ABSTRACT

LANGER, TIMOTHY JOSEPH. Population estimates with age and genetic structure of a harvested bear population in eastern North Carolina. (Under the direction of Phillip David Doerr.)

Noninvasive genetic sampling (NGS) is appealing because it facilitates the use of more robust, capture-recapture models to estimate population size. NGS is expensive, however, and current sub-sampling approaches, though made *a priori*, are made with incomplete knowledge of the ramifications. I compared model selection and population estimates from all hair samples to those from subsets of samples chosen by simulating 4 published sub-sampling approaches. I used 4 weeks of samples collected from black bears (*Ursus americanus*) at scented DNA hair traps during Spring 2003 and again during Spring 2004 in Hyde County, North Carolina. I found that follicle filters deleted individuals from the data set without altering sex ratio, but random sub-sampling both deleted capture histories and altered the sex ratio. Collectively, these decisions biased population estimates low and produced inconsistent model selection among 10 replications.

I also conducted a 13-week study in Spring/Summer 2004 to investigate effects of using food and scent to lure bears to DNA hair traps. Food and scent collected twice as many hair samples as just scent, but produced similar estimates. I do not recommend using follicle filters or sub-sampling; my data suggest they may reduce NGS to an expensive population index. Instead, I recommend using only scent to lure bears, identifying all samples for gender, and genotyping just female samples. This approach estimates the female population size and, combined with ages from trapped bears and ages with fecundity data from hunter harvested bears, allows estimation of reproductive rate, which are especially valuable for population monitoring.

Model M_o fit females best and model M_b fit males best for both 2003 and 2004 and produced population estimates of 223 females and 160 males. Using reproductive tract data from hunter harvested bears and Spring estimates of breeding-age females, I estimated yearly cub production as 97 cubs of each sex for a total population estimate of 577 bears in our 404.3 mi^2 (1,047.2 km^2) study area. My study area has averaged about 120 hunter harvested bears the past 15 years. Because I estimated the net reproductive rate was 1.0, the maximum sustainable yield appeared to be 20.7 %.

POPULATION ESTIMATES WITH AGE AND GENETIC STRUCTURE OF A HARVESTED BEAR POPULATION IN EASTERN NORTH CAROLINA

by

TIMOTHY JOSEPH LANGER

A dissertation submitted to the Graduate Faculty of
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in partial fulfillment of the
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APPROVED BY:

KEN POLLOCK	**BRUCE WEIR**
Chair of Advisory Committee **PHIL DOERR**	**DAVID COBB**

DEDICATION

To my beautiful wife, Karma, who sacrificed so much for me to accomplish this degree. When I needed help both in the field and in the lab, re-assurance, patience, understanding, support… you gave all willingly and unconditionally. You are such a special person and I love you so very much! Thank you!

BIOGRAPHY

Timothy Joseph Langer was born April 2, 1971, to Patricia Kay and Henry Joseph Langer in St. Paul, Minnesota. Tim grew up in Edina, MN with his younger siblings: Sarah and Phillip. Tim graduated from Edina High School in 1989, earned a B.A. in Biology from Carleton College in 1993, and earned a M.S. in Fisheries and Wildlife Sciences from North Carolina State University in 1999. Sarah earned a MBA and currently lives in Japan with her husband, Atsushi, while Phillip is an orthopedic surgeon living in Providence, Massachusetts. In Minnesota Tim's mom teaches piano as a nationally certified teacher of music and Tim's dad is a certified fraud examiner and forensic accountant.

Tim marred Karma Kay Magnuson on May 2, 1998. They celebrated their 8th wedding anniversary in 2006 and are happily anticipating the birth of their first child in November. Karma has taught in Raleigh for 9 years and is currently teaching 6th grade science at Magellan Charter School. Karma's younger brother, Seth, lives in Gilroy, California where they grew up and runs facilities maintenance at Bonfante Gardens Theme Park. Karma's parents, Mary and Steve, currently live in Florida and are enjoying semi-retirement. When they are not driving around the country, Steve is breeding radishes and building an airplane from scratch, while Mary enjoys sewing, shelling, and singing.

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LIST OF NOMENCLATURE

Aldrich foot snare: A physically restraining trap that is designed to catch and hold a bear to a tree by use of a cable and throwing arm.

Allele: A genetic variant at a locus.

Capture history: A series of 1s and 0s for every bear in the dataset, which denotes whether an individual was (a 1) or was not (a 0) sampled during each session of a sampling period.

Closed population: Refers to an interval of time during which it is assumed that there is no immigration, emigration, births, or deaths of individuals.

Culvert trap: A physically restraining trap that catches a bear when it walks into a modified culvert, pulls a lever baited with food, and the door at the other end falls shut.

DNA hair traps: Are corrals of double-stranded barbed wire stapled16 to 20 inches (40.6 to 50.8 cm) above the ground and around trees to encircle an area 6-10 meters across the polygon. They are used to collect hair samples from bears non-invasively, i.e. without physically restraining them.

Electrophoresis: A methods for separating proteins or DNA fragments in a gel according to their charge, shape, and/or size.

Expected heterozygosity: The heterozygosity expected if a population is in Hardy-Weinberg equilibrium.

Genetic drift: Changes in the genetic composition of a population due to random sampling in small populations.

Genotype: The unique set of alleles at each loci that identify a particular individual.

Genotyping #: A number arbitrarily assigned to a bear's unique genotype. This number differentiates the 897 different bears in this study. Note: if tattoo and genotyping # were the same it would only be coincidence.

GPS: Global positioning systems used to locate positions on Earth via information from satellites. Ideal satellite geometry for positional accuracy would be evenly spaced satellites around the position in a plane 45 degree above the horizon.

Hardy-Weinberg Equilibrium: The equilibrium genotype frequencies achieved in a random mating population with no strong forces from mutation, selection, migration.

LIST OF NOMENCLATURE (cont.)

Heterogeneity: Variation in capture probabilities between individuals due to age, gender, or other inherent differences, excluding temporal variation and behavioral response associated with initial capture.

Heterozygosity: Number of heterozygous individuals at a locus divided by number of individuals.

Heterozygote: An individual with two different alleles at a locus.

Homozygosity: Number of homozygous individuals at a locus divided by number of individuals.

Homozygote: An individual with two copies of the same allele at a locus.

Locus: A particular section of DNA.

Loci: More than one locus.

Microsatellite: A locus with a tandem repeat of 1 to 5 base pairs of DNA.

NCWRC: North Carolina Wildlife Resources Commission

Noninvasive genetic sampling (NGS): Sampling a bear without catching it in a physically restraining trap, such as collecting a hair sample via a hair trap.

PCR: Polymerase chain reaction is a process in which DNA is replicated.

PDOP: Precision dilution of precision value for indexing accuracy of a GPS position.

Polymorphic: The presence of several alleles at a locus.

Primer: A short nucleotide sequence that binds to DNA during the PCR process and facilitates replication of a locus.

Sampling period: A sampling period consists of consecutive sampling sessions. The sampling period commonly used in this research was five sessions, during which time the bear population was assumed to be closed. During the first session of each period, no samples were collected, the lure was placed, and the barbed wire was sterilized.

LIST OF NOMENCLATURE (cont.)

Sampling session: A unit of time during which each DNA hair trap was visited once. In 2002 the length of sampling sessions was 5 days. During 2003-2004 the sampling session was 7 days long, since the number of corrals increased from 85 to 204 when the study area increased.

Tattoo #: A three-digit number that was tattooed to an inside upper lip of bears that were captured in physically restraining traps, i.e. Aldrich foot snares or culvert traps. The first of 74 tattooed bears was given # 701. Note: if the tattoo and genotyping # were the same it would only be coincidence.

Trap response: Variation in capture probabilities between individuals due to behavioral response associated with initial capture.

PREFACE

My investigations of black bears in eastern North Carolina began with the goals of determining if population size could be estimated using genetic markers and then to apply this knowledge to bear management. Black bears have for generations been extremely popular game for hunters and more recently with wildlife watchers in coastal North Carolina. In addition, bear numbers are subject to numerous environmental and anthropogenic pressures that impact the landscapes they occupy. Humans in this area intentionally or unintentionally impact bears in many ways, sometimes by direct feeding or baiting, or by manipulating crop production. My educational and research goals were explore these relationships. Thus, 5 years ago I began a journey of exploration that would inform me scientifically but which would also teach much about people and landscapes.

Scientific discovery often leads to more questions than answers, though it begins with results and untested questions of past research: a thorough literature review leads to the design and implementation of an experiment to test hypotheses. We are conservative by choice, requiring sufficient evidence to reject the possibility that what we observed in our experiment occurred due to chance alone. Acknowledging bias and sources of error, we strive objectively to advance knowledge in a particular field, even though we cannot prove, only support, the predictions of our hypothesis testing.

If experiments cannot prove results, what is scientific truth? Especially for wildlife studies in field settings where few variables can be controlled, “truth” seems exceptionally difficult to define. Is truth a defensible description of the way something works in nature, or a description that can be supported by numerous citations? The prevailing view may be wrong. I have often heard professors and wildlife professionals lament how often poor

research gets published. Given the concise nature of scientific writing, I wonder how well the limitations of other studies are communicated, considered, and understood. We have all been taught theoretically that decisions on how to interpret data may be appropriate for one application, but inappropriate for another. We must be careful and thoughtful when we dive into the literature and look for papers to corroborate an approach, trusting their "truths".

Primary literature provided me with a basic understanding of bear (*Ursus spp.*) monitoring programs. Bear populations have traditionally been monitored via indices, such as hanging sardine cans every half mile along trails and returning 5 days later to count bear visits. However, there is not a demonstrated relationship between the number of bait stations visited by bears and size of the bear population (i.e. the index lacks validation). Mammal populations are traditionally estimated by catching individuals in physically restraining traps, releasing those individuals with a mark, and then re-sampling. This approach has not worked for bears, however, because too few marked (previously caught) individuals are re-caught and the resulting population estimate is erroneously high. Presumably the few re-captures are due to "trap shyness", or avoidance of traps after initial capture.

Previously captured, "trap shy" bears may return to a trap site, but avoid being caught again. Could bears be re-captured another way, without having to be restrained physically in a trap? If bears were fitted with ear streamers when they were trapped the first time, cameras instead of traps could potentially capture return visits to a trap site. The NCWRC tried this approach prior to funding this study. Statistically speaking, while the first time a bear is caught it is identifiable individually, a picture of a bear with ear streamers would not identify it individually, but only as one of the group that was trapped. Without individual identification, capture rates and statistical results are imprecise (Seber 1982). In addition,

unmarked individuals are not marked during the camera re-sight period (White 1996). Furthermore, identifying streamers are temporary, subject to loss at an unknown rate, and photographs of black bears marked with ear streamers are often inconclusive (Minta and Mangel 1989) (M. Jones, NCWRC, personal communication). For population estimation, remote cameras can be used more effectively for species with naturally identifiable characteristics, such as the striping patterns of tigers (*Panthera tigris*) or propeller scars of manatees (*Trichechus manatus*) (Karanth and Nichols 1998).

Noninvasive genetic sampling (NGS), a technique that uses DNA to mark and re-capture individual animals with less trap shyness, burst onto the wildlife management scene in the mid-1990s. This promising method was used to assess grizzly bear (*Ursus arctos*) population status on a large scale in western North America. Instead of using physically restraining traps, bears were sampled via barbed wire at DNA hair traps. Using DNA identification, researchers were able to provide minimum population sizes for grizzly bear populations, as well as assess genetic isolation necessary to address conservation concerns. Because by definition it should not produce a trap response, non-invasive sampling was also attractive as an approach because many more bears throughout a much larger study area could be sampled than if physically restraining traps had been used.

Black bear (*Ursus americanus*) managers have also been intrigued by the potential of non-invasive genetic sampling and DNA hair sampling studies have become common. I wonder, though, if we are using this new technique appropriately. Because the grizzly bear is endangered, those projects often have large budgets to spend on hair analysis. Black bear researchers using food as a lure may be exacerbating their need to sub-sample by collecting unnecessary samples. They may also be jeopardizing the ability of modeling programs to fit

their data by introducing a trap happy response for bears that visit a DNA hair trap first and receive a food reward, while the other bears that visit receive no food reward.

In Chapter 1, I investigated the effects of 4 follicle filter and sub-sampling protocols on population estimates and genetic tests using NGS via DNA hair traps. If NGS is to be widely applied, cost savings from analyzing a portion of samples is necessary, but the impacts must be minimized and understood. Otherwise, the validity of results and the management decisions based upon them are questionable. Caution is required in the application of all new tools in conservation. The best science dictates we employ skeptical approaches that avoid the temptation of uncritical bandwagon biology.

In Chapter 2, I evaluated complementary aspects of sampling via NGS, hunter harvests, and traditional trapping. While NGS has many advantages, age determination requires a tooth, commonly collected via trapping or after a bear has been hunter harvested or otherwise killed. Density estimates from NGS require home range estimates while hair samples were collected. Besides monitoring fine-scale movement patterns of bears, radio-telemetry collars also provided critical information, such as whether the population was closed during sampling. Integrating all available monitoring data is important for improving bear management.

Chapter 3 is a testament to the hundreds of supporters that helped in myriad ways and made this research project their own. Specifically, I commented on the benefits of public involvement in scientific research and the limitations of the traditional approach to scientific research. I argued that the real scientific “truth” is not whether you can get your research published, but if you can improve others’ values of wildlife and wild places through your research. While these goals complement one another, my hope is more scientists would work

as hard to facilitate public involvement in their research as they do to publish it. We, as scientists, may gain strong statistical support for hypotheses, but I believe gaining public support for wildlife and wild places is far more significant.

Chapters 4 and 5 are comments from the field for improving bear monitoring techniques. First, I discuss the advantages of using culvert traps to trap black bears over Aldrich foot snares. Then I examine fix rates and accuracy of GPS collar locations from a simulated performance study while collars were placed on sticks in habitats with a range of canopy openness.

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CHAPTER 1

EFFECTS OF FOLLICLE FILTERS AND SUB-SAMPLING ON POPULATION ESTIMATES FROM NONINVASIVE DNA SAMPLING

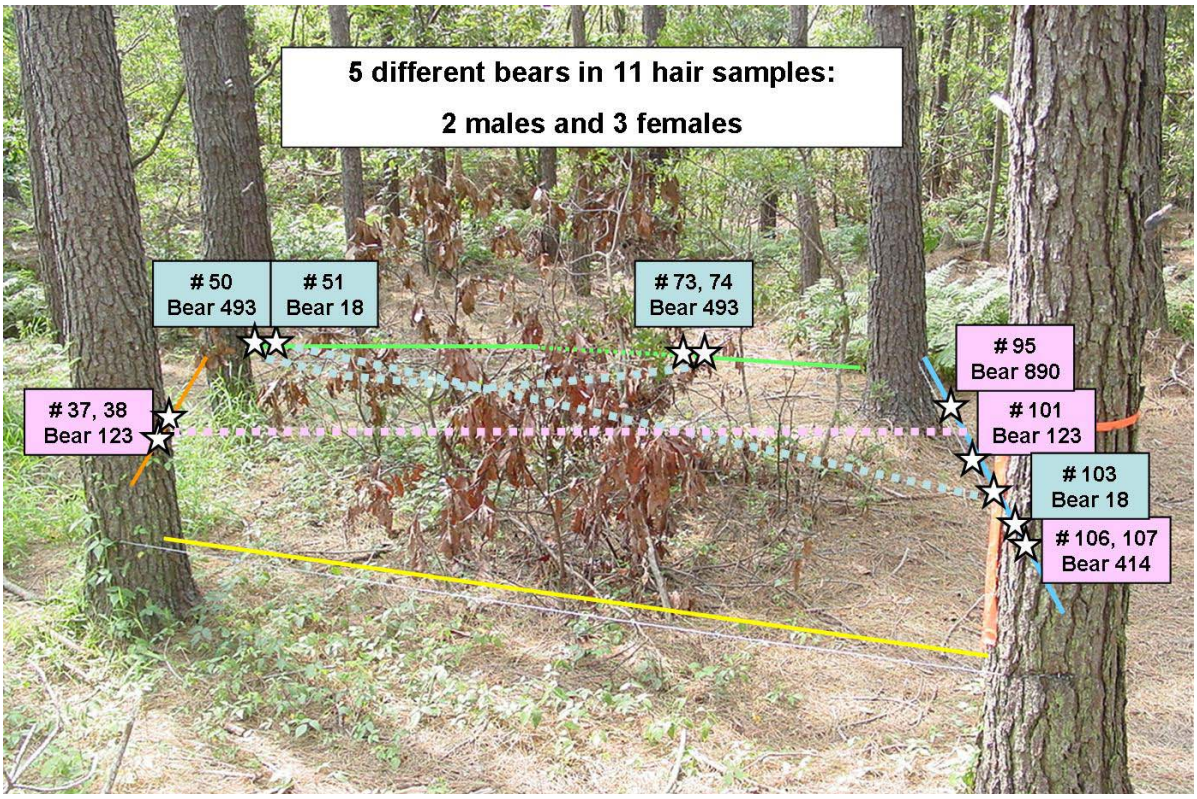

Figure 1.1. This DNA hair trap, baited with 1.5 ounces (42.6 ml) of scent, collected 11 hair samples from 5 bears during a 7-day sampling period in Spring 2004 in Hyde County, NC.

ABSTRACT

Noninvasive genetic sampling (NGS) appeals to researchers because NGS can overcome limitations of physically restraining traps and facilitate the use of more robust, capture-recapture models to estimate population size. Though made *a priori*, current sub-sampling approaches of researchers using NGS are made with incomplete knowledge of the ramifications on population estimates. We compared model selection and population estimates when using all hair samples to those from subsets of samples chosen by simulating 4 published sub-sampling approaches. We used 4 weeks of samples collected from black bears (*Ursus americanus*) at scented DNA hair traps during Spring 2003 and again during Spring 2004 in Hyde County, North Carolina. We found that follicle filters deleted individuals from the data set without altering sex ratio, but random sub-sampling both deleted capture histories and altered the sex ratio. Collectively, these decisions biased population estimates low and produced inconsistent model selection among 10 replications. We also conducted a 13-week study in Spring/Summer 2004 to investigate the effect of using food with scent to lure bears to DNA hair traps. Using food with scent averaged collecting twice as many hair samples as just scent, but produced similar estimates. To minimize error and bias in population estimates derived from NGS, we do not recommend using any follicle filter or sub-sampling. Instead, we recommend using only scent to lure bears, identifying all samples for gender, and then genotyping just the female samples. This approach specifically estimates the female population size and, when combined with age and fecundity data from hunter harvested bears, allows estimation of net reproductive rate, both important for population monitoring.

Key words: Noninvasive genetic sampling, follicle filters, sub-sampling, population estimates, capture probability, heterogeneity, precision, bias, bears, *Ursus* spp.

INTRODUCTION

Repeated captures of large mammals are a foundation of many studies conducted to estimate population size and enhance knowledge of these animals to produce scientifically based management (Cronin et al. 2005, Mowat et al. 2005, Taberlet et al. 1997). If initial capture probabilities are low and a trap shy response results in even lower re-capture probabilities, using physically restraining traps to sample individuals will often produce erroneously high population estimates in mark-recapture studies (Schwarz and Seber 1999, Seber 1982, 1986, 1992). Consequently, wildlife researchers often opted to use indices of relative abundance for population monitoring of black bears (*Ursus americanus*) (Abler 1988, Johnson 1992, Miller et al. 1994, Powell et al. 1996). Surveys based on indices are frequently less expensive and require less effort than those based on mark-recapture studies (Williams et al. 2002c). However, Nichols and Pollock (1983) used simulations and statistical theory to demonstrate the limitations of inferences from indices compared to capture-recapture models.

The use of NGS to monitor bear populations has grown rapidly in the past ten years (Boulanger et al. 2004a, Mowat et al. 2005, Woods et al. 1999). NGS appeals to researchers because NGS can overcome limitations of physically restraining traps and facilitate the use of capture-recapture models to estimate population size. Because samples are collected without the negative experiences produced from drugging and handling, NGS reduces the potential for a trap shy response. In addition, DNA hair traps of NGS can sample many

individuals at once, while a physically restraining trap can only catch one. DNA hair traps do not require daily monitoring like physically restraining traps, so researchers can study a much larger area and with greater sampling intensity. All of these reasons suggest a larger sample of individuals, sampled at a higher rate, can be collected using NGS than with physically restraining traps. If used properly, NGS can produce reliable population estimates of bear populations (see Chapter 2).

Applying NGS has presented new challenges, however. Only 1 sample per individual per sampling period is necessary for a complete capture history to calculate population estimates. All additional samples are extraneous and increase time, cost, and possible error. DNA hair traps are checked periodically and an individual animal may visit 1 or more DNA hair traps more than once and leave multiple samples within a sampling period. Population estimates from data sets with capture histories from more individuals and with more re-captures are more reliable than smaller data sets, but there are trade-offs between maximizing capture information and cost. Depending on the number of samples and research objectives, genotyping costs average $35 to $50 per sample (in 2006). Research budgets are often not large enough to analyze all hair samples and researchers have used different strategies to choose samples for analysis. Current sub-sampling approaches, though made *a priori*, are made with incomplete knowledge of the ramifications of sub-sampling on capture histories of individuals. By comparing results when using all and subsets of samples, we investigated the impact of sub-sampling on population estimates.

Limitations of statistical models: While capture-recapture, statistical analysis programs like MARK and CAPTURE can adjust for unequal capture probabilities between individuals with a suite of models that include heterogeneity and trap response, they can not

account for individuals with no chance of capture (Pollock et al. 1990). Individuals in the population with zero chance of capture cause a serious negative bias. DNA hair traps are typically placed at a density that all individuals should have a non-zero chance of capture. However, sub-sampling may reduce the capture probabilities to the point where effectively they have zero chance of capture. For instance, if 2 bears were only sampled once and both were sampled at the same corral during the same sampling period, if 1 sample or less per corral was chosen for analysis, at least 1 of those bears would not have a capture event.

Furthermore, researchers may increase the heterogeneity between individuals via study design. Some black bear researchers have assumed that capture rates would be too low if food was not used to lure bears to DNA hair traps in addition to scent (Boersen et al. 2003, Dobey et al. 2005, Thompson 2003, Tredick 2005). Using food as a lure may create 2 problems. First, the number of hair samples collected may increase, which will exacerbate the fiscal necessity for sub-sampling. Second, using food might also make the re-capture rate for individuals who visit the trap first different than the re-capture rate for subsequent individuals, because the first bear will get a food reward and associate the scent with a reward, whereas subsequent bears will not make that association. This potential trap response and difference in re-capture rates can not be accounted for without knowing which bears got the food reward, which is not generally possible, and might therefore increase heterogeneity.

If heterogeneity exists between individuals, sub-sampling may create a bias. Anderson (2001) proposed that research and management biologists may not realize how untrustworthy inferences from non-probabilistic samples can be. First, there is no valid basis for an inductive inference from the sample data to the population of interest (Anderson 2001).

Second, there is no valid basis to assess precision of estimated population parameters (Anderson 2001). The result could be "biased but apparently precise" estimates of population size and variance (White et al. 1982) that are highly undesirable if the estimates are to be used for management decisions (Boulanger et al. 2004b).

We evaluated the effects of different sub-sampling approaches on population estimates when using NGS via samples from DNA hair traps. We also compared the effectiveness of scented DNA hair traps baited with and without food when sampling black bears. To accomplish this, we compared model selection and population estimates when using all hair samples to those from subsets of samples chosen by simulating 4 sub-sampling approaches reported in the literature. We concluded by recommending how best to reduce the number of analyzed hair samples while maintaining the validity of population estimates.

METHODS

To collect the DNA samples that would allow us to estimate the black bear population via mark-recapture in our Hyde County study area, we distributed 192 hair corrals to include most occupied bear habitat (see Chapter 2 for complete description of study area). This number of corrals allowed us to locate corrals at a density of about 1 per square mile (2.6 km^2) of contiguous forest and approximate the area of a small weekly home range for black bears in eastern North Carolina (Jones 1996). To test the effects of sub-sampling protocols, we used our DNA hair trap data from Spring 2003 and Spring 2004 (Figure 1.2). Reported sub-sampling approaches use 2 criteria: minimum number of DNA follicles per sample and the number of random samples chosen per corral per sampling period. We simulated the follicle filtering and sub-sampling protocols reported by 4 recent black bear studies in the

southeast (Table 1.1). For simplicity, we refer to these protocols as A-D in the text to reflect that the total number of samples analyzed decreased from A to D. Because all protocols involved choosing samples randomly after follicle filtering, we wrote a computer program in C++ language for Microsoft visual studio 6.0 (Dr. Bjarne Stroustrup, AT&T Labs, 1985) and replicated each protocol 10 times to investigate robustness. We also incrementally tested alternative levels of follicle filtering and sub-sampling for sensitivity analysis. In addition, we chose samples from corrals in a modified random manner that avoided choosing samples from adjacent barbs, if possible, because adjacent barbs samples were more likely to be from the same individual.

We evaluated population estimates and genetic results for every set of samples. Our computer program produced output files to run in Programs MARK and CAPTURE for population estimates (Rexstad and Burnham 1991, White 1996, White and Burnham 1999), as well as counted the total number of individuals and capture history events. We defined a capture event as a 1 given to a bear in its capture history if it was sampled at least once during a secondary sampling period. In Program Mark we used Akaike's information criterion (AICc), corrected for small sample size, to evaluate trap response (M_b), heterogeneity (M_h), and time (M_t) models (Akaike 1973, Burnham and Anderson 1998). Our computer program also produced output files to run in GENEPOP 3.4 to perform exact tests of Hardy-Weinberg equilibrium, test for linkage disequilibrium, and test if allelic distributions were identical between protocols and replications (Raymond and Rousset 1995, Rousset and Raymond 1997). Within each replication of a protocol, the computer program also calculated the Probability of Identity for each genotype, as refined by Waits et al. (2001), to estimate the chance of mis-identifying highly related individuals (i.e. siblings) as

one individual. Our goal was to find a follicle filter and sub-sampling approach that required analyzing as few samples as possible, but that gave results for 10 replications that were consistent with results when all hair samples were analyzed.

Because age information is not available from hair samples and we wanted to examine the ages of bears sampled in DNA hair traps, we used DNA to determine which bears we also sampled via hunter harvests or physical restraining traps and had pulled a tooth for aging. Of the 705 unique bears sampled via DNA hair traps, we obtained ages for 106 bears. Some of these known-age bears were sampled in more than 1 year via DNA hair traps, which provided 158 known-age bears when they were sampled in DNA hair traps. We used SAS for Windows (version 9.1.3, SAS Institute, Cary, N.C.) to test whether the number of follicles in a hair sample was correlated with age, gender, or number of periods a bear had been sampled via DNA hair traps.

Test of using food with scented DNA hair traps: We used 12 of the 192 DNA hair traps used for the entire study area in Spring 2004 as non-tangibly baited corrals and built 12 additional DNA hair traps spaced between those to bait tangibly (Figure 1.2). We simultaneously collected hair samples from these 2 sets of DNA hair traps every 7 days for 13 weeks from May 16 to August 15, 2004. At non-tangibly baited corrals, we alternated raspberry or meat scent for the first 8 weeks and then used peanut butter (# 2020) scent for the last 5 weeks. At tangibly baited corrals we used 5 ounces (142.1 ml) of food, consisting of 3.5 ounces (99.4 ml) of peanut butter and 1.5 ounces (42.6 ml) of honey in a paper cup hung between trees 5 feet (1.5 m) above the ground in the middle of the corral. In addition, we sprayed tangibly baited corrals with 1.5 ounces (42.6 ml) of peanut butter scent for the last 9 weeks.

Our 3 experimental manipulations lasted 4, 4, and 5 weeks. The last manipulation was extended to a 5th week, because after the first week of dry weather we received heavy rainfall continually. We reasoned that because the first 2 manipulations had 4 weeks of consistent (dry) weather, the last one should also be 4 weeks of consistent (wet) weather and extended that manipulation by 1 week. In addition, during these manipulations we tracked the movements of 7 bears with GPS telemetry to investigate closure and heterogeneity. The GPS collars we deployed on 4 females and 3 males during May 1–10 were programmed to attempt positions every 5 minutes from May 16 to August 9 and then fall off (see Chapter 2 for more information). We used minimum convex polygons to quantify weekly home range size because we did not want to exclude information that would show whether a bear had a non-zero chance of capture via a DNA hair trap.

RESULTS

We successfully genotyped 3,051 of 3,296 (92.6 %) hair samples with 1 or more follicles collected during 2001-2004. Samples with 3 or more follicles yielded a genotype at least 88.3 % of the time, compared to 58.7 % for 1 follicle samples and 82.0 % for 2 follicle samples. Samples with 10 follicles yielded a genotype most often at 96.1 % (Table 1.2). Once we identified all genotypes, we labeled digital photographs of DNA hair traps with barb numbers and unique bear numbers to discern patterns of hair collection (Figure 1.1). There were 585 sequences of up to 9 consecutive barbs that had hair. We analyzed how often hair samples collected from adjacent barbs were the same bear; 83.8 % of the time the same bear accounted for both samples when only 2 adjacent barbs had hair samples. Within all consecutive barb sequences with hair samples, on average 80.7 % of the time adjacent

barbs were identified as the same bear (Table 1.3).

We sampled 705 bears via DNA hair traps during a total of 1,564 secondary sampling periods: 316 females during 745 secondary sampling periods (average 2.4, median 1.0, standard deviation 2.7, maximum 18) and 389 males during 819 secondary sampling periods (average 2.1, median 1.0, standard deviation 2.0, maximum 13). The significance of these results is that there was heterogeneity in the number of periods individual bears were sampled via DNA hair traps, which means that sub-sampling could create a negative bias by reducing capture events in an individual's capture history. Most males and females were only sampled during one secondary period, meaning that if a sub-sampling protocol only chooses 1 sample per corral per period, and 2 bears were only sampled at the same corral during the same period, then at least 1 of them would be eliminated from the data set. If a third bear was present and its sample was randomly chosen, both of the other bears would be eliminated from the data set.

We also investigated whether follicle filters were biased towards age or gender. Mean follicles per sample was not correlated with age ($p = 0.6857$), gender ($p = 0.9789$), or age*gender ($p = 0.9809$). Because a follicle filter excludes all samples with less than a certain number of follicles, we conducted additional analyses to determine whether an individual would remain in the dataset using the highest number of follicles for all samples from a bear during a sampling period. For all bears, that highest number was independent of age ($p = 0.6737$), gender ($p = 0.8572$), or age*gender ($p = 0.7244$). For bears with more than 1 capture event, we investigated that highest number for the first and last sampling period. The mean number for the first period was 8.0 follicles (standard deviation 2.4, minimum 1, maximum 10) and the mean for the last period was 7.3 follicles (standard deviation 3.1,

minimum 1, maximum 10). The last period had a significantly lower mean (t-test, p = 0.0016). However, age (p = 0.8196), gender (p = 0.9741), and age*gender (p = 0.0690) were not correlated (even though the age*gender interaction was close to our alpha level of 0.05, few individuals in older age classes biased the result). These results suggest bears of all ages and both sexes were equally likely to be affected by sub-sampling protocols. Furthermore, if an individual animal was sampled during more than 1 period, sub-sampling protocols could remove a capture event from an individual's capture history as likely in the last sampling period as the first.

We genotyped 440 of 584 (75.3 %) samples from Spring 2003 and 593 of 710 (83.5 %) samples from Spring 2004 collected during 4 secondary sampling periods each year using scent to attract bears to DNA hair traps. In 2003, 262 samples (59.5 %) were males, as compared to 280 samples (47.2 %) in 2004. We identified a total of 193 bears in 2003 (114 males, 59.1 %) sampled with 223 capture events and 227 bears in 2004 (119 males, 52.4 %) sampled with 288 capture events.

Using all samples, we estimated males and females separately for each year. The M_o model was chosen best for females in both years and estimated 239 females (S.E. 58.6) in 2003 and 207 (S.E. 27.4) in 2004. Similarly, the M_b model was chosen best for males in both years and estimated 164 (S.E. 26.8) in 2003 and 156 (S.E. 18.3) in 2004 (See Chapter 2 for more information). We ran the simulations of protocols A-D for both data sets, but only present 2004 results here because they were consistent with 2003 and had better precision from higher capture rates due to less rainfall which flooded the study area in 2003. In addition, because we could only assess differences in results using samples that were genotyped, only genotyped samples were available for selection by different protocols. For

example, of the 338 samples chosen by Thompson et al. (2005) for analysis, 52 (15.4 %) could not be genotyped, which is consistent with our failure rate, but which provides less information than if all 338 samples had been successfully genotyped. Our results are also conservative because we had the computer program select slightly more samples than researchers indicated attempting for 3 protocols (Table 1.1).

The first step of protocols A-D involved applying a follicle filter. This step could not be replicated, as it involved discarding all samples that had less than a certain number of follicles, but using all samples that remained. Population estimates for females, using model M_o, decreased from 207 (S.E. 27.4) with no follicle filter to 149 (S.E. 27.9) with a 10 only follicle filter. Similarly, population estimates for males, using model M_b, decreased from 156 (S.E. 18.3) with no follicle filter to 118 (S.E. 20.3) with a 10 only follicle filter (Table 1.4).

The second step of protocols A-D involved randomly choosing a certain number of samples and thus we did 10 replications. Protocol A used a 5-10 follicle filter, followed by randomly choosing 2 samples per corral per sampling period. On average, protocol A deleted 30 % of individuals (Figure 1.3) and 35 % of total capture events (Figure 1.4), when compared to using no follicle filter and all samples. Even if all samples were chosen after using a 5-10 follicle filter, 19 % of individuals (Figure 1.3) and 21 % of capture events (Figure 1.4) would still have been deleted. The other protocols progressively analyzed fewer samples and deleted more information, capped by protocol "D" that averaged an 85 % loss of individuals and an 88 % loss in total capture events.

The effect on population estimates of individual and capture event losses varied among replications. For example, of the 119 males sampled in Spring 2004, a 5-10 follicle filter

removed 22 of them from the data set completely and reduced capture events for 6 remaining males (Figure 1.5). Randomly choosing 1 sample per corral per sampling period, and then 70 % of those samples, produced different population estimates for similar losses of individuals and capture events. One replication produced an estimate of 57 males (S.E. 6.4) when 42 maintained complete capture histories, 7 had reduced capture events, and 70 were eliminated. Another replication produced an estimate of 87 males (S.E. 36.2) when 37 maintained complete capture histories, 12 had reduced capture events, and 70 were eliminated. Generally speaking, pooled results for each protocol were more precise than using separate models for males and females (Table 1.5). Within the set of pooled results, though capture rates remained fairly constant, average population estimates and precision decreased, while coefficients of variation increased, as fewer samples were selected (protocol A (highest) to protocol D (fewest)). Model selection also was less consistent as sub-sampling increased.

Using an alpha level of 0.05 and after Bonferroni correction, no genetic tests on the complete data set, or data sets from the replications of simulated protocols, were significant. All data sets were in Hardy-Weinberg equilibrium, without linkage disequilibrium, and had similar allelic distributions. In addition, genotypes within each data set had $P.I._{sibs}$ (Probability of Identity for sibling pairs) values in the recommended range (less than 0.0001) for population estimation. These results suggested that follicle filters and sub-sampling did not affect genetic tests, the appropriateness of genetic assumptions, or the ability to identify individuals with the same set of micro-satellites.

Test of using food with scented DNA hair traps: In the 13-week study investigating results from 2 sets of DNA hair traps with different lures, we collected a total of 1,243 hair samples and successfully genotyped 982 (79.0 %) of them. We used all the data, without any

sub-sampling protocols to compare differences. A total of 143 different bears (73 males, 70 females) were sampled: 100 bears (47 males, 53 females) at non-tangible corrals and 108 bears (56 males, 52 females) at tangible corrals. Tangible corrals sampled more bears on average per week (1.8 vs. 1.4), represented by higher numbers of bears per week and fewer weeks with no bear visits (Table 1.6). Tangible corrals also averaged twice as many hair samples when they were baited with scent and food, as compared to non-tangible corrals baited with just scent: 34.8 to 16.8 (4 weeks of dry weather) and 13.8 to 8.2 (5 weeks of wet weather). If tangible corrals just had food without scent, however, they had half the number of samples as non-tangible corrals baited with scent: 10.1 to 19.8 (4 weeks of dry weather).

We used the M_o model to compare results because Program MARK generally fit it best, except when we analyzed tangible corrals for 8 weeks and the lure changed after 4 weeks (in that case, we used the 5 parameter M_{tb} model). Non-tangible corrals estimated 52 males (S.E. 16.4) for weeks 1-4 and 56 males (S.E. 7.2) for weeks 1-8. Tangible corrals estimated 54 males (S.E. 5.7) for weeks 5-8 and 54 males (S.E. 5.6) for weeks 1-8. Three hurricanes accounted for excessive rainfall during weeks 10-13, including 13 inches (33.0 cm) of rain in 3 days. Estimates dropped to 17 males (S.E. 6.9) for both tangible and non-tangible corrals. Female estimates were less affected. Non-tangible corrals estimated 53 females (S.E. 4.2) for weeks 1-8 and 46 females (S.E. 10.6) for weeks 10-13. Tangible corrals estimated 45 females (S.E. 3.4) for weeks 1-8 and 44 females (S.E. 4.1) for weeks 10-13 (Table 1.7).

Six bears (2 males, 4 females) in this area wore GPS collars during the first 12 weeks of this study, but 1 male dropped his collar after 8 weeks. All bears stayed within the perimeter of the tangible/non-tangible study area for the entire time, except 1 male that

temporarily emigrated for 1 week. There was heterogeneity in movements between sexes. Males averaged 2.7 (S.E. 0.4) non-tangible and 3.2 (S.E. 0.4) tangible corrals per weekly home ranges that averaged 18.8 km^2 (S.E. 2.8) using a minimum convex polygon estimator (Figure 1.6). Females averaged 1.4 (S.E. 0.1) non-tangible and 1.1 (S.E. 0.1) tangible corrals per weekly home ranges that averaged 5.6 km^2 (S.E. 0.6) using a minimum convex polygon estimator (Mohr 1947).

DISCUSSION

The simulated sub-sampling protocols produced different results from one another, different results among replications of a given protocol, and biased results when compared to those from using all hair samples. However, because there was heterogeneity between individual animals, capture probabilities remained fairly constant as the number of samples was reduced and this concealed bias. For example, comparing no follicle filter with a 5-10 follicle filter, the capture rate for females was slightly lower (0.17 vs. 0.15), but with males it was actually higher (0.30 vs. 0.35) and the population estimate had better precision (11.3 vs. 18.3) even though a total of 19 % of individuals (Figure 1.3) and 21 % of capture events (Figure 1.4) had been deleted from the data set. Furthermore, the female estimate dropped from 183 to 149 between a 5-10 and 10 only follicle filter with the same capture rate and similar precision (Table 1.4). Significant information was contained in samples with 1-3 follicles, as demonstrated by deletions of 14 % of individuals and 16 % of capture history events when they were filtered (Figures 1.3, 1.4). For this reason, even though those samples are more likely to produce erroneous genotypes (Waits 2004) and are more expensive to analyze because of the low levels of DNA present (Waits and Paetkau 2005), we recommend

not using a follicle filter.

Follicle filters and random sub-sampling affected results differently. The sex ratio of genotypes remaining in the data set after follicle filtering remained constant, which was consistent with our result that number of follicles in a sample was not correlated with gender. Without filtering, 55.2 % of bears in the data set were males. With a 5-10 follicle filter, 55.5 % of bears in the data set were males, and with a 10 only follicle filter, 56.7 % of bears in the data set were males. However, random sub-sampling not only further decreased the number of individuals left in the data set, it often changed the sex ratio significantly, even among replications of the same protocol (Table 1.5). We ran 10 replications of each simulated protocol and the coefficient of variation increased as the number of samples decreased. Researchers that use sub-sampling protocols have only have 1 replication, which means that simply due to chance they could get good (estimated) precision for a model within any protocol. This fact leads to inconsistent model selection for results from different study areas in the same year or the same study area in multiple years, as demonstrated by Tredick (2005) who averaged different "best" models chosen by Program MARK for different study areas and the same study area in different years.

Tredick (2005) analyzed the most samples (56 %, protocol A) and even analyzed gender (protocols B-D did not), but ended up pooling genders anyway to improve precision. Pooling genders introduced a negative bias for all 4 protocols, however. For example, the average female (190) and male (107) estimates totaled 297, compared to 341 for the average pooled estimate (Protocol A, Table 1.5). Average precision was also less for the pooled estimate (6.5) than for females (21.9) and males (13.7) separately. It is important to note, however, that with pooled estimates, the "best" model often changed between replications.

Because our results suggested that males and females were best fit by different models, it makes sense that random sub-sampling would produce data sets with different sex ratios that would be fit better by different models.

