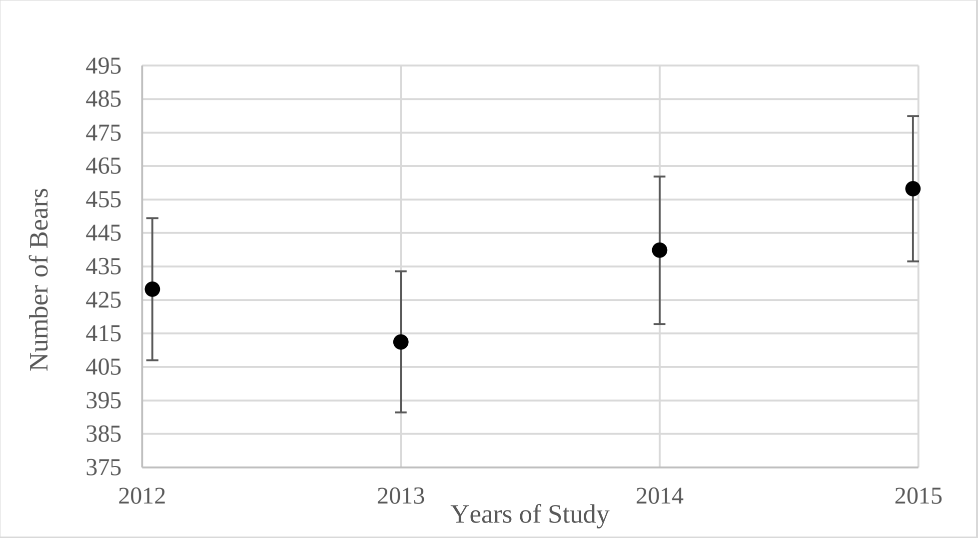


Figure 2.11. Yearly overall abundance estimates across the region of interest (1,126.97 km^2) of the central Georgia black bear population based on the best fit model and region.N calculations.