Pooling genders also hurts inferences, such as the number of females in the population estimate. Obviously, knowing this number is important for monitoring. In addition, Boersen et al. (2003), Dobey et al. (2005), Thompson et al. (2005), and Tredick (2005) all reported estimates from Program MARK as the population size and were not aware of individuals that may have been excluded from their models, including individuals that were not sampled (such as cubs). Because we had a female population estimate, we could use other information to estimate the number of cubs in the population and add that number to the estimated population size (see Chapter 2). Program MARK can also not account for individuals that were sampled (but eliminated by protocol decisions). When genders were estimated separately, there was more information to assess the accuracy of estimates. As we discovered, severely biased estimates may still have good precision.

Even if follicle filters did not remove any bears, sub-sampling would have, given the density of DNA hair traps. Randomly choosing 1 sample per corral per weekly sampling period implies that only 1 bear would visit a DNA hair trap each week. However, black bear home ranges overlap and we sampled as many as 6 bears at a non-tangible corral and 9 bears at a tangible corral in a week. Protocols B-D chose less than 1 sample per corral per weekly sampling period. For 2003 and 2004, our collared female bears had 1.6 corrals in their weekly home ranges, compared to 4.4 for males (see Chapter 2). Even if bears were sampled at more than 1 corral during a sampling period, the number of bears would have to be extremely low not to introduce heterogeneity.

We recommend not using food as a lure to hair traps. Capture rates did not change over time significantly for non-tangible corrals, suggesting that bears did not become indifferent to the scent lures either during or between study years. Also, using only a small amount of food, we doubled the number of samples. Given closure is assumed for modeling, an alternative approach would be to use non-tangible corrals and double the study area size to use natural barriers to movement, if possible. Data from tangible corrals produced similar estimates as those from non-tangible corrals. Precision from non-tangible corral data was better sometimes, but that could possibly be explained by heterogeneity in the marked population that could not be modeled since only the first bear to visit a corral each week was rewarded. Alternatively, there may have been an interaction of the lures for the 2 sampling methods that produced trap responses for an individual based on which type DNA hair trap they visited first. We plan to explore these possibilities in the future. One positive of tangible corrals was that they had 10.9 % more weekly periods when at least 1 bear was sampled. We attributed this to the fact that tangible food might keep its attractiveness longer, especially after rain, than a liquid scent.

Filtering and sub-sampling decisions can also affect the appropriateness of genetic estimators. For example, because Woods et al. (1999) asserted that the probability of identity for siblings ($P.I._{sibs}$) is the most conservative estimate of mistaking two closely related individuals for the same individual, Boersen et al. (2003), Dobey et al. (2005), Thompson et al. (2005), and Tredick (2005) all calculated $P.I._{sibs}$. However, $P.I._{sibs}$ is the most conservative estimator only if you suspect a high probability of sibling pairs in your dataset (Woods et al. 1999). Woods et al. (1999) analyzed all samples with visible follicles (1,836 of 2,200 total samples, 83.5%) and these 4 researchers (protocols A-D) analyzed 56 % down to 6 % of their

samples. There were also other differences in the studies. Woods et al. (1999) studied both black and grizzly bears. Grizzly bear offspring stay with their mother for 2-3 years, compared to 1 year for black bears, so there are an extra 1-2 years to sample sibling pairs together, before one or all possibly disperse out of the study area (Nowak 1999). Also, we did not sample black bear cubs in our DNA hair traps until Fall and even then not often. Furthermore, the minimum number of samples for a sibling pair would be 2 per corral per sampling period. Protocols B-D analyzed less than 1 sample per corral per sampling period and sampling a sibling pair at a given corral in a particular sampling period would seem to be the most realistic scenario. In summary, as a result of follicle filters and sub-sampling, sibling pairs in the analyzed dataset are much less certain and choosing $P.I._{sibs}$ as the most conservative estimator may be suspect.

The proper approach to ecological data is probabilistic, in which subjectivity and convenience sampling are replaced by some type of random selection (Anderson 2001). However, we believe our data suggest follicle filtering and random sub-sampling of NGS hair samples do not achieve biological randomness. In fact, the expense of analyzing all samples has created several sets of haphazard criteria which reduce samples and costs but which lack rigor. Pollock et al. (1990) argued that estimators are preferable to indices because indices have more bias, confound population size and capture probability, and make spatial and temporal trends likely subject to bias. Our data suggest follicle filters and sub-sampling may reduce NGS to an expensive index. Effective wildlife management can only be enhanced by precise population estimates if they are not biased (Mace and Waller 1997b, Miller et al. 1997). Currently, researchers use different sub-sampling protocols but compare

density estimates for inferences. We believe a standardized approach to selecting hair samples collected via NGS is preferable.

RECOMMENDATIONS

To minimize error and bias in population estimates derived from NGS, we do not recommend using any follicle filter or sub-sampling. Instead, we propose an approach that will not necessarily cost more than the protocols we simulated, but will provide more useful, reliable, and cost effective results. We recommend using only scent to lure bears to DNA hair traps, identifying all samples for gender, and then genotyping just the female samples. This approach specifically estimates the female population size and, when combined with age and fecundity data from hunter harvested bears, allows estimation of net reproductive rate, both important for population monitoring. Even without considering the bias or precision problems, protocols A-D only estimate numbers of bears, not females.

The following protocol illustrates this recommendation. By using only scent as a lure, half as many samples will be collected, compared to using food and scent, with little effect on results. Approximately 12 % of collected samples would have no follicles and be discarded when viewed under a microscope. We then suggest identifying the gender of all remaining samples and, on average, 9 % will not have enough DNA. Of those with adequate DNA, 47 % of samples will be from females. We propose completing the genotyping of all female samples. Our lab costs were such that we could identify the gender of 4 samples for the same price as completely genotyping 1 sample. Thus, our recommendations to use only scent as a lure, identify all samples for gender, and then genotype only female samples is comparable in cost to completely genotyping 25 % of samples collected when using food and

scent as a lure to DNA hair traps (the 4 protocols we simulated that did this averaged analyzing 23 % of the samples they collected: 6 %, 14 %, 17 %, and 56 %).

Our recommended approach preserves all (male) samples for possible analysis at a later date and facilitates genetic investigations using mitochondrial DNA (only in females). In addition, when samples are randomly chosen for analysis and the others discarded, it is not possible to replace samples that were attempted but not able to be genotyped, which could have contributed further to the negative bias. Furthermore, our results suggested that population estimates from 8 weeks of dry weather had good precision (Table 1.7). Three of the 4 protocols we simulated collected hair samples for more than 8 weeks, so using fewer weeks could significantly reduce samples without affecting results.

FUTURE RESEARCH

When we used our full data set to analyze the effects on genetic results of sub-sampling protocols A-D, the allele frequencies of all sub-populations were not significantly different from one another and still in Hardy-Weinberg equilibrium for all replications. If too many individuals had been randomly removed from a data set, genetic differences could have been falsely detected due to chance. Filters and sub-sampling might be analogous to genetic drift, which operates on chance, is a strong evolutionary force at low population sizes, and creates genetically distinct sub-populations. In this analogy, the population bottleneck and genetic distinctions are not real, but artifacts of decisions to reduce cost via the number of samples analyzed.

We should investigate whether the genetic results given sub-sampling protocols would have been different if our study area had been smaller. For example, Thompson et al. (2005)

used 2 study areas of 110 km^2 that were each 10 % of our study area. We could split our study area into 5 parts, replicate protocol B 10 times, and examine whether allele frequencies varied significantly from each other and from when all samples were used for the entire study area. Thompson et al. (2005) observed distinct and consistent patterns of allele occurrence between small and adjacent study areas. Biologically, we would not have expected sub-population structure, because there was not a physical barrier to movement between them and individuals were found using both areas with NGS and telemetry (Kindall 2004).

We propose collaborating with other researchers using NGS who also analyzed all samples collected from DNA hair traps. We would like to examine whether model selection in Program MARK is consistent for other bear populations, both with pooled data and each gender individually. Heterogeneity is difficult to model, but we accounted for some of it by analyzing genders individually. If other research produced similar results, then we would feel stronger about that facet of experimental design. We are also interested in replicating our simulations of sub-sampling protocols and believe that the data set of the Northern Divide Grizzly Bear (*Ursus arctos*) Project is one possibility. If population estimates from sub-sampling protocols are biased to a similar extent, we could possibly generalize a correction factor. Also, the study area for that project is so large that there may be sub-populations, which would provide the opportunity for a more robust test of how sub-sampling protocols may alter allele frequencies, because our study area did not have sub-population structure.

Table 1.1. Four protocols used by black bear researchers to reduce the number of hair samples collected via noninvasive genetic sampling to analyze for population estimates.

Protocol	Research project	Follicle filter	Random sub-sampling approach	Total samples collected	# of analyzed samples	We simulated using this random sub-sampling approach
A	Tredick (2005)	5-10	2 or more samples/corral/period	5,242	2,946 (56.2 %)	2 samples/corral/period
B	Thompson et al. (2005)	5-10	1 sample/corral/period, then 25 samples/period (which was about 65 % of those samples)	1,926	338 (17.5 %)	1 sample/corral/period, then 70 % of those samples
C	Dobey et al. (2005)	5-10	1 sample/corral/period, then 8 samples/period (which was about 45 % of those samples	1,177	168 (14.3 %)	1 sample/corral/period, then 50 % of those samples
D	Boersen et al. (2003)	Only 10	1 sample/corral/period, then 25 % of those samples	1,939	116 (6.0 %)	1 sample/corral/period, then 30 % of those samples

Table 1.2. Genotyping success rates for 3,286 hair samples grouped by number of DNA follicles.

# of DNA follicles	# of samples	# that yielded a genotype	% that yielded a genotype	# insufficient DNA	% insufficient DNA	# > 1 bear	% > 1 bear
1	75	44	58.7%	31	41.3%	0	0.0%
2	111	91	82.0%	18	16.2%	2	1.8%
3	267	242	90.6%	24	9.0%	1	0.4%
4	246	227	92.3%	13	5.3%	6	2.4%
5	257	227	88.3%	20	7.8%	10	3.9%
6	236	215	91.1%	15	6.4%	6	2.5%
7	193	175	90.7%	12	6.2%	6	3.1%
8	164	152	92.7%	4	2.4%	8	4.9%
9	106	101	95.3%	3	2.8%	2	1.9%
10	1,631	1,567	96.1%	31	1.9%	33	2.0%
Totals	3,286	3,041	92.6%	171	5.2%	74	2.2%

Table 1.3. The likelihood an adjacent barb had hair from the same bear for barb sequences of varying length, using all samples collected via DNA hair traps during 2001-2004 in Hyde County, NC.

# of consecutive barbs with hair	# of adjacent pairs for same bear		# of adjacent pairs for different bears		Total
	#	%	#	%	#
2	382	83.8 %	74	16.2 %	456
3	152	78.4 %	42	21.6 %	194
4	42	77.8 %	12	22.2 %	54
5	14	58.3 %	10	41.7 %	24
6	20	66.7 %	10	33.3 %	30
7	6	100.0 %	0	0.0 %	6
9	7	87.5 %	1	12.5 %	8
Total	623	80.7 %	149	19.3 %	772

Table 1.4. Using follicle filters to determine samples for genotyping, population estimates (N) and initial capture probabilities (p) using 2004 data, the M_o model for females, and the M_b model for males (The M_b, or trap response, model also has a capture probability (c) for previously captured individuals). Note: S.E. is the standard error.

Follicle filter	Females N (S.E.) with p (S.E.)	Males N (S.E.) with p (S.E.) and c (S.E.)
1-10	207 (27.4) with 0.17 (0.03)	156 (18.3) with 0.30 (0.06) and 0.13 (0.02)
2-10	194 (25.4) with 0.17 (0.03)	145 (15.9) with 0.32 (0.06) and 0.14 (0.02)
3-10	196 (28.2) with 0.16 (0.03)	137 (13.8) with 0.33 (0.06) and 0.13 (0.02)
4-10	184 (28.3) with 0.16 (0.03)	131 (14.7) with 0.32 (0.06) and 0.12 (0.02)
5-10	183 (30.8) with 0.15 (0.03)	118 (11.3) with 0.35 (0.06) and 0.12 (0.02)
Only 10	149 (27.9) with 0.15 (0.03)	118 (20.3) with 0.27 (0.07) and 0.09 (0.02)

Table 1.5. Using hair samples from Spring 2004, Program MARK results for pooled results using all models, for females using M_o model, and for males using M_b model, averaged over 10 replications of 4 sub-sampling protocols. (N = population estimate, C.V. = coefficient of variation, S.E. = standard error, p = initial capture rate, and c = re-capture rate).

Part a. Pooled gender results				
Protocol*	Avg. N (C.V.)	Avg. S.E. / N (C.V.)	Avg. p (C.V.)	"Best" model
A	341 (2.3)	6.5 (1.0)	0.14 (3.8)	M_b (9 times)
B	228 (5.5)	8.0 (2.4)	0.12 (6.0)	M_b and M_{bh} (4 times each)
C	171 (5.3)	9.3 (2.5)	0.11 (4.5)	M_{bh} (6 times)
D	87 (11.1)	13.8 (15.1)	0.12 (13.7)	M_o, M_b and M_{bh} (3 times each)
Part b. Females only, M_o model results				
Protocol*	Avg. N (C.V.)	Avg. S.E. / N (C.V.)	Avg. p (C.V.)	
A	190 (7.5)	21.9 (7.3)	0.12 (10.9)	
B	221 (39.2)	41.5 (25.1)	0.07 (41.5)	
C **	225 (36.6)	61.7 (26.1)	0.05 (36.6)	
D ***	79 (64.1)	69.9 (28.3)	0.07 (42.2)	
Part c. Males only, M_b model results				
Protocol*	Avg. N (C.V.)	Avg. S.E. / N (C.V.)	Avg. p (C.V.)	Avg. c (C.V.)
A	107 (6.1)	13.7 (15.1)	0.31 (8.1)	0.08 (10.0)
B	77 (14.7)	30.4 (41.3)	0.24 (25.5)	0.04 (64.5)
C	52 (31.4)	31.9 (102.0)	0.30 (34.0)	0.04 (38.8)
D **	29 (25.2)	29.4 (88.9)	0.34 (32.8)	0.01 (165.0)

* Protocols A-D were described in Table 1.1 on page 29.

** 1 replication could not fit the model and was ignored.

*** 2 replications could not fit the model and were ignored.

Table 1.6. For the 2 sets of 12 non-tangible and 12 tangible corrals, the frequency unique bears visited each week with the average and median number of hair samples left.

# of bears	Frequency		Average # of samples		Median # of samples	
	Non-tangible corrals	Tangible corrals	Non-tangible corrals	Tangible corrals	Non-tangible corrals	Tangible corrals
9	0 (0.0 %)	1 (0.6 %)	n/a	23.0	n/a	23
6	2 (1.3 %)	4 (2.6 %)	10.5	14.3	10.5	14
5	2 (1.3 %)	4 (2.6 %)	12.0	18.0	12	16
4	10 (6.4 %)	13 (8.3 %)	8.2	7.7	8	7
3	14 (9.0 %)	23 (14.7 %)	6.9	6.6	5	6
2	32 (20.5 %)	29 (18.6 %)	4.0	3.9	4	3
1	43 (27.6 %)	46 (29.5 %)	2.0	2.3	2	2
0	53 (34.0 %)	36 (23.1 %)	n/a	n/a	n/a	n/a

Table 1.7. We used the M_o model to estimate populations of males and females during the 13-week lure study. (N = population estimate, S.E. = standard error, p = initial capture rate, and c = re-capture rate).

Part a. Males				
Non-tangible corrals	Bait	N (S.E.)	p (S.E.)	c (S.E.)
Weeks 1-4	Raspberry or meat scent	52 (16.4)	0.15 (0.05)	
Weeks 5-8	Raspberry or meat scent	43 (10.8)	0.19 (0.06)	
Weeks 1-8 (combined)	Raspberry or meat scent	56 (7.2)	0.14 (0.02)	
Weeks 10-13	Peanut butter scent	17 (6.9)	0.19 (0.09)	
Tangible corrals	Bait	N (S.E.)	p (S.E.)	c (S.E.)
Weeks 1-4	Food only	32 (12.0)	0.16 (0.07)	
Weeks 5-8	Food & peanut butter scent	54 (5.7)	0.32 (0.05)	
Weeks 1-8 (combined)*	Food only, then food & peanut butter scent	54 (5.6)	0.08 (0.02), 0.38 (0.11)	0.21 (0.09), 0.28 (0.04)
Weeks 10-13	Food & peanut butter scent	17 (6.9)	0.19 (0.09)	
Part b. Females				
Non-tangible corrals	Bait	N (S.E.)	p (S.E.)	c (S.E.)
Weeks 1-4	Raspberry or meat scent	34 (6.2)	0.26 (0.06)	
Weeks 5-8	Raspberry or meat scent	54 (9.0)	0.24 (0.05)	
Weeks 1-8 (combined)	Raspberry or meat scent	53 (4.2)	0.20 (0.03)	
Weeks 10-13	Peanut butter scent	46 (10.6)	0.20 (0.05)	
Tangible corrals	Bait	N (S.E.)	p (S.E.)	c (S.E.)
Weeks 1-4	Food only	21 (4.6)	0.27 (0.08)	
Weeks 5-8	Food & peanut butter scent	49 (5.2)	0.32 (0.05)	
Weeks 1-8 (combined)*	Food only, then food & peanut butter scent	45 (3.4)	0.09 (0.02), 0.43 (0.11)	0.35 (0.11), 0.31 (0.04)
Weeks 10-13	Food & peanut butter scent	44 (4.1)	0.36 (0.05)	

* Since the bait was changed after 4 weeks, we used the M_{tb} model modified to estimate only 5 parameters: N, p1, p2, c1, and c2.

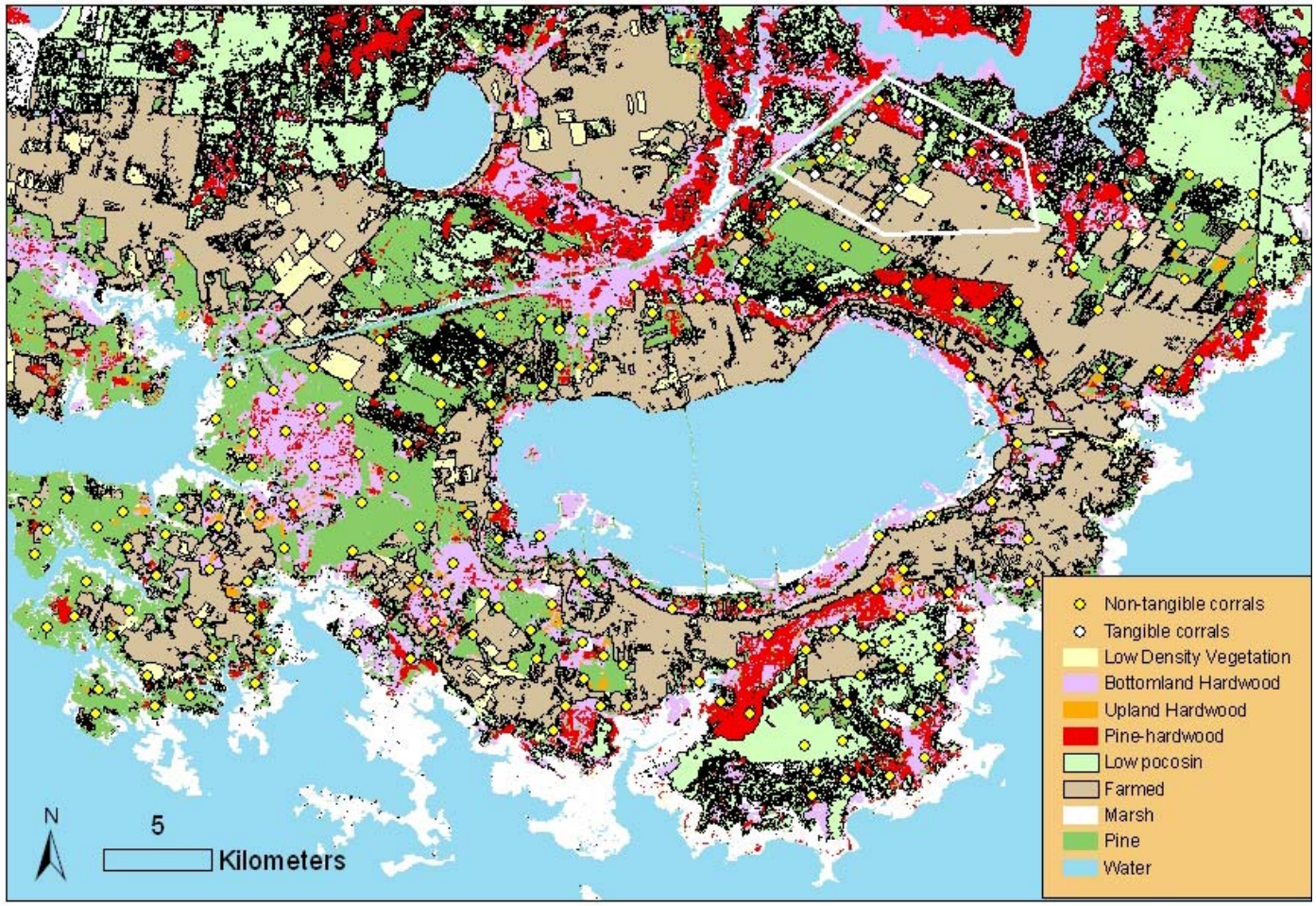

Figure 1.2. Non-tangible corrals located around Lake Mattamuskeet and used in Spring 2003 and Spring 2004 to non-invasively sample black bears in Hyde County, North Carolina. The white box delineates 12 tangible and 12 non-tangibly baited corrals used for an additional experiment to study the attractiveness of scented corrals with and without food.

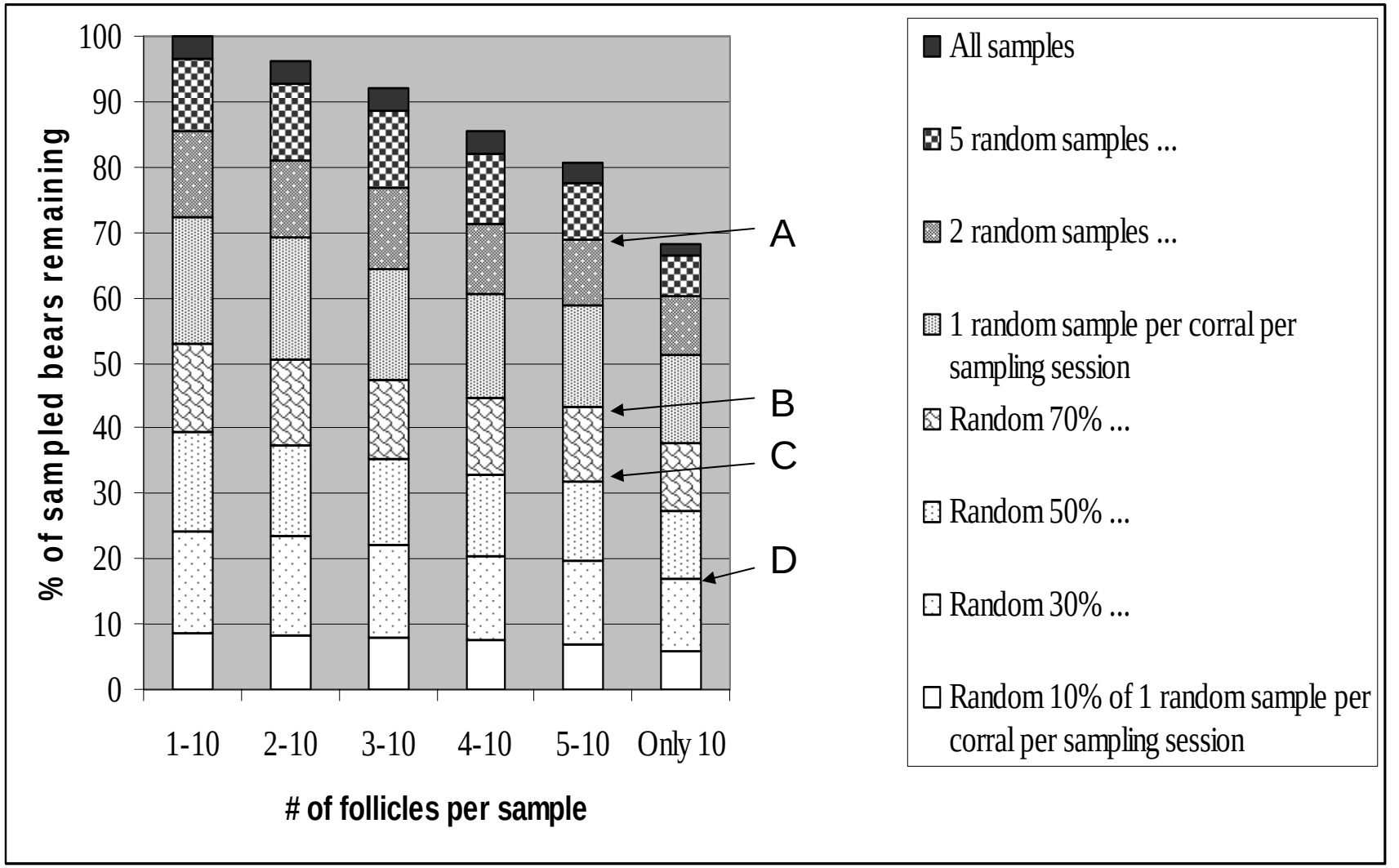

Figure 1.3. Of the 227 individuals sampled in Spring 2004, the % of bears remaining in the dataset after filtering and sub-sampling, averaged over 10 replications for 4 protocols (A-D).

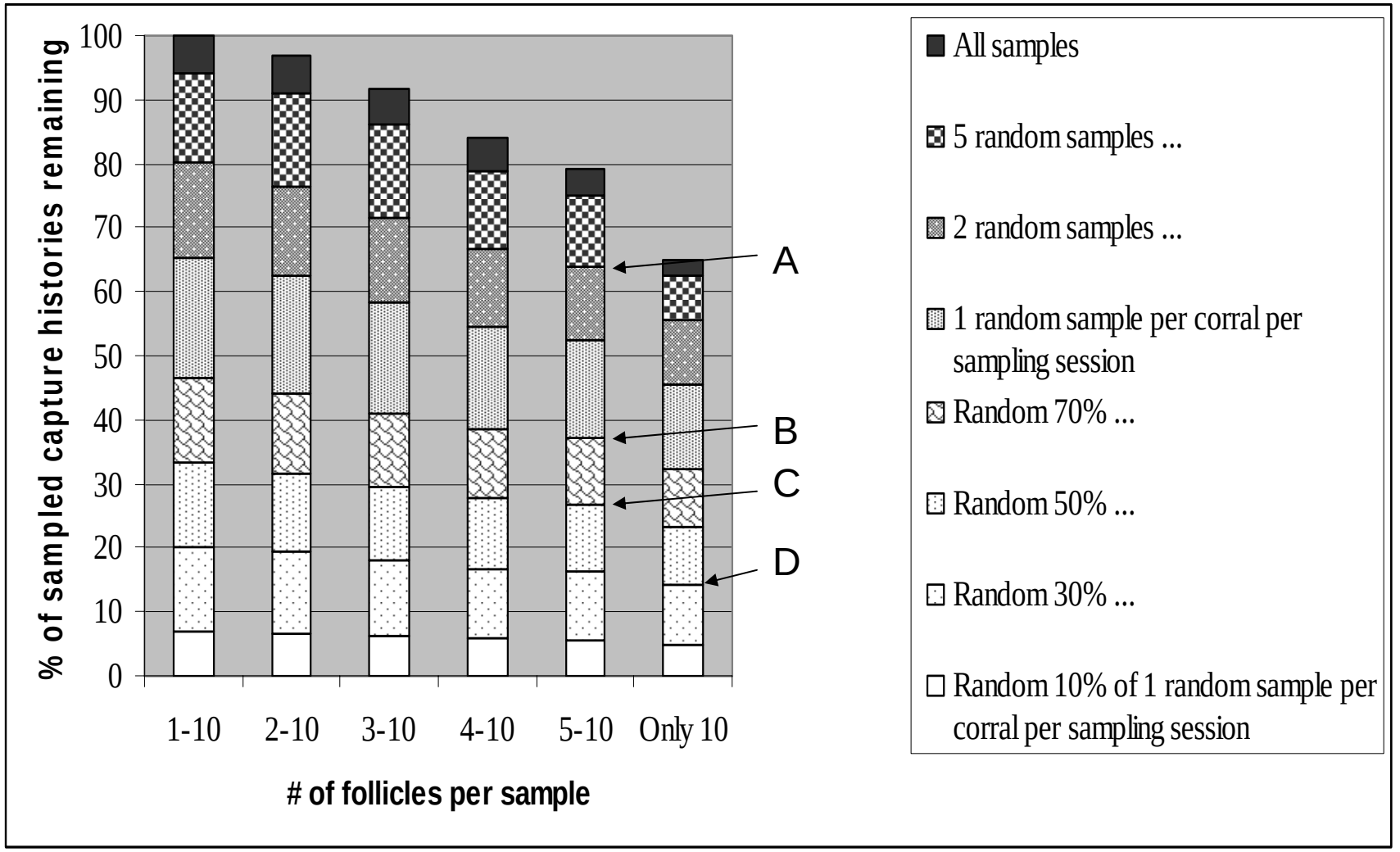

Figure 1.4. Of the 288 total capture events from non-invasive hair sampling in Spring 2004, the % remaining in the dataset after filtering and sub-sampling, averaged over 10 replications for 4 protocols (A-D).

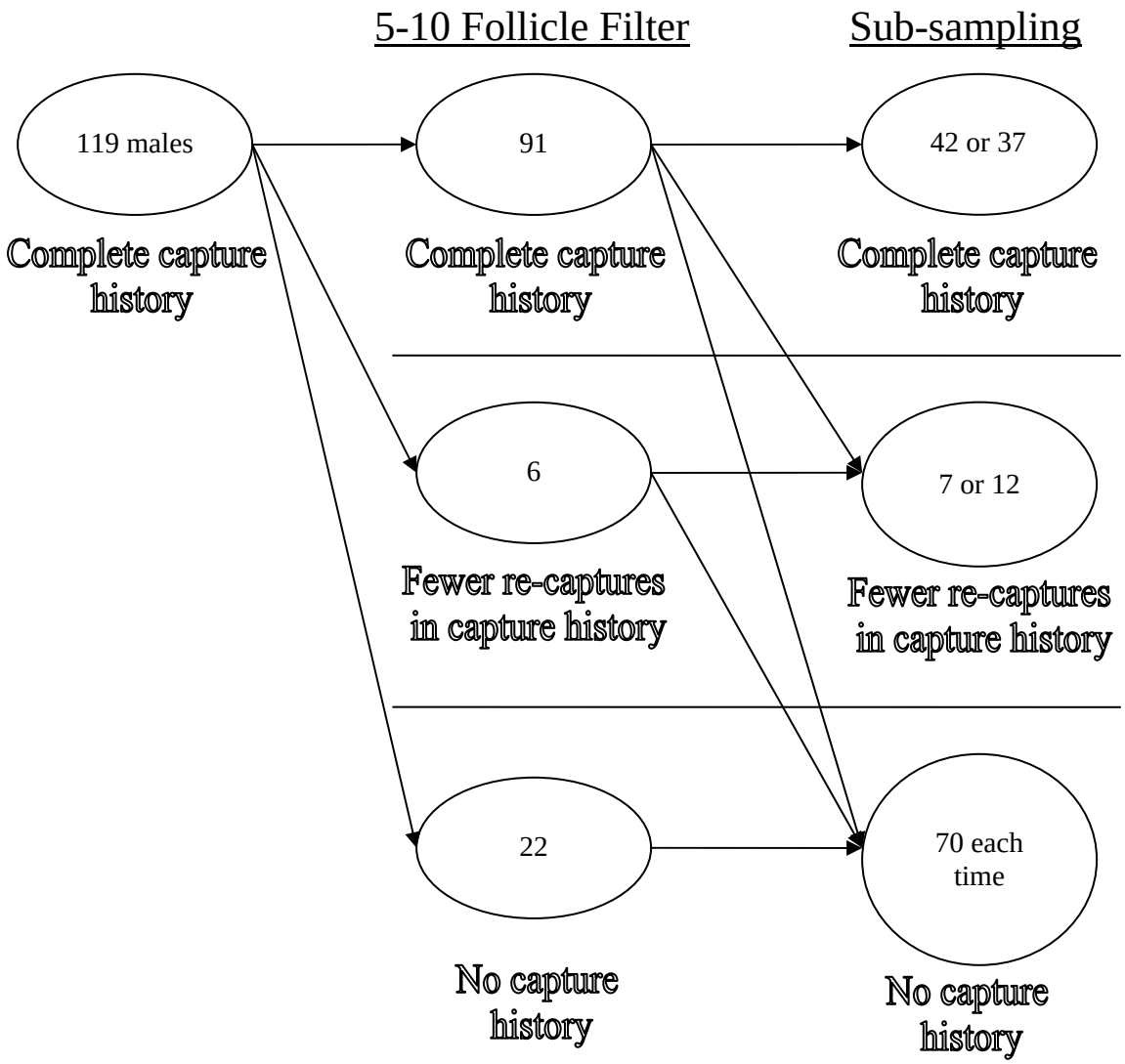

Figure 1.5. The effect on capture histories for males sampled in Spring 2004 from 2 replications of protocol "B", which consisted of filtering 5-10 follicle samples and then randomly choosing 70% of 1 random samples per DNA hair trap per secondary sampling period to genotype.

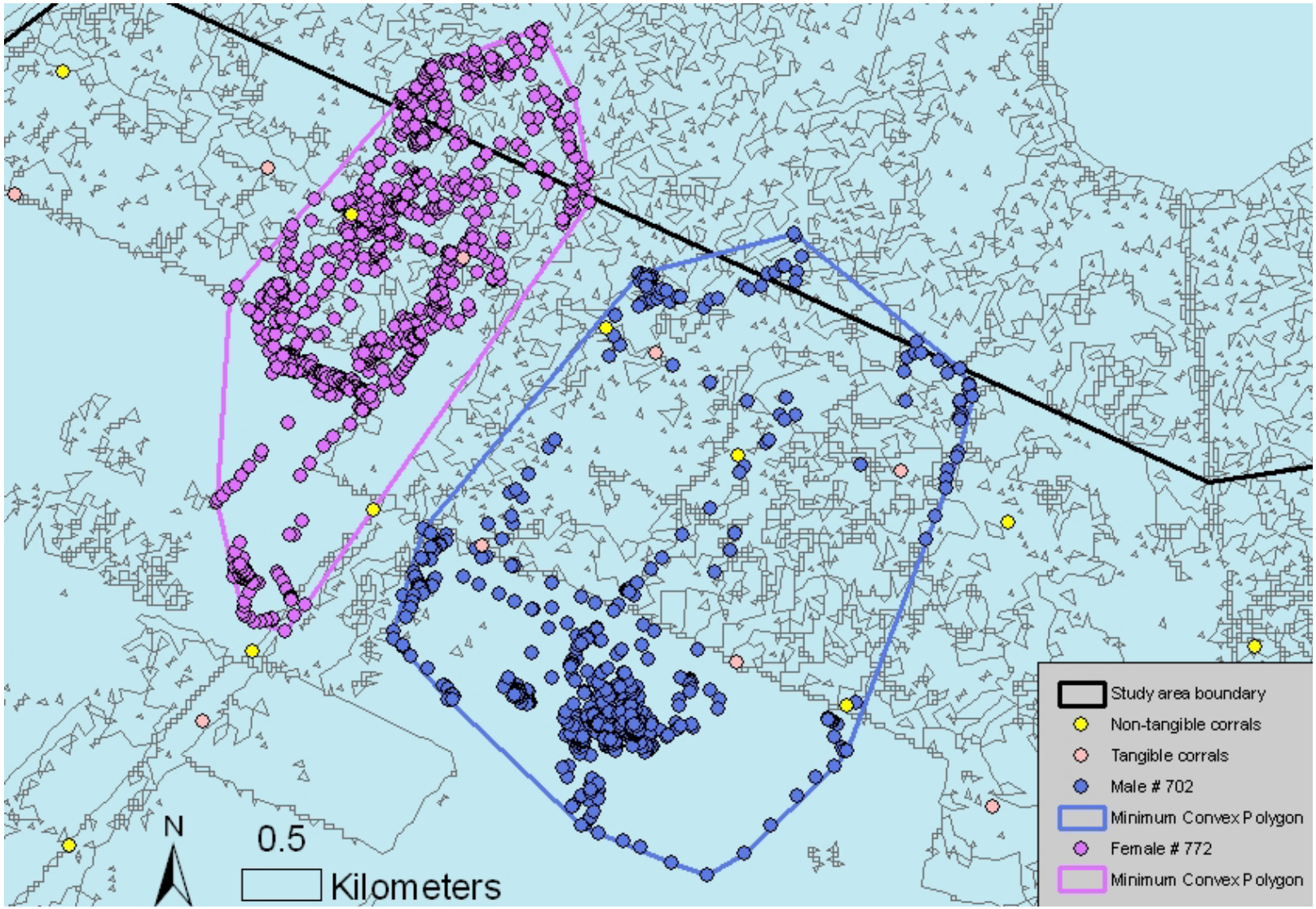

Figure 1.6. Example of weekly home ranges for a male and female bear during food lure study of 2004 in Hyde County, NC.

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CHAPTER 2

CHARACTERISTICS OF A HARVESTED BLACK BEAR POPULATION IN EASTERN NORTH CAROLINA

Figure 2.1. A 610 lb. (277 kg.), 12.75 year old, male bear harvested on December 13, 2003 by David Eakes (kneeling third from left) in Hyde County, NC.

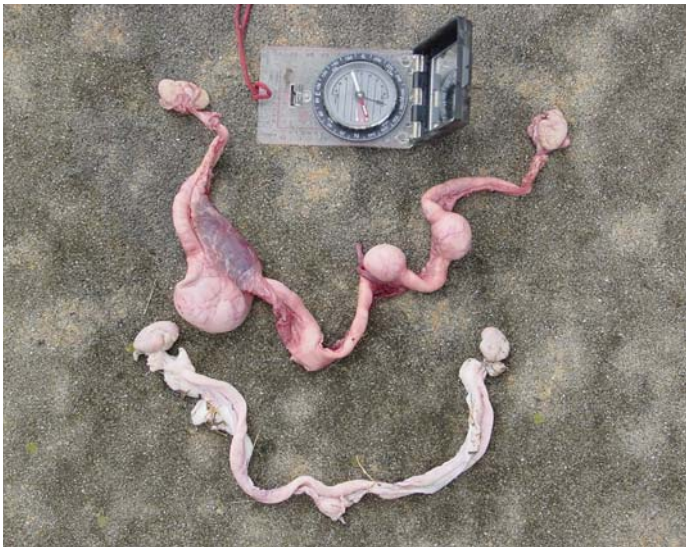

Figure 2.2. Two reproductive tracts collected by Tim Langer from female black bears harvested in 2003 in Hyde County, NC.

ABSTRACT

Noninvasive genetic sampling (NGS) has wide application for genetic and mark-recapture studies. When used in combination with trapping for age determination, hunter harvests for fecundity data, and GPS telemetry to assess closure and heterogeneity, NGS can be an extremely valuable for population monitoring. Bears were sampled via NGS in eastern North Carolina, south and east of the intra-coastal waterway in Hyde County during 2001-2004. Bears were also trapped to deploy 36 GPS collars and sampled from hunter harvests during 2002-2004. We analyzed all samples and determined that cubs were not sampled during NGS in Spring. Model M_o fit females best and model M_b fit males best for both Spring 2003 and Spring 2004. Population estimates for each gender were similar between years, but we estimated more females than males: 223 females and 160 males. Using reproductive tract data from hunter harvested bears and Spring estimates of the number of breeding-age females, we estimated yearly cub production and added 97 cubs of each sex for a total population estimate of 577 bears in our 404.3 mi^2 (1,047.2 km^2) study area. The 2:1 ratio of estimated females to males was consistent with the 2:1 ratio of males to females in the reported harvest. Our study area averaged about 120 hunter harvested bears for 15 years, suggesting the sustainable yield was 20.7 %. Because we estimated the net reproductive rate for females as 1.0, we suggest that hunter harvest in our study area is at maximum sustainable yield for current recruitment and harvest rates. We recommend conducting NGS in Spring to minimize the risk of sampling cubs and being rained out by thunderstorms and hurricanes that prevail during Fall in the Southeast. It is crucial to analyze all hair samples and for sex so that precise estimates of both genders are possible.

Key words: Black bear, *Ursus americanus*, noninvasive genetic sampling, population size, management, monitoring, hunter harvest, survivorship, fecundity, net reproductive rate

INTRODUCTION

Management of large carnivores, such as the American black bear (*Ursus americanus*), by hunting is a challenge because these animals require substantial landscapes to support sustainable populations suitable for harvesting, and their reproductive potential is relatively low. Black bear populations in many states, including North Carolina, have a checkered history that reflects these challenges. In the mid-1960s, the North Carolina Wildlife Resources Commission (NCWRC) hired its first bear biologist project leader to monitor state-wide bear populations. The average age of female bears that were harvested was 3.75 years old, which jeopardized recruitment (M. Jones, NCWRC, unpublished data). Bear population sizes dropped and by the late-1960s county commissioners voted to close bear hunting seasons across the state. In 1971, the NCWRC created 28 bear sanctuaries to protect bears and serve as population sources to re-colonize formerly occupied areas. Bear populations rebounded and hunting seasons re-opened in the early 1980s, largely subject to NCWRC control. Black bears are expanding their range throughout North Carolina and record harvests have been common in recent years. Hunting seasons have increased from 3 to 18 days in the coastal region and are even longer in the mountains. At some point we must ask "What level of harvest can bear populations sustain?"