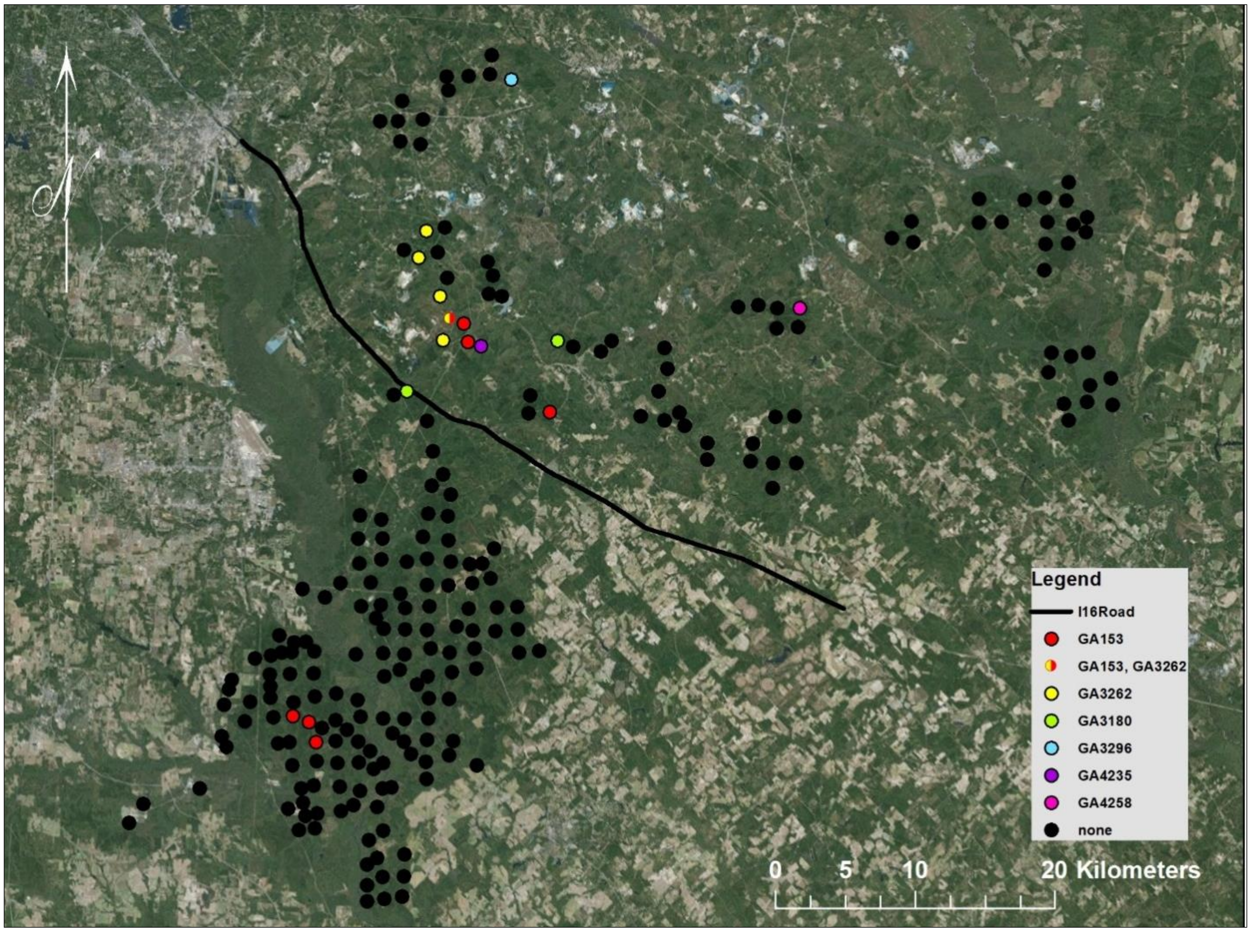


Figure 2.12. Locations in central Georgia during 2012-2015 where each of 6 bears were detected north of I-16. We detected GA153 (red) in the southern grid in 2012 and again in the northern grid in 2015. We detected GA3180 (green) in the southeastern grid in 2014 and again in the northern grid in 2015. All other individuals were only detected in the northern grid.

Table 2.2. Observed (*H_O*) and expected (*He*) heterozygosity, number of alleles (*A*), probability of identity (*PI*), and probability of sibling identity (*PI_{sibs}*) statistics of microsatellite markers used to establish individual identity of black bears in the central Georgia black bear population. Overall PI and PI_{sibs} values were computed including the gender marker.

Locus	*Ho*	*He*	*A*	*PI*	*Pisib*
G1A	0.68	0.66	5	0.16	0.46
G10L	0.52	0.54	5	0.27	0.55
G10M	0.55	0.56	3	0.29	0.54
CXX20	0.46	0.46	4	0.37	0.61
MU59	0.49	0.50	4	0.37	0.59
G10X	0.50	0.54	6	0.27	0.55
CXX110	0.50	0.50	3	0.37	0.59
D123	0.58	0.62	5	0.21	0.49
D1A	0.74	0.71	5	0.14	0.43
G10U	0.65	0.57	3	0.27	0.53
$\bar{x}$	0.57	0.56	4.3	0.27	0.53
Overall PI	-	-	-	1.4×10^{-6}	1.8×10^{-3}

Table 2.3. Summary of chi-square (X^2) tests with associated degrees of freedom (*DF*) for Hardy-Weinberg equilibrium for 10 loci used for individual identification of black bears in the central Georgia black bear population. Reported P-values are the significance values for chi-square tests comparing observed (H_O) and expected (H_E) heterozygosity for each locus.

Locus	*DF*	X^2	*P*-value
G1A	10	7.00	0.73
G10L	10	622.02	0.00
G10M	3	2.66	0.45
CXX20	6	1.66	0.95
MU59	6	2.68	0.85
G10X	15	627.20	0.00
CXX110	3	0.91	0.82
D123	10	15.26	0.12
D1A	10	10.60	0.39
G10U	3	3.82	0.28

Table 2.4. Truncated list of candidate models used to estimate density of the central Georgia black bear population from 2012-2015, and summary of model selection procedures based on corrected Akaike's Information Criterion for small sample sizes (AIC_c). Densities (D) were modeled by year (session), habitat, and sex (g), capture probabilities (g_0) were modeled by sex and behavior (b), and sigma (σ) was modeled by sex.

model	*detectfn*	*npar*	*logLik*	*AIC*	*AICc*	*ΔAICc*	*AICcwt*
M23.2.noAnthro: D~(g+habitat) g_0~(g+bk+session) σ~g	halfnormal	11	-5826.57	11675.13	11675.77	0.00	0.72
M25.noAnthro: D~(session+g+habitat) g_0~(g+bk+session) σ~g	halfnormal	14	-5824.33	11676.67	11677.69	1.92	0.28
noAnthro2: D~(g +habitat) g_0~g+b+session σ~g	halfnormal	11	-6348.93	12719.87	12720.50	1044.73	0.0
M25.noAnthro.B: D~(session + g + habitat) g_0~(g + b + session) σ~g	halfnormal	14	-6346.49	12720.99	12722.00	1046.24	0.000

Table 2.5. Density estimates (bears/km^2) of female and male black bears for the 2 habitat covariates (Upland and Bottomland) within the region of interest (1,126.97 km^2) for the central Georgia black bear population during 2012-2015.