Effective wildlife management requires reliable population estimates (Mace and Waller 1997a, Miller et al. 1997). However, absolute population estimates have not existed for many populations of large carnivores, including black bears and grizzly bears (*Ursus*

arctos). Traditional mark-recapture studies to estimate populations are inappropriate for bears because they are difficult to catch more than once in a physically restraining trap. Hence, these populations have been traditionally managed using population indices, from which actual densities are not calculable (Nichols and Pollock 1983).

DNA marking using hair or feces samples is a new technique that aims to reduce heterogeneity and increase capture probabilities (Foran et al. 1997, Hoss et al. 1992, Waits et al. 1999, Woods et al. 1996). Genetic tagging has many of the attributes of an ideal mark, which would be non-invasive, invisible, clearly read, inexpensive, and permanent (Woods et al. 1999). Though genetic analysis is expensive, both hair and feces samples are relatively easy to collect and this facilitates population monitoring over a large area. Because black bears do not defend territories where feces would be concentrated, however, DNA can be more systematically and efficiently collected from free-ranging black bears using hair traps (Woods 1998). Hair samples with follicles (roots) can yield sufficient DNA for identifying a species, an individual, and its sex (Waits 2004). Genetic tagging is applicable to all eukaryotic organisms and unambiguous if enough genetic loci are utilized to distinguish between individuals (Paetkau and Strobeck 1994). Hair samples with follicles (roots) can yield sufficient DNA for identifying a species, an individual, and its sex (Waits 2004). Mason (1997) used DNA analysis to study potoroo (*Potorous tridactylus*) populations, while Palsboll et al. (1997) used genetic tagging to study a population of humpback whales (*Megaptera novaeangliae*). Thus, DNA marking has wide application for genetic and mark-recapture studies. However, because DNA marking is non-invasive, age determination is not possible. Physically catching bears allows removal of a tooth to age animals (Stoneberg and Jonkel 1966), as well as deployment of telemetry collars to track bear movements. As a

result, genetic tagging should be used to complement traditional monitoring methods.

Other complications in monitoring large mammal populations are that they may be threatened with extinction or have isolated sub-populations. DNA identification can be used to evaluate genetic status and conservation protocols (Randi et al. 1994, Waits et al. 2000). Taberlet (1996) reported genetic data suggesting European brown bears from sub-populations should not be intermixed, but recommended 3 conservation units be maintained to maximize genetic diversity. Paetkau et al. (1995) raised concerns that gene flow between the 12 geographically isolated, polar bear (*Ursus maritimus*) populations in Canada was too low. Similarly, using DNA analysis from hair samples, Hartl et al. (1996) reported that Asian and African elephants are distinct from one another, but isolated populations within those continents have not separated.

Conservation and management of large carnivores can be complicated by many uncertainties, including those involving the population impacts of harvesting by highly mobile hunters and by year to year changes in habitat quality and configuration. Black bears often thrive in human impacted landscapes where agricultural, forested, and semi-natural habitats intermix (Jones 1996, 2003, Jones and Pelton 2003). In eastern North Carolina black bears benefit from farming practices that produce abundant foods (e.g., corn, wheat, soybeans) adjacent to dense forested habitats and bear hunters from around the state and nation are attracted by the high density and large size of bears found in coastal North Carolina. The world record black bear, weighing 880 lbs. (400 kg.) was harvested in 1998 in Craven County.

Clear understanding is needed of population responses by bears to such a dynamic set of influences. Such knowledge for this important game species is especially critical in areas

where agriculture and artificial feeding may seasonally inflate resources and where harvest pressure may be intense. We tested the efficacy of using DNA hair traps and genetic marking to compile population estimates of black bears on a large scale in the North Carolina Coastal Plain. We chose to study bears in Hyde County because of the diversity of habitat types, range of public and private lands with and without bear hunting, and because Hyde County has sustained the highest annual harvest of bears in the State over the past 15 years, averaging 150 bears per year and 16 % of the coastal bear harvest. In addition, NCWRC personnel invest significant time and resources into collecting age and fecundity information from hunter harvested bears in Hyde County. We estimated net reproductive rate for the estimated number of females to assess if current harvest levels are sustainable. We also discuss whether modeling programs estimate all individuals in a population and whether our population estimates could be accurate.

METHODS

Study area: Bears were collared and sampled via noninvasive genetic sampling (NGS) in eastern North Carolina, south and east of the intra-coastal waterway in Hyde County during 2001-2004 (Figure 2.3). In addition, with the help of NCWRC personnel we collected DNA, age, and reproductive data from hunter harvested bears in Hyde and Tyrrell counties during 2002-2004 (Figures 2.1, 2.2). We used natural water boundaries to delineate most of our study area boundary to bolster assumptions of closure. Where there was not a water boundary, we added half the distance between DNA hair traps, 0.5 miles (0.8 km), beyond their perimeter to delineate the study area (Tredick 2005). Our study area included 3 State game lands and portions of 3 National Wildlife Refuges (Figure 2.4); public land

comprised 20.1 % (210.5 km^2) of the 404.3 mi^2 (1,047.2 km^2) study area. Private land comprised the other 79.9 % (836.7 km^2) and had been extensively drained for agriculture or forestry (Table 2.1). Farming, fishing, and hunting were the primary sources of income for the local community. Cotton increased in recent years as a prominent agricultural crop, with corn, soybeans, and wheat having long been staple crops. Vegetation in pine plantations under the loblolly pine (*Pinus taeda*) overstory included American holly (*Ilex opaca*), red maple (*Acer rubrum*), sweet gum (*Liquidambar styraciflua*), and tulip poplar (*Liriodendron tulipifera*). Hardwood stands contained overstory species such as black gum (*Nyssa sylvatica*), northern red oak (*Quercus rubra*), red bay (*Persea borbonia*), red maple, sweet gum, tulip poplar, and willow oak (*Quercus phellos*). All forest stands were characterized by thick understory vegetation including devil's walking stick (*Aralia spinosa*), greenbrier (*Smilax* spp.), poison ivy (*Toxicodendron radicans*), switchcane (*Arundinaria* spp.), and various bay (*Persea* spp.) and brambles (*Rubus* spp.).

Climate in the study area was temperate. Summers were generally hot and humid with frequent afternoon thunderstorms and temperatures often exceeding daily highs of 38 degrees Celsius, while winters were cool, rainy, and temperatures rarely dropped below freezing. The study area was flat with low topography within a few meters of sea level and often flooded during periods of heavy rainfall or hurricanes. Most roads were bordered by a canal or ditch used to build up the road and promote drainage. State highway 94 and U.S. highway 264 bisected the study area, but there were few other paved roads.

The base land cover map we used was the most recent available from the North Carolina Gap Analysis Land Cover project, a 1992 era map with 70 cover classes represented in the state of North Carolina (McKerrow and Williams 2006). The estimated overall

accuracy of the map when generalized to 15 land cover classes was 87.7 %, with a 95 % confidence interval between 84.9 % and 90.5 %. We reduced cover classes to the 8 used by Jones and Pelton (2003) for black bear habitat analyses in eastern North Carolina and summarized the distribution and relative occurrence of these 8 land cover classes on public and private land in our study area (Table 2.1). Low pocosin and marsh were the most common land cover classes on public land, while crop land and upland hardwoods were the most common cover classes on private land.

Noninvasive genetic sampling: Mowat and Strobeck (2000) urged that DNA hair trap sites systematically cover the entire study area, so we placed traps at a density of 1 per sq. mi. (2.6 km^2) in forested areas of suitable habitat within 100 meters of roads or trails traversable with a truck or 4-wheeler. We attempted to place DNA hair traps around borders of contiguous blocks of clear cuts or farmland. We avoided marsh, heavily fragmented, and human populated areas to maximize capture probabilities. We secured access to and placed DNA hair traps on 63 private properties, 2 State Game Lands, and 3 National Wildlife Refuges.

DNA hair traps consisted of a single strand of 15.5-gauge barbed wire with barbs spaced 5 inches (12.5 cm) apart and stapled 16-20 inches (40.6 to 50.8 cm) off the ground in a polygon 5-10 meters across the middle using 3-8 trees (Figure 1.1, page 7) (Mowat and Strobeck 2000). We used a pick and shovel to level the ground under the wire and maintain an appropriate height for the wire, as well as recording the location of each trap with GPS (Global Positioning System, Mowat and Strobeck 2000). DNA hair traps were baited with 1.5 ounces of liquid scent dispensed with a spray bottle on vegetation in the middle of the corral. We alternated raspberry (# 2205) or meat (# 007083) flavor lures (Mother Murphy's,

Greensboro, North Carolina). We collected hair samples over 4 years to estimate population sizes: in a 2001 pilot study we used 42 corrals (September 3-October 9); in 2002 (north half of study area) we used 85 corrals during four 5-day intervals (May 10-June 3), two 5-day intervals (August 14-August 28), and four 5-day intervals (September 12-October 6); in 2003 we used 191 corrals during four 7-day intervals (May 16-June 19) and (September 5-17, abbreviated by Hurricane Isabel); and in 2004 we used 192 corrals during four 7-day intervals (May 30- July 3), as well as 2 sets of 12 corrals for thirteen 7-day intervals (May 16-August 17) for a food lure study (Figures 2.5 and 1.2, on page 36).

During the pilot study in 2001, we placed corrals at higher densities and checked them at varying intervals. For all other sampling periods, we visited hair traps for 5 consecutive secondary sampling periods. In 2002, we used 5 sampling periods of 5 days each for a 25-day, primary sampling period. In 2003 and 2004, we used 5 sampling periods of 7 days each for a 35-day, primary sampling period. We had to lengthen the secondary sampling period from 5 to 7 days because of the greater number of DNA hair traps in 2003 and 2004. Hair snare periods of 5-7 days were long enough to sample bears, while captured hair would have minimal DNA degradation and minimal chance of being blown off the barbed wire by wind (Mowat and Strobeck 2000). We collected hair at a single barb as 1 sample and preserved DNA follicles by drying the hair samples with indicating silica dessication while in the field (Roon et al. 2003). After removing a hair sample, we burned the barbed wire with a propane torch to eliminate any genetic material at the beginning of the next hair collection period.

We also collected hair samples from bears trapped in physically restraining traps during 2002-2004. In addition, NCWRC personnel assisted us in collecting hair samples

from harvested bears in Hyde and Tyrrell counties during the November and December hunting seasons of 2002 to 2004. All hair samples were collected according to protocol # 01-135, approved by the Institutional Animal Care and Use Committee at North Carolina State University.

DNA hair analysis: We cut all hair samples from NGS, physically trapped, and hunter harvested bears to include 1 to 10 DNA follicles per sample. We genotyped 248 hunter harvested bears to determine the allele frequency distribution within the population and identify which and how many primers we should analyze to distinguish closely related individuals (Paetkau 1998, Waits et al. 2001). Analyzing too few genetic markers could produce a "shadow effect" and an underestimate of the population, as new individuals would be misidentified as marked (known) individuals (Donnelly 1995, Lewontin and Hartl 1991, Mills et al. 2000, Nichols and Balding 1991). Analyzing too many genetic markers could produce genotyping errors and an overestimate of the population, as a subsequent sample from a known individual would be mistaken as originating from a (fictitious) individual (Paetkau 2004). Also, erroneous amplification of DNA in non-optimized reactions can produce false genotypes (Goosens et al. 1998, Paabo et al. 1990, Taberlet et al. 1999).

Only hairs with the hair follicle (root) are useful because the root is the only viable source of DNA in a hair sample (Roon et al. 2003). DNA is extracted from hair follicles and polymerase chain reaction (PCR) allows minute quantities of DNA to be replicated many times and supplies sufficient quantities of DNA for analysis (Waits et al. 2000). Particular regions of DNA (loci) were isolated with appropriate primers, amplified using PCR, separated on an acrylamide gel, and visualized with fluorescence (Goosens et al. 1998). Gender was identified for all unknown genotypes using a PCR-based method based on

identification of specific regions of the X and Y chromosomes of nuclear DNA (Ennis and Gallagher 1994, Gibson et al. 1991). If the sample is from a female, it will show just 1 band on a gel (XX), but if the sample is from a male, it will show 2 bands (XY). Nuclear DNA analysis at 4-6 genetic loci generally permits identification of individuals (Jarne and Lagoda 1996, Paetkau and Strobeck 1995). I used 248 hunter harvested bears to determine the allele distribution for the population and identified 5 genetic markers to use to distinguish individuals: G1A, G10B, C10C, G1D, and G10L, as well as provide known gender samples to verify sex results (Paetkau et al. 1998).

DNA was extracted from hair follicles using the DNAeasy Tissue Kit and cleaned and concentrated using a DNA QIamp spin column (Qiagen, Valencia, CA) (Waits et al. 2000). We added 2 uL of carrier DNA (2 kb of dI/dC, or polydeoxyinosinic-deoxycytidylic acid sodium) to add bulk to the DNA in solution and increase its retention when flushed through the spin column. We ran 10 uL PCR reactions with 0.3 uL of BSA (Bovine Serum Albumin) to stabilize DNA, 5.0 uL of Qiagen multiplex PCR solution, 0.08-0.25 µM of each primer, 4.3 µl of genomic DNA extract, and distilled water, as necessary. Even though we ran single PCR reactions, we used the multiplex mix because the patented concentration of salts in the mix produced more consistent results. We used fluorescent labels from ABI (Applied Biosystems, Foster City, CA) dye set D to label PCR products. The amplification cycle consisted of an initial denaturing at 95° C for 15 minutes followed by 30-42 cycles of 95° C denaturing for 30 seconds, 54.5 - 60° C annealing for 50 seconds, and 72° C extension for 2 minutes (the number of cycles and annealing temperature varied by primer). Cycling culminated with a 30-minute extension at 72° C and then held at 4 degrees indefinitely. We added 3 cycles to PCR reactions when the initial set of reactions did not produce amplified

products. One µl of PCR product was added to 1 ul of a mixture containing 50 % formamide, 15 % loading buffer, and 30 % Genescan-500 Rox internal size standard. We ran each PCR reaction in its own lane, and did not put the same primer in an adjacent lane. The mixture was subjected to capillary electrophoresis through an acrylamide gel on an ABI PRISM 377 Genetic Analyzer (i.e., automated sequencer). Fluorescently labeled DNA fragments were analyzed and genotype data generated using Genescan software (ABI) (Waits et al. 2000).

Genetic analysis also required substantial experience and was time consuming (Roon 1999). We optimized PCR reactions for 10 months by running 70 gels of non-precious DNA samples. We followed the precautions outlined by Taberlet et al. (1996) and Waits (2004) for processing low volume hair samples. We had 2 separate lab spaces in different buildings, so amplified DNA could not contaminate our hair extraction. In addition, I did not use automated fragment identification and scored all alleles myself. We re-ran all ambiguous primer results at least once more. Once I accepted results of all 5 loci for each sample, we re-ran and re-analyzed samples with genotypes that varied at 1 allele or locus. Once I had identified all genotypes, we ran sex identification reactions for each genotype with 4 known males and 4 known females on each gel.

Genetic analysis: For NGS and hunter-harvest hair samples from 2003 and 2004, we used GENEPOP 3.4 (Raymond and Rousset 1995) to perform exact tests of Hardy-Weinberg equilibrium to investigate possible sub-population structure, and linkage disequilibrium tests to investigate whether genotypes at one locus were independent from genotypes at another locus. We also tested if the hunter harvest samples were genetically different than the NGS samples by testing whether the allelic distribution was identical across these sampled

populations (Raymond and Rousset 1995, Rousset and Raymond 1997). Because bear sampling is often non-random, there is a high probability that DNA samples will contain near-relatives (Taberlet and Luikart 1999). This situation requires statistical tests that assume the likelihood of parent-offspring and sibling-sibling pairs within the data set (Paetkau et al. 1995, Paetkau and Strobeck 1994). We calculated $P.I._{sibs}$ values < 0.0001, identified by Waits (2001) as ideal for population estimation when the data set includes sibling pairs.

Physical trapping of bears: We caught 30 different bears during June 7–12, June 15-21, June 27-July 15, and August 10-11, 2002 to deploy 10 Telonics GPS collars (model TGW-3500, Mesa, Arizona). We caught 39 different bears during April 5 - 17, June 21 – July 9, and August 14 - Sept 5, 2003 to deploy 19 Telonics GPS collars and 9 bears during May 1-10, 2004 to deploy 7 Lotek GPS collars (model 3300L, Newmarket, Ontario). In 2002 collars were programmed to time-release on November 22, in 2003 collars were programmed to time-release on December 31, and in 2004 collars were programmed to time release on August 9. We placed cotton spacers in 2002 and leather spacers in 2003-2004 in collar belting as back-up releases. Bears were trapped using culvert traps and Aldrich foot snares (Margo Supplies Ltd., High River, Alberta, Canada) modified with automobile hood springs to reduce injuries (Johnson and Pelton 1980). Captured bears were immobilized with an intra-muscular injection of zolazepam-tiletamine at a dosage of 4.4 mg per kg of estimated body weight (Cattet et al. 2003). We applied a wetting agent (Aqua tears$_{TM}$) to eyes of bears to prevent desiccation and monitored body temperature, respiration, and pulse rate throughout the handling. One pre-molar tooth was removed from each bear for aging

(Matson's Lab, Milltown, Montana). All bears received lip tattoos with a unique identification number between 701 and 775. We handled bears according to protocol # 01-136 approved by the Institutional Animal Care and Use Committee at North Carolina State University.

Home range analysis: GPS collars were programmed to attempt 30 minute locations during Spring and Fall periods of NGS and beginning on November 1 (to correspond with hunting seasons) in 2002 and 2003. During other periods the collars were programmed to attempt locations every 3 hours to save battery life. Each year hunting seasons consisted of 3 6-day periods: one in November and two in December. In 2002, hunting seasons were November 11–16, December 16-21, and December 23-28. In 2003, hunting seasons were November 10-15, December 8-13, and December 15-20. In 2004, hunting seasons were November 9-14, December 6-11, and December 13-18. In 2004 we switched to Lotek collars because of superior battery life and programmed collars to attempt a location every 5 minutes from May 16 to August 9 because we were investigating finer-scale bear movement patterns. We used Arcview 3.3 to generate minimum convex polygons of bear movements during each secondary sampling period of NGS, as well as calculate the area for those polygons (Mohr 1947). We chose minimum convex polygons because we had many locations per day (up to 288) and did not want to exclude areas where a bear might have passed a DNA hair trap. We were not interested in size of core areas, but the amount of possible area traversed to assess whether an individual may have had a zero probability of capture. As Garshelis (1998) pointed out, closed models available in Program CAPTURE (and now Program MARK) can account for heterogeneity of capture probabilities, but not violations of the assumptions of

demographic and geographic closure that will cause overestimation of density. The radio-telemetry data were necessary to assess geographic closure (Garshelis 1998, McLellan 1989).

Population estimates: We assumed closed populations during primary sampling periods and used programs MARK and CAPTURE to fit time, heterogeneity, and trap response models and calculate population estimates (Schwarz and Seber 1999, Seber 1982, 1986, 1992). We generated capture histories for each bear based on whether they were sampled during each of the 4 weeks of sampling. We calculated population estimates for each year for both sexes together, as well as males and females separately (Rexstad and Burnham 1991, White 1996, White and Burnham 1999). Survival estimates from life tables provide an independent estimate from that provided by the robust design in Program Mark, which yielded estimates of apparent survival (Table 2.2, Appendices 1,2). We picked the best model in Program Mark to estimate population size and then used that model structure in the robust design to estimate apparent survival, which included all animal disappearance, that is, all mortality plus emigration. We did not estimate temporary emigration with the robust design because we only had two years of data for the large study area of 2003-2004

Estimating fecundity: To estimate the number of reproductive age females and cub production in our population, we used composite dynamic life table descriptions of our bear population, derived from the harvest data as used by fisheries and wildlife biologists generally to describe the life histories of vertebrates with multiple age classes. This analysis assumes a stable population with a stable age structure (Williams et al. 2002b). Williams et al. (2002b) were critical of this method and urged caution in making inferences from these data. In these analyses, the age structure of harvested animals was used to generate a "virtual population" that assumes a stable age structure (Dinsmore and Johnson 2005, Williams et al.

2002a). Specifically, we used the age at death frequency (Table 2.3) from 181 bears harvested by hunters in our study area (age at catch in fish literature) to generate an l_x (number alive at start of age interval) for the known number of bears alive at some previous time. This is a "composite" dynamic life table (age at death) approach to describing life history, as the bears we used were harvested over more than one year, specifically 2002-2004 (Caughley 1977, Seber 1973). For each gender, we then calculated age specific survival probabilities and age structures. We assumed that ages were accurately determined by teeth sent to Matson's lab (Milltown, Montana) and that the age at harvest sample was representative. Though they were not used to calculate age specific survivorship, we also aged trapped bears so that their ages could be used to identify known-age individuals that were also sampled in DNA hair traps.

Because it is illegal to harvest cubs and none were reported harvested, and too few yearlings were reported as harvested to be an accurate representation of the size of that cohort, we could not use hunter harvest data for those 2 age classes. Miller et al. (2003) estimated cub mortality as 43 % and 66 % for grizzly bears. M. Jones (NCWRC, unpublished data) provided percentages of females with both placental scars and corpora lutea. If we assumed that those females lost their cubs prior to breeding season and cubs of the remaining females just with placental scars survived, cub mortality was 30 %. However, that estimate may be low, as cubs may have died after breeding season, for instance as a result of their mother being harvested. We used a cub mortality rate of 50 % for both sexes. We then distributed the number of individuals for each sex per age class so that total individuals at least 1 year old added up to our population estimates of 223 females and 160 males (Table 2.4).

To estimate cub production, we assigned fecundity information to age classes of breeding females. According to M. Jones (NCWRC, unpublished data), 80% of 3 year old female bears living in the coastal plain of North Carolina reproduce and average 2 cubs. Furthermore, coastal bears average litters every 2 years, 4 year olds average 2.3 cubs and 5 year olds and older average 2.5 cubs (M. Jones, NCWRC, unpublished data). Because an average of 66.5 % of females were harvested with placental scars (and the average % of reproducing females can not exceed 50 % without consecutive age litters, which has only been documented anywhere once), we assumed that 50% of 4 year old and older females reproduced in any given year and calculated reproductive values for each age class (Table 2.5) (M. Jones, NCWRC, unpublished data).

Estimating apparent survivorship: Using the M_o model for females and M_b model for males for both Spring 2003 and Spring 2004, we calculated the apparent survivorship for each gender. We also set parameters in Program Mark so that capture rates for the M_o model were the same in both years, as well as initial and re-capture rates in the M_b model as the same for both years (White 1996, White and Burnham 1999).

RESULTS

For NGS sampling in both Spring 2003 and Spring 2004, 109 DNA hair traps each year sampled 1 or more bears. During Spring 2003, 59.1 % of the unique bears were male, compared to 52.0 % during Spring 2004 (Table 2.6). In Spring 2003, 79 females had 91 capture history events and 114 males had 132 capture history events. In Spring 2004, 108 females were captured 139 times and 119 males were captured 149 times. Pooling sexes, 193 bears had 223 capture history events in 2003 and 227 bears had 288 capture history

events in 2004. (We defined a capture history event as whether a bear was sampled at least once during a secondary sampling period). We mapped the number of unique bears per corral for each gender and each year (Figures 2.7 - 2.10). In general, 2004 produced higher capture rates and more precise estimates. For example, the initial capture rate was 0.09 in 2003 vs. 0.17 in 2004 for females using M_o model, with standard errors of 58.6 in 2003 vs. 27.4 in 2004 (Tables 2.7-2.10).

For females alone, the M_o model fit the data better in Programs Mark and Capture, producing estimates of 207 (S.E. 27.4) to 239 (S.E. 58.6). Population estimates from the modified Lincoln-Peterson were slightly lower with less precision (Tables 2.3 and 2.4). For males alone, the M_b model fit the data better in Programs Mark and Capture, producing estimates of 156 (S.E. 18.3) to 164 (S.E. 26.8). When M_{bh} and M_b models produced the same results, we chose M_b as the better fitting model because it was less complex (Tables 2.7 and 2.8). Because the male data were best fit with a trap response model and specifically a trap shy response, estimated rates of capture for marked individuals were less than unmarked individuals. Alternately, AICc criterion in Program Mark suggested that the female data were best fit without modeling trap, time, and heterogeneity (Tables 2.9, 2.10).

Averaging the appropriate model result from 2003 and 2004 (M_o model results for females: 207 and 239; M_b model results for males: 156 and 164), we estimated there were 223 females and 160 males for a total of 383 bears in the modeled population during Springs 2003 and 2004. When we pooled gender data into one dataset, the M_h model was the best model suggested for 2003, but the finite version had poor precision in Program Mark (population estimate of 724 (S.E. 185.9) and the jackknife version in Program Capture, which produced a population estimate of 432 (S.E. 25.0), was not programmable into

Program Mark and thus could not be used in the Robust Design). In 2004, the M_b model was chosen by both programs and estimated 317 bears (S.E. 33.4). The inconsistency in estimates, precision, and model selection suggested that the pooled data were difficult to fit (Tables 2.11 and 2.12). For example, models with nearly identical criteria values produced vastly different results. In 2004, the M_o model estimated 457 bears (S.E. 43.9), the M_{bh} model estimated 348 bears (S.E. 59.4), and both had identical AICc values. These results suggested heterogeneity between males and females and hence better results when genders were analyzed separately.

Movement data from GPS collars also supported heterogeneity, both among and within sexes. We calculated the area of minimum convex polygons for the 4 week periods of NGS sampling during Spring 2003 and Spring 2004 (Table 2.13). Seven males averaged 5.6 mi^2 (14.6 km^2) weekly home ranges, while 4 females averaged 3.1 mi^2 (7.9 km^2) weekly home ranges. Capture probabilities were inevitably influenced by an animal's movements relative to DNA hair traps. There were 4.4 corrals on average in male weekly home ranges (range 0 - 10), compared to 1.6 corrals for females (range 0 - 4). In addition, within both genders the weekly home ranges and number of corrals within them varied greatly for 3.25 year olds. Male bear (tattoo) # 769 averaged 11.1 mi^2 (28.8 km^2) and 7.8 corrals per week, while male bear (tattoo) # 734 averaged 1.6 mi^2 (4.1 km^2) and 1.3 corrals per week, including 2 weeks without a corral within his weekly home range. Female bear (tattoo) # 771 averaged 3.8 mi^2 (9.8 km^2) and 1.8 corrals per week, while female bear (tattoo) # 770 averaged 1.1 mi^2 (2.7 km^2) and 0.5 corrals per week, including 2 weeks without a corral within her weekly home range. Small home range sizes (weeks 1 and 2, Figure 2.13) and high degree of linearity in home range size (weeks 1 and 3, Figure 2.15) resulted in weeks with no corrals within the

home range, which violated the assumption of non-zero capture probability.

Movement of bears outside of the study area and in areas within the study area without DNA hair traps was important to assess closure and heterogeneity. The four times males (Figures 2.11, 2.12) and 5 times females (Figure 2.13) moved outside of the study area, they returned to the study area and enclosed an area with more than 1 DNA hair trap during that week's home range. In addition, 2 collared male bears (tattoo #s 731 and 732) that were in the study area before and after the Spring 2003 sampling period for DNA hair traps remained outside of the study area the entire time of NGS sampling (Figure 2.14). Within the study area, some of Gull Rock Game Lands could not be sampled because there was no access. Collared bears appeared not to use those areas (Figure 2.15) or when they did, those week's home ranges still enclosed several DNA hair traps (Figure 2.16). These movement data supported our assumption of closure and our assumption of non-zero capture probabilities for bears during our 4-week, Spring, primary sampling periods.

Hunter harvested bears were sampled with the help of NCWRC personnel. During 2002-2004 hunting seasons, a total of 181 bears (123 males, 58 females) were harvested in our study area and checked by biologists. We collected hair for DNA identification, teeth for aging, and recorded harvest location (Figures 2.17 - 2.19). Hunter harvest was highest north and east of Lake Mattamuskeet. Using DNA identification we mapped the multiple locations for individual bears sampled more than once via our different techniques (Figure 2.20). We recorded GPS coordinates for locations of DNA hair traps, culvert traps, and Aldrich foot snares and used the geographic center of 1 square mile (2.6 km^2) areas of the Quad, Block, Square system used by the Forest Service to approximate harvest locations. Of the 897 total bears in our DNA database for 2001-2004, 28.7% were sampled in more than 1 sampling

session and 23.9 % were sampled in more than 1 year. Bears sampled via more than one sampling method included 110 bears sampled via DNA hair traps, 77 bears sampled via hunter harvest, and 60 bears sampled via culvert traps or Aldrich foot snares (Table 2.14).

DISCUSSION

NGS sampling was biased towards males, though population estimates produced a female bias in the population when all hair samples were analyzed. The average annual harvest of 150 bears the past 15 years in Hyde County suggests stability (M. Jones, NCWRC, unpublished data) and averaging results for Springs 2003 and 2004, 55.5 % (233 of 420) of the sampled bears were males, though 41.8 % (160 of 383) of the estimated population were males. This suggested that males were sampled more often via DNA hair traps than females and, in fact, 2.8 more DNA hair traps were in a male's weekly home range than a female's weekly home range, on average. We dealt with this heterogeneity between genders by analyzing all samples and estimating male and female population sizes separately. Different models fit the data better for males and females. As a result, we were able to obtain more precise estimates and consistent model selection among study years analyzing each gender separately.

Model M_b fit the data best for males and model M_o fit the data best for females. Most bear researchers in North America have used food and scent to lure bears to DNA hair traps to collect hair samples (Boersen et al. 2003, Dobey et al. 2005, Thompson et al. 2005, Tredick 2005). We did not use food and only used scent. The rationale for using food is that bears might become "apathetic" towards DNA hair traps if only scent was used (Tredick 2005). Our results did not support this conclusion. For example, model M_t for females in

Spring 2003 had rates of capture between 0.09 and 0.10 for all 4 secondary sampling periods. Capture rates were higher in 2004 as there was less rain, but still the M_t model was the 6th model chosen by AICc criteria in Program Mark and rates of capture only varied between 0.15 and 0.20. These results were consistent for males as well (Appendices 3-8). Furthermore, most investigators use an amount of food that the first bear to the corral can easily consume. When such is the case, scent is the only lure available to subsequent bears. Rewarding only the first bear to visit a DNA hair trap baited with scent and food could create heterogeneity in captured individuals and affect population estimates.

Our results are fundamentally different from bear researchers who do not analyze sex of hair samples and estimate the population of males and females together (Boersen et al. 2003, Dobey et al. 2005, Thompson et al. 2005, Tredick 2005). When we pooled genders, all models struggled to fit the data. As a result, population estimates and precision varied widely between sampling sessions. This suggested an outcome that analyzing subsets of all samples might produce significant impacts on model selection and behavior. Because males were generally sampled at a higher rate in our DNA hair trap sessions and the random selection of samples and thus individuals could favor one sex over another, chance could affect how different models would be favored and chosen by Program Mark due to the different individuals and sex ratio in the unknown and pooled analysis. Furthermore, because models only apply to individuals with non-zero capture probabilities and capture rates were already small when we used all samples, we expected negative impacts on population estimates from sub-sampling.

Most bear researchers accept the model estimates as applying to the entire population (Boersen et al. 2003, Dobey et al. 2005, Thompson et al. 2005, Tredick 2005). We used

complementary sampling methods to test this assumption for our estimates of 223 females (M_o model) and 160 males (M_b model) in our study area. Of the 705 unique bears sampled via DNA hair traps, 106 bears were aged. Some of these known-age bears were sampled in more than 1 year via DNA hair traps, which provided 158 known-age bears when they were sampled in DNA hair traps. We did not sample any cubs (defined as less than 1 year of age) in Spring sampling periods, but did sample 3 in Fall sampling periods (2 males, 1 female). Yearling bears were sampled 18 times and 8 of those were "captured" in Spring sampling periods (3 males, 5 females). These results suggest that Spring sampling was better than Fall sampling because cubs are only a few months old and apparently too small to be sampled by DNA hair traps in the Spring, while yearlings of both sexes were sampled in the Spring. As a result, we were convinced our Spring population estimates of 223 females and 160 males represented bears one year old and older for Spring 2003 and Spring 2004.

We estimated the 151, breeding-age females in the population produced 97 male and 97 female cubs each year, given a 1:1 sex ratio in black bear offspring (Clark and Smith 1994). This produced the population estimate of bears in our study area of 577 bears (320 females and 257 males) for Spring 2003 and Spring 2004. For females in the estimated population, mean life span was 4.8 years for all females and 8.6 years if a female lived to be 3 years old. Thus, on average, each female that reached breeding age subsequently had 3 litters. For males in the estimated population size, mean life span was 3.3 years for all males and 6.9 years if a male lived to be 3 years old.

Using 50 % mortality of cubs, 48 yearlings of each gender were added each year. Our study area was 2/3 the area of Hyde County. If 80 % of the 150 annual reported harvest of bears in Hyde County occurred in our study area (not all bears are checked by biologists and

assigned harvest locations) and the ratio of males to females was 2:1, then 80 males were harvested each year. If 48 are added each year via reproduction, more males are harvested than produced, which could explain the female bias in the population estimate. If cub survivorship increased to 60% with a stable population size, there would be 6 fewer breeding females and 4 fewer cubs of each sex produced. Cub survivorship would be difficult to study, but of interest. We trapped a 12.5 year old female bear (tattoo) # 709 weighing 126 pounds on June 18, 2002 that was lactating. When she was hunter harvested on November 11, 2003, she weighed 200 pounds and was also lactating. We believe the best explanation was she lost her cubs in 2002, was bred again, and had another litter in 2003. Because she was harvested in Fall 2003, that second litter may also have died. Thus, this population appeared robust to mortality in the first 2 age classes, with survivorship of 50% for cubs and 48% for yearling females.

The population was likely stable as the net reproductive rate for the population we calculated to be exactly 1.0, given our age specific survival probabilities and recruitment schedules (Tables 2.4, 2.5) (Dinsmore and Johnson 2005). Hyde County has sustained an annual harvest rate of 150 bears for 15 consecutive years, so assuming a stable age structure seemed reasonable, as populations tend towards a stable age structure over time. The 2:1 ratio of males to females in the hunter harvest is consistent with the approximate 1:2 ratio (160:240) of males to females in our estimated population size. Bears exhibited sexual dimorphism in weight in our study area and heavier bears were exclusively male bears. Hunters claimed they often choose not to kill smaller bears (personal observation) and this choice likely resulted in fewer females being harvested. A common criterion for some hunters in Hyde County is to only harvest bears weighing over 300 pounds and this may help

select for males, as only 2 of over 400 females harvested since 1996 in Hyde County weighed more than 300 pounds (M. Jones, NCWRC, personal communication).

Relative to quality management of bears in Hyde County, only males get larger than 400 pounds or grow skulls wide and long enough to make the trophy record book. Minimum skull measurements totaling 21 inches (53.3 cm) for the all-time Boone and Crockett trophy book have been reached by males as young as 6.75 years old in Hyde County (Reneau and Byers 1998). We estimated that 44 of the 160 (27.5 %) males at least one year old (and thus legally available for harvest) were at least 6.75 years old. Of the heaviest 11 bears harvested in North Carolina, three weighing 680 pounds or more were harvested in our study area and were at least 9.75 years old (M. Jones, NCWRC, unpublished data). We estimated that 18 of 160 (11.3 %) males greater than one year old were at least 9 years of age in our population. Of the entire estimated population of 577 bears, males at least 6 years old were 7.6 % of the population and males at least 9 years old were 3.1 % of the population.

For the age classes (2 and older) for which we estimated annual survivorship, females averaged 83 % and males averaged 77 %. Lower survival of males could be explained in part by gender-selective harvesting, as hunting is the primary source of mortality in this bear population. Under-reporting of bears would not likely change our age structures and annual survivor probabilities, unless the under-reporting only varied for specific ages. The most likely age classes to be under-reported were cubs and 1 year olds (it is illegal to harvest a bear less than 50 pounds), which again supported our decision to use harvest data beginning with the 2 year old age class. Interestingly, if we doubled the harvest of 1 year old females and incorporated that age class into the stable age structure analyses, the result was 14 additional breeding females (165 total) and 9 additional cubs of each sex (106 total), which

yields more bears to harvest with the same population size. Lee and Vaughan (2005) reported 1-, 2-, and 3-year-old female survivorship was 0.87 (95 % C.I. 0.78-0.92), compared to 1-year-old male survivorship as 0.32 (95 % C.I. 0.20-0.47) and 2- and 3-year-old male survivorship as 0.59 (95 % C.I. 0.47-0.71). They attributed 98 % of subadult bear mortality to hunters, which were higher than our harvest rates for subadult males. Weights of adult males in the Appalachian mountains are considerably less than weights of adult males on the coast of North Carolina (M. Jones, NCWRC, unpublished data). Perhaps this reduced size difference results in higher mortality for subadult males in the mountains.

The best model for males was M_b for both years, and the M_b model with initial and re-capture probabilities set equal for both years performed better than estimating them separately for each year. This result was positive because it suggested consistent sampling effectiveness and trap response. The best model for females was M_o for both years, with equal capture probabilities for marked and unmarked individuals within a primary period but different among primary periods.

If we can accept the validity of the survivorship estimates, the difference between them estimates emigration and/or mortality beyond reported harvest. If annual average male survivorship for 1 year olds and older is 0.75, and apparent survival from Program MARK is 0.40, then the difference is 0.35. Similarly, if annual average female survivorship for 1 year olds and older is 0.81, and apparent survival from Program MARK is 0.51, then the difference is 0.30. Qualitatively, these results are consistent with the notion that males disperse more than females. We mapped the locations where individual male and female bears were sampled via the same or different techniques over the entire study (Figure 2.16). Because the only sampling outside of the study area was hunter harvest, and more males

were reported harvested than females, and females were sampled less often in all sampling techniques, female movements were under-represented. However, males showed larger and more frequent movements over large distances.

Projecting these apparent survival estimates with the estimated population sizes produced interesting results. Male results fit the reported harvest data well. If 80 males were harvested each year from the estimated number of 160 males, this explained most of loss of 96 males projected by the apparent survival estimate of 40 %. The other 16 males suggested as lost could be accounted for by unreported harvests, emigration, or other mortality. On the other hand, female results did not fit the reported harvest data well, because the unaccounted for difference between reported hunter harvests and annual loss to apparent survivorship is larger for females and females were believed to disperse less often. Apparent survivorship of 51 % of an estimated female population of 223 produced an annual loss of 109 individuals, of which 40 on average were believed to be accounted for by reported harvest. Using data from only the smaller study area of Spring 2002 sampling, which was the north half of the larger study area used in 2003 and 2004, for all 3 years, we used the robust design in Program Mark to estimate apparent survival of females. We used the M_o model for all 3 years because the M_o models were the best for the 2003-2004 comparison. Apparent survival was estimated as 60% (S.E. 15%) for 2002-2003 and 58% (15%) for 2003-2004. The precision for both estimates was poor, as expected because it was less than half the larger study area with fewer data (Appendices 9, 10). However, the data suggested a similar, and slightly higher, apparent survival rate for females. The increased apparent survivorship accounted for another 20 individuals lost annually, which reduced the difference between

estimated annual loss and reported harvest to 49 females. Perhaps they are under-reported in the harvest or die from other mortality factors.

Female bear (tattoo) # 730 was harvested and not reported. We knew she died because the GPS collar she was wearing was later returned. Even though we were told she was not weighed when she was harvested, when we trapped her 3 months before she weighed 100 pounds (45.5 kg). This experience suggested that females could be under-reported. Possibly there are other sources of mortality for females. We observed 2 bears killed by other bears while in Aldrich foot snares during this study, and both were young females. The apparent survival estimate could be negatively affected by the lower capture rates for females than males in DNA hair traps and would be more believable if we had more study years, but it does suggest that females are under-reported in the hunter harvest.

Comparing the spatial distribution of bears sampled via hunter harvest and DNA hair traps, hunter harvests occurred most often north and east of Lake Mattamuskeet NWR, while DNA hair traps sampled bears throughout the study area (Figures 2.7–2.10). Hunter harvest was not as uniform and representative of the entire study area, especially for females which are most important for population monitoring (Figures 2.17–2.19). For both males and females, few bears over all 3 years were reported harvested by hunters near Gull Rock Game Lands. Many males and females were sampled in that area via DNA hair traps and males were shown to move to other parts of our study area from there (Figure 2.20). These data supported the notion that Gull Rock Game Lands, a bear sanctuary, served as a population source for the rest of the study area. This finding was consistent with the results of Beringer et al. (1998), who reported that another bear sanctuary in North Carolina, located in the mountains, functioned as a population source.

Movement of bears throughout and outside of the study area corroborated the genetic results of absence of population sub-structure. Only 1 bear per 3 generations must immigrate to maintain genetic diversity (L. Waits, University of Idaho, personal communication). We documented plenty of movement within one generation (Figure 2.20). Bear populations on Alligator River NWR and Pocosin Lakes NWR were also determined to not be genetically different (Tredick 2005) and this result is consistent with our findings. These 2 National Wildlife Refuges are located partly in Hyde County, but mostly in counties adjacent to Hyde County and our study area. For the set of 5 loci we tested on 4 populations (NGS and hunter harvest samples in 2003 and 2004), we noted one deviation from Hardy-Weinberg expectations following Bonferroni correction (i.e. the p-value of locus A was 0.001 (S.E. 0.0004) for hunter harvest, 2004 samples; Appendix 11). In addition, Fisher's global test produced a p-value of 0.0216 for Spring 2003, NGS samples and 0.0120 for hunter harvest, 2004 samples (Appendix 11). Only 1 pair of loci in 1 population was significant for linkage disequilibrium following Bonferroni correction (Appendix 12). Loci C and D were highly significant for the Spring 2003 NGS sample, but possibly limited data meant the model produced a boundary estimate of "highly significant" because an actual value was not calculated. Lastly, when comparing the 4 populations, only the B locus was significantly different following Bonferroni correction (p-value = 0.0027, S.E. = 0.00118, Appendix 13). We can not explain these departures other than by chance.

Regarding density of bears in our study area, our estimates would not change, but the interpretation of them would. We did not calculate density for the following reasons. First, the size of male and female home ranges varied. Jones (2000) used the mean radius of annual home range sizes for male and female black bears on the Neuse-Pamlico Peninsula of

eastern North Carolina, as reported by Jones (1996), and circumscribed all trap sites with a radius of 1.6 km to determine effective study area. We believed that weekly home range size was most relevant, since DNA hair traps were checked every 7 days. Furthermore, our GPS collar data showed that weekly home ranges during NGS sampling varied greatly among individuals of same age and gender. Would an average be the proper area to use? What about the linearity of bear home ranges? Clearly, there are important questions to consider.

Some areas in our study area were likely rarely used by bears, such as the 14 % classified as marsh (Table 2.1). There were also areas of other habitat with DNA hair traps in which no bears were sampled, as well as areas that did not have DNA hair traps and were therefore not sampled (Figures 2.7–2.10). Should those areas be included in the area for a density estimate? Our study area encompassed land around a large, centrally located lake of 62.5 mi^2 (161.9 km^2). Lake Mattamuskeet NWR affects interpretation of density, as it creates edge habitat and implications for dispersal and movement. Size of study area also impacts density estimates. For example, Tredick (2005) used study areas of 60 km^2, 40 km^2 and a 15 km wide transect to connect them in Pocosin Lakes NWR. DNA traps in these areas covered approximately 25.0 % of the 460 km^2 refuge (Tredick 2005). Extrapolating density estimates would be problematic, because small areas do not have the range of habitat types and may be biased towards higher density habitats such as farm land or lower density habitats such as marsh.

We studied bears on public and private land to sample contiguous areas evenly. We also used the advantage of NGS over physically restraining sampling methods to sample a large area, which allowed us to choose a study area of sufficient size to use natural barriers to movement and facilitate closure assumptions (White et al. 2000). Water encircled more than

85 % of our 1,047.2 km^2 study area. Extending half a home range beyond the perimeter would mean that the center of an individual's home range would have been located in water. While we documented bears swimming the intra-coastal waterway, this centering assumption would imply regular crossings that are not supported by data from our collared bears. Furthermore, if an individual whose home range was located mostly outside of the perimeter of the DNA hair traps came into the area enclosed by the DNA hair traps briefly, it would have minimal effect of population estimates. This situation most likely fit male bears because they had larger weekly home ranges. For collared bears with weekly home ranges inside the perimeter of the DNA hair traps, 7 males averaged leaving hair samples at only 5.6 % of DNA hair traps (7 of 124) and 4 collared females averaged leaving hair at only 11.5 % of DNA hair traps (3 of 26). As a result, we believed this apparent inefficiency of sampling at DNA hair traps actually was beneficial because bears with marginal home range areas inside the study area were likely to have zero capture probabilities and thus were not part of the population estimate. For all of these reasons, we believed the area enclosed by the water, and 0.5 mile (0.8 km) buffer beyond the perimeter of DNA hair traps without a proximate water boundary, was reasonable for the area of our population estimates in Spring 2003 and Spring 2004.

If the bear population fluctuates about 577 bears with 120 bears harvested per year, we believe a harvest of 20.7 % of bears is sustainable for this bear population, assuming recruitment and harvest rates do not change significantly. M. Jones (NCWRC, personal communication) indicated that bear managers previously thought that only up to 15 % harvest of bears was sustainable, but there are other unpublished data that also suggest in highly agricultural areas along the east coast of the United States that bear harvests above 20

% are indeed sustainable.

RECOMMENDATIONS

For NGS via DNA hair traps of black bears in eastern North Carolina, we suggest sampling during Spring to minimize the chances of sampling cubs and being rained out by fall hurricane and thunderstorm systems. We suggest implementing uniformity in the micro-satellite primers that researchers in eastern North Carolina use to identify individuals. The areas used by Tredick (2005), Thompson et al. (2005), and us to study bears were within 50 miles (80 km) of each other, but we could not identify common individuals in our data sets because we all used different sets of micro-satellites. We suggest it would not be difficult to determine which loci would be best to use in the future, coordinating that could be done when State research permits were issued, and a standard set of primers for analysis would not increase lab costs. In addition, we propose that NCWRC personnel collect hair samples from hunter harvested bears across the State. These data would facilitate genetic inquiries across a large scale. Bear biologists in South Carolina are also interested if bears are dispersing south from North Carolina. DNA marking has a lot of potential to enhance bear management.

We attempted to identify pair-wise relationships, but 5 loci were not enough even for first-order relationships. If genetic relatedness is a research objective, a trade-off between more primers and fewer samples may be warranted. We did not do a formal error test, but there were 23 tattooed bears that were handled twice (either trapped twice or trapped and then hunter harvested). DNA hair samples were taken each handling and ran without knowledge of which other sample belonged to the bear with the same tattoo number. Genotyping results matched all samples correctly.

Table 2.1. Land type and ownership in study area within Hyde County, North Carolina.

	sq. mi.	sq. km.	Of total	On public land	On private land
Farm land	116.1	300.7	28.7 %	0.9 %	99.1 %
Upland hardwoods	4.2	10.9	1.0 %	1.3 %	98.7 %
Low density vegetation	11.2	29.0	2.8 %	2.3 %	97.7 %
Pine	82.2	212.9	20.3 %	6.4 %	93.6 %
Bottomland hardwoods	46.6	120.6	11.5 %	26.2 %	73.8 %
Pine - hardwoods	31.2	80.9	7.7 %	31.4 %	68.6 %
Low pocosin	56.3	145.7	13.9 %	46.0 %	54.0 %
Marsh	56.5	146.3	14.0 %	46.9 %	53.1 %
Total	404.3	1047.2	100.0 %	20.1 %	79.9 %

Table 2.2. Apparent survival estimates of male and female bears using the Robust design between primary DNA sampling periods in Spring 2003 and Spring 2004 in Hyde County, North Carolina.

Part a. Males

Model	AICc criteria	Delta AICc	AICc weight	Model likelihood	# of parameters	Apparent survival estimate	Apparent survival standard error
p1 = p2 & c1 = c2	- 684.89	0.00	0.61	1.00	5	0.40	0.07
M_b M_b	- 683.36	1.54	0.28	0.46	7	0.38	0.07
M_o M_b	- 680.09	4.80	0.06	0.09	6	0.38	0.07
M_b M_o	- 679.51	5.38	0.04	0.07	6	0.61	0.12
M_o M_o	- 676.23	8.66	0.01	0.01	5	0.61	0.12
p1 = p2 = c1 = c2	- 675.69	9.20	0.01	0.01	4	0.70	0.13

Part b. Females

Model	AICc criteria	Delta AICc	AICc weight	Model likelihood	# of parameters	Apparent survival estimate	Apparent survival standard error
M_o M_o	- 466.55	0.00	0.35	1.00	5	0.51	0.11
M_o M_b	- 465.79	0.76	0.24	0.68	6	0.39	0.10
p1 = p2 = c1 = c2	- 464.76	1.79	0.14	0.41	4	0.59	0.13
M_b M_o	- 464.50	2.05	0.12	0.36	6	0.51	0.11
M_b M_b	- 463.72	2.83	0.08	0.24	7	0.39	0.10
p1 = p2 & c1 = c2	- 463.15	3.40	0.06	0.18	5	0.50	0.15

Table 2.3. Ages of 181 black bears harvested by hunters in our study area during 2002-2004 in Hyde County, NC.

Age class	Total	% of total	Cumulative % of total	Males	% of males	Cumulative % of males	Females	% of females	Cumulative % of females
0.75	0	0	0.0 %	0	0	0.0 %	0	0	0.0 %
1.75	13	7.2 %	7.2 %	6	4.9 %	4.9 %	7	12.1 %	12.1 %
2.75	22	12.2 %	19.3 %	15	12.2 %	17.1 %	7	12.1 %	24.1 %
3.75	21	11.6 %	30.9 %	17	13.8 %	30.9 %	4	6.9 %	31.0 %
4.75	20	11.0 %	42.0 %	15	12.2 %	43.1 %	5	8.6 %	39.7 %
5.75	14	7.7 %	49.7 %	12	9.8 %	52.8 %	2	3.4 %	43.1 %
6.75	14	7.7 %	57.5 %	10	8.1 %	61.0 %	4	6.9 %	50.0 %
7.75	10	5.5 %	63.0 %	7	5.7 %	66.7 %	3	5.2 %	55.2 %
8.75	15	8.3 %	71.3 %	12	9.8 %	76.4 %	3	5.2 %	60.3 %
9.75	9	5.0 %	76.2 %	6	4.9 %	81.3 %	3	5.2 %	65.5 %
10.75	9	5.0 %	81.2 %	6	4.9 %	86.2 %	3	5.2 %	70.7 %
11.75	10	5.5 %	86.7 %	7	5.7 %	91.9 %	3	5.2 %	75.9 %
12.75	9	5.0 %	91.7 %	5	4.1 %	95.9 %	4	6.9 %	82.8 %
13.75	1	0.6 %	92.3 %	0	0.0 %	95.9 %	1	1.7 %	84.5 %
14.75	1	0.6 %	92.8 %	1	0.8 %	96.7 %	0	0.0 %	84.5 %
15.75	4	2.2 %	95.0 %	1	0.8 %	97.6 %	3	5.2 %	89.7 %
16.75	2	1.1 %	96.1 %	1	0.8 %	98.4 %	1	1.7 %	91.4 %
17.75	1	0.6 %	96.7 %	1	0.8 %	99.2 %	0	0.0 %	91.4 %
18.75	1	0.6 %	97.2 %	0	0.0 %	99.2 %	1	1.7 %	93.1 %
19.75	4	2.2 %	99.4 %	1	0.8 %	100.0 %	3	5.2 %	98.3 %
20.75	1	0.6 %	100.0 %	0	0.0 %		1	1.7 %	100.0 %
Total	181			123	males		58	females	

Table 2.4. Age structure and individuals per age class for the estimated bear population at least one year old in Hyde County, North Carolina. Age structures for 1.75 year olds were not calculated because hunter harvest mortality data were used to calculate these age structures and hunter harvest of that age class was not considered to be the major source of mortality.

Age class	Age structure		# of individuals	
	Females	Males	Females	Males
1.75			49	49
2.75	0.134	0.188	23	21
3.75	0.115	0.164	20	18
4.75	0.105	0.137	18	15
5.75	0.092	0.113	16	13
6.75	0.087	0.093	15	10
7.75	0.076	0.077	13	9
8.75	0.068	0.066	12	7
9.75	0.060	0.047	11	5
10.75	0.052	0.037	9	4
11.75	0.045	0.027	8	3
12.75	0.037	0.016	6	2
13.75	0.026	0.008	5	1
14.75	0.024	0.008	4	1
15.75	0.024	0.006	4	1
16.75	0.016	0.005	3	1
17.75	0.013	0.003	2	0
18.75	0.013	0.002	2	0
19.75	0.010	0.002	2	0
20.75	0.003	0.000	0	0
Totals			223	160

Table 2.5. Given proportional survivorship generated from our hunter harvest data, the reproductive rates per age class using age specific fecundity data from M. Jones (North Carolina Wildlife Resources Commission, unpublished data).

Age class	Proportional survivorship	Age specific fecundity	Proportional reproductive rates
0.75	1.00	0.00	0.00
1.75	0.50	0.00	0.00
2.75	0.24	0.00	0.00
3.75	0.21	0.80	0.17
4.75	0.19	0.58	0.11
5.75	0.17	0.63	0.10
6.75	0.16	0.63	0.10
7.75	0.14	0.63	0.09
8.75	0.12	0.63	0.08
9.75	0.11	0.63	0.07
10.75	0.09	0.63	0.06
11.75	0.08	0.63	0.05
12.75	0.07	0.63	0.04
13.75	0.05	0.63	0.03
14.75	0.04	0.63	0.03
15.75	0.04	0.63	0.03
16.75	0.03	0.63	0.02
17.75	0.02	0.63	0.01
18.75	0.02	0.63	0.01
19.75	0.02	0.63	0.01
20.75	0.00	0.63	0.00
Total net reproductive rate			1.00

Table 2.6. Using 2003-2004 study area, sampling success of unique bears via DNA hair traps for 4 weeks during 2003-2004 in Hyde County, NC.

	Week 1	Week 2	Week 3	Week 4	Total
Spring 2003					
Total samples that were genotyped	128	120	96	96	440
Unique bears sampled	63	61	51	48	193
# of males (%)	41 (65.1%)	40 (65.6%)	27 (52.9%)	24 (50.0%)	114 (59.1%)
Unique corrals with hair (%)	51 (26.7%)	50 (26.2%)	46 (24.1%)	34 (17.8%)	108 (56.5%)
Range in total samples per corral	1-8	1-10	1-7	1-15	1-18
Range in unique bears per corral	1-5	1-4	1-3	1-8	1-8
Average # of samples for corrals with hair	2.6	2.4	2.1	2.8	4.1
Average # of bears for corrals with hair	1.4	1.3	1.2	1.4	2.0
Spring 2004					
Total samples that were genotyped	165	151	150	127	593
Unique bears sampled	84	77	67	60	227
# of males (%)	49 (58.3%)	36 (46.8%)	35 (52.2%)	28 (46.7%)	118 (52.0%)
Unique corrals with hair (%)	59 (30.7%)	54 (28.1%)	39 (20.3%)	41 (21.4%)	109 (56.8%)
Range in total samples per corral	1-20	1-12	1-18	1-21	1-44
Range in unique bears per corral	1-8	1-6	1-6	1-7	1-16
Average # of samples for corrals with hair	2.8	2.8	3.8	3.1	5.4
Average # of bears for corrals with hair	1.5	1.5	1.8	1.5	2.5

Table 2.7. Results for 114 males caught 132 times in 2003, using Program Mark, Program Capture, and modified Lincoln-Peterson.

Mark						95% Confidence Interval	
Model	AICc Criteria	Estimate	SE	p-hat	c-hat	Lower	Upper
M_{tb}	-421.06	114	0.00	0.36 - 0.53	0.05 - 0.17	114	114
M_{bh}	-420.65	167	29.23	0.25 & 0.58	0.06 & 0.87	133	259
M_b	-418.81	164	26.81	0.26	0.09	133	248
M_h - finite	-418.52	475	163.29	0.06 & 0.73		269	955
M_t	-417.19	331	65.42	0.07 - 0.12		236	501
M_{tbh}	-415.83	114	0.00			114	114
M_o	-415.47	337	66.84	0.10		239	510
M_{th}	-414.53	967	1660.57			187	10030

Capture						95% Confidence Interval	
Model	Criteria	Estimate	SE	p-hat	c-hat	Lower	Upper
M_{bh}	1.00	164	26.76	0.26		133	247
M_{tbh}	0.95						
M_o	0.86	337	66.50	0.10		240	508
M_b	0.85	164	26.80	0.26	0.09	133	247
M_h - jackknife	0.75	257	19.30	0.13		225	300
M_{tb}-burnham	0.75	236	649.51	0.12 - 0.17		118	4591
M_{th}-chao	0.59	560	182.77	0.04 - 0.07		321	1079
M_t	0.00	331	64.58	0.07 - 0.12		237	498

Lincoln-Peterson (Chapman modification)						95% Confidence Interval	
Week		Estimate	Variance	Avg. Estimate		Lower	Upper
2nd	M = 41, n = 40, m = 7	214	3354	304		101	328
3rd	M = 74, n = 27, m = 6	299	7650			128	470
4th	M = 95, n = 24, m = 5	399	16286			149	649

Table 2.8. Results for 119 males caught 149 times in 2004, using Program Mark, Program Capture, and modified Lincoln-Peterson.

Mark						95% Confidence Interval	
Model	AICc Criteria	Estimate	SE	p-hat	c-hat	Lower	Upper
M_b	-404.03	156	18.28	0.30	0.13	134	211
M_{tb}	-403.12	119	0.00	0.40 - 0.60	0.11 - 0.16	119	119
M_{bh}	-402.00	156	18.28	0.30 & 0.62	0.13 & 0.38	134	211
M_t	-401.06	246	34.04	0.11 - 0.20		195	332
M_o	-400.11	249	34.69	0.15		197	336
M_h - finite	-398.08	249	34.69	0.15 & 0.28		197	336
M_{tbh}	-397.45	119	0.00			119	119
M_{th}	-391.83	235	33.90			185	322

Capture						95% Confidence Interval	
Model	Criteria	Estimate	SE	p-hat	c-hat	Lower	Upper
M_{bh}	1.00	156	18.25	0.30		134	211
M_b	0.99	156	18.23	0.30	0.13	134	211
M_{tbh}	0.82						
M_o	0.66	249	34.51	0.15		197	335
M_{tb}-burnham	0.65	203	177.13	0.16 - 0.24		126	1196
M_h - jackknife	0.54	239	18.30	0.16		209	280
M_{th}-chao	0.51	242	35.99	0.12 - 0.20		189	334
M_t	0.00	246	33.58	0.11 - 0.20		196	330

Lincoln-Peterson (Chapman modification)						95% Confidence Interval	
Week		Estimate	Variance	Avg. Estimate		Lower	Upper
2nd	M=49, n=36, m=8	205	2622	231		104	305
3rd	M=77, n=36, m=11	240	2544			141	338
4th	M=102, n=28, m=11	248	2468			151	345

Table 2.9. Results for 79 females caught 91 times in 2003, using Program Mark, Program Capture, and modified Lincoln-Peterson.

Mark						95% Confidence Interval	
Model	AICc Criteria	Estimate	SE	p-hat	c-hat	Lower	Upper
M_o	-230.96	239	58.57	0.09		159	400
M_b	-228.98	301	342.77	0.07	0.10	104	2013
M_{bh}	-226.93	301	342.77	0.07 & 0.83	0.01 & 0.10	104	2013
M_h - finite	-226.89	253	152.80	0.09 & 0.24		119	845
M_{tb}	-226.79	79	0.00	0.28 - 0.53	0.09 - 0.10	79	79
M_t	-225.14	239	58.49	0.09 - 0.10		159	399
M_{tbh}	-219.31	79	0.00			79	79
M_{th}	-218.18	305	98.80			178	592

Capture						95% Confidence Interval	
Model	Criteria	Estimate	SE	p-hat	c-hat	Lower	Upper
M_o	1.00	239	58.14	0.10		160	398
M_h - jackknife	0.86	175	15.89	0.13		149	211
M_{tbh}	0.68						
M_{bh}	0.60	301	342.90	0.07		105	2013
M_{th}	0.43	262	88.42	0.08 - 0.09		154	528
M_b	0.35	301	343.84	0.07	0.10	105	2019
M_{tb}	0.32	142	104.16	0.16 - 0.22		86	677
M_t	0.00	239	57.40	0.09 - 0.10		161	395

Lincoln-Peterson (Chapman modification)						95% Confidence Interval	
Week		Estimate	Variance	Avg. Estimate		Lower	Upper
2nd	M=22, n=21, m=2	168	5341	199		24	311
3rd	M=41, n=24, m=4	209	5180			68	350
4th	M=61, n=24, m=6	220	3915			98	343

Table 2.10. Results for 108 females caught 139 times in 2004, using Program Mark, Program Capture, and modified Lincoln-Peterson.

Mark						95% Confidence Interval	
Model	AICc Criteria	Estimate	SE	p-hat	c-hat	Lower	Upper
M_o	-329.28	207	27.36	0.17		166	276
M_h - finite	-328.95	4667	114562.22	0.00 & 0.33		139	661742
M_b	-328.60	160	28.96	0.24	0.16	127	252
M_{tb}	-327.91	108	0.00	0.32 - 0.54	0.14 - 0.16	108	108
M_{bh}	-326.90	183	84.79	0.15 & 0.32	0.00 & 0.31	121	552
M_t	-325.23	206	27.20	0.15 - 0.20		166	275
M_{tbh}	-321.80	108	0.00			108	108
M_{th}	-321.23	165	20.20			137	220

Capture						95% Confidence Interval	
Model	Criteria	Estimate	SE	p-hat	c-hat	Lower	Upper
M_h - jackknife	1.00	224	17.64	0.16		194	263
M_o	0.77	207	27.22	0.17		167	275
M_{tbh}	0.61						
M_{bh}	0.57	160	28.90	0.24		127	251
M_b	0.39	160	28.90	0.24	0.16	127	251
M_{th}	0.38	318	78.87	0.10 - 0.13		212	536
M_{tb}	0.36	130	19.08	0.27 - 0.40		114	203
M_t	0.00	206	26.79	0.15 - 0.20		166	273

Lincoln-Peterson (Chapman modification)						95% Confidence Interval	
Week		Estimate	Variance	Avg. Estimate		Lower	Upper
2nd	M=35, n=41, m=5	251	6480	210		93	409
3rd	M=71, n=31, m=11	191	1477			116	266
4th	M=91, n=32, m=15	189	901			130	248

Table 2.11. Results for 193 bears caught 223 times in 2003, using Program Mark, Program Capture, and modified Lincoln-Peterson.

Mark						95% Confidence Interval	
Model	AICc Criteria	Estimate	SE	p-hat	c-hat	Lower	Upper
M_h - finite	-913.00	724	185.87	0.07 & 0.67		466	1227
M_{tb}	-912.47	193	0.00	0.33 - 0.53	0.07 - 0.14	193	193
M_b	-911.45	356	80.97	0.18	0.09	258	602
M_o	-911.24	579	89.40	0.10		440	798
M_{bh}	-909.43	356	80.97	0.18 & 1.0	0.03 & 0.09	258	602
M_t	-908.42	577	88.93	0.08 - 0.11		438	794
M_{th}	-904.68	713	154.30			487	1112
M_{tbh}	-902.15	193	0.00			193	193

Capture						95% Confidence Interval	
Model	Criteria	Estimate	SE	p-hat	c-hat	Lower	Upper
M_h - jackknife	1.00	432	25.00	0.13		389	486
M_o	0.98	579	89.13	0.10		441	796
M_{tbh}	0.86						
M_{bh}	0.85	356	80.91	0.18		259	601
M_b	0.66	356	81.10	0.18	0.09	259	602
M_{th}	0.57	802	193.41	0.06 - 0.08		525	1311
M_{tb}	0.54	622	2917.88	0.08 - 0.10		203	20326
M_t	0.00	577	88.09	0.08 - 0.11		440	791

Lincoln-Peterson (Chapman modification)						95% Confidence Interval	
Week		Estimate	Variance	Avg. Estimate		Lower	Upper
2nd	M=63, n=61, m=9	396	10129	528		199	593
3rd	M=115, n=51, m=10	547	17884			285	809
4^{th}	M=156, n=48, m=11	640	22048			349	931

Table 2.12. Results for 227 bears caught 288 times in 2004, using Program Mark, Program Capture, and modified Lincoln-Peterson.

Mark						95% Confidence Interval	
Model	AICc Criteria	Estimate	SE	p-hat	c-hat	Lower	Upper
M_b	-1050.63	317	33.39	0.27	0.14	272	409
M_{tb}	-1048.86	227	0.00	0.37 - 0.57	0.13 - 0.15	227	227
M_o	-1046.62	457	43.91	0.16		385	560
M_{bh}	-1046.29	348	59.39	0.22 & 1.0	0.12 & 0.36	275	528
M_t	-1046.17	454	43.58	0.13 - 0.18		384	557
M_h - finite	-1043.39	687	810.12	0.06 & 0.24		272	4948
M_{th}	-1041.83	1792	8872.21			267	61485
M_{tbh}	-1041.20	227	0.00			227	227

Capture						95% Confidence Interval	
Model	Criteria	Estimate	SE	p-hat	c-hat	Lower	Upper
M_{bh}	1.00	317	33.36	0.27		272	409
M_b	0.95	317	33.37	0.27	0.14	272	409
M_{tbh}	0.76						
M_o	0.59	457	43.78	0.16		386	559
M_{tb}	0.57	320	82.40	0.26 - 0.27		249	640
M_h - jackknife	0.56	464	25.42	0.16		419	519
M_{th}	0.41	537	84.13	0.11 - 0.16		411	749
M_t	0.00		43.25	0.13 - 0.18		384	555

Lincoln-Peterson (Chapman modification)						95% Confidence Interval	
Week		Estimate	Variance	Avg. Estimate		Lower	Upper
2nd	M=84, n=77, m=13	473	10247	450		274	671
3rd	M=148, n=67, m=22	440	4525			308	571
4th	M=193, n=60, m=26	437	3292			325	550

Table 2.13. Weekly home ranges (calculated as minimum convex polygons) of male and female black bears during 4 weeks of non-invasive genetic sampling in Hyde County, North Carolina. Data from 4 of the 7 males are from Spring 2003, while data from the remaining 3 males and all 4 females are from Spring 2004.

	Average mi^2 (km^2)	Minimum mi^2 (km^2)	Maximum mi^2 (km^2)	Average # of corrals	Minimum # of corrals	Maximum # of corrals
7 males						
Week 1	7.9 (20.5)	1.0 (2.7)	21.8 (56.4)	5.0	0 (Closest < 290 m)	10
Week 2	4.9 (12.8)	1.9 (4.8)	7.0 (18.1)	4.7	3	7
Week 3	5.1 (13.3)	0.8 (2.1)	11.7 (30.4)	4.3	0 (Closest < 290 m)	9
Week 4	4.6 (11.9)	2.4 (6.1)	8.8 (22.7)	3.7	1	7
All weeks	5.6 (14.6)	0.8 (2.1)	21.8 (56.4)	4.4	0 (twice)	10
4 females						
Week 1	2.6 (6.8)	0.4 (0.9)	5.5 (14.2)	1.5	0 (Closest < 350 m)	2
Week 2	2.6 (6.8)	0.9 (2.4)	4.8 (12.3)	1.8	0 (Closest < 160 m)	4
Week 3	4.6 (12.0)	1.5 (4.0)	9.7 (25.1)	2.0	1	3
Week 4	2.4 (6.1)	1.1 (2.7)	3.8 (9.8)	1.3	1	2
All weeks	3.1 (7.9)	0.4 (0.9)	9.7 (25.1)	1.6	0 (twice)	4

Table 2.14. Comparison of sampling results for bears using DNA hair traps, hunter harvests, and trapping (culvert traps or Aldrich foot snares) during 2001-2004 in Hyde County, North Carolina.

	# of bears	**% of capture method**
Of the total bears sampled via DNA hair traps	**705**	
DNA hair traps only	595	84.4%
DNA hair traps + hunter harvest	56	7.9%
DNA hair traps + trapping	39	5.5%
DNA hair traps + hunter harvest + trapping	15	2.1%
Total # of bears sampled via hunter harvest	**250**	
hunter harvest only	173	69.2%
hunter harvest + DNA hair traps	56	22.4%
hunter harvest + trapping	6	2.4%
hunter harvest + trapping + DNA hair traps	15	6.0%
Total # of bears sampled via trapping	**73**	
trapping only	13	17.8%
trapping + DNA hair traps	39	53.4%
trapping + hunter harvest	6	8.2%
trapping + DNA hair traps + hunter harvest	15	20.5%

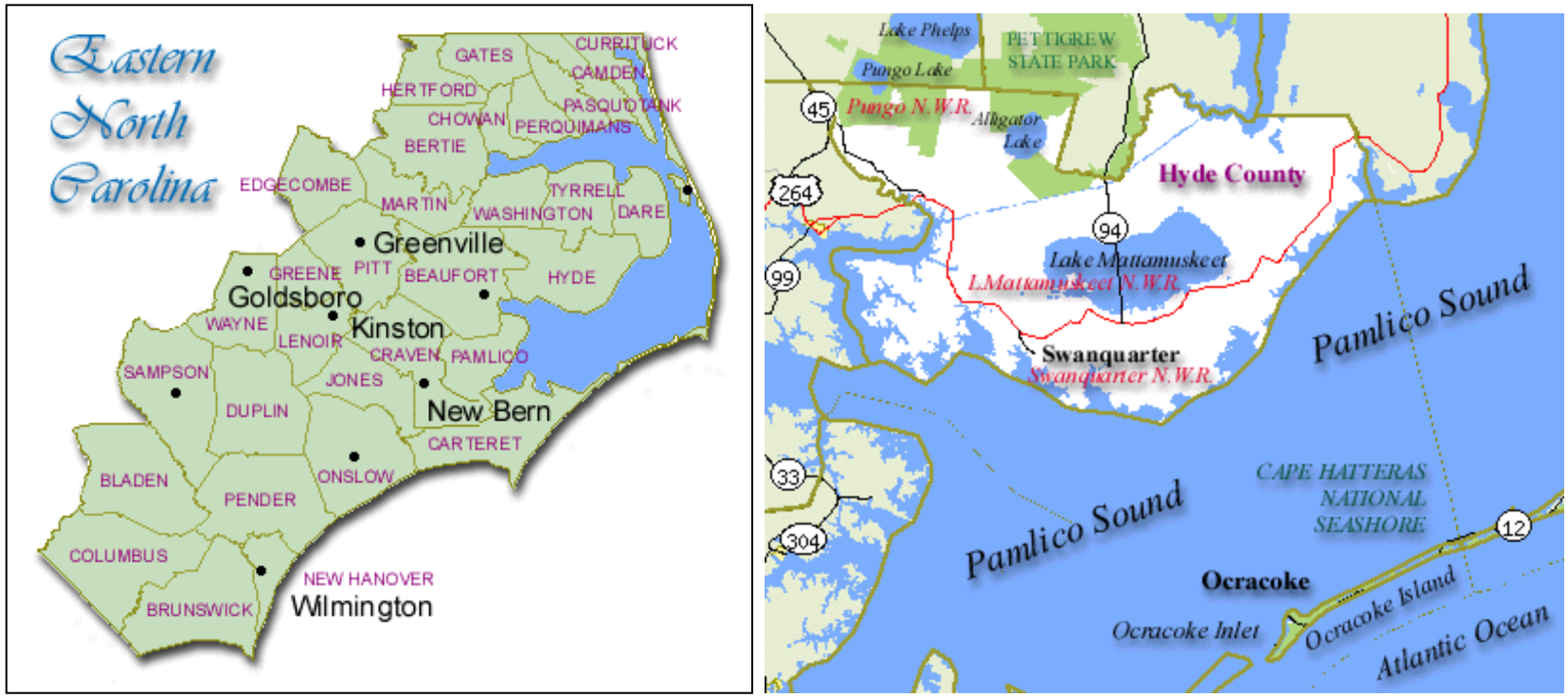

Figure 2.3. Eastern North Carolina, with inset of Hyde County (http://www.waywelivednc.com/maps/eastern.htm presented by The North Carolina Office of Archives and History in association with The University of North Carolina Press, 2004).

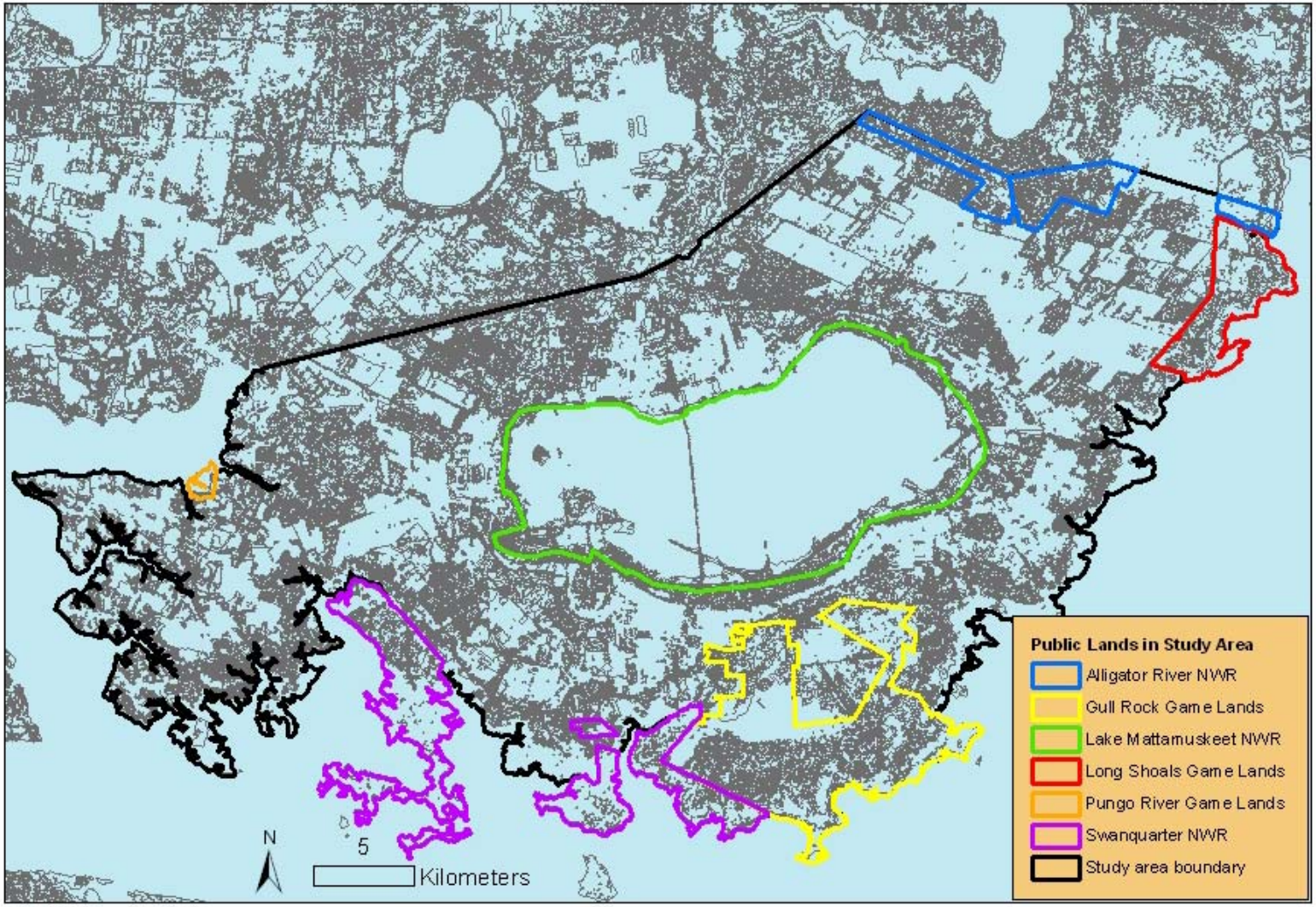

Figure 2.4. State game lands and National Wildlife Refuges (NWR) in our study area south and east of the intra-coastal waterway in Hyde County, NC.

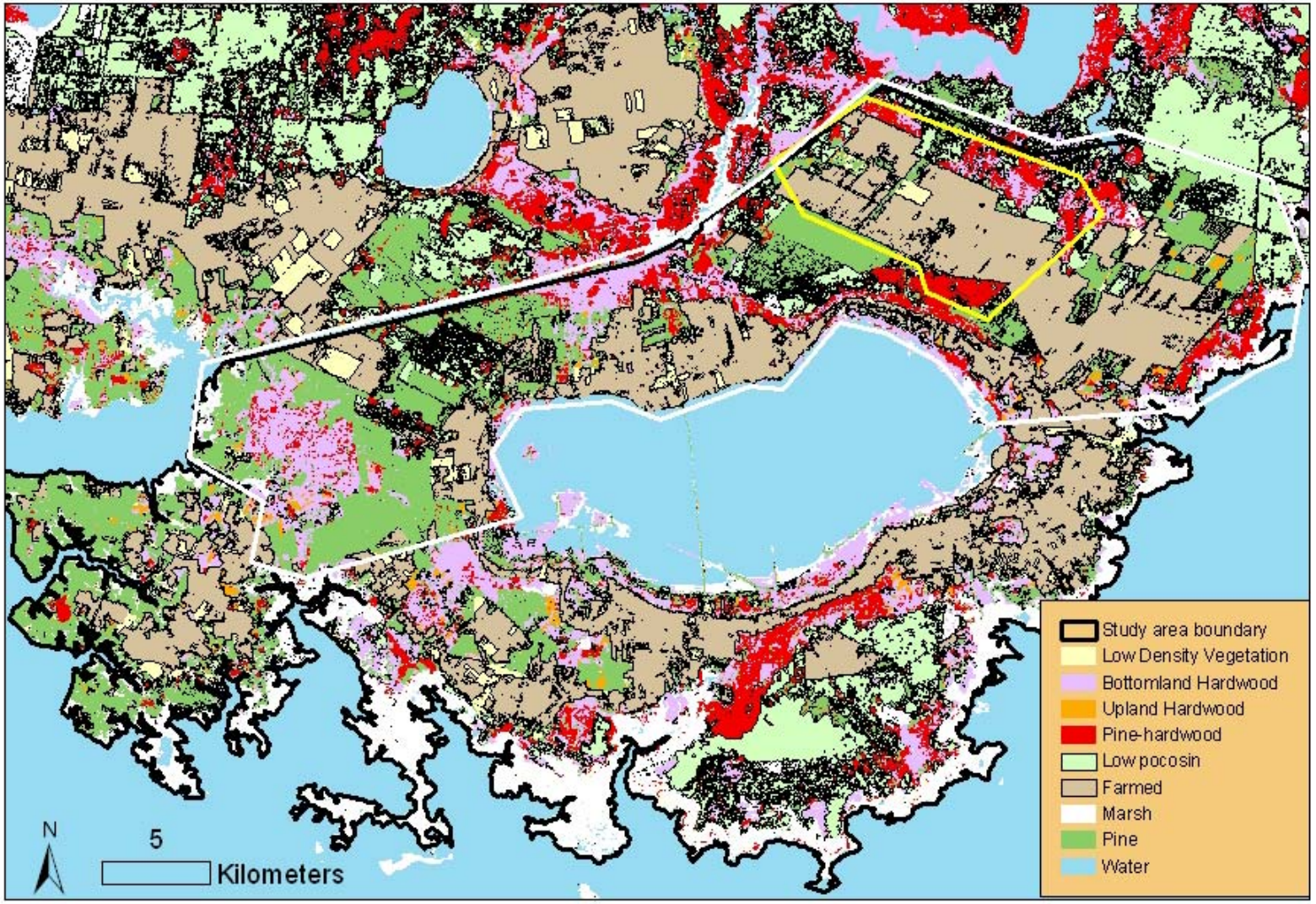

Figure 2.5. Study areas for noninvasive genetic sampling: 2001 (yellow), 2002 (white), and 2003-2004 (black) in Hyde County, NC.