	Males	*Females*
Upland	0.117	0.194
Bottomland	0.040	0.066

Table 2.6. Annual expected abundance (*R.N*) estimates of female black bears within the region of interest (1,126.97 km^2) of the central Georgia black bear population, based on the number of individuals identified (*n*) during 2012-2015. Standard Error (*SE*), Lower (*LCL*) and Upper (*UCL*) Confidence Intervals are also included.

Year	*R.N*	*SE*	*LCL*	*UCL*	*n*
2012	240.85	18.14	209.68	281.31	105
2013	232.54	18.03	201.61	272.78	99
2014	247.85	18.84	215.46	289.81	106
2015	256.60	18.58	224.66	298.02	117

Table 2.7. Annual expected abundance (*R.N*) estimates of male black bears within the region of interest (1,126.97 km^2) of the central Georgia black bear population, based on the number of individuals identified (*n*) during 2012-2015. Standard Error (*SE*), Lower (*LCL*) and Upper (*UCL*) Confidence Intervals are also included.

Year	*R.N*	*SE*	*LCL*	*UCL*	*n*
2012	187.35	11.04	168.39	211.99	105
2013	179.95	10.93	161.19	204.36	99
2014	191.99	11.34	172.48	217.22	106
2015	201.63	11.23	182.32	226.65	117

DISCUSSION

The abundance and density estimates we generated were developed under 4 basic assumptions: bears did not lose marks, bears were correctly identified, the bear population was demographically and geographically closed, and all bears had an equal chance of being captured. Because we used unique genetic markers, we offer that marks were not lost. Likewise, results from assessment of PI_{sibs} and testing of conformity to the Hardy-Weinberg equilibrium principle both yielded acceptable results, suggesting that bears were correctly identified. Our sampling periods were designed to satisfy the third assumption, as the 8-week sampling period occurred when the study population experienced no recruitment and high survival. However, we recognize that some movement of males in and out of the study area may have occurred given that breeding season overlapped our sampling (Hamilton and Marchinton 1977, Powell et al. 1997, Eiler et al. 1989); this could perhaps have resulted in the sporadic samples (all from males) collected in the northern grid. Finally, we recognize that all bears did not likely have equal chances of being captured, which secr accounts for by allowing for individual heterogeneity in capture probability (g_0) (Otis et al. 1978, Tredick et al. 2007).

Our overall (males and females combined) estimate of density for the CGP was 0.417 bears/km^2, slightly higher than the 0.232 and 0.24 bears/km^2 estimates reported by Hooker et al. (2015). Our abundance estimates (428.2, 412.5, 439.84, and 458.2 bears from 2012-2015) were higher than those reported in Hooker et al. (2015) and Sanderlin (2009). However, in both of these studies the area in which density was calculated was smaller than the 1,126.97 km^2 study area we sampled. Specifically, Sanderlin (2009) estimated population abundance to be 192 bears (95% BCI = 143-280) in 2006 for a 184 km^2 study area encompassing the Ocmulgee and Oaky Woods WMAs, yielding an estimated population density of 1.04 bears/km^2 (CI = 0.78-1.52).

Hooker et al. (2015) estimated a density of 0.232 and 0.240 bears/km^2 for 2012 and 2013, respectively, across a 1,020 km^2 study area, yielding an estimated population abundance of 236 and 244 bears, respectively. In contrast to Sanderlin (2009) who focused only on state-managed WMAs, and Hooker et al. (2015) who focused estimates only on a portion of undeveloped lands on our study site, we estimated a density surface across the entire natural landcover of the state space, the geographic scale of which was considerably larger than that used in previous works on our study area. Hence, it is reasonable that our estimates of density and abundance are higher than previously reported.

Bear densities vary considerably across the southeastern United States, hence direct comparison of our estimates to those published previously are difficult because of different methods of estimation, time, and spatial scales used in each study. However, of studies using spatially explicit estimation methods, our estimates were similar to those reported for Lewis Ocean Bay, North Carolina (0.339 bears/km^2; Drewry et al. 2013). Conversely, our estimates were slightly lower than those reported for coastal North Carolina, USA (0.46-0.77 bears/km^2; Tredick and Vaughan 2009), but higher than those reported for Carvers Bay, North Carolina (0.046 bears/km^2; Drewry et al. 2013), and White River National Wildlife Refuge, Arkansas, USA (0.262 bears/km^2 in 2004 to 0.136 bears/km^2 in 2007; Clark et al. 2010).