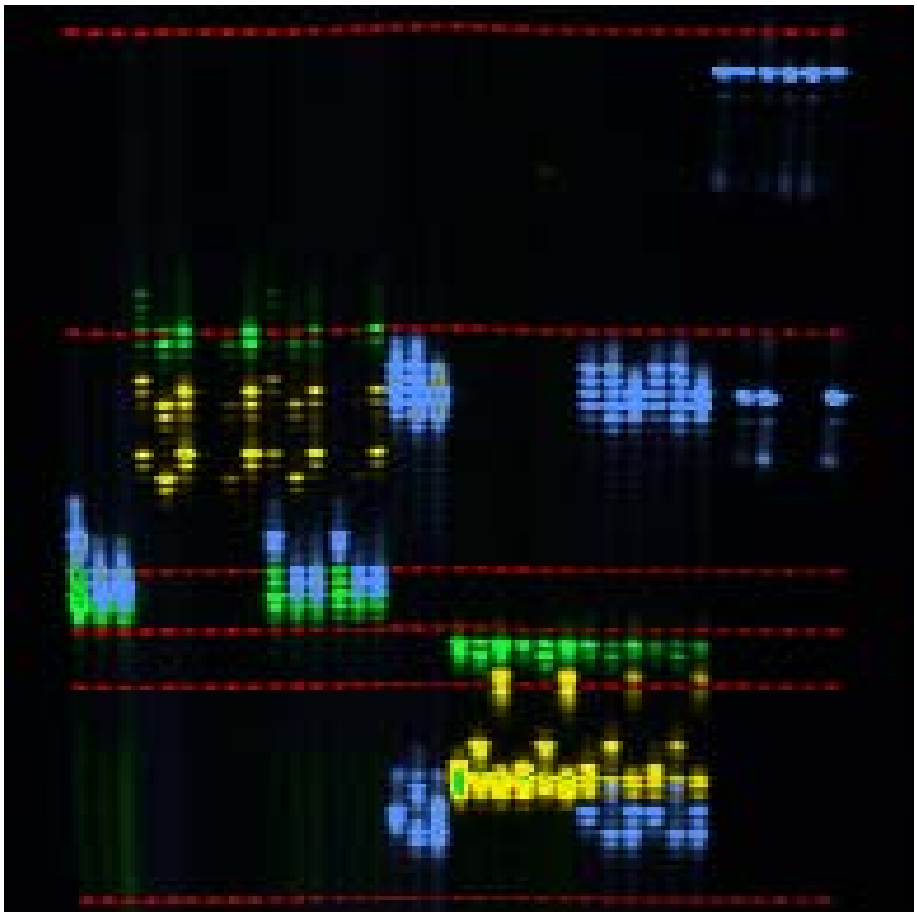

Figure 2.6. An example of spectral interference and other difficulties when trying to multiplex micro-satellite reactions and run them in adjacent lanes on an acrylamide gel.

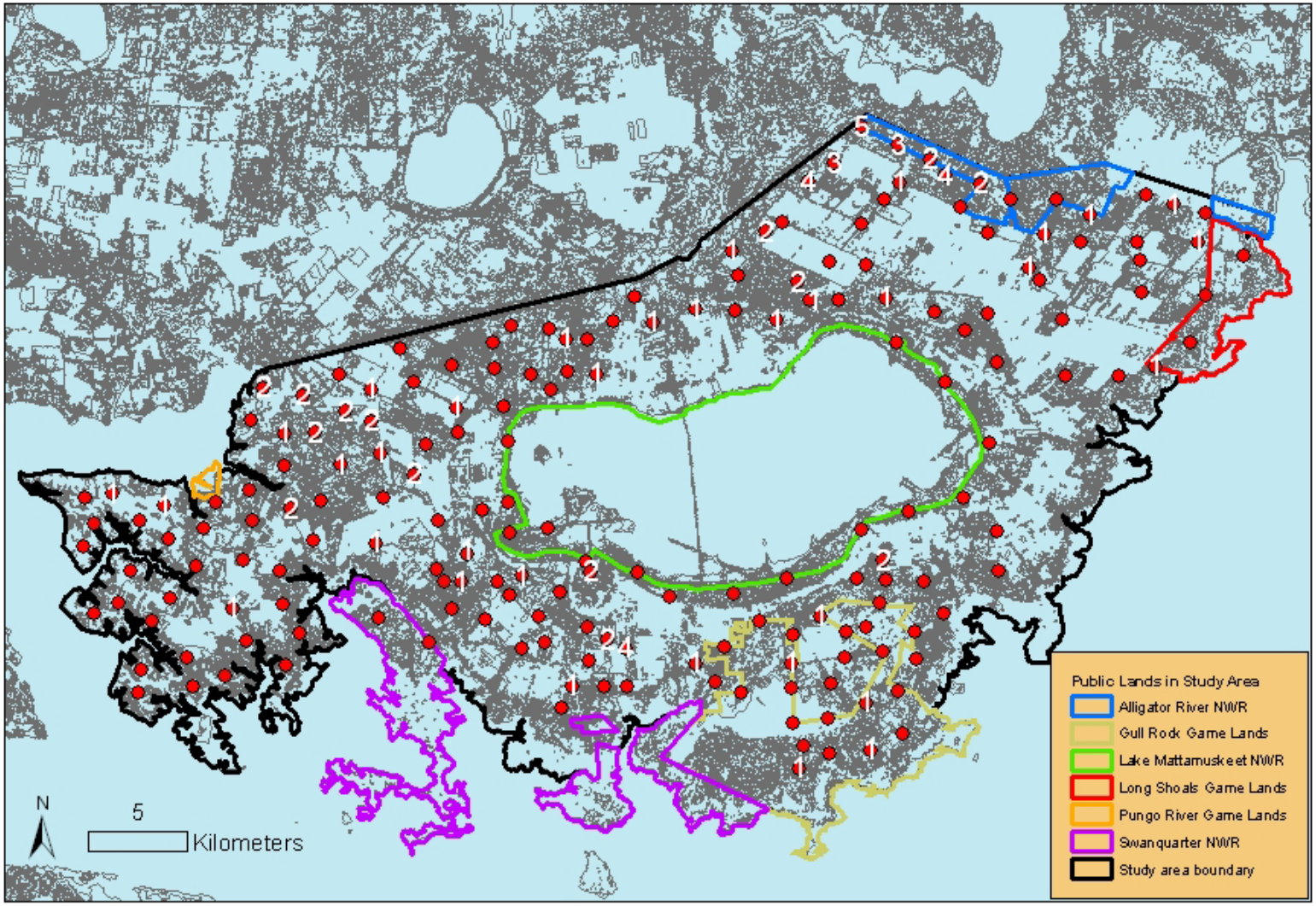

Figure 2.7. Number of unique females sampled at each DNA hair trap during Spring 2003 in Hyde County, North Carolina.

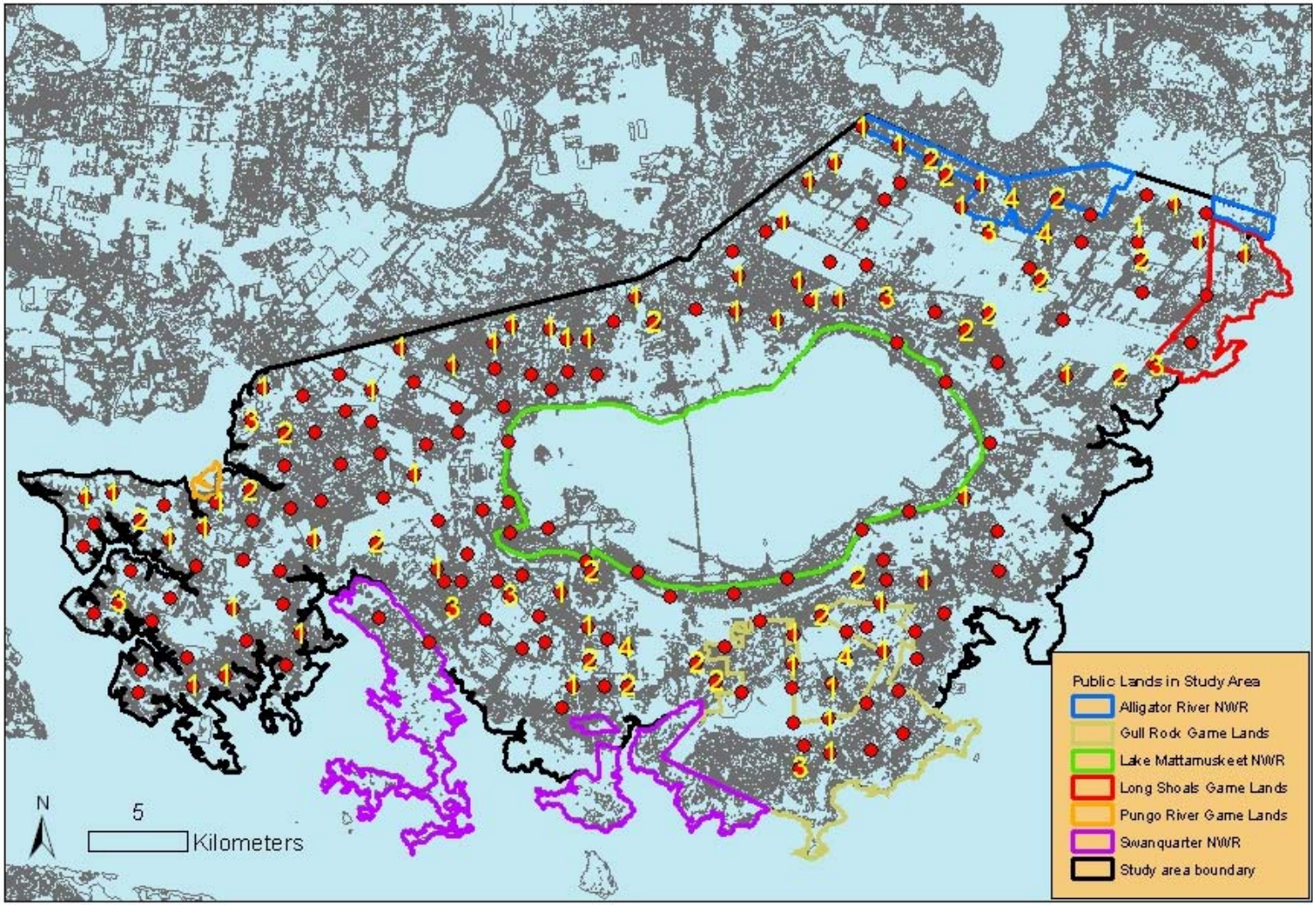

Figure 2.8. Number of unique males sampled at each DNA hair trap during Spring 2003 in Hyde County, North Carolina.

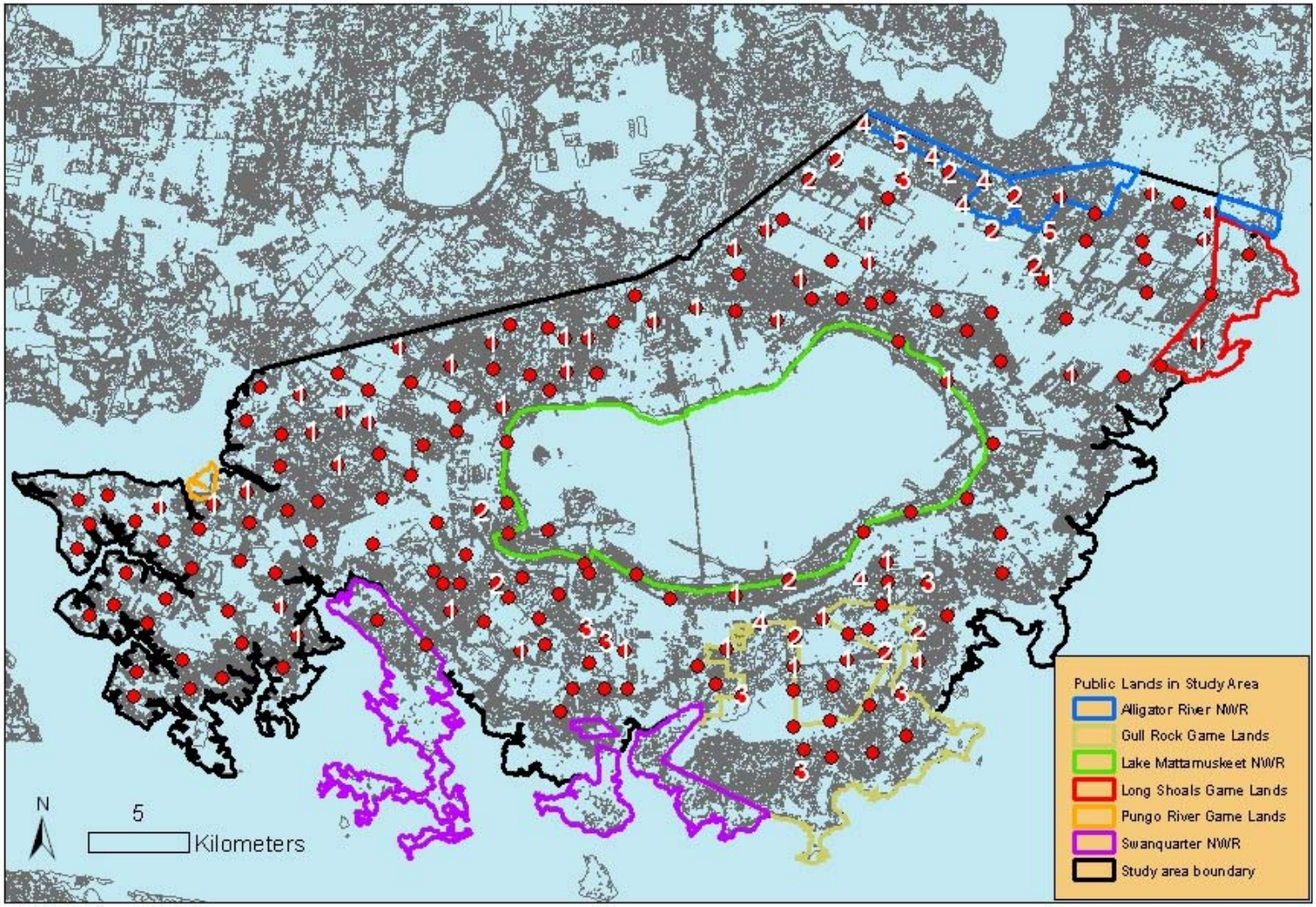

Figure 2.9. Number of unique females sampled at each DNA hair trap during Spring 2004 in Hyde County, North Carolina.

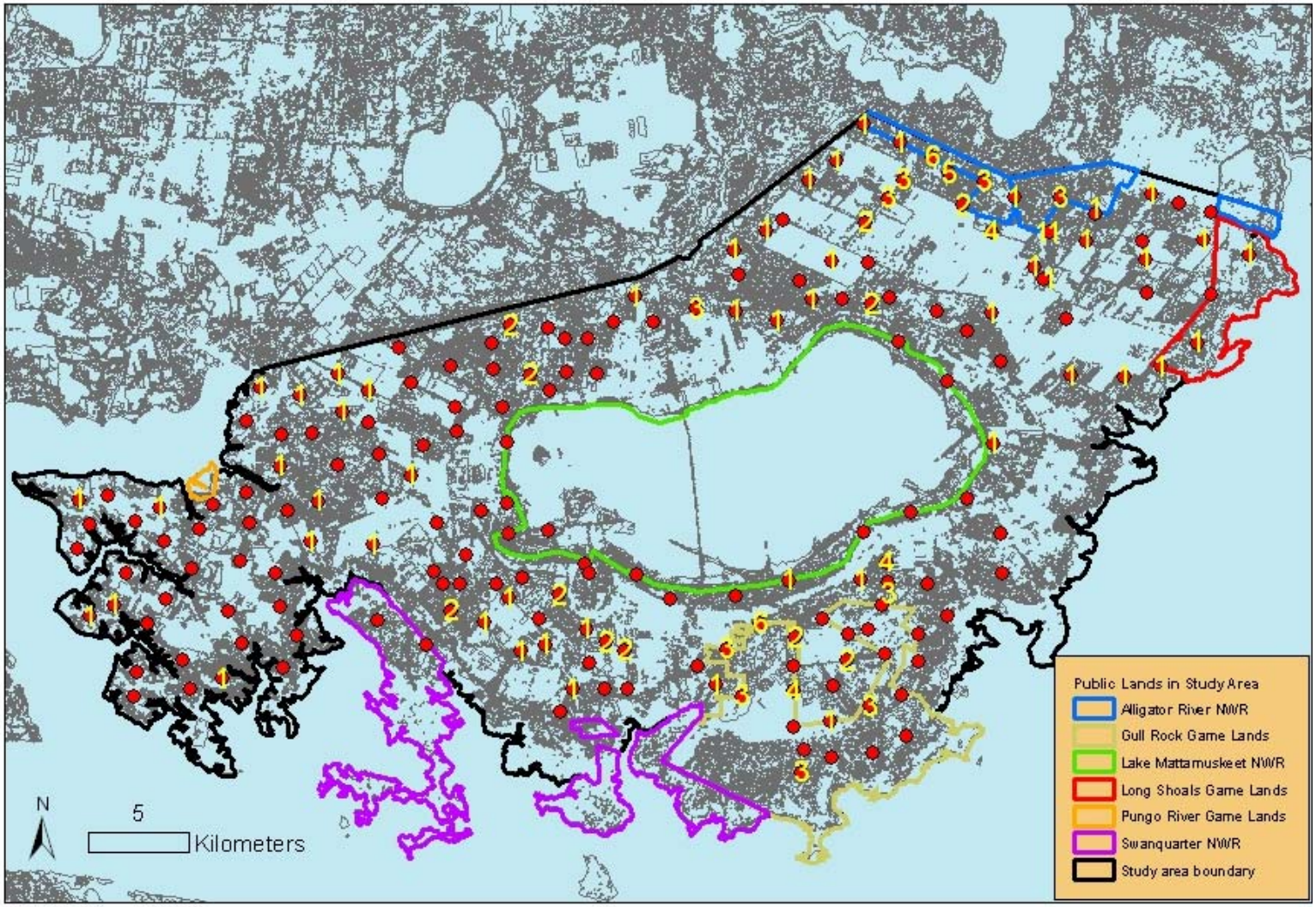

Figure 2.10. Number of unique males sampled at each DNA hair trap during Spring 2004 in Hyde County, NC.

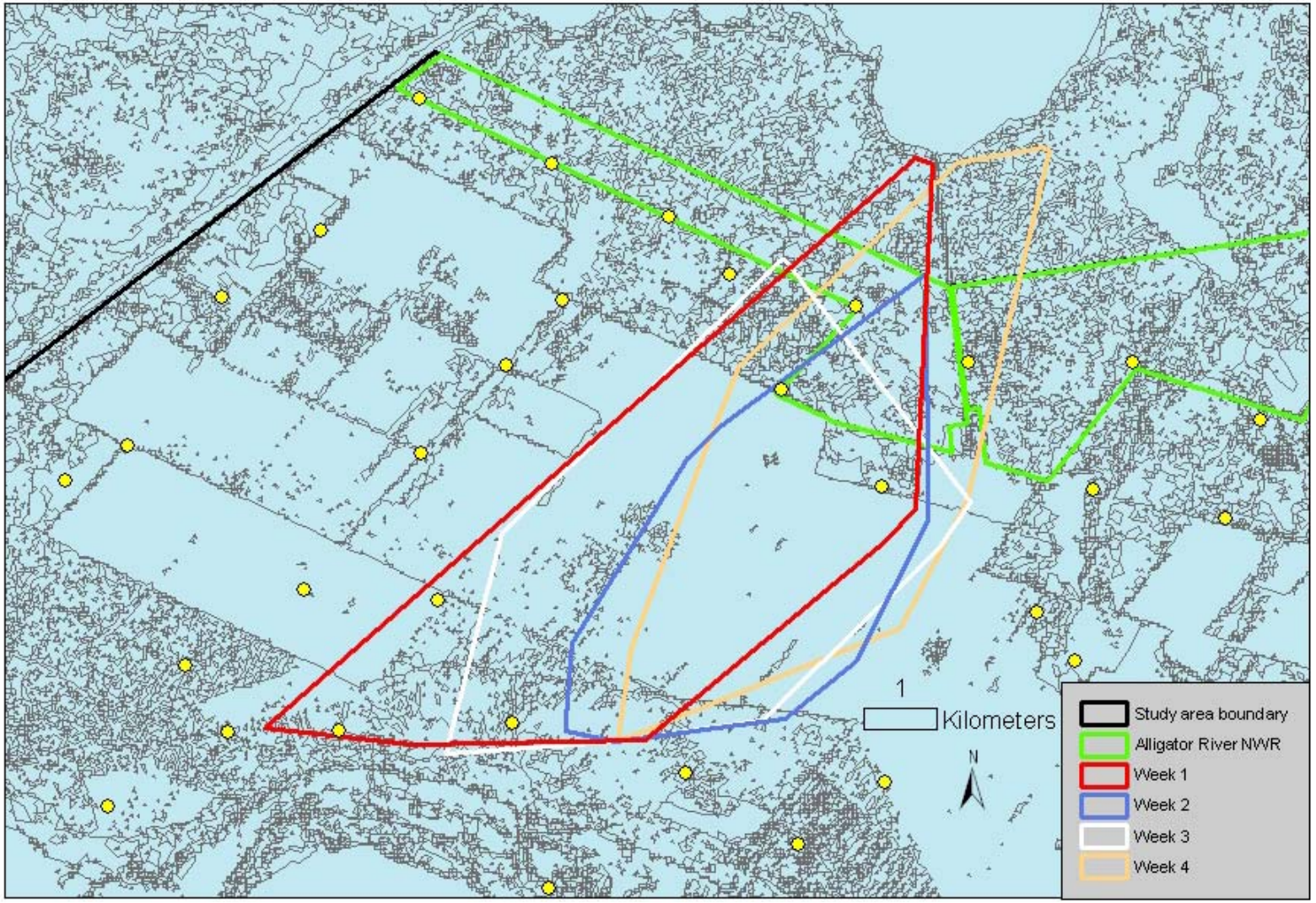

Figure 2.11. Minimum convex polygons of 4 week periods for 1 male black bear during Spring 2003 in Hyde County, North Carolina.

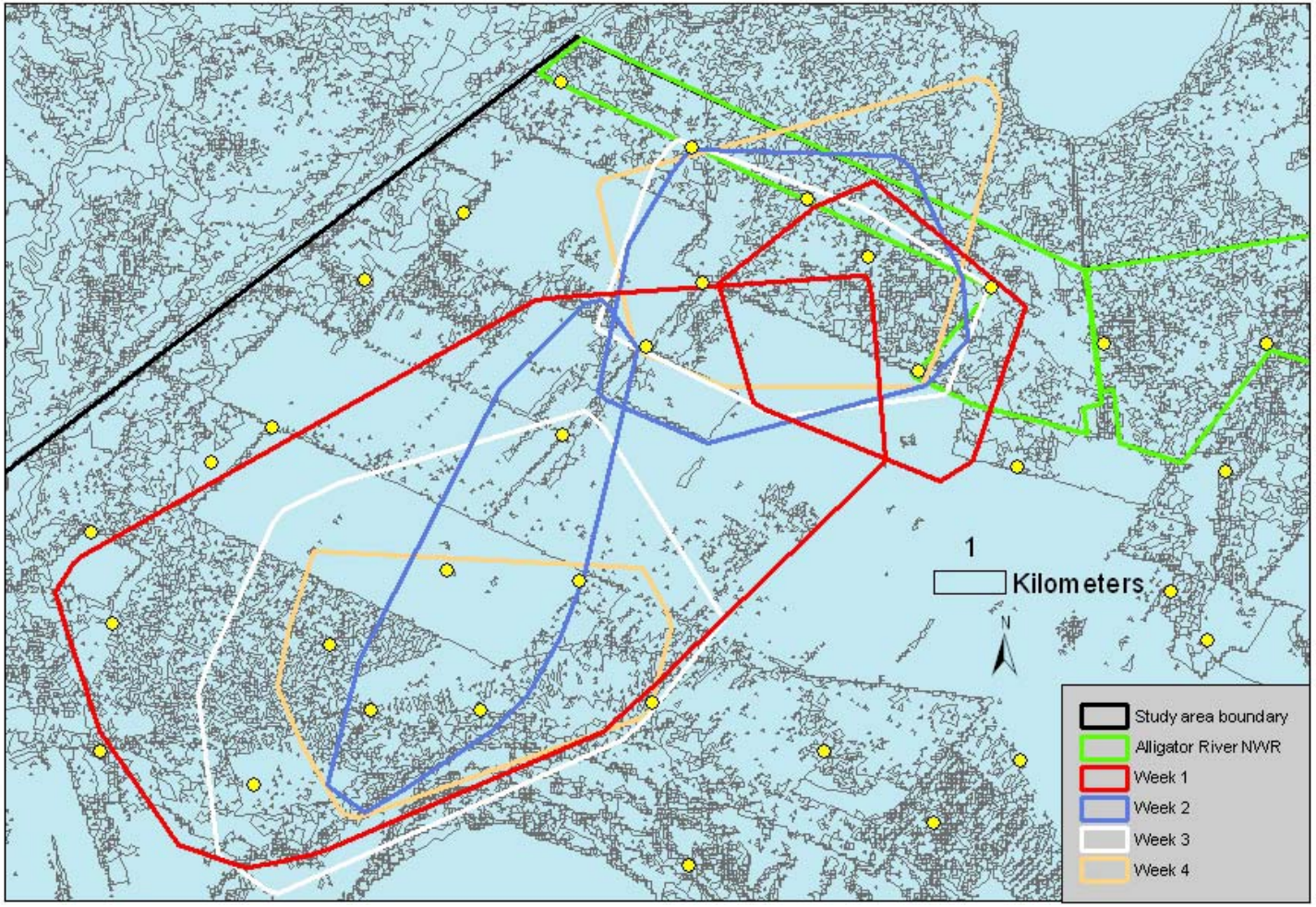

Figure 2.12. Minimum convex polygons of 4 week periods for 2 male black bears during Spring 2004 in Hyde County, NC.

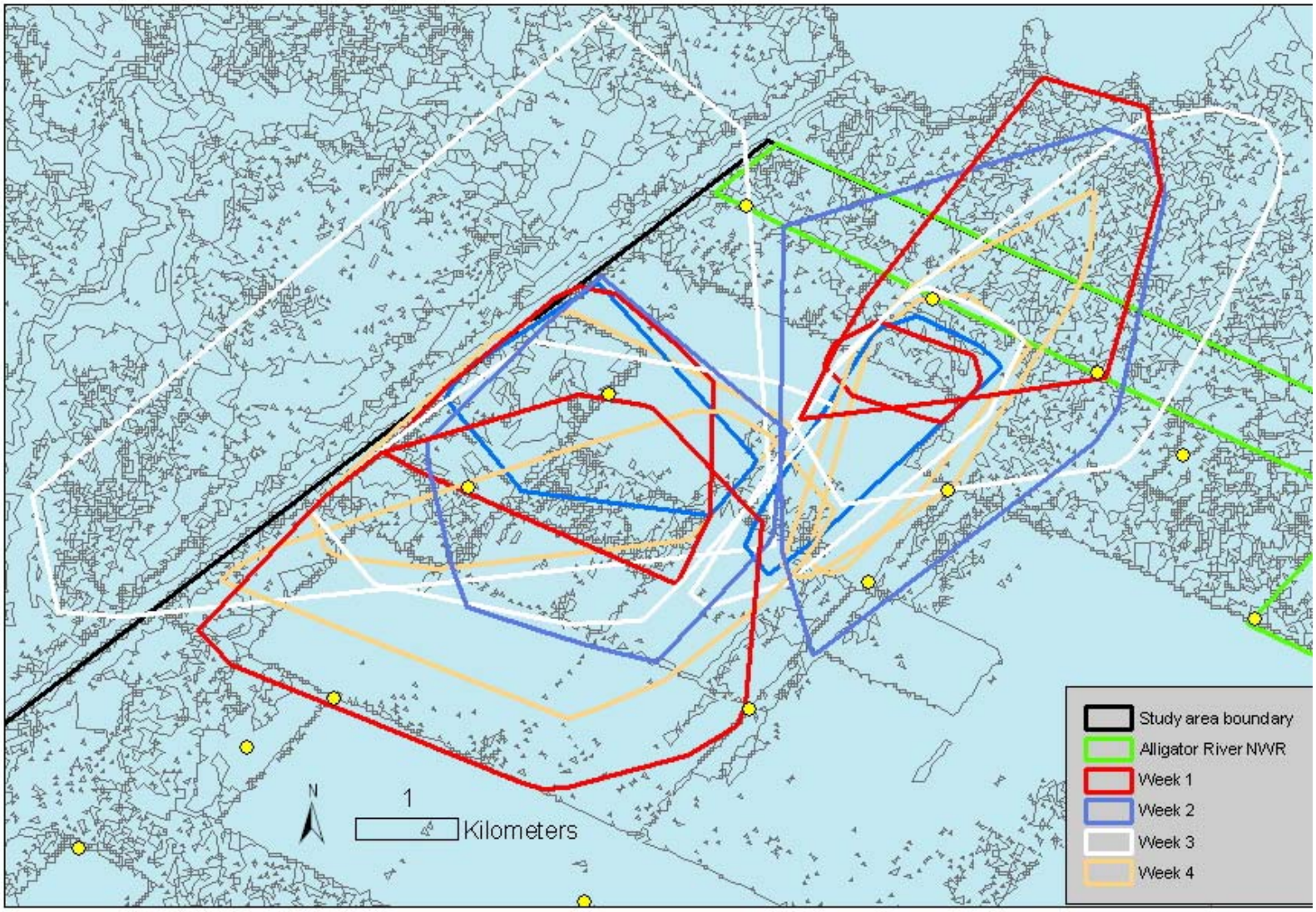

Figure 2.13. Minimum convex polygons of 4 week periods for 4 female black bears during Spring 2004 in Hyde County, NC.

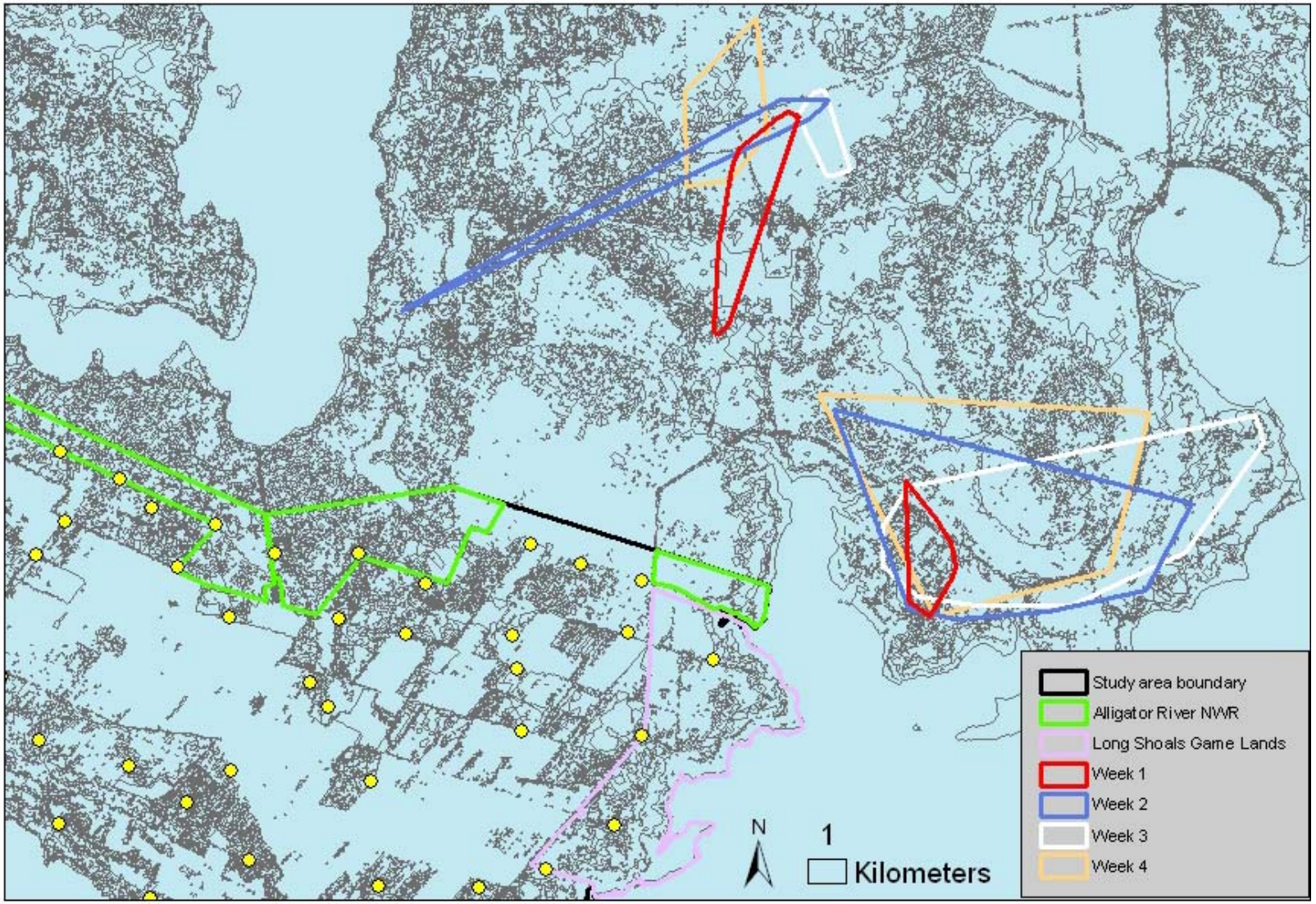

Figure 2.14. Minimum convex polygons of 4 week periods for 2 male black bears during Spring 2003 in Dare County, NC.

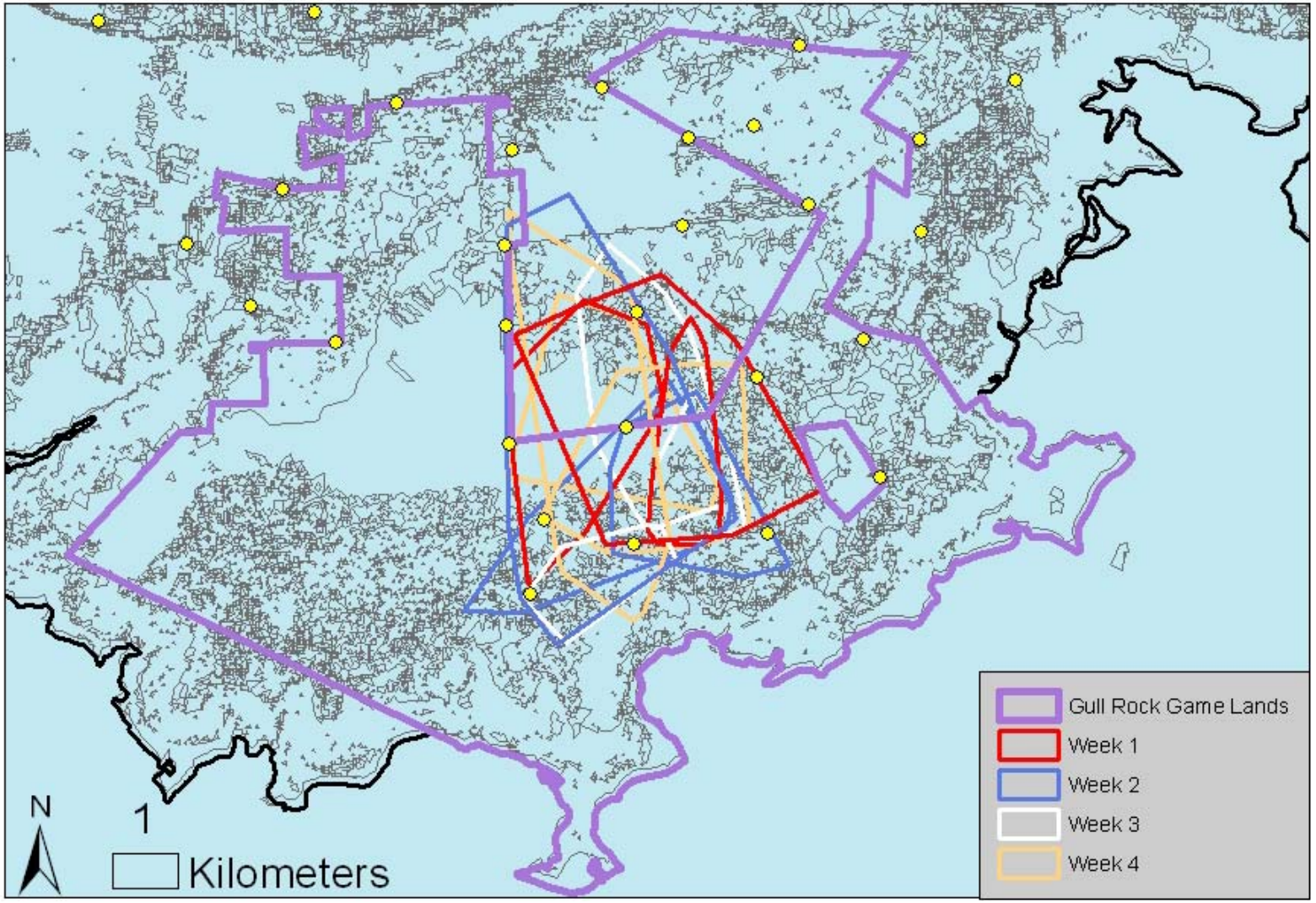

Figure 2.15. Minimum convex polygons of 4 week periods for 3 male black bears during Spring 2003 in Hyde County, NC.

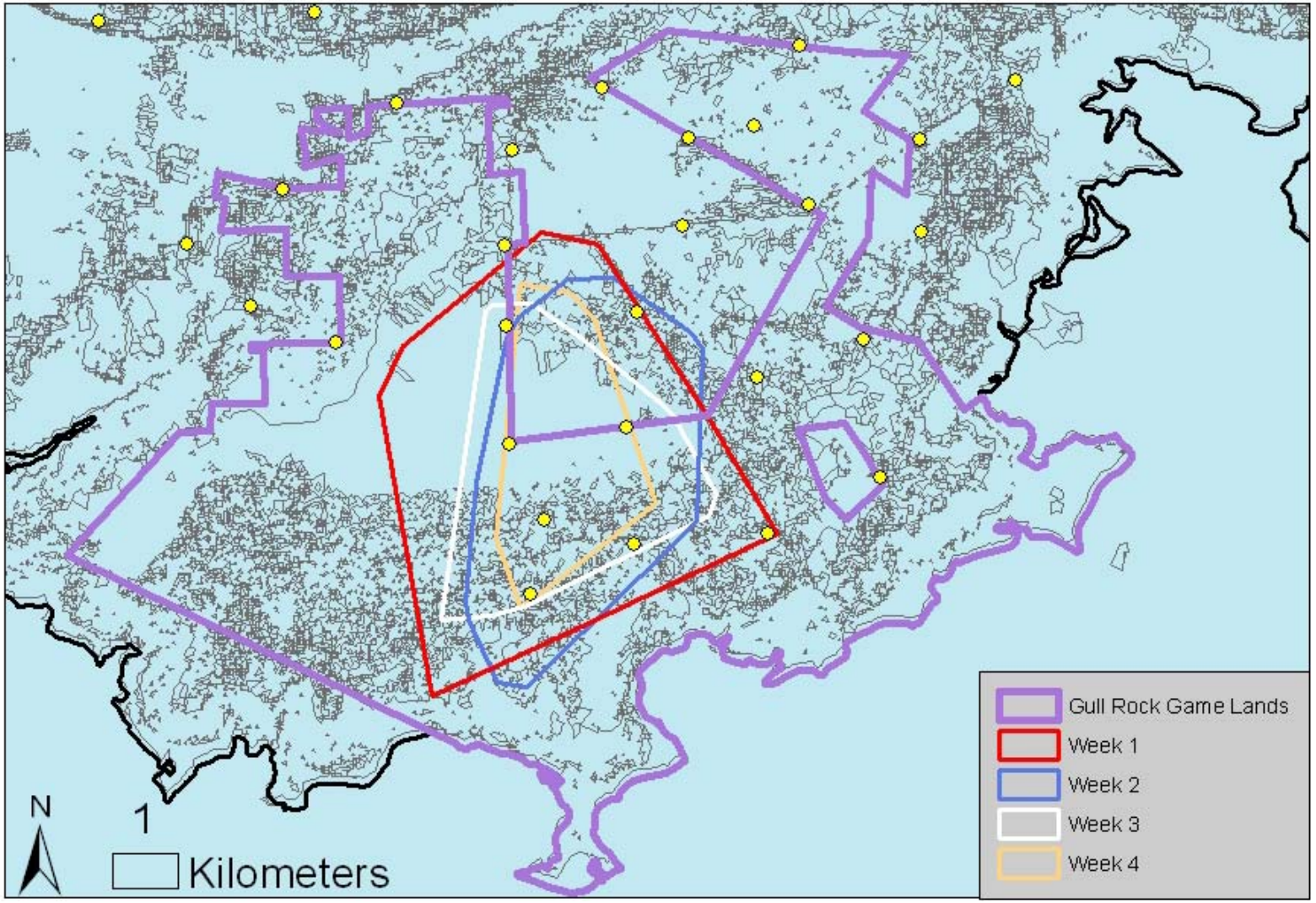

Figure 2.16. Minimum convex polygons of 4 week periods for 1 male black bear during Spring 2004 in Hyde County, NC.

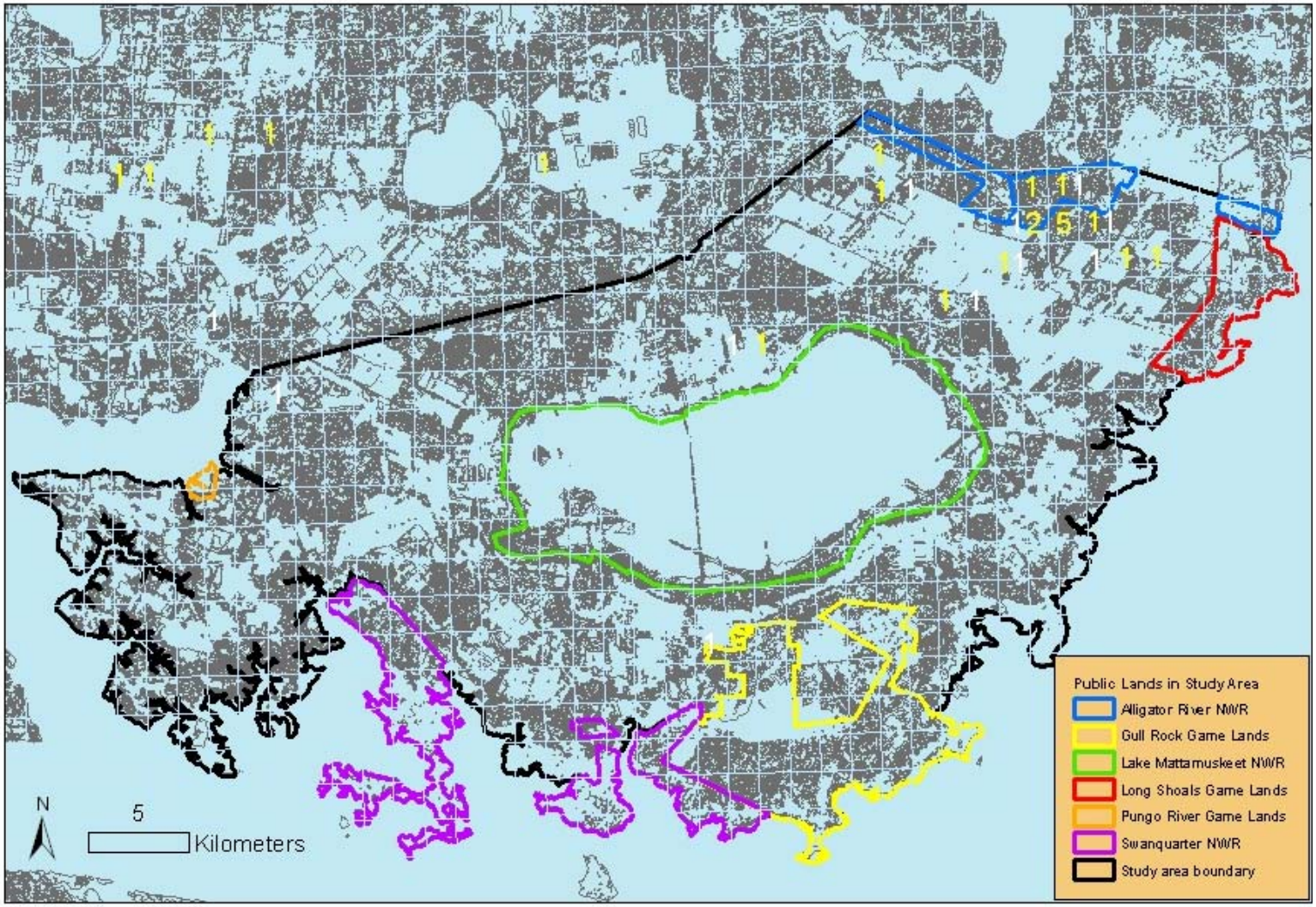

Figure 2.17. Number of males (yellow) and females (white) that were hunter harvested and sampled in 2002 in Hyde County, NC.

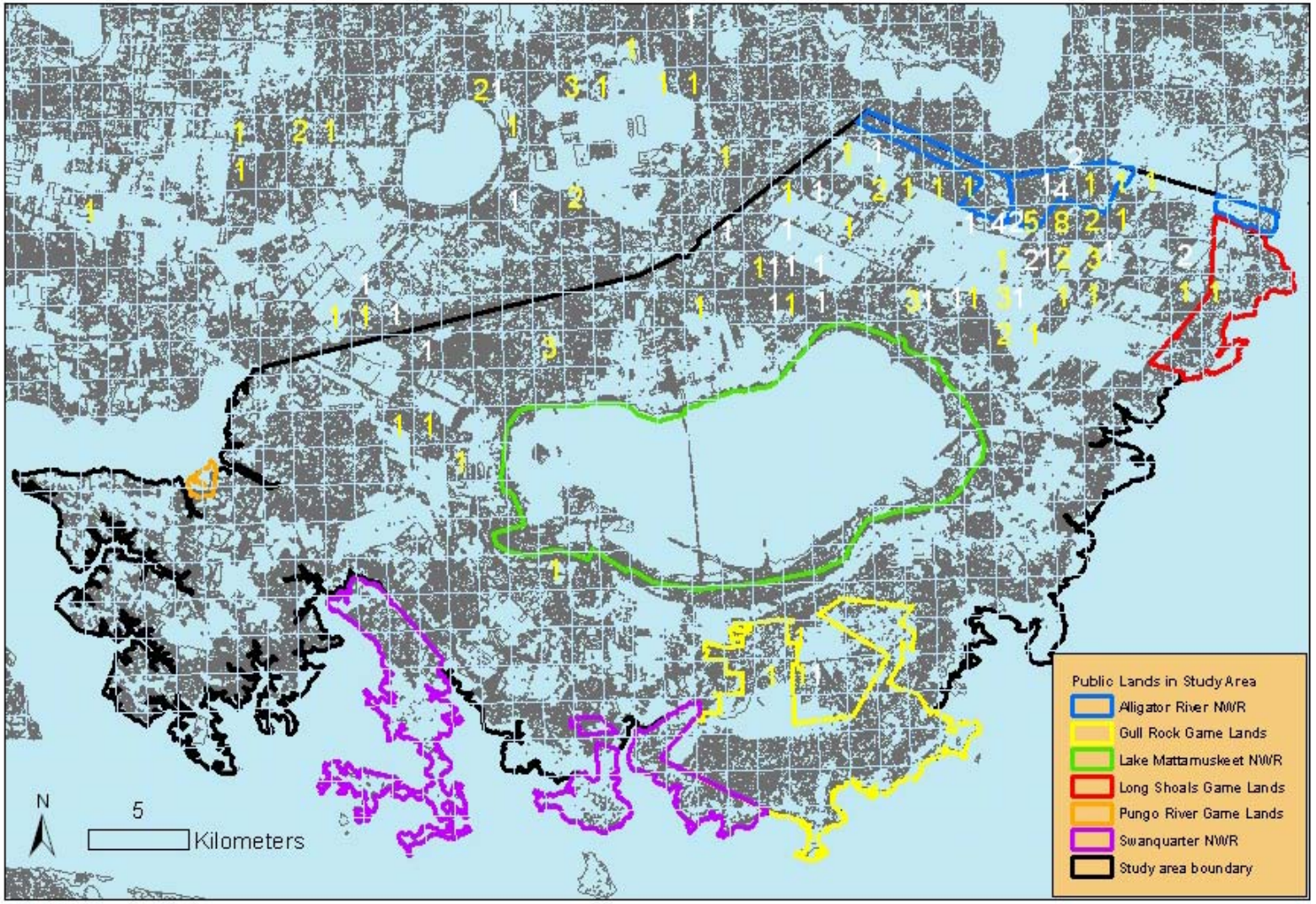

Figure 2.18. Number of males (yellow) and females (white) that were hunter harvested and sampled in 2003 in Hyde County, NC.

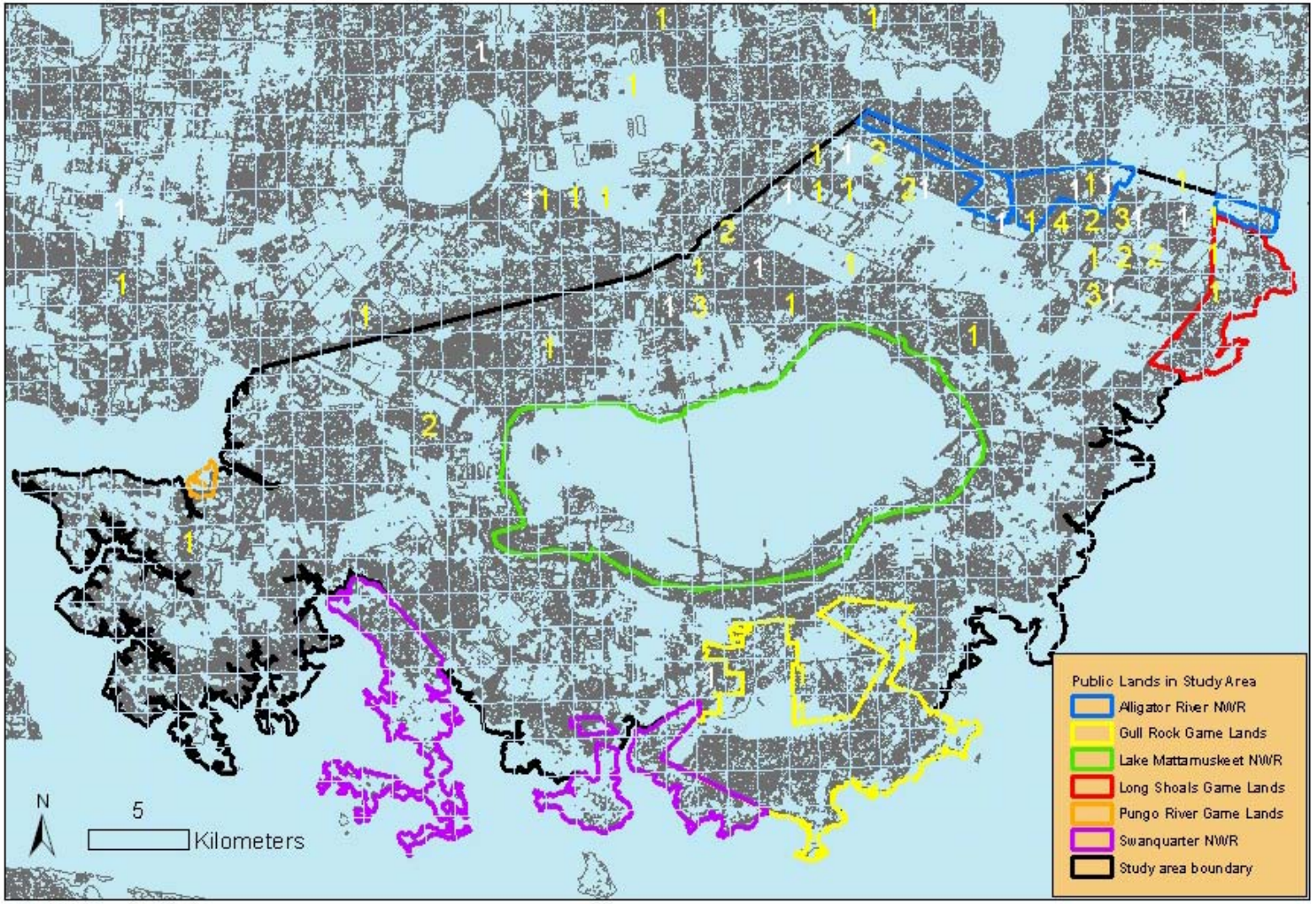

Figure 2.19. Number of males (yellow) and females (white) that were hunter harvested and sampled in 2004 in Hyde County, NC.

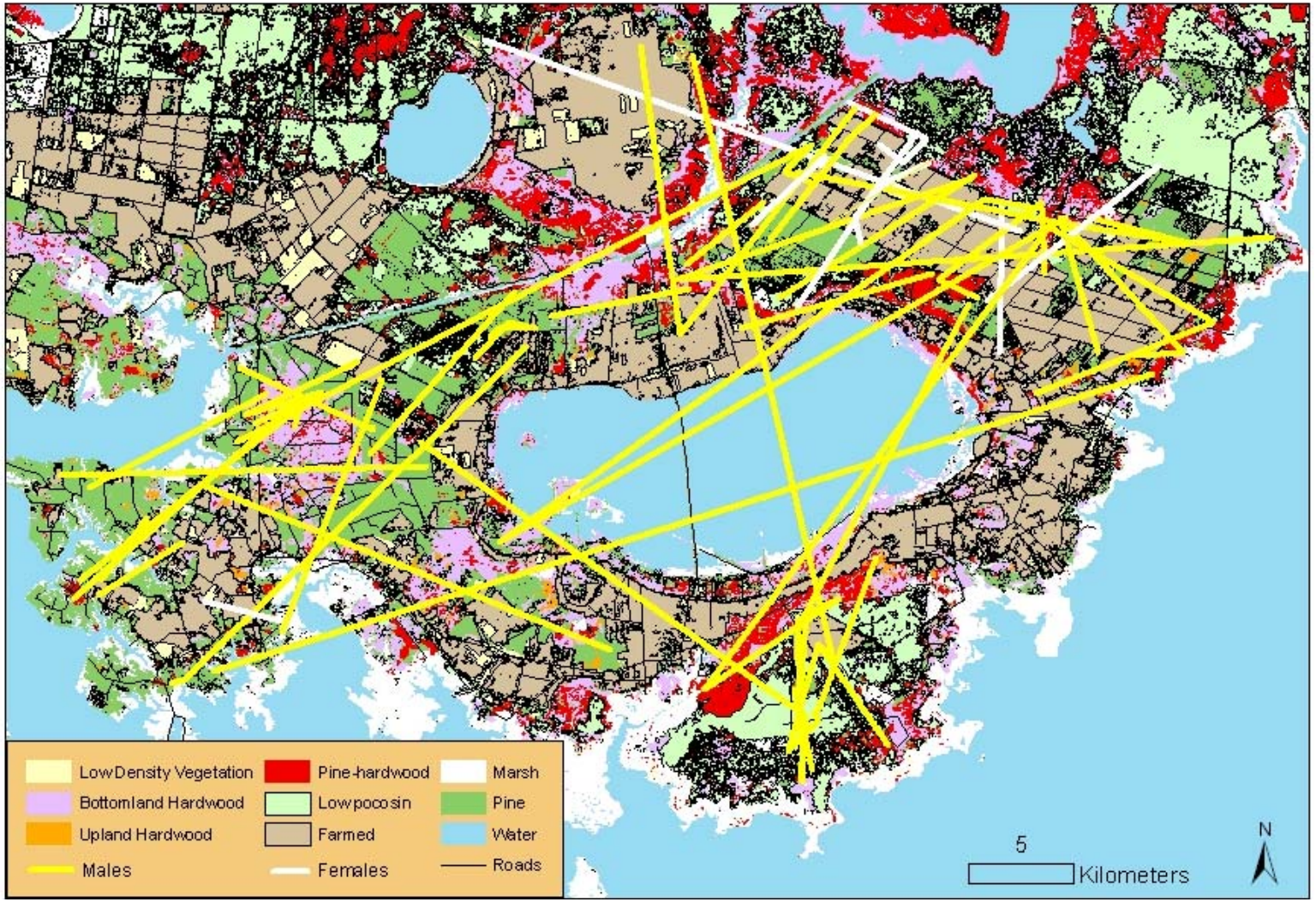

Figure 2.20. Depictions of extreme distances between multiple locations for individual bears, sampled via DNA hair traps, Aldrich foot snares, culvert traps, and/or hunter harvest during 2001-2004 in Hyde and Tyrrell counties, NC.

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CHAPTER 3

PRIVATE INVOLVEMENT ENHANCES WILDLIFE RESEARCH

Figure 3.1. People of all ages experienced bear trapping and supported bear research.

ABSTRACT

Wildlife research has traditionally been conducted with little awareness or involvement by the private sector. Principal investigators often respond to a request for proposals from a public agency with research designed for public lands and present their findings at professional conferences and in peer-reviewed journals. I feel wildlife researchers need to expand this approach and involve the public. Private individuals can provide land access, research ideas, local knowledge, financial, and monetary support if we make an effort to develop personal relationships with them via public talks, informal reports, and invitations to participate in the research. Among the biggest challenges facing us is how to conserve our natural resources for future generations, given the growing human population and its impacts on the environment. In this paper I explain how wildlife researchers can conduct rigorous science and also improve wildlife conservation by using examples from my black bear (*Ursus americanus*) research in North Carolina. It is well understood among conservation biologists that conserving natural resources only on public land is insufficient. I believe that engaging, not just educating, the public positively affects their values of wildlife and wild places, which is what I propose as the ultimate goal of wildlife research in the 21st century.

Key words: Wildlife research, funding, values, conservation, public policy

Researchers play a vital role in objectively discovering, understanding, and describing effects generated by events or interactions with respect to wildlife (Riley et al. 2002). Though technology advances relentlessly, Keppie (1990) and Mason (1983) were not

convinced better research equates to better decisions. Riley et al. (2002) stated that knowledge is insufficient for effective wildlife management without integrating human dimensions and White (2001) reported that data and logical arguments cannot defuse some of the emotional issues that are the basis of wildlife management conflicts. Leopold realized this deficiency long ago: "One of the anomalies of modern ecology is the creation of two groups, each of which seems barely aware of the existence of the other. The one studies the human community, almost as if it was a separate entity, and calls its findings sociology, economics, and history. The other studies the plant and animal community and comfortably relegates the hodge-podge of politics to the liberal arts. The inevitable fusion of these two lines of thought will, perhaps, constitute the outstanding advance of the present century" (Meine 1988). By involving the public, who have entrusted wildlife to management by wildlife agencies, wildlife researchers can conduct more robust science, as well as leave a longer lasting legacy by bridging the gaps between wildlife research, human dimensions, wildlife management and public policy.

Changing bear management challenges in western North Carolina: The traditional focus of wildlife managers has often been to restore populations to biological carrying capacities and provide benefits to a relatively narrow range of "stakeholders", defined as anyone who will be affected by, or will affect, wildlife or wildlife management (Decker et al. 1996, Organ and Ellingwood 2000). In North Carolina there were perceived to be so few bears that citizens legislated control of bear management away from the North Carolina Wildlife Resources Commission (NCWRC) and closed bear hunting statewide via county initiatives in the late 1960s. In 1970 NCWRC responded with many actions to restore bear populations, most significant of which was the establishment of 28 bear sanctuaries

statewide. The bear population rebounded and bear hunting opened again in the 1980s, largely subject to NCWRC control. Since then record harvests and range expansion of bears have been reported (M. Jones, NCWRC, personal communication).

Wildlife managers would seem to have already overcome the toughest obstacles to managing bears at this point. However, times change and the 21st century has brought new challenges. Facing more diverse interests and conflicting expectations of a broader stakeholder base, managers have to consider the Wildlife Stakeholder Acceptance Capacity, or WSAC (Organ and Ellingwood 2000). Ellingwood and Spignesi (1986) first described WSAC as a "cultural" carrying capacity and explained it can be significantly lower than the Biological Carrying Capacity (BCC) for some species. Management decisions are made even more difficult by the complex nature of the WSAC. While both are dynamic in the long-run, BCC is usually fixed at a given point in time, while WSAC can simultaneously be at different extremes among various stakeholder groups (Organ and Ellingwood 2000, Siemer and Decker 1991). From their survey on stakeholders' attitudes towards black bear management practices, Teel et al. (2002) reported such diverse attitudes within the non-user group regarding wildlife-related issues that it was often difficult to generalize orientations.

Bears in the mountains of North Carolina seem to be above WSAC. As people move into core bear areas, and bears expand their range into suburban areas, conflicts between bears and humans increase and management becomes more difficult. During mast crop failures, bear complaints become particularly problematic, as bears may look to anthropogenic sources of food to fill the void in natural sources. In North Carolina, part of the human population increase is comprised of transplants from states without bears or a bear hunting tradition. This change in the human constituency affects WSAC and acceptable

management decisions, due to values that vary with demographics, level of education, and length of residency. For example, urban sprawl makes traditional means of control (hunting and trapping) difficult, even if control was supported by a majority of constituents (Organ and Ellingwood 2000, Teel et al. 2002).

Education is one way to raise the WSAC. Bowman et al. (2001) concluded that educational programs are needed to improve the knowledge about black bear natural history and management. Bowman et al. (2001) also reported that with education, positive attitudes toward black bears are possible, even at high bear population levels. A greater understanding of underlying motives and values that affect the dynamics of WSAC is essential to insure that agency programs will be responsive and generate long-term public support (Organ and Ellingwood 2000). The NCWRC currently conducts public hearings on a yearly basis, but Bleiker and Bleiker (2000) reported such hearings are the least desirable type because they have the narrowest representation of stakeholders. Credibility is the main currency of public agencies for keeping support of stakeholders, which Beck et al. (1995) argued wildlife agencies will lose if they do not rapidly develop a philosophy for decision-making that includes constituents which have historically been left out of the process. The sufficiency-of-biology and expert-authority precepts used effectively by wildlife managers in the 20th century must be expanded to include stakeholders throughout the decision-making process (Riley et al. 2002). I believe educating the public needs to evolve into engaging the public, which seeks input and not just acceptance.

Another solution to a bear population that is higher than WSAC in the mountains of NC is to increase harvest. The NCWRC reported the mountain bear population can support a higher bear harvest and currently proposes allowing hunting on land currently designated as a

bear sanctuary (M. Jones, NCWRC, personal communication). Beyond the potential reactions from non-user groups to expanded hunting, this proposal has upset some hunter groups, which hold the sanctuaries as sacred and insurance that there will be bears to hunt in the future. At the same time, non-hunting NC residents in the mountains have been urging managers to increase the minimum weight for harvested bears from 50 to 100 pounds (M. Jones, NCWRC, personal communication), because how the hunt is conducted is a powerful factor in their acceptance of hunting (Beck et al. 1995). Raising the minimum size could result in fewer bears being harvested and possibly higher densities. In general, wildlife managers certainly can use help shaping societal values, given the growing disapproval of many traditional forms of predator management. "Protectionist" values towards wildlife may already be firmly established in hunters and traditionally supportive groups, as well as the general population (Pacelle 1998). Education can help constituents understand management proposals. However, if most members of the public are opposed, education alone is likely to prove ineffective (Teel et al. 2002). Clearly, bear management decisions in NC are becoming more complicated.

A model for more robust wildlife research: Wildlife researchers can and should do more to help wildlife managers. White (2001) pointed out that currently the human dimensions wizards in wildlife management are often asked to resolve impossible conflicts. All stakeholders are right, given the assumptions each brings to the issue (White 2001). Managers depend on researchers to provide reliable information and use information as the foundation of wildlife management decisions (White 2001). Diminished confidence in science is one reason given by Decker and Chase (1997) why stakeholders have become more involved in wildlife management and have even taken authority away from professional

wildlife managers through judicial, legislative, and referendum processes (Loker et al. 1998, Riley et al. 2002). Beck et al. (1995) reported that the ballot initiative in Colorado over bear hunting occurred because the agency failed to listen to all constituents, not because the general constituency believed the agency was not committed to protecting the black bear population.

By involving the public in wildlife research, trust and credibility are fostered not only in research, but also management and policy. Organ and Ellingwood (2000) reported that direct contact with stakeholders in an informal setting is ideal. Most state agencies likely do not have enough time or personnel to maintain such contact at a large scale. However, wildlife researchers in the field embody scientific knowledge and may interact often with the lay public, especially when working on private lands. I believe wildlife researchers should include private involvement at multiple levels. Relationships with the private and public sectors can produce various forms of support, ranging from local knowledge, land access, volunteer work, logistical help, monetary, and in-kind support (Figure 3.2).

Research funding: While agency funding may continue to be the life blood of wildlife research, support from the private and business sectors can certainly enhance wildlife research because traditional funding sources receive more proposals than can be fully funded (Anderson et al. 2003). For example, by building a web of private support I supplemented my initial budget from the State wildlife agency with large sums of monetary and in-kind support from private individuals, organizations, and businesses. To achieve this level of private support I actively sought out and interacted with people. Additional funding enabled me to expand my research objectives and address important assumptions of experimental design, which in turn increased the credibility and perception of the research

among citizens and conservation groups in North Carolina. Long-term, I believe such private support could also lead to agency funding.

Land access and more: Building personal relationships not only increases funding support, but also facilitates private land access. Black bears thrive on a mix of habitat types and studying bears only on public land might bias results, especially in eastern North Carolina where agricultural crops on private lands are an important food source for bears. To study bears over a large scale and include all land use and habitat types, I began relationships with over 60 private landowners in eastern North Carolina to gain land access. Over time these relationships can be personally satisfying and educational, but also powerful tools for generating funding and political support for conservation. As demonstrated in the ornithological community, "citizen science" has enabled research on a national scale by fostering success of the Christmas and great backyard bird counts, as well as the annual breeding bird surveys (Cornell Lab of Ornithology). When people believe your research is theirs as well, they will volunteer to help in a variety of ways that can strengthen your research. Researchers, however, must make the initial effort.

Broaden the audience: Schmutz (2002) reported that many federal wildlife biologists do not attend professional conferences. I suspect even fewer members of the lay public attend professional conferences than do wildlife biologists. I have used other opportunities to present my information to both groups by speaking at museums, an estuarium, university, elementary schools, a home owner's association meeting, and various wildlife and hunting clubs over 40 times in 5 years, all across North Carolina. I also organized my own annual event in my study area that provides free food and drink to encourage people to come out, learn about my research, and contribute money if they are

able and interested. I believe wildlife researchers need to present their research in forums other than professional conferences.

Anderson et al. (2003) urged scientists to relate their findings to legislators, agency administrators, and the lay public in such a way that high quality science is demanded and integral for social, judicial, and political matters. The emphasis of Research One universities, and the scientific community in general, has traditionally been to publish or perish (Clapman 2005). Schmutz (2002) reported that many federal wildlife biologists do not read scientific literature, potentially leading to failure to recognize important and relevant scientific contributions and an absence of adaptive management. I also suspect the lay public rarely reads primary literature, unless it is Open Access and available via an internet search. This disconnect suggests a communication gap. I assert that publishing only in peer-reviewed journals is too narrow a focus for wildlife researchers in the 21st century. Reports can, and should, be made available and intelligible to the public. We can and should condense our findings for a local newspaper or popular magazine. I produced annual reports to send to interested parties, written without scientific format and jargon to help address this communication gap. Such progress reports with interesting pictures and information can be extremely effective at building relationships with the private and business sectors.

Example of wildlife research affecting public policy: While conducting bear research I became aware of the use of blocks of candy weighing up to a ton that were legally put out to feed bears. Wildlife managers had been monitoring the increase of such excessive feeding for several years. Though this issue was beyond my original research objectives, I recorded biological data and behavioral observations of bears which suggested candy blocks contributed to poor health and disrupted normal behavior of bears. Teel et al. (2002) noted

the importance of determining public attitudes regarding topics before policies are developed, implemented, or revised, due to the controversial nature of predator management issues. Accordingly, I presented my information to the board of the North Carolina Bear Hunter's Association in February, 2003. This group is largely comprised of hunters who use dogs to hunt bears and would definitely be affected by a change in allowable feeding practices, as they often feed bears to facilitate training of their dogs before hunting season. Next, I asked landowners and property managers in my study area to write position statements relative to the appropriateness of feeding bears with candy blocks. I showed pictures of teeth from bears we trapped at candy blocks to obtain feedback from dentists and veterinarians on health implications. When NCWRC wildlife managers contacted me in August to complement their efforts on this issue, I provided both biological and human dimensions data. A meeting of biologists, wildlife managers, and politicians on August 26, 2003 resulted in a press release on October 3, 2003 describing a law resolution forbidding the use of candy blocks to feed bears (Figure 3.3).

Later that fall some people expressed frustration to me about the new resolution. I anticipated as much, given that Beck et al. (1995) noted the history of natural resource management in America clearly indicates that change often occurs in non-incremental steps rather than gradually, which makes resistance to change strong and acceptance difficult. Engaging, and not just educating, the public paid dividends here because established relationships facilitated trust in my information and my credibility parlayed into support for this policy change. I did not lose any access privileges because of the law resolution, even though some landowners opposed the resolution. Being honest, familiar, and forthright

increased trust. I had informed affected groups well beforehand, which positively influenced their reactions to the policy change.

As a fledging biologist I was once advised to be the best biologist I could, but to leave politics to politicians. I now reject this notion. Are politicians inherently good biologists? The passion and knowledge of wildlife researchers need to be a larger part of the public policy process. Wildlife research, wildlife management, and public policy should be less separated. I believe the traditional approach to wildlife research (diagrammed as the left column in Figure 3.2) has detrimentally confined the responsibility of wildlife researchers to only producing reliable information. We can and should do more.

Concluding remarks: "Too bad you don't have a big grant to pay for your project", said a tenured faculty member to me after one of my public presentations. Actually I had 2, large, agency supported grants, but that is not the point. Engaging the public is about more than just raising money. Natural resources are hard to assign dollar values and politics operate on dollar values and public endorsements. Van Putten (2005) reported that often neither robust science nor thoughtful solutions drive public policy: politics drives policy. I believe that a personal donation from disposable income is the strongest endorsement of support for research. Hundreds of individuals have contributed to my bear research. One supporter commented that the broad support for my research gives it credibility with the public as being pure science, rather than research with a hidden agenda funded by a narrow representation of stakeholders. Credibility and trust from the public are earned continually, not given with a terminal degree.

Stakeholders are increasingly expecting to participate in wildlife management decisions (Riley et al. 2002). I believe citizens will be more supportive of management decisions if

they participate in, or are at least familiar with, wildlife research. I actively encouraged guests of all ages to experience bear trapping (Figure 3.1) and have repeatedly been told my ability to generate support is because people feel that my research project is theirs as well. I often provide gift copies of A Sand County Almanac and use public interactions as opportunities to promote Leopold's Land Ethic (Leopold 1949). Conservation on private land is critical to achieving long-term and large-scale goals (McNaught and Nickens 2003). As evidenced by the success of Al Gore's movie ("An Inconvenient Truth"), people are warming up to the idea that climate change is a real concern and needs to be addressed. Publications in primary literature have stated the problem for many years, but were not as effective at affecting public opinions as Gore's film. We owe it to future generations to improve society's values for wildlife and wild places. I believe that increasing public awareness and involvement in wildlife research by broadening our approach will not only benefit conservation, but wildlife research itself.

Figure 3.2. Traditional approach to scientific research is depicted in the left column and proposed inclusive approach integrating the private sector is given in the right column.

Press Releases/What's New

NORTH CAROLINA WILDLIFE RESOURCES COMMISSION

Wildlife Resources Commission Clarifies Bear-Baiting Prohibition

Remains of a candy block (foreground) entice a black bear to feed.

Candy blocks, which can weigh up to 2,000 pounds, can be made of gum, licorice, hard candies, or in this instance, chocolate and peanut butter.

In addition to suffering from tooth decay, bears addicted to candy can develop behavioral disorders.

All photos by Stan Hutchens, N.C. State University wildlife technician.

Figure 3.3. Example of how engaging the public through wildlife research can help wildlife managers adopt public policy to protect bears and other wildlife.

RALEIGH (Oct. 7, 2003)—The N.C. Wildlife Resources Commission on Oct. 3 took aggressive action to protect black bears in North Carolina by unanimously passing a resolution to interpret more strictly the state's "bear-baiting statute." This law prohibits the taking of bears "with the use or aid of any salt, salt lick, grain, fruit, honey, sugar-based material, animal parts or products, or other bait."

The new interpretation of the bear-baiting statute makes it illegal to place candy blocks and subsequently hunt bears in that area.

The action was prompted by a written request from the N.C. Bear Hunters Association and information provided by researchers at N.C. State University who were concerned about the health and behavioral development of bears. Some bear hunters and guides had circumvented the bear-baiting statute by hauling and dumping blocks of candy weighing up to 2,000 pounds onto their leased hunting tracts during the off-season, allowing black bears to get "hooked" on the candy, then removing the candy prior to opening day of bear-hunting season.

Before Oct. 3, the practice of "sugar hooking" — so-called because of the addictive effects of sugar on bears — was considered legal by some hunters because the candy was removed prior to the beginning of the bear season. But questions arose about the effects of candy blocks on: the health of black bears, management of bears, bear populations and distribution, and the ethics of hunting sugar-addicted bears.

“The Wildlife Commission first heard of this practice three years ago, and use of candy blocks has escalated every year since then,” said David Cobb, chief of the Commission’s Wildlife Management Division. “Around these bait sites, we are seeing bears with health and behavioral problems.”

Along with a decline in dental health, black bears hooked on the candy blocks also change their behavior, losing their fear of humans and staying in close proximity to the enormous blocks of candy, which can be made of bubble gum, licorice, chocolates or assorted hard candies.

Cobb and an N.C. State University doctoral student, Tim Langer, in July observed bears behaving strangely and in close proximity to a candy block.

“It’s very unusual to see adult bears so near each other, but that’s what’s happening at these candy blocks,” said Langer, whose research into Hyde County black bear populations is funded in part by a Commission grant. “The bears didn’t run away when we approached them. They appeared too sick to move.”

Hyde County isn’t the only place where bears are tempted by candy blocks. Earlier this year, the Commission received a report of a trucking company that was asked to deliver candy blocks to Hyde, Bladen and Haywood counties — a statewide arrangement that caught the attention of the N.C. Bear Hunters Association (NCBHA).

"North Carolina has recently become [subject to] a number of ill-advised or unscrupulous individuals and organizations who have taken to the practice of 'sugar hooking' … intended as a means of circumventing our current prohibitions on hunting bear with the use or aid of bait," wrote Jim Noles, president of NCBHA, in a Sept. 9 letter to the Commission. "The unrelenting feeding of sugar-rich substances caused a pattern of bear behavior that results in the bears' continued visitation to the feeding sites long after the sugary substances are visually removed to coincide with the commencement of bear-hunting season." Noles' letter also requested that the Commission "undertake appropriate measures for injunctive relief."

Now, with the Commission's more specific interpretation of the existing bear-baiting statute, candy blocks no longer will be allowed. Wildlife enforcement officers will begin issuing citations to individuals who hunt in areas where candy blocks are used to bait bear. Violation of the law constitutes a Class 1 misdemeanor, which is punishable by a two-year revocation of a hunting license, a fine of $2,000 or more, court costs, and a $2,232 replacement fee, if a bear is killed.

Since its inception in 1947, the N.C. Wildlife Resources Commission has been dedicated to the wise-use, conservation, and management of the state's fish and wildlife resources. Nineteen wildlife commissioners create and maintain laws and regulations governing hunting, fishing and boating activities based on input from the Commission's wildlife and fisheries biologists, wildlife enforcement officers, educators, engineers and administrative staff.

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CHAPTER 4

FROM THE FIELD:

ADVANTAGES OF CULVERT TRAPS FOR TRAPPING BLACK BEARS

Figure 4.1. Using 2 Aldrich foot snares successfully on the same bear trail.

Figure 4.2. Releasing a bear from a culvert trap after it has fully recovered from anesthesia.

ABSTRACT

Aldrich foot snares have traditionally been used to trap black bears (*Ursus americanus*) for field studies. We also used culvert traps and caught bears 95 times during 2002-2005 in coastal North Carolina. Culvert traps averaged catching a bear every 4.1 trap nights and 1.2 bear visits, compared to 7.3 trap nights and 3.3 bear visits for Aldrich foot snares, and caught 2 bears previously trapped in Aldrich foot snares. Two bears trapped in Aldrich foot snares were killed by another bear (3.1 %), while all injuries of bears trapped in culvert traps were minor. Culvert traps also allowed us to release animals without drugging or handling them and allowed an anesthetized animal to fully recover, while protected inside the trap, before release. Relatively speaking, culvert traps were easier to move, set and reset, and open and close. We also found culvert traps could be checked from a distance, were more effective in rainy or flooded conditions, and significantly reduced the risk to staff when drugging a trapped animal. We propose expanding the use of culvert traps when researchers can borrow them from a State or Federal agency and deploy them in an area with adequate road coverage and limited access (e.g., locked gates).

Key words: Aldrich foot snare, culvert trap, *Ursus americanus*, black bear, efficiency, injury

INTRODUCTION

Wildlife researchers often focus on the health of the overall population, but while trapping we must focus on the health of each individual. We are ethically compelled as researchers to continually evaluate performance and injury risk of trapping techniques (Powell and Proulx 2003, Shivik et al. 2005), especially when studying small and threatened

populations where accidents and injuries associated with trapping are a major concern (Kaczensky et al. 2002). Aldrich foot snares are spring activated and have been used for many years to efficiently catch bears, but little information is available in the primary literature on rates of major trapping injuries (Johnson and Pelton 1980). Kaczensky et al. (2002) used Aldrich foot snares in combination with a trap transmitter system to guarantee that handling of brown bears (*Ursus arctos*) started within 1-2 hours of initial capture. This approach minimized trapping injuries, but was demanding. Beyond the risk of trapping mortality or broken bones (defined as major trapping injuries), physiological effects from using Aldrich foot snares should also be considered. Cattet et al. (2003) reported that catching grizzly bears with Aldrich foot snares may result in significant muscle damage in the short-run, and poorer body condition over time, when compared to bears drugged from helicopters.

Culvert traps protect the trapped individual from other animals and confine the movements of an animal after it has been drugged. Culvert traps also offer the advantage of allowing a drugged animal the opportunity to fully recover from anesthesia while being protected inside the trap before being released. This is an important consideration, because anesthesia is not an exact science, drug combinations like Telazol are often used that are not fully reversible, and many factors can affect an individual's recovery (M. Stoskopf, N.C. State University, personal communication). We evaluated trapping efficiency, selectivity, and rates of injury for Aldrich foot snares and culvert traps for black bears in eastern North Carolina to assess if expanded use of culvert traps is warranted.

METHODS

Bears were trapped in eastern North Carolina, south and east of the intra-coastal waterway in Hyde County (Figure 4.3). The 404.3 mi^2 (1,047.2 km^2) of land in our study area encircled 62.5 mi^2 (161.9 km^2) of water within Lake Mattamuskeet National Wildlife Refuge. The base land cover map we used was the North Carolina Gap Analysis Land Cover Data, a 1992 era map with 70 cover classes represented in the state of North Carolina (McKerrow and Williams 2006). The estimated overall accuracy of the map when generalized to 15 land cover classes was 87.7 %, with a 95 % confidence interval between 84.9 and 90.5 %. We reduced cover classes to the 8 used by Jones and Pelton (2003) for black bear habitat analyses in eastern North Carolina and summarized the relative occurrence of each land cover class (Table 4.1). Comprising 28.7 % of the study area, farm land was most common and covered 116.1 mi^2 (300.7 km^2).

Bears were trapped using culvert traps and Aldrich foot snares (Margo Supplies Ltd., High River, Alberta, Canada), modified with automobile hood springs to reduce injuries (Johnson and Pelton 1980). An Aldrich foot snare cost $40 (in 2003) and could be re-used once the throw cable was replaced after a capture ($1 each). Alternatively, culvert traps only needed to be cleaned out before re-used. They required a truck or trailer to move, however, and cost several thousand dollars each, so we did not buy our own and borrowed up to three at a time from the North Carolina Wildlife Resources Commission, which required logistical coordination.

We caught 31 bears during June 7 - August 11, 2002 using Aldrich foot snares to deploy 10 GPS collars. In 2003, we trapped 29 bears between April 5 and August 17 using Aldrich foot snares and trapped 14 bears during August 14 – September 5 using culvert traps

to deploy 19 GPS collars. In 2004, we used Aldrich foot snares and culvert traps from May 1 to 10 and caught 9 bears to deploy 7 GPS collars. In 2005 we trapped only to recover a GPS collar and used culvert traps to catch 12 bears between April 6 and May 24.

Trap sites were pre-baited for 2 weeks (Johnson and Pelton 1980), and replenished daily, with concentrated scents of peach, coconut, or green apple as lures (Mother Murphy's, Greensboro, N.C.) and pastries (Krispy Kreme Doughnuts). We checked traps at least once a day between 08:00 and 09:30. If the predicted mid-day temperature exceeded 90 degrees Fahrenheit, we closed traps from 12:00 to 16:00. Some days we checked traps a second time between 16:00 and 17:30. Captured bears were handled immediately and immobilized with an intra-muscular injection of Telazol (zolazepam-tiletamine) at a dosage of 4.4 mg per kg of estimated body weight (Cattet et al. 2003). We applied a wetting agent to the eyes of bears to prevent desiccation, checked for trap injuries, tattooed an upper lip, and removed a pre-molar tooth for aging (Matson's Lab, Milltown, Montana). We also monitored body temperature, respiration rate, and pulse rate throughout the handling, as outlined by protocol # 01-136 approved by the Institutional Animal Care and Use Committee of North Carolina State University.

RESULTS

We did not plan to use culvert traps in our research originally, which is why we did not use them at all in 2002 and not until August 14 in 2003. Rain and flooded conditions in 2003 made it impossible to set Aldrich foot snares, so we were forced to try an alternative trapping approach and began using culvert traps. We used both trap types in 2004. One

female bear in each of 2003 and 2004 was killed while in Aldrich foot snares. Consequently, we only used culvert traps in 2005 to avoid that risk.