Behavioral response to capture at baited traps 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 corn was available as bait at our sites. While CMR studies account for behavioral responses, estimates based on those models can be affected when data are missing, as in the case of subsampling or genotyping failures (Laufenberg et al. 2013, Augustine et al. 2014). Augustine et al. (2014) developed a modeling approach that explicitly accounted for processes causing missing data. However, that approach was based on a complete random sampling design and differs from our subsampling based on Laufenberg et al. (2013). Subsampling data affects g_0 because subsampled data may or may not identify an animal at its first capture, which can result in estimates of abundance being biased high. Likewise, we also noted low capture probabilities (g_0) for both sexes, which likely inflated the estimated number of bears across all 4 years of sampling. Violation of the geographic closure assumption could negatively bias capture probabilities and artificially inflate abundance estimates. Furthermore, we detected few individuals in the northern grid, despite extensive sampling across a broad spatial extent. While informative, the data collected in the northern grid were too sparse to use in an expanded state-space calculation, hence we excluded these data from the modeling process. However, by excluding male samples collected in the northern grid, we also negatively affected σ estimation for males, hence g_0 would decrease more rapidly as distances from hair-snares increased, further biasing abundance estimates high. Regardless, our estimates of abundance indicate that bear numbers in the CGP are larger than previously believed, but we suspect our estimates of abundance are biased high given the above.

Finally, it is plausible that continued sampling across a broader spatial grid in the north could be useful and would perhaps detect more individual bears. However, the low number of male-only hair samples we collected, coupled with a general lack of sign noted during our field work, suggests that the state space we used encompassed the geographic extent of the CGP. We offer that individuals found north of I-16 were either dispersing yearling males or adult males travelling during the breeding season, and that these animals are likely residents of the CGP within the southern study region.

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CHAPTER 3

CONCLUSIONS AND MANAGMEMT IMPLICATIONS

We collected sparse data from the northern grid (i.e., area north of I-16), and conclude that these samples likely come from dispersing male bears, rather than indicating a range expansion of the CGP. The total absence of female samples suggests that currently, the breeding portion of the CGP fails to extend north of I-16. However, we recommend that DNR continue monitoring bear activity in the area encompassed by the northern grid. Our findings suggest that the entire breeding range of the CGP, and hence the range containing all resident bears, is encompassed within the spatial extent we used.

We found densities of bears to be lower in bottomland natural areas and higher in upland natural areas. This is consistent with findings reported in Gray (2015), who noted the importance of upland habitats to denning ecology of females. Likewise, ongoing work using GPS data from collared bears in the CGP is demonstrating the importance of upland habitats to bears (M. Hooker, UGA, unpublished data). Our overall (males and females combined) estimate of density for the CGP was 0.417 bears/km^2. Overall estimates of abundance did not vary significantly across years, with estimates 428.20 (SE=21.24), 412.49 (SE=21.08), 439.84(SE=21.99), and 458.23(SE=21.71) bears from 2012-2015, respectively. These estimates were higher than previously reported estimates of 236 and 244 bears for 2012 and 2013, respectively (Hooker et al. 2015). However, our estimates were based on a 1,126.97 km^2 area of interest, whereas estimates reported by Hooker et al. (2015) were based on a 1,020 km^2 area of interest. Moreover, due to our low observed capture probabilities, we suspect that our models overestimated density and abundance. Likewise, the potential that we violated geographic closure assumptions in our modeling efforts could have negatively biased capture probabilities, and hence affected density estimates.

Our estimates of bear abundance can be used to inform management decisions for the CGP, particularly in regards to habitat management and harvest regulations. While our estimates of abundance are higher than the most recent published estimates (Sanderlin 2009, Hooker et al. 2015), we suggest continued monitoring of the CGP given that harvest continues annually and mortalities attributable to roadkill are persistent. Miller (1990) noted that a maximum harvest rate of 14% for black bear populations could be managed for sustainable yield, but this rate assumes optimal conditions for reproduction, natural mortality, and a male-biased harvest rate. Gray (2015) observed male-biased litters and smaller than average litters, and a female-biased harvest, all of which could negatively affect the overall population growth rate. Since female survival and recruitment drive population growth for black bears, the removal of females coupled with an apparent lack of recruitment of females is concerning (Jonkel and Cowen 1971, Beecham 1980, Elowe and Dodge 1989, Powell et al. 1997, Oli and Dobson 2003, Wildt et al. 2003). Currently, bear hunting in the CGP occurs in mid-December, but moving the hunt to mid-January could continue to decrease the chance of female harvest. Gray (2015) noted that mean den entrance for females was January 7. By delaying the hunt until mid-January, managers could capitalize on female denning behavior, particularly decreased movement, to decrease female harvest rates.

We recommend that a Population Viability Analysis (PVA) be conducted to develop a potential risk assessment and better inform DNR of potential population trends of the CGP. Bayesian statistical methods can account for survival and recruitment within the population, and can better handle multiple types of data currently available from concurrent studies focused on the CGP, including hair-snare, live-capture, and denning data.

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