Trapping effort and efficiency: We trapped northeast of Lake Mattamuskeet in all years, but also trapped west and south of the Lake in 2003 (Figure 4.3). Pooling all trapping results, we accumulated 592 trap nights (defined as a 24-hour period) over 129 days (average 4.6 and range 1 – 15 trap nights/day). Aldrich foot snares were used for 465 trap nights over 71 days (average 6.5 and range 1 – 15 trap nights/ day) and culvert traps for 127 trap nights over 64 days (average 2.0 and range 1 – 3 trap nights/day). Of the 95 bears captured in 2002-2005, 64 were in Aldrich foot snares and 31 were in culvert traps. We used Aldrich foot snares in 2002-2004 (averaging a bear every 7.3 trap nights) and used culvert traps in 2003-2005 (averaging a bear every 4.1 trap nights, Table 4.2).

On average we caught 3 bears every 4 days (0.74 bears per day). However, we did catch 4 bears in 10 Aldrich foot snares on June 8, 2002, 4 bears in 6 Aldrich foot snares on July 8, 2002, and 6 bears in 10 traps (7 Aldrich foot snares and 3 culvert traps) on May 1, 2004. For locations with evidence of high bear traffic (such as scats, tracks, and sightings), we set two Aldrich foot snares or two culvert traps and caught bears in both traps on the same day (Figure 4.1).

Trapping selectivity: Incidental animals were caught with both Aldrich foot snares and culvert traps. One red wolf (*Canis rufus*) and one feral pig (*Sus scrofa*) were caught in Aldrich foot snares for a total of two catches in 465 trap nights (0.004 %), compared to one red wolf and six raccoons (*Procyon lotor*) (two at once) caught in culvert traps for a total of six catches in 127 trap nights (0.05 %). However, culvert traps may just have been more efficient at catching incidental animals than Aldrich foot snares, which is logical considering

that bear snares were too large to catch raccoons, but raccoons were tall enough to reach the bait in culvert traps and release the trap door. Using physical evidence such as scats, tracks, size of hole in snare set, and whether hung bait was removed, we recorded 91 non-bear visits in 465 trap nights to Aldrich foot snares (19.6 %), compared to 9 non-bear visits in 64 total trap nights (during 2003-2004) to culvert traps (14.1 %, Table 4.2).

Trapping injuries: We analyzed the frequency and type of trapping injuries for bears caught in Aldrich foot snares and culvert traps separately and for each year. Though uncommon, some bears had more than one minor trapping injury. "No injuries" was most common for Aldrich foot snares (43.8 %), while culvert traps more often had bears with bloody claws (60.0 %) or one or two cuts on a foot or their face (35.0 %) than no injuries (30.0 %). However, we considered these injuries as minor. They probably resulted from bears scraping their paws along the metal grate at the end of the culvert trap or swatting the metal treadle arm that released the door. Because culvert traps do not involve a snare, bears handled in culvert traps experienced no swelling or punctures of a snared foot. In 2005, we culvert trapped 12 bears and released the first 11 without handling them because our field work was completed except for catching a bear to remove a GPS collar. As a result, we calculated rates for minor trapping injuries ignoring these bears, but used them for calculating rates of major trapping injury because that could be assessed without handling (Table 4.3).

DISCUSSION

Our overall prevalence of minor trapping injuries in 57.1 % of captures (48 of 84) was similar to the 58.7 % reported by Johnson and Pelton (1980) and our overall rate of

major injury in 2.1 % of captures (2 of 95) was similar to their rate of 3.7 %. Although NCWRC personnel (unpublished data) reported bears trapped in older designs of culvert traps often damaged their teeth, we observed no damaged teeth in 20 captures of bears caught in these new and re-designed culvert traps. Generally speaking, one improvement we made to our handling methods over time was to use ice during warm weather. Initially we cooled bears with canal water and four bears we handled in 2002 had sustained and elevated temperatures over 103.0 degrees Fahrenheit (normal temperature for a bear is 101.5 degrees Fahrenheit). Beginning in August of 2002 we used ice and ice packs to cool bears, if necessary, and reduced that type of trapping stress.

Culvert traps offered us an opportunity to trap bears in flooded conditions of 2003, when the ground in wooded areas was too wet to effectively set Aldrich foot snares. Even when we caught a bears with an Aldrich foot snare, we had to carry the bear to find a dry enough place in the woods for handling it. Unlike Aldrich foot snares, we set culvert traps directly on roads, which were elevated and relatively dry. Culvert traps also were more efficient than Aldrich foot snares, both in trap nights per catch and bear visits per catch. This means we could use fewer traps, which was important since we were borrowing them and there were a limited number available. Culvert traps were also easier to set, re-set, check at a distance, and open and close during a hot day. The effectiveness of culvert traps may be explained by the fact that bears in our study area have large home ranges they travel using roads (Figure 4.4). However, because culvert traps are set on roads, they are best used when access is limited with locked gates, as trapped bears could potentially be agitated by humans.

We used culvert traps to complement the use of Aldrich foot snares in 2003 and 2004, but then used them exclusively in 2005 to protect trapped bears after we experienced a

second trapping mortality. Both dead bears were females caught in Aldrich foot snares. In 2003, a 3-year-old female, weighing 55 pounds, was killed and partially consumed and, in 2004, a 2-year-old female was completely consumed except for the skull, feet, and some hide. As a result, the bear could not be weighed and its gender had to be determined genetically. On July 8, 2002, we caught a 6.5-year-old female and a 10.5-year-old male in Aldrich foot snares at the same trapping location (Figure 4.1). We had missed a capture the day before and set a second Aldrich foot snare along the trail, catching two animals the next day. Given how agitated the female seemed with the male so close, it is possible catching the male in the second snare kept him from harassing her, as she was lactating and it was breeding season.

Tietje et al. (1986) described cases of cannibalism (defined as the killing and eating of a conspecific) of both denning and active black bears. They suggested that cannibalism may not be strongly selected against in adult male bears, given that females and sub-adult males are smaller, are likely to be unrelated to cannibalistic males, and that adult male fitness is negatively related to bear density. Lunn and Stenhouse (1985) also documented cannibalism of an adult female polar bear by an adult male polar bear. Culvert traps not only protect trapped bears, but bears recovering from anesthesia. After the second mortality, we routinely pulled recovering bears back into culvert traps, shut the door, and returned a couple hours later to release the bear after it had fully recovered (Figure 4.2).

We found one bear that had had no trapping injuries, only one dose of Telazol, and released in apparently excellent condition drowned the next day in a canal when we were monitoring the signal of its GPS collar. We spoke with veterinarian M. Stoskopf (N.C. State University, personal communication) about this and he felt that either the 5.5-year-old female

was still ataxic when she tried to swim away and drowned, or the drug anesthetized her a second time after the initial recovery. This instance provided another reason to allow bears to fully recover inside culvert traps before releasing them.

Culvert traps re-caught at least two individuals previously trapped in Aldrich foot snares and were effective in an area trapped for four consecutive years. In flooded conditions culvert traps provided us the only viable option to catch bears. Also, in 2005 when we were targeting one particular bear, culvert traps afforded us the option of releasing other bears without drugging them. This feature eliminated costs, time, and reduced handling risks to bears and personnel. Though training personnel reduces risk, drugging a bear in an Aldrich foot snare certainly has greater risk than drugging a bear inside a culvert trap.

Since culvert traps are expensive, we suggest borrowing them and planning trapping periods during their availability. We recommend trapping bears during March and April in coastal agricultural areas. We observed bears active that time of year, winter wheat was not yet edible, and little natural food was available, which we believed increased the attractiveness of our trapping lures. Late winter/early spring was also was a good time to trap because daily high temperatures did not exceed 90 degrees Fahrenheit, so we could keep traps open 24 hours a day and not worry about trapped animals overheating. Coincidentally, that time period was a good time to borrow culvert traps from our State game agency, because they mainly use culvert traps during summer and fall to respond to nuisance bear complaints. We recommend using culvert traps to catch black bears either exclusively or in addition to Aldrich foot snares, depending on their availability, road coverage, and your capability to limit access. Culvert traps were more effective, reduced our number of trapping

days, and eliminated the risk of trapping mortality from another bear, which was a major concern for us in agricultural areas with high bear densities.

Table 4.1. Occurrence of 8 land cover classes within our study area in Hyde County, North Carolina.

Land cover type	sq. mi.	sq. km.	Of total
Farm land	116.1	300.7	28.7 %
Pine	82.2	212.9	20.3 %
Marsh	56.5	146.3	14.0 %
Low pocosin	56.3	145.7	13.9 %
Bottomland hardwoods	46.6	120.6	11.5 %
Pine - hardwoods	31.2	80.9	7.7 %
Low density vegetation	11.2	29.0	2.8 %
Upland hardwoods	4.2	10.9	1.0 %
Total	404.3	1047.2	100.0 %

Table 4.2. Trapping efficiency and selectivity of Aldrich foot snares and culvert traps used to catch black bears during 2002-2005 in Hyde County, North Carolina.

Year	Trap type	# of trap nights	# of bear visits	# of bear catches	Trap nights per bear capture	Bear visits per bear capture	Incidental catches
2002	Aldrich foot snares	183	83	31	5.9	2.7	none
2003	Aldrich foot snares	272	121	29	9.4	4.2	red wolf, feral pig
2004	Aldrich foot snares	10	5	4	2.5	1.3	none
	Total	465	209	64	7.3	3.3	
2003	Culvert traps	41	17	14	2.9	1.2	none
2004	Culvert traps	23	5	5	4.6	1.0	6 raccoons
2005	Culvert traps	63	not recorded	12	5.3	n/a	red wolf
	Total	127	22	31	4.1	1.2*	

* Bear visits were not recorded in 2005, so this average for culvert traps is only for 2003 and 2004.

Table 4.3. Rates of trapping injuries for Aldrich foot snares and culvert traps during bear trapping in 2002-2005 in Hyde County, NC.

Year	Trap type	# of bears	Type of trapping injury							
			None	Major	Minor					
				Mortality	1 or 2 punctures on foot	Swelling	1 or 2 cuts on a foot or scratches on face	Bloody claws	Cut gum or lost tooth	Too hot
2002	Aldrich foot snares	31	12	0	2	4	8	0	3	4
2003	Aldrich foot snares	29	15	1	6	2	7	0	1	0
2004	Aldrich foot snares	4	1	1	1	0	0	1	0	0
	Total	64	28 (43.8 %)	2 (3.1 %)	9 (14.1 %)	6 (9.4 %)	15 (23.4 %)	1 (1.6 %)	4 (6.3 %)	4 (6.3 %)
2003	Culvert traps	14	4	0	n/a	n/a	5	8	0	0
2004	Culvert traps	5	1	0	n/a	n/a	2	4	0	0
2005	Culvert traps	1 + 11*	1	0	n/a	n/a	unknown	unknown	unknown	unknown
	Total	20 + 11*	6 (30.0 %)	0	0	0	7 (35.0 %)	12 (60.0 %)	0	0

* These bears were released without handling and did not have a major injury, but minor injuries were unknown.

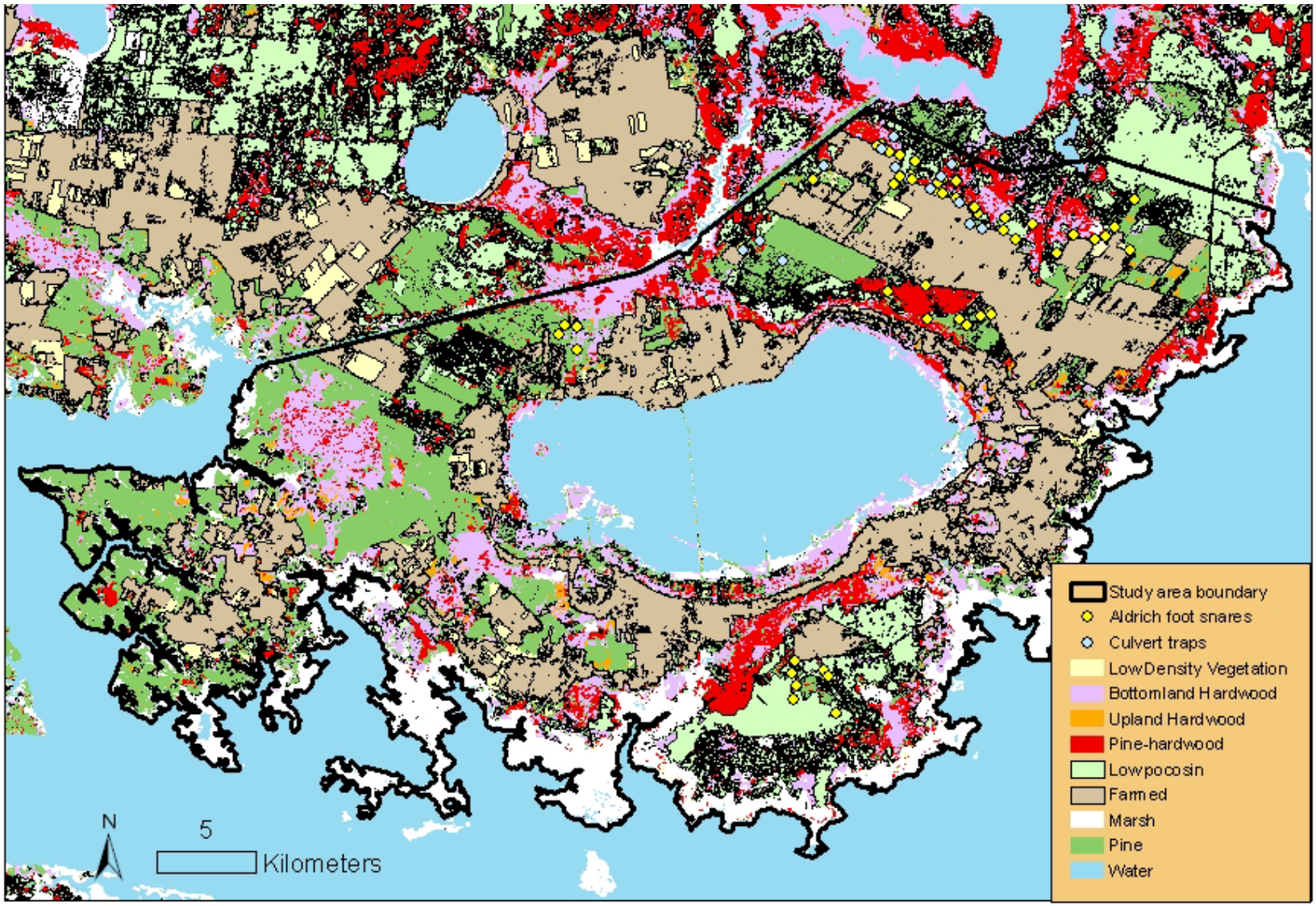

Figure 4.3. Trap locations for Aldrich foot snares and culvert traps used to catch bears during 2002-2005 in Hyde County, NC.

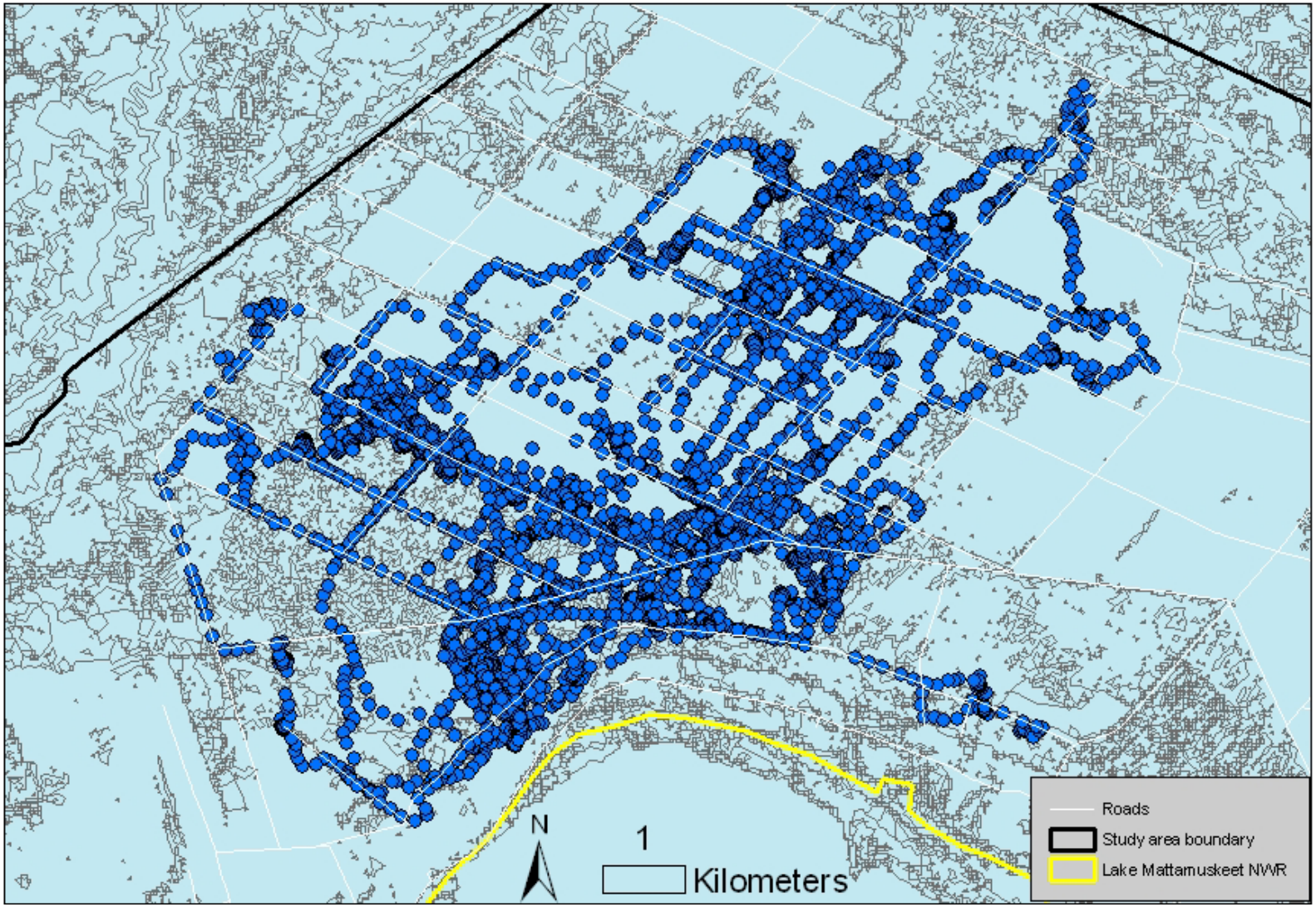

Figure 4.4. GPS locations of a 3.5-year-old, male bear during May 16–July 10, 2004 in Hyde County, NC, were often associated with farm roads.

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CHAPTER 5

EFFECTS OF HABITAT ON FIX RATES AND DISTANCE ERRORS

FOR GPS COLLAR LOCATIONS

Figure 5.1. Telonics GPS collars (model TGW-3500) were put on a stand to assess the accuracy of locations.

ABSTRACT

Global Positioning System (GPS) collars offer exciting opportunities to monitor wildlife and are being used to monitor bear (*Ursus spp.*) home range and habitat use around the globe. However, prior to such analyses, GPS collar performance and effects that interactions with habitat have on positional accuracy should be investigated. We tested GPS collar performance using 11 Telonics collars programmed to attempt positions at 1 or 3 hour intervals during March 26-April 5 and August 22-29, 2003. We used 22 test sites chosen to represent the range from 0.0 % to 100.0 % of canopy openness. Though the success rate of location attempts was almost 100.0 % at test sites at or above 53.8 % of canopy openness, the highest mean and maximum errors for locations with PDOP (Positional Dilution of Precision) values of 1.0 to 5.0 was at 58.3 % canopy openness. Locations with PDOP values from 1.0 to 2.0 removed 795 of 849 (93.6 %) successful fixes, but had the lowest mean (8.8 m) and lowest maximum (31.4 m) error. Specific research questions should be considered when choosing the PDOP filter because there was a trade-off between decreasing the distance errors of GPS locations and losing biological information from locations that may be less accurate.

Key words: GPS collars, Telonics, positional accuracy, fix rates, canopy cover

INTRODUCTION

GPS (Global Positioning System) collars offer exciting opportunities to monitor wildlife. Biggs et al. (2001) reported that GPS collars were more effective and efficient for tracking elk than VHF (very-high-frequency) collars because GPS collars can be

programmed to obtain fixes automatically, have fewer logistical problems, and are more economical for long-term data collection efforts. GPS collars are being used to monitor black (*Ursus americanus*) and brown bear (*Ursus arctos*) home range and habitat use (Belant and Follmann 2002), but it is wise for researchers to evaluate GPS collar performance and effects that interactions with habitat have on positional accuracy before conducting such analyses (Rempel et al. 1995). Accordingly, we tested how the rate of successful fixes and positional accuracy for GPS collar locations was affected by canopy openness in our study area.

METHODS

We conducted this test of GPS collar performance in eastern North Carolina, south and east of the intra-coastal waterway in Hyde County during 2003 (Figure 2.3, page 92). We used 11 GPS collars programmed to attempt positions at 1 or 3 hour intervals during March 26-April 5 and August 22-29 (Telonics, model TGW-3500, Mesa, Arizona). We used 22 test sites chosen to represent the range from 0.0 % to 100.0 % of canopy openness, because GPS signals can not go through objects and the amount of structural interference may affect fix rates and positional accuracy. Accordingly, we located one test site in a field and split the others between a pine stand and a hardwood stand within the area also used for our pilot study of bears (Figure 2.5, page 94). At each test site a stand was placed to hold the GPS antenna of a collar at 29.5 inches (74.9 cm) above the ground, a mean shoulder height of bears when we deployed GPS collars in 2002. A digital Nikon camera with a fish-eye lens converter was used to take hemispherical photographs of the canopy from this height using a tri-pod and bubble level on the camera (Englund et al. 2000). We used the automatic settings

for aperture width and shutter speed and took photographs when the sky was uniformly overcast at the beginning and end of each test period (Englund et al. 2000). Photographs were analyzed using GAP Light Analyzer software (Version 2.0, Simon Fraser University and the Institute of Ecosystem Studies) (Holder 2003). Canopy structure from 0 to 10 degrees above the horizon does not affect collar performance (Telonics Inc., Mesa, Arizona), so we ignored canopy cover in that range.

We downloaded data after retrieving collars and projected locations from decimal degrees to NAD (North America Datum)_1983_StatePlane with meter units, because North Carolina is wider from east to west than north to south. We then used ArcView GIS 3.3 and ArcMap of ArcGIS Desktop 9.1 (Environmental Systems Research Institute, Inc., Redlands, California) to obtain projected x,y coordinate positions for collar locations. For the "true" location of test sites, rather than use the GPS coordinates from a hand-held unit, which is still another approximation, we used the x,y location for the geometric mean of all successful test locations as the "true" location. This is a more robust approach, as locations from multiple days and time of day represent more satellite configurations and the average from these should be more accurate when at least 20 locations are used (G. Catts, N.C. State University, personal communication). Error distances between the geometric mean and individual test locations were calculated by taking the square root of the sum of the squared x,y coordinate differences (Figure 5.2).

RESULTS

Indices of canopy openness at an individual test site decreased from 0.4 % to 9.2 % due to phenological changes between the beginning and end of a testing period. We

therefore averaged estimates when reporting the canopy openness for a particular test site. Canopy openness ranged from 4.2 to 100.0 % at 16 test sites for 951 attempts, 102 of which (10.7 %) were unsuccessful. An additional 6 test sites and 191 attempts were excluded from analyses, because we did not know when the stand fell over at 1 test site (47 attempts), when collars were moved from 4 test sites by animals (104 total attempts), or 3 test sites did not have enough successful positions to use a geometric mean as the "true" location (40 total attempts). For example, 1 collar was moved over 155 meters from its test site within a 2 day period by an unknown animal.

Over 30 % of location attempts were unsuccessful for 2 of 3 test sites with less than 15 % canopy openness. However, between 7 test sites with 53.8 % to 100.0 % canopy openness, only 1 attempt out of 307 was unsuccessful (0.003 %, Table 5.1). Mean and median error distances were smallest for the test site with 100.0 % canopy openness, both when all successful fixes were used (mean = 4.7 m, median = 3.9 m) and using only fixes with Precision Dilution of Precision (PDOP) values from 1.0 to 5.0 (mean = 11.7 m, median = 8.2 m). Using all successful fixes, the highest mean error (21.7 m) and maximum error (146.2 m) were at the test site with 25.0 % canopy openness. Using only successful fixes with PDOP values from 1.0 to 5.0, the highest mean error (15.4 m) and maximum error (98.9 m) were at the test site with 58.2 % canopy openness (Table 5.2).

Pooling all successful fixes, we analyzed mean, median, and maximum errors by range of PDOP values (Table 5.3). Locations with PDOP values from 1.0 to 2.0 removed 795 of 849 (93.6 %) successful fixes, but had the lowest mean (8.8 m) and lowest maximum (31.4 m) error. Locations with PDOP values from 1.0 to 4.0 also had a median error of 7.4 meters after removing 422 of 849 (49.7 %) successful fixes. Locations with PDOP values of

1.0 to 5.0 only removed 240 of 849 (28.3 %) successful fixes and had the same maximum error distance (98.9 m) as locations with PDOP values of 1.0 to 4.0.

DISCUSSION

There are trade-offs between decreasing the distance errors of GPS locations and losing biological information from locations that may be less accurate. A PDOP filter is one approach to decreasing distance errors and our data supported that the most restrictive filter (PDOP values from 1.0 to 2.0) had the smallest mean and maximum errors, but only left 6.4 % of locations. Specific research questions should be considered when choosing the PDOP filter. We used a filter of 1.0 to 5.0 when calculating weekly home ranges because the maximum error of GPS collar locations was less than 100 meters, median error was about 8 meters, and we wanted to preserve the biological information from over 70% of the successful attempts. M. Jones (NCWRC, unpublished data) reported that the mean error for telemetry locations using VHF (very high frequency) collars on black bears in a similar agricultural setting in eastern North Carolina was 180 meters. We were comfortable that our acceptable maximum error for GPS locations was less than half the average of VHF locations. We used the same PDOP filter for weekly home range calculations in all study years, though we switched to GPS collars manufactured by Lotek (Newmarket, Ontario, Canada) in 2004 after using GPS collars manufactured by Telonics in 2002 and 2003. To be certain, we should have tested whether accuracy of collar locations varied by manufacturer.

Though fix rate success was almost 100.0 % at test sites at or above 53.8 % of canopy openness, the highest mean and maximum errors for locations with PDOP values of 1.0 to 5.0 was at 58.3 % canopy openness. This can be explained by the fact that GPS telemetry

degrades over a continuum. Beginning with a test site with 100.0 % canopy openness, there is a high probability for a successful attempt and an accurate location. As canopy closure increases, the geometry of satellite signals is detrimentally affected, but not so much that a fix attempt is not successful. As a result, in the middle range of canopy openness, locations are successful, but have more error than test sites with 100.0 % canopy openness. As canopy closure increases further, signals are degraded to the point that more attempts are unsuccessful and those that are also have poorer accuracy than those at test sites with 100.0 % canopy openness.

These results are for locations that were not differentially corrected. Because the bias and degraded satellite geometry of selective availability was removed in 2000, for most applications differential correction is not necessary. Graves and Waller (2006) reported that differential correction decreased mean error in locations by 0.99 meters, but only 5 % of locations were corrected by more than 8 meters. Furthermore, error actually increased with differential correction for over 30 % of locations (Graves and Waller 2006). Relative to PDOP thresholds, locations with greater than 8.0 PDOP values improved more with differential correction than those with less. Graves and Waller (2006) also noted the accuracy of GPS technology exceeds that of most habitat maps.

Successful rates for location attempts varied by bear and year when collars were actually deployed on bears. The first 8 collars we deployed in 2002 only averaged 14.5 % successful fix rate and we sent the remaining 2 collars for that year back for improvements before deploying them. Subsequent collars performed much better, with a maximum success rate of 80.1 %, though even 14.5 % was still a large number of fixes because GPS collars can attempt so many locations. This simulated study was conducted with collars placed on a

stand at a fixed height. Obviously, this condition does not reflect the position of a collar placed on a bear, when additional factors affect GPS collar performance. Graves and Waller (2006) reported that sizes (weight, girth, and neck circumference) of grizzly bears (*Ursus arctos*) were negatively associated with location success. If it were possible to put GPS collars on captive bears and observe them at all times, we could investigate habitat biases and compare how bear activity affects GPS locations. Moen et al. (1996) approximated this research design by monitoring 1 free-ranging moose in an enclosure. Anecdotally, one collared female bear (tattoo # 754) spent the bulk of her time in the area used for our simulation study and the success rate of location attempts for her collar was 60.0 % (Table 5.4).

A research opportunity worth exploring would be to assess the differences between GPS and VHF locations made at the same time for individual animals with known locations, because GPS collars also have VHF transmitters. GPS collars could be programmed to attempt locations on a schedule when personnel could also be out triangulating the individual animal via VHF signals.

In conclusion, GPS collars represent a significant improvement over VHF collars in the amount and quality of data that can be acquired about animal movements. GPS collars can attempt prodigious numbers of locations at regular intervals, during any weather conditions, at any time of day (or night), and in areas without access. Furthermore, because accuracy and precision of GPS collar locations are quite good compared to VHF collar locations, the higher initial investment is almost trivial given the richness of the data generated.

Table 5.1. Summary from 16 test sites used to examine how fix rates of GPS collars vary with canopy openness in Hyde County, North Carolina.

Canopy openness	Habitat type	Total attempts	Unsuccessful attempts	
			#	%
4.2	hardwoods	117	36	30.8 %
8.8	hardwoods	164	20	12.2 %
13.7	pines	51	16	31.4 %
13.9	hardwoods	74	9	12.2 %
15.0	pines	27	2	7.4 %
19.1	hardwoods	50	8	16.0 %
25.0	pines	40	0	0.0 %
26.4	pines	40	5	12.5 %
28.1	hardwoods	81	5	6.2 %
53.8	pines	24	0	0.0 %
58.2	hardwoods	63	0	0.0 %
75.2	pines	39	0	0.0 %
80.6	hardwoods	43	0	0.0 %
91.3	hardwoods	55	1	1.8 %
93.2	pines	40	0	0.0 %
100.0	field	43	0	0.0 %
Total		951	102	10.7 %

Table 5.2. Error distances for 16 test sites used to assess the accuracy of GPS collar locations by canopy openness in Hyde County, North Carolina. (PDOP = positional dilution of precision).

Canopy openness	Using all successful fixes (PDOP = 1.0 to 18.0)				Successful fixes with PDOP values of 1.0 to 5.0			
	#	Median (m)	Mean (m)	Maximum (m)	#	Median (m)	Mean (m)	Maximum (m)
4.2	81	9.9	14.6	131.1	54	8.7	10.9	39.7
8.8	144	13.8	16.9	102.7	85	11.2	14.7	78.5
13.7	35	11.8	13.1	35.5	24	12.1	11.4	20.6
13.9	65	11.5	15.1	70.1	48	8.9	12.5	60.9
15.0	25	8.9	11.9	69.0	18	8.4	11.7	68.6
19.1	42	11.3	12.8	47.8	26	8.5	10.6	30.1
25.0	40	12.7	21.7	146.2	31	9.4	13.6	58.9
26.4	35	7.0	8.3	23.4	24	7.3	8.7	22.4
28.1	76	10.5	16.8	74.5	52	8.4	14.6	68.4
53.8	24	5.3	6.3	15.7	18	5.6	6.2	15.8
58.2	63	10.9	16.0	98.0	47	10.6	15.4	98.9
75.2	39	5.6	6.5	14.1	29	5.5	6.3	13.9
80.6	43	6.8	11.6	64.9	36	7.0	12.9	64.9
91.3	54	8.4	13.1	80.2	44	8.0	14.0	79.5
93.2	40	5.3	6.8	25.8	35	5.4	6.9	25.9
100.0	43	3.9	4.7	15.1	38	4.2	4.7	14.8
ALL	849	9.2	13.4	146.2	609	8.2	11.7	98.9

Table 5.3. Error distances for GPS collar locations grouped by PDOP values in Hyde County, NC. (PDOP = Positional Dilution of Precision).

PDOP range	1.0 – 18.0	1.0 – 5.0	1.0 – 4.0	1.0 – 3.0	1.0 – 2.0
Median (m)	9.2	8.2	7.4	7.3	7.4
Mean (m)	13.4	11.7	10.9	10.1	8.8
Maximum (m)	146.2	98.9	98.9	78.5	31.4
	n = 849	n = 609	n = 427	n = 246	n = 54

Table 5.4. GPS collar deployment and successful fix rates for 34 bears during 2002-2004 in Hyde County, NC.

Bear tattoo #	Date collar started collecting positions of bear	Date collar stopped collecting positions of bear	# of days	Frequency of attempts (minutes)	# of attempts	# of successful locations	% total success	# 3D fixes (1-7 PDOP)	% 3D success (1-7 PDOP)	# 2D fixes (1-5 PDOP)	% 2D success (1-5 PDOP)
706	15-Jun-02	9-Aug-02	56	60 or 180*	759	70	9.2%	41	5.4%	29	3.8%
709	17-Jun-02	11-Sep-02	87	60 or 180*	2,337	501	21.4%	290	12.4%	211	9.0%
711	18-Jun-02	22-Nov-02	158	60 or 180*	3,969	650	16.4%	339	8.5%	311	7.8%
713	19-Jun-02	22-Nov-02	157	60 or 180*	3,957	596	15.1%	354	8.9%	242	6.1%
716	29-Jun-02	6-Aug-02	39	60 or 180*	501	71	14.2%	36	7.2%	35	7.0%
718	2-Jul-02	19-Sep-02	80	60 or 180*	2,468	690	28.0%	477	19.3%	213	8.6%
723	8-Jul-02	1-Nov-02	117	60 or 180*	2,804	231	8.2%	111	4.0%	120	4.3%
726	11-Jul-02	22-Nov-02	135	60 or 180*	3,788	119	3.1%	42	1.1%	77	2.0%
729	11-Aug-02	22-Nov-02	104	60 or 180*	3,112	1,551	49.8%	944	30.3%	607	19.5%
730	11-Aug-02	11-Nov-02	93	60 or 180*	2,565	1,290	50.3%	761	29.7%	529	20.6%
731	5-Apr-03	31-Dec-03	271	60 or 180*	4,100	2,590	63.2%	1,812	44.2%	778	19.0%
732	5-Apr-03	23-Aug-03	141	60 or 180*	1,603	560	34.9%	271	16.9%	289	18.0%
734	13-Apr-03	31-Dec-03	263	60 or 180*	4,034	2,457	60.9%	1,702	42.2%	755	18.7%
705	14-Apr-03	31-Dec-03	262	60 or 180*	4,021	2,301	57.2%	1,543	38.4%	758	18.9%
737	14-Apr-03	31-Dec-03	262	60 or 180*	4,025	2,297	57.1%	1,450	36.0%	847	21.0%
738	15-Apr-03	24-Jun-04	437	60 or 180*	5,444	3,228	59.3%	2,163	39.7%	1,065	19.6%
739	22-Jun-03	23-Aug-03	63	60 or 180*	1,473	701	47.6%	466	31.6%	235	16.0%
745	30-Jun-03	10-Oct-03	103	60 or 180*	2,444	1,028	42.1%	696	28.5%	332	13.6%
746	2-Jul-03	7-May-04	311	60 or 180*	7,436	4,601	61.9%	3,129	42.1%	1,472	19.8%
747	3-Jul-03	31-Dec-03	182	60 or 180*	4,337	2,747	63.3%	1,795	41.4%	952	22.0%

Table 5.4 (cont.)

Bear tattoo #	Date collar started collecting positions of bear	Date collar stopped collecting positions of bear	# of days	Frequency of attempts (minutes)	# of attempts	# of successful locations	% total success	# 3D fixes (1-7 PDOP)	% 3D success (1-7 PDOP)	# 2D fixes (1-5 PDOP)	% 2D success (1-5 PDOP)
750	5-Jul-03	31-Oct-03	119	60 or 180*	2,820	1,263	44.8%	895	31.7%	368	13.0%
754	16-Aug-03	14-Nov-03	91	60 or 180*	2,158	1,294	60.0%	1,019	47.2%	275	12.7%
755	16-Aug-03	31-Dec-03	138	60 or 180*	3,295	1,782	54.1%	1,255	38.1%	527	16.0%
758	17-Aug-03	31-Dec-03	137	60 or 180*	3,263	639	19.6%	415	12.7%	224	6.9%
762	24-Aug-03	31-Dec-03	130	60 or 180*	3,101	2,327	75.0%	1,866	60.2%	461	14.9%
764	27-Aug-03	31-Dec-03	127	60 or 180*	3,033	2,429	80.1%	1,935	63.8%	494	16.3%
767	31-Aug-03	31-Dec-03	123	60 or 180*	2,933	1,976	67.4%	1,445	49.3%	531	18.1%
768	5-Sep-03	31-Dec-03	118	60 or 180*	2,809	1,201	42.8%	688	24.5%	513	18.3%
702	16-May-04	9-Aug-04	86	5	24,575	13,473	54.8%	6,452	26.3%	7,021	28.6%
764	16-May-04	9-Aug-04	86	5	24,368	18,043	74.0%	12,874	52.8%	5,169	21.2%
769	16-May-04	10-Jul-04	56	5	15,871	9,891	62.3%	5,410	34.1%	4,481	28.2%
770	16-May-04	9-Aug-04	86	5	24,575	17,706	72.0%	11,990	48.8%	5,716	23.3%
771	16-May-04	9-Aug-04	86	5	24,563	18,768	76.4%	14,509	59.1%	4,259	17.3%
772	16-May-04	9-Aug-04	86	5	24,575	14,991	61.0%	8,021	32.6%	6,970	28.4%

* Collars were programmed to attempt a location fix every hour during sampling periods of DNA hair traps and hunter harvest and every 3 hours otherwise. In addition, for the 2 collars deployed in 2003 and still on in 2004, a location fix was attempted every hour.

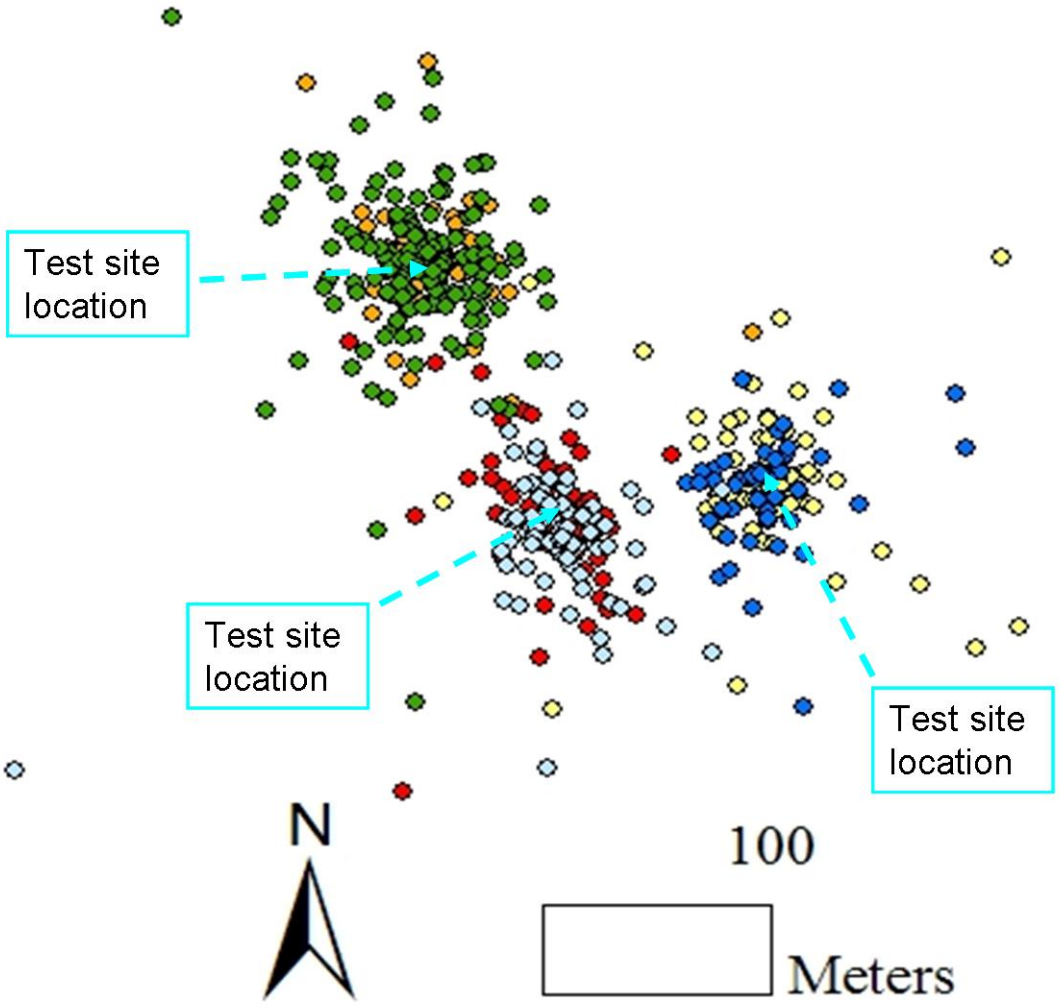

Figure 5.2. An example of GPS collar locations from 3 test sites that were each used during two different periods (Spring and Summer data are represented in different color dots for a particular test site: green and orange, red and light blue, yellow and dark blue) to represent different degrees of canopy openness.

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CONCLUDING COMMENTS

"Coalescing into an amorphous mass of nothing much" was how Caughley (1980) described most large mammal studies. Better tools, such as DNA markers and radio-telemetry, have since afforded scientists greater opportunity to conduct rigorous research, but we must use them carefully (Romesburg 1981, 1991). I hope I have shaken the status quo approach of uncritically using haphazard sub-sampling protocols for NGS application. Follicle filtering, random sub-sampling, and using food as a lure should not be used without careful consideration of the consequences. Anderson et al. (2000) pointed out that Akaike's Information Criterion (AIC) generated in Program MARK and used by researchers to choose the "best" model of population estimation is not a test in any sense. Furthermore, the true model is not assumed to be contained within the set of candidate models (Anderson et al. 2000). If data are collected or analyzed in ways that are fundamentally flawed, no analytical theory will allow valid inferences about populations of interest (Anderson 2001). If some animals are not part of the data set, modeling programs can not account for them.

I believe an analogy can be drawn from follicle filtering and sub-sampling in NGS to radio-telemetry performed via VHF or GPS collars. Man power and logistical constraints limit the number of locations that can be collected per VHF collar, and these locations are filtered by time of day, time of year, area, and weather conditions amenable to data collection. Several orders of magnitude separate the number of locations possible, and more than 1-2 orders of magnitude separate the accuracy of locations. I think that using VHF collars and using a follicle filter with random sub-sampling both introduce bias and limit inferences. Research must be designed with sufficient resources to analyze enough hair

samples or use GPS collars to collect adequate movement data, to address hypotheses. Both of these new technologies still have problems to resolve, but offer the potential to conduct more amazingly rigorous science, especially when used to complement one another.

Graduate students should never quit learning, learn to recognize when they do not know, and strive to fill in knowledge gaps (White 2001). I believe this advice applies to all wildlife professionals and hope everyone agrees that involving the lay public is both necessary and critical for successful wildlife research and management in the 21st century. The home range and movement data available via GPS collars that were privately funded complemented well the initial broad research questions funded by the state agency (Keppie 1990). Furthermore, if private support is sought, the research will certainly be of interest to the public and thus valuable to wildlife managers. My goal throughout my graduate career has been to rigorously pursue high-quality research, while developing the "scientific attitude" as defined by Leopold (Meine and Knight 1999). I hope that "imponderable combination of curiosity, skepticism, and objectivity" to which he was referring always describes my scientific endeavors.

FUTURE RESEARCH

With the help of a colleague I am currently conducting a survey regarding GPS collar performance. Our goal is to summarize experiences to provide new GPS collar users realistic expectations and recommendations for study design, given the suite of variables that impact the use of GPS collars. I also will be further analyzing the GPS collar data from this research, looking at seasonal home ranges of bears in relation to habitats and hunting seasons. I am also interested in further understanding the efficiency of sampling via DNA hair traps by analyzing how often bears approach a DNA hair trap and leave hair samples.

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APPENDICES

LIST OF APPENDICES

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Appendix 1. Program Mark results for robust design of male bears sampled in Spring 2003 and Spring 2004 via DNA hair traps in Hyde County, North Carolina.

Real Function Parameters of p1 = p2 & c1 = c2

Parameter	S Estimate	S Standard Error	95% Confidence Interval Lower	Upper	
1:S	0.3966396	0.0684273	0.2729106	0.5351747	
2:Gamma"	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:p Session 1	0.2790335	0.0441712	0.2010712	0.3731073	
10:p Session 2	0.2790335	0.0441712	0.2010712	0.3731073	
11:c Session 1	0.1095890	0.0149259	0.0835738	0.1424437	
16:c Session 2	0.1095890	0.0149259	0.0835738	0.1424437	
17:N Session 1	155.70261	16.083461	134.09957	200.52464	
18:N Session 2	162.55371	16.709808	140.06650	209.04465	

Real Function Parameters of M_b M_b

Parameter	S Estimate	S Standard Error	95% Confidence Interval Lower	Upper	
1:S	0.3799571	0.0692562	0.2561816	0.5215991	
2:Gamma"	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:p Session 1	0.2553000	0.0646930	0.1496341	0.4004450	
7:p Session 2	0.3014320	0.0604150	0.1973670	0.4309090	
11:c Session 1	0.0857143	0.0193178	0.0546674	0.1319327	
14:c Session 2	0.1315789	0.0223867	0.0935475	0.1819680	
17:N Session 1	164.13339	26.810381	132.75939	247.97862	
18:N Session 2	155.69555	18.278791	133.58379	211.33285	

Real Function Parameters of M_o M_b

Parameter	S Estimate	S Standard Error	95% Confidence Interval Lower	Upper	
1:S	0.3799571	0.0692562	0.2561815	0.5215991	
2:Gamma"	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:p Session 1	0.0980105	0.0210772	0.0637551	0.1477663	
11:c Session 1	0.0980105	0.0210772	0.0637551	0.1477663	
10:p Session 2	0.3014320	0.0604150	0.1973670	0.4309090	
16:c Session 2	0.1315789	0.0223867	0.0935475	0.1819680	
17:N Session 1	336.69867	66.844263	239.23040	510.02762	
18:N Session 2	155.69556	18.278803	133.58379	211.33290	

Appendix 1 (cont.)

Real Function Parameters of M_b M_o

Parameter	S Estimate	S Standard Error	95% Confidence Interval Lower	Upper	
1:S	0.6066227	0.1158733	0.3731826	0.7997709	
2:Gamma"	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:p Session 1	0.2552998	0.0646930	0.1496340	0.4004449	
11:c Session 1	0.0857143	0.0193178	0.0546674	0.1319327	
10:p Session 2	0.1496725	0.0237284	0.1088448	0.2023376	
16:c Session 2	0.1496725	0.0237284	0.1088448	0.2023376	
17:N Session 1	164.13346	26.810418	132.75941	247.97880	
18:N Session 2	248.87665	34.688310	196.64033	336.25751	

Real Function Parameters of M_o M_o

Parameter	S Estimate	S Standard Error	95% Confidence Interval Lower	Upper	
1:S	0.6066230	0.1158736	0.3731823	0.7997715	
2:Gamma"	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:p Session 1	0.0980105	0.0210772	0.0637551	0.1477663	
11:c Session 1	0.0980105	0.0210772	0.0637551	0.1477663	
10:p Session 2	0.1496725	0.0237284	0.1088447	0.2023376	
16:c Session 2	0.1496725	0.0237284	0.1088447	0.2023376	
17:N Session 1	336.69872	66.844285	239.23042	510.02773	
18:N Session 2	248.87672	34.688352	196.64035	336.25770	

Real Function Parameters of p1 = p2 = c1 = c2

Parameter	S Estimate	S Standard Error	95% Confidence Interval Lower	Upper	
1:S	0.6997754	0.1258176	0.4188327	0.8828835	
2:Gamma"	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:p Session 1	0.1249434	0.0160366	0.0967459	0.1599042	
10:p Session 2	0.1249434	0.0160366	0.0967459	0.1599042	
11:c Session 1	0.1249434	0.0160366	0.0967459	0.1599042	
16:c Session 2	0.1249434	0.0160366	0.0967459	0.1599042	
17:N Session 1	275.08387	34.792741	219.99568	358.80254	
18:N Session 2	287.17093	36.071692	229.97344	373.84894	

Appendix 2. Program Mark results for robust design of female bears sampled in Spring 2003 and Spring 2004 via DNA hair traps in Hyde County, North Carolina.

Real Function Parameters of M_o M_o

Parameter	S Estimate	S Standard Error	95% Confidence Interval Lower	Upper	
1:S	0.5105097	0.1117602	0.3026855	0.7147633	
2:Gamma"	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:p Session 1	0.0949916	0.0250864	0.0559297	0.1568035	
13:c Session 1	0.0949916	0.0250864	0.0559297	0.1568035	
7:p Session 2	0.1679456	0.0257308	0.1233416	0.2245483	
14:c Session 2	0.1679456	0.0257308	0.1233416	0.2245483	
17:N Session 1	239.49480	58.565669	159.26035	399.93779	
18:N Session 2	206.91221	27.361834	166.09074	276.41970	

Real Function Parameters of M_o M_b

Parameter	S Estimate	S Standard Error	95% Confidence Interval Lower	Upper	
1:S	0.3944419	0.1002491	0.2224758	0.5972305	
2:Gamma"	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:p Session 1	0.0949916	0.0250865	0.0559297	0.1568036	
11:c Session 1	0.0949916	0.0250865	0.0559297	0.1568036	
7:p Session 2	0.2443327	0.0672125	0.1367476	0.3975772	
14:c Session 2	0.1573604	0.0259439	0.1128964	0.2150904	
17:N Session 1	239.49475	58.565644	159.26033	399.93767	
18:N Session 2	159.75505	28.958931	126.60818	251.94665	

Real Function Parameters of p1 = p2 = c1 = c2

Parameter	S Estimate	S Standard Error	95% Confidence Interval Lower	Upper	
1:S	0.5926964	0.1272818	0.3411251	0.8035342	
2:Gamma"	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:p Session 1	0.1382389	0.0185060	0.1057915	0.1786500	
7:p Session 2	0.1382389	0.0185060	0.1057915	0.1786500	
13:c Session 1	0.1382389	0.0185060	0.1057915	0.1786500	
16:c Session 2	0.1382389	0.0185060	0.1057915	0.1786500	
17:N Session 1	175.64307	23.722679	139.15528	234.26290	
18:N Session 2	240.30361	30.709394	192.44604	315.28318	

Appendix 2 (cont.)

Real Function Parameters of M_b M_o

Parameter	S Estimate	S Standard Error	95% Confidence Interval Lower	Upper	
1:S	0.5105098	0.1117602	0.3026856	0.7147634	
2:Gamma"	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:p Session 1	0.0732644	0.0934968	0.0052902	0.5402659	
11:c Session 1	0.0967742	0.0265502	0.0557804	0.1627034	
7:p Session 2	0.1679456	0.0257308	0.1233415	0.2245482	
14:c Session 2	0.1679456	0.0257308	0.1233415	0.2245482	
17:N Session 1	300.57150	342.77395	104.38780	2012.7603	
18:N Session 2	206.91225	27.361846	166.09076	276.41977	

Real Function Parameters of M_b M_b

Parameter	S Estimate	S Standard Error	95% Confidence Interval Lower	Upper	
1:S	0.3944415	0.1002489	0.2224758	0.5972298	
2:Gamma"	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
6:p Session 1	0.0732646	0.0934966	0.0052903	0.5402633	
7:p Session 2	0.2443330	0.0672124	0.1367479	0.3975773	
11:c Session 1	0.0967742	0.0265502	0.0557805	0.1627035	
14:c Session 2	0.1573604	0.0259439	0.1128964	0.2150904	
17:N Session 1	300.57074	342.77120	104.38786	2012.7426	
18:N Session 2	159.75493	28.958843	126.60815	251.94623	

Real Function Parameters of p1 = p2 & c1 = c2

Parameter	S Estimate	S Standard Error	95% Confidence Interval Lower	Upper	
1:S	0.4952141	0.1465356	0.2372006	0.7558021	
2:Gamma"	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:p Session 1	0.1750152	0.0548134	0.0915733	0.3086560	
10:p Session 2	0.1750152	0.0548134	0.0915733	0.3086560	
11:c Session 1	0.1339564	0.0190107	0.1008692	0.1757751	
16:c Session 2	0.1339564	0.0190107	0.1008692	0.1757751	
17:N Session 1	146.67196	35.585030	104.69354	257.23523	
18:N Session 2	200.69767	47.988110	143.66898	348.90562	

Appendix 3. Mark results for NGS of 79 female black bears caught 91 periods during Spring 2003 in Hyde County, NC.

UUReal Function Parameters of M_o

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.0949917	0.0250865	0.0559297	0.1568036
2:N	239.49472	58.565638	159.26031	399.93763

Real Function Parameters of M_b

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.0732645	0.0934966	0.0052902	0.5402642
2:c	0.0967742	0.0265502	0.0557805	0.1627035
3:N	300.57111	342.77233	104.38785	2012.7497

Real Function Parameters of M_{bh}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.3349697E-14	0.2007717E-07	-0.3935125E-07	0.3935125E-07
2:p	0.8337322	0.3971115E-07	0.8337322	0.8337323
3:p	0.8337322	0.3971115E-07	0.8337322	0.8337323
4:p	0.8337322	0.3971115E-07	0.8337322	0.8337323
5:p	0.8337322	0.3971115E-07	0.8337322	0.8337323
6:p	0.0732645	0.0934969	0.0052902	0.5402663
7:p	0.0732645	0.0934969	0.0052902	0.5402663
8:p	0.0732645	0.0934969	0.0052902	0.5402663
9:p	0.0732645	0.0934969	0.0052902	0.5402663
10:c	0.0077769	0.1619237E-16	0.0077769	0.0077769
11:c	0.0077769	0.1619237E-16	0.0077769	0.0077769
12:c	0.0077769	0.1619237E-16	0.0077769	0.0077769
13:c	0.0967742	0.0265502	0.0557805	0.1627034
14:c	0.0967742	0.0265502	0.0557805	0.1627034
15:c	0.0967742	0.0265502	0.0557805	0.1627034
16:N	300.57119	342.77357	104.38776	2012.7584

Appendix 3 (cont.)

Real Function Parameters of M_h

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.0233515	0.4813338	0.3320588E-12	1.0000000
2:p	0.2405455	1.2618214	0.4180323E-06	0.9999958
3:p	0.0862141	0.0990003	0.0079722	0.5255446
4:N	253.29002	152.79975	118.67451	844.65563

Real Function Parameters of M_{tb}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.2784807	0.0504322	0.1909328	0.3869715
2:p	0.3333337	0.0624391	0.2237651	0.4644517
3:p	0.5263157	0.0809983	0.3701833	0.6774660
4:p	1.0000000	0.4609675E-05	0.9999910	1.0000090
5:c	0.0909089	0.0612908	0.0228394	0.2996402
6:c	0.0975605	0.0463397	0.0371032	0.2327203
7:c	0.0983599	0.0381294	0.0448619	0.2021520
8:N	79.000000	0.4850113E-05	79.000000	79.000004

Real Function Parameters of M_t

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.0919545	0.0292293	0.0485169	0.1674385
2:p	0.0877748	0.0281979	0.0460293	0.1609913
3:p	0.1003140	0.0312831	0.0534985	0.1802935
4:p	0.1003140	0.0312831	0.0534985	0.1802935
5:N	239.24864	58.488482	159.12598	399.49068

Appendix 3 (cont.)

Real Function Parameters of M_{tbh}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.1437631	0.0873449	0.0401120	0.4028463
2:p	0.6666667	0.1924501	0.2681041	0.9161044
3:p	0.3144742E-13	0.1786432E-06	-0.3501406E-06	0.3501407E-06
4:p	1.0000000	0.2728503E-04	0.9999465	1.0000535
5:p	0.0797728	0.0000000	0.0797728	0.0797728
6:p	0.2133042	0.0632884	0.1146253	0.3621831
7:p	0.3570473	0.0686031	0.2361453	0.4993810
8:p	0.4739032	0.0966850	0.2963869	0.6582711
9:p	1.0000000	0.2479614E-05	0.9999951	1.0000049
10:c	0.2641478	0.2083853	0.0420551	0.7458818
11:c	0.3102146E-14	0.3702012E-07	-0.7255944E-07	0.7255945E-07
12:c	0.5282955	0.3223719	0.0814945	0.9339381
13:c	0.2690719E-15	0.2362033E-07	-0.4629584E-07	0.4629584E-07
14:c	0.1196584	0.0577763	0.0443332	0.2848233
15:c	0.1150501E-14	0.1059911E-07	-0.2077425E-07	0.2077426E-07
16:N	79.000000	0.1366406E-04	79.000000	79.000012

Real Function Parameters of M_{th}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.0090371	0.0068580	0.0020288	0.0393018
2:p	1.0000000	0.2813169E-05	0.9999945	1.0000055
3:p	0.3330974	0.3243362	0.0277637	0.8972882
4:p	0.3335187E-11	0.1556557E-05	-0.3050848E-05	0.3050855E-05
5:p	1.0000000	0.1046378E-03	0.9997949	1.0002051
6:p	0.0637544	0.0265183	0.0277169	0.1399058
7:p	0.0665238	0.0261625	0.0302624	0.1399634
8:p	0.0794988	0.0302262	0.0370139	0.1625186
9:p	0.0703793	0.0286784	0.0310682	0.1516465
10:N	304.64432	98.799740	178.29608	591.76302

Appendix 4. Mark results for NGS of 108 female black bears caught 139 periods during Spring 2004 in Hyde County, NC.

Real Function Parameters of M_o

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.1679456	0.0257309	0.1233415	0.2245482
2:N	206.91223	27.361850	166.09074	276.41976

Real Function Parameters of M_h

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.9871339	0.3083683	0.1065531E-08	1.0000000
2:p	0.0032891	0.0834432	0.4582931E-13	1.0000000
3:p	0.3264220	0.1095340	0.1543562	0.5626710
4:N	4666.5354	114562.22	139.40745	661742.27

Real Function Parameters of M_b

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.2443328	0.0672125	0.1367477	0.3975772
2:c	0.1573604	0.0259439	0.1128964	0.2150904
3:N	159.75503	28.958918	126.60818	251.94659

Real Function Parameters of M_{tb}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.3240740	0.0450360	0.2426727	0.4177195
2:p	0.4931506	0.0585151	0.3807789	0.6062187
3:p	0.5405403	0.0819289	0.3812951	0.6919157
4:p	1.0000000	0.3357523E-05	0.9999934	1.0000066
5:c	0.1428575	0.0591486	0.0607379	0.3004854
6:c	0.1549297	0.0429422	0.0879197	0.2585357
7:c	0.1648352	0.0388947	0.1018856	0.2556086
8:N	108.00000	0.6618843E-05	108.00000	108.00000

Appendix 4 (cont.)

Real Function Parameters of M_{bh}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.3234350	0.2594233	0.0447164	0.8299973
2:p	0.3556961	0.1642355	0.1193399	0.6922178
3:p	0.3556961	0.1642355	0.1193399	0.6922178
4:p	0.3556961	0.1642355	0.1193399	0.6922178
5:p	0.3556961	0.1642355	0.1193399	0.6922178
6:p	0.1487778	0.1334816	0.0216670	0.5797188
7:p	0.1487778	0.1334816	0.0216670	0.5797188
8:p	0.1487778	0.1334816	0.0216670	0.5797188
9:p	0.1487778	0.1334816	0.0216670	0.5797188
10:c	0.3136656	0.0889845	0.1689353	0.5067788
11:c	0.3136656	0.0889845	0.1689353	0.5067788
12:c	0.3136656	0.0889845	0.1689353	0.5067788
13:c	0.8581357E-13	0.2240125E-06	-0.4390644E-06	0.4390646E-06
14:c	0.8581357E-13	0.2240125E-06	-0.4390644E-06	0.4390646E-06
15:c	0.8581357E-13	0.2240125E-06	-0.4390644E-06	0.4390646E-06
16:N	182.84362	84.788097	120.60920	552.24434

Real Function Parameters of M_t

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.1697896	0.0344329	0.1124563	0.2481797
2:p	0.1988964	0.0382304	0.1342981	0.2843605
3:p	0.1503851	0.0318353	0.0979739	0.2238750
4:p	0.1552362	0.0324906	0.1015868	0.2299662
5:N	206.13744	27.196566	165.58232	275.25546

Appendix 4 (cont.)

Real Function Parameters of M_{tbh}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.3053806	0.2094683	0.0596772	0.7528114
2:p	0.5994329	0.2029830	0.2220412	0.8869558
3:p	0.5018068	0.2599432	0.1160115	0.8854626
4:p	1.0000000	0.7952562E-05	0.9999844	1.0000156
5:p	0.0157133	806.41685	0.2217093E-12	1.0000000
6:p	0.2030160	0.0761725	0.0919313	0.3905930
7:p	0.4912381	0.0819768	0.3367197	0.6474490
8:p	0.4411258	0.1397044	0.2063161	0.7055954
9:p	1.0000000	0.1778590E-05	0.9999965	1.0000035
10:c	0.2529090	0.1458688	0.0693767	0.6058710
11:c	0.3230973	0.1536411	0.1075054	0.6541498
12:c	0.4484945	0.1821330	0.1611099	0.7749511
13:c	0.2126102E-12	0.2756714E-06	-0.5403158E-06	0.5403162E-06
14:c	0.0553903	0.0705493	0.0041555	0.4517566
15:c	0.0035877	0.1260476	0.5000516E-13	1.0000000
16:N	108.00000	0.9566591E-05	108.00000	108.00001

Real Function Parameters of M_{th}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.8694134	0.0536015	0.7252047	0.9438074
2:p	0.2435680	0.0536357	0.1539695	0.3629388
3:p	0.1351218	0.0442548	0.0692261	0.2470914
4:p	0.2116715	0.0480216	0.1325110	0.3206423
5:p	0.2226908	0.0503746	0.1393807	0.3363361
6:p	0.3701656E-14	0.2401456E-07	-0.4706854E-07	0.4706855E-07
7:p	1.0000000	0.5693214E-04	0.9998884	1.0001116
8:p	0.0270315	0.0894027	0.3550301E-04	0.9560249
9:p	0.1522312E-13	0.8270044E-07	-0.1620928E-06	0.1620929E-06
10:N	165.28042	20.198153	137.28202	220.04986

Appendix 5. Mark results for NGS of 114 male black bears caught 132 periods during Spring 2003 in Hyde County, NC.

Real Function Parameters of M_{tb}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.3596491	0.0449465	0.2769967	0.4515608
2:p	0.4520548	0.0582509	0.3422469	0.5667377
3:p	0.5250001	0.0789581	0.3727356	0.6727537
4:p	1.0000000	0.2016621E-05	0.9999960	1.0000040
5:c	0.1707317	0.0587642	0.0836349	0.3171399
6:c	0.0810810	0.0317309	0.0368813	0.1689585
7:c	0.0526315	0.0229098	0.0220762	0.1202765
8:N	114.00000	0.4017770E-17	114.00000	114.00000

Real Function Parameters of M_{bh}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.0180573	0.0169621	0.0028122	0.1070720
2:p	0.5840790	0.5195356	0.0207926	0.9893473
3:p	0.5840790	0.5195356	0.0207926	0.9893473
4:p	0.5840790	0.5195356	0.0207926	0.9893473
5:p	0.5840790	0.5195356	0.0207926	0.9893473
6:p	0.2460683	0.0672069	0.1382702	0.3989953
7:p	0.2460683	0.0672069	0.1382702	0.3989953
8:p	0.2460683	0.0672069	0.1382702	0.3989953
9:p	0.2460683	0.0672069	0.1382702	0.3989953
10:c	0.8705924	0.2641846	0.0635727	0.9985023
11:c	0.8705924	0.2641846	0.0635727	0.9985023
12:c	0.8705924	0.2641846	0.0635727	0.9985023
13:c	0.0585049	0.0196631	0.0299437	0.1111863
14:c	0.0585049	0.0196631	0.0299437	0.1111863
15:c	0.0585049	0.0196631	0.0299437	0.1111863
16:N	166.60527	29.227113	133.03382	259.38935

Real Function Parameters of M_{b}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.2552998	0.0646930	0.1496339	0.4004450
2:c	0.0857143	0.0193178	0.0546674	0.1319327
3:N	164.13346	26.810433	132.75940	247.97887

Appendix 5 (cont.)

Real Function Parameters of M_h

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.0075286	0.0075866	0.0010358	0.0525795
2:p	0.7276518	0.2904857	0.1312171	0.9792801
3:p	0.0645383	0.0251651	0.0295763	0.1350761
4:N	474.61134	163.28517	268.67936	954.71033

Real Function Parameters of M_t

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.1238117	0.0304269	0.0753999	0.1966946
2:p	0.1207919	0.0298342	0.0734027	0.1924225
3:p	0.0815346	0.0220355	0.0474977	0.1364676
4:p	0.0724751	0.0201983	0.0415589	0.1234287
5:N	331.14794	65.415887	235.86373	500.93404

Real Function Parameters of M_{tbh}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.0636672	0.0375557	0.0193966	0.1894586
2:p	0.6888887	0.3652856	0.0727182	0.9842575
3:p	0.4428569	0.7435798	0.0021580	0.9965887
4:p	1.0000000	0.4502946E-04	0.9999117	1.0000883
5:p	0.0391450	0.0000000	0.0391450	0.0391450
6:p	0.3372620	0.0470014	0.2520569	0.4345361
7:p	0.4523484	0.0630355	0.3340521	0.5762850
8:p	0.5095754	0.0910980	0.3371180	0.6797834
9:p	1.0000000	0.3167769E-05	0.9999938	1.0000062
10:c	0.4000001	0.2190891	0.1002282	0.7995946
11:c	1.0000000	0.2052848E-05	0.9999960	1.0000040
12:c	0.3333333	0.1924501	0.0838956	0.7318958
13:c	0.1388889	0.0576384	0.0590150	0.2931854
14:c	0.7011264E-15	0.9308351E-08	-0.1824437E-07	0.1824437E-07
15:c	0.0294118	0.0204891	0.0073675	0.1100985
16:N	114.00000	0.1013358E-04	114.00000	114.00001

Appendix 5 (cont.)

Real Function Parameters of M_o

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.0980105	0.0210772	0.0637551	0.1477663
2:N	336.69872	66.844283	239.23042	510.02773

Real Function Parameters of M_{th}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.0175724	0.0134505	0.0038694	0.0760957
2:p	0.6577636	0.3421936	0.0889861	0.9742383
3:p	0.4984328	0.3816776	0.0474869	0.9519428
4:p	0.3728679	0.3085866	0.0428411	0.8876149
5:p	0.2127642	0.1576489	0.0409685	0.6309821
6:p	0.0313919	0.0670453	0.4301026E-03	0.7093920
7:p	0.0331891	0.0648132	0.6546536E-03	0.6427200
8:p	0.0217511	0.0430191	0.4225595E-03	0.5390599
9:p	0.0214570	0.0414262	0.4585034E-03	0.5117624
10:N	967.01116	1660.5713	187.38083	10029.779

Appendix 6. Mark results for NGS of 119 male black bears caught 149 periods during Spring 2004 in Hyde County, NC.

Real Function Parameters of M_b

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.3014320	0.0604150	0.1973669	0.4309091
2:c	0.1315789	0.0223867	0.0935475	0.1819680
3:N	155.69557	18.278815	133.58379	211.33296

Real Function Parameters of M_{tb}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.4117647	0.0451156	0.3270077	0.5021001
2:p	0.4000000	0.0585540	0.2924207	0.5181734
3:p	0.5952381	0.0757392	0.4426319	0.7314147
4:p	1.0000000	0.1661749E-05	0.9999967	1.0000033
5:c	0.1632653	0.0528011	0.0838085	0.2938890
6:c	0.1428571	0.0398779	0.0809081	0.2398600
7:c	0.1078431	0.0307126	0.0607323	0.1843268
8:N	119.00000	0.1986768E-05	119.00000	119.00000

Real Function Parameters of M_{bh}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.1364035E-14	0.1966194E-07	-0.3853740E-07	0.3853741E-07
2:p	0.6208635	0.0000000	0.6208635	0.6208635
3:p	0.6208635	0.0000000	0.6208635	0.6208635
4:p	0.6208635	0.0000000	0.6208635	0.6208635
5:p	0.6208635	0.0000000	0.6208635	0.6208635
6:p	0.3014320	0.0604150	0.1973670	0.4309091
7:p	0.3014320	0.0604150	0.1973670	0.4309091
8:p	0.3014320	0.0604150	0.1973670	0.4309091
9:p	0.3014320	0.0604150	0.1973670	0.4309091
10:c	0.3798006	0.0000000	0.3798006	0.3798006
11:c	0.3798006	0.0000000	0.3798006	0.3798006
12:c	0.3798006	0.0000000	0.3798006	0.3798006
13:c	0.1315789	0.0223867	0.0935475	0.1819680
14:c	0.1315789	0.0223867	0.0935475	0.1819680
15:c	0.1315789	0.0223867	0.0935475	0.1819680
16:N	155.69556	18.278806	133.58379	211.33291

Appendix 6 (cont.)

Real Function Parameters of M_t

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.1993456	0.0375682	0.1356695	0.2831183
2:p	0.1464580	0.0303298	0.0963724	0.2163415
3:p	0.1464580	0.0303298	0.0963724	0.2163415
4:p	0.1139118	0.0256801	0.0724228	0.1746923
5:N	245.80432	34.038657	194.61377	331.65089

Real Function Parameters of M_o

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.1496725	0.0237284	0.1088448	0.2023376
2:N	248.87669	34.688343	196.64033	336.25765

Real Function Parameters of M_h

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	1.0000000	0.9325335E-06	0.9999982	1.0000018
2:p	0.1496725	0.0237284	0.1088448	0.2023376
3:p	0.2755930	179.79372	0.5283520E-11	1.0000000
4:N	248.87668	34.688336	196.64032	336.25761

Appendix 6 (cont.)

Real Function Parameters of M_{tbh}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.6167827	0.0000000	0.6167827	0.6167827
2:p	0.3556560	0.0000000	0.3556560	0.3556560
3:p	0.4670852	0.0000000	0.4670852	0.4670852
4:p	0.9919398	0.0000000	0.9919398	0.9919398
5:p	0.9999999	0.0000000	0.9999999	0.9999999
6:p	0.5020709	0.0000000	0.5020709	0.5020709
7:p	0.2602782	0.0000000	0.2602782	0.2602782
8:p	0.2041557E-11	0.4611096E-05	-0.9037747E-05	0.9037751E-05
9:p	1.0000000	0.5212074E-05	0.9999898	1.0000102
10:c	0.3064649	0.1674936	0.0861749	0.6743361
11:c	0.2001979E-15	0.5046028E-08	-0.9890215E-08	0.9890215E-08
12:c	0.1502855	0.0540916	0.0715853	0.2886113
13:c	0.1213911E-13	0.4830689E-07	-0.9468149E-07	0.9468151E-07
14:c	0.3818648	0.2396510	0.0778739	0.8188105
15:c	0.1142633E-13	0.4557978E-07	-0.8933635E-07	0.8933637E-07
16:N	119.00000	0.2864083E-04	119.00000	119.00003

Real Function Parameters of M_{th}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.0737814	0.1940328	0.3049455E-03	0.9541334
2:p	0.1430138E-12	0.4408980E-06	-0.8641600E-06	0.8641603E-06
3:p	0.1752906E-13	0.1071742E-06	-0.2100615E-06	0.2100615E-06
4:p	0.2665671	0.2532350	0.0279004	0.8215080
5:p	0.4714406	0.9946146	0.3569118E-03	0.9995514
6:p	0.2253732	0.0685102	0.1188063	0.3856905
7:p	0.1655804	0.0523026	0.0863333	0.2941506
8:p	0.1443459	0.0407778	0.0811547	0.2436916
9:p	0.0912303	0.0329811	0.0440069	0.1796083
10:N	234.73629	33.898732	184.95737	322.08403

Appendix 7. Mark results for NGS of pooled results for 193 male and female bears caught 223 periods during Spring 2003 in Hyde County, NC.

Real Function Parameters of M_h

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.0067069	0.0088246	0.5031160E-03	0.0830512
2:p	0.6718134	0.3319115	0.0967218	0.9750834
3:p	0.0729687	0.0219765	0.0399741	0.1295227
4:N	724.16596	185.86876	465.85151	1227.0323

Real Function Parameters of M_{tb}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.3264249	0.0337525	0.2640003	0.3956747
2:p	0.4000000	0.0429669	0.3194368	0.4863612
3:p	0.5256410	0.0565394	0.4153764	0.6334606
4:p	1.0000000	0.3215590E-05	0.9999937	1.0000063
5:c	0.1428571	0.0440867	0.0760378	0.2523574
6:c	0.0869564	0.0262753	0.0474247	0.1541095
7:c	0.0705128	0.0204971	0.0394752	0.1228331
8:N	193.00000	0.5860634E-16	193.00000	193.00000

Real Function Parameters of M_b

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.1770149	0.0538415	0.0943970	0.3073972
2:c	0.0898204	0.0156451	0.0635114	0.1255662
3:N	356.07589	80.974456	257.98069	602.25615

Real Function Parameters of M_o

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.0962056	0.0160559	0.0690072	0.1325971
2:N	579.48794	89.398619	440.05901	797.60425

Appendix 7 (cont.)

Real Function Parameters of M_{bh}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.4368803E-13	0.7735184E-07	-0.1516096E-06	0.1516097E-06
2:p	0.9971599	67.362877	0.4876136E-08	1.0000000
3:p	0.9971599	67.362877	0.4876136E-08	1.0000000
4:p	0.9971599	67.362877	0.4876136E-08	1.0000000
5:p	0.9971599	67.362877	0.4876136E-08	1.0000000
6:p	0.1770150	0.0538414	0.0943971	0.3073971
7:p	0.1770150	0.0538414	0.0943971	0.3073971
8:p	0.1770150	0.0538414	0.0943971	0.3073971
9:p	0.1770150	0.0538414	0.0943971	0.3073971
10:c	0.0296964	193.96723	0.4250443E-12	1.0000000
11:c	0.0296964	193.96723	0.4250443E-12	1.0000000
12:c	0.0296964	193.96723	0.4250443E-12	1.0000000
13:c	0.0898203	0.0156451	0.0635114	0.1255662
14:c	0.0898203	0.0156451	0.0635114	0.1255662
15:c	0.0898203	0.0156451	0.0635114	0.1255662
16:N	356.07579	80.974302	257.98072	602.25546

Real Function Parameters of M_t

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.1091628	0.0212472	0.0739487	0.1582798
2:p	0.1056974	0.0207135	0.0714277	0.1536876
3:p	0.0883699	0.0180280	0.0588387	0.1306652
4:p	0.0831717	0.0172156	0.0550696	0.1237365
5:N	577.11947	88.927993	438.45195	794.12688

Appendix 7 (cont.)

Real Function Parameters of M_{th}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.0055374	0.0048118	0.0010034	0.0299442
2:p	0.7568023	0.3379666	0.0784335	0.9912878
3:p	1.0000000	0.1620091E-04	0.9999682	1.0000318
4:p	0.6135510	0.4638224	0.0331869	0.9865651
5:p	0.5964027	0.4654013	0.0323229	0.9849338
6:p	0.0846082	0.0225323	0.0496638	0.1405050
7:p	0.0804343	0.0222519	0.0462599	0.1362484
8:p	0.0684874	0.0180883	0.0404702	0.1136042
9:p	0.0643532	0.0171166	0.0379052	0.1071990
10:N	713.23120	154.30131	487.46042	1112.1065

Real Function Parameters of M_{tbh}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.0408748	1.1605892	0.5918586E-12	1.0000000
2:p	0.2766967	7.8571650	0.5312777E-11	1.0000000
3:p	0.1788300	7.0213290	0.3024442E-11	1.0000000
4:p	0.2884658	13.793042	0.5630364E-11	1.0000000
5:p	1.0000000	0.4032998E-04	0.9999210	1.0000790
6:p	0.3285405	0.3989968	0.0139284	0.9442867
7:p	0.4101496	0.7403309	0.0017243	0.9964404
8:p	0.5407855	1.6529257	0.2542814E-05	0.9999982
9:p	1.0000000	0.1230378E-04	0.9999759	1.0000241
10:c	1.0000000	0.1922303E-03	0.9866327E-03	1.0000000
11:c	0.7205342	0.3956973	0.0519345	0.9918266
12:c	0.7540386	0.4600895	0.0231579	0.9974839
13:c	0.1120898	0.0472756	0.0473993	0.2425864
14:c	0.0688016	0.0259225	0.0323493	0.1403712
15:c	0.0499509	0.0223568	0.0204553	0.1169020
16:N	193.00000	0.6363532E-04	193.00000	193.00010

Appendix 8. Mark results for NGS of pooled results for 227 male and female bears caught 288 times during Spring 2004 in Hyde County, NC.

Real Function Parameters of M_b

			95% Confidence Interval	
Parameter	Estimate	Standard Error	Lower	Upper
1:p	0.2689320	0.0452109	0.1898847	0.3660184
2:c	0.1435294	0.0170072	0.1133022	0.1801821
3:N	317.26991	33.392733	271.74046	409.13170

Real Function Parameters of M_{tb}

			95% Confidence Interval	
Parameter	Estimate	Standard Error	Lower	Upper
1:p	0.3700440	0.0320456	0.3097117	0.4347275
2:p	0.4475524	0.0415814	0.3681434	0.5297300
3:p	0.5696203	0.0557064	0.4588257	0.6738555
4:p	1.0000000	0.3696847E-05	0.9999928	1.0000072
5:c	0.1547619	0.0394623	0.0920370	0.2485337
6:c	0.1486486	0.0292418	0.0999188	0.2154550
7:c	0.1347150	0.0245759	0.0933733	0.1905147
8:N	227.00000	0.1462446E-04	227.00000	227.00002

Real Function Parameters of M_o

			95% Confidence Interval	
Parameter	Estimate	Standard Error	Lower	Upper
1:p	0.1577059	0.0174026	0.1265100	0.1948781
2:N	456.54596	43.914181	385.30164	559.85409

Appendix 8 (cont.)

Real Function Parameters of M_{bh}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.0379332	0.0302915	0.0076900	0.1670902
2:p	1.0000000	0.1098856E-04	0.9999785	1.0000215
3:p	1.0000000	0.1098856E-04	0.9999785	1.0000215
4:p	1.0000000	0.1098856E-04	0.9999785	1.0000215
5:p	1.0000000	0.1098856E-04	0.9999785	1.0000215
6:p	0.2245957	0.0628802	0.1249061	0.3701911
7:p	0.2245957	0.0628802	0.1249061	0.3701911
8:p	0.2245957	0.0628802	0.1249061	0.3701911
9:p	0.2245957	0.0628802	0.1249061	0.3701911
10:c	0.3649765	0.1419761	0.1474830	0.6562939
11:c	0.3649765	0.1419761	0.1474830	0.6562939
12:c	0.3649765	0.1419761	0.1474830	0.6562939
13:c	0.1208068	0.0230395	0.0824153	0.1736968
14:c	0.1208068	0.0230395	0.0824153	0.1736968
15:c	0.1208068	0.0230395	0.0824153	0.1736968
16:N	347.54735	59.386223	275.34783	527.56497

Real Function Parameters of M_t

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.1848815	0.0254206	0.1401268	0.2399415
2:p	0.1694747	0.0239599	0.1275276	0.2217131
3:p	0.1474650	0.0218357	0.1095789	0.1955729
4:p	0.1320582	0.0203160	0.0970633	0.1771941
5:N	454.34513	43.582826	383.66593	556.91096

Real Function Parameters of M_h

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.2640432	0.2937159	0.0182075	0.8740692
2:p	0.2352758	0.1300155	0.0694543	0.5591193
3:p	0.0580145	0.1547916	0.2389659E-03	0.9407191
4:N	686.89719	810.11555	271.80087	4948.0118

Appendix 8 (cont.)

Real Function Parameters of M_{th}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.1332833	0.6463342	0.2656381E-05	0.9998877
2:p	0.3034858	0.1068499	0.1392542	0.5399129
3:p	0.1643953	0.0613524	0.0757696	0.3207124
4:p	0.2240907	0.0783801	0.1066404	0.4113365
5:p	0.1950247	0.0706786	0.0911148	0.3692879
6:p	0.0074250	0.0461628	0.3484335E-07	0.9993777
7:p	0.0243063	0.1452411	0.1525079E-06	0.9997543
8:p	0.0086865	0.0552900	0.3000156E-07	0.9996094
9:p	0.0086484	0.0537276	0.4040559E-07	0.9994694
10:N	1791.6210	8872.2139	266.96295	61484.715

Real Function Parameters of M_{tbh}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:pi	0.5063132	0.3372246	0.0679251	0.9352037
2:p	0.5668648	0.1619468	0.2643050	0.8266191
3:p	0.3643989	0.3105509	0.0397596	0.8881209
4:p	0.9999999	0.0012128	0.9511661E-04	1.0000000
5:p	0.9908422	50.008366	0.1502629E-08	1.0000000
6:p	0.1681899	0.1750191	0.0171157	0.7012952
7:p	0.4919585	0.1335936	0.2535413	0.7340904
8:p	0.2820753	0.3487895	0.0132557	0.9199450
9:p	1.0000000	0.3499609E-05	0.9999931	1.0000069
10:c	0.1995349	0.1063178	0.0633358	0.4788791
11:c	0.2269707	0.0793525	0.1079417	0.4160397
12:c	0.2130379	0.0978033	0.0794304	0.4592633
13:c	0.9316601E-10	0.1001077E-04	-0.1962101E-04	0.1962120E-04
14:c	0.0478332	0.1147927	0.3592865E-03	0.8753365
15:c	0.0194056	0.1077188	0.3005405E-06	0.9992332
16:N	227.00000	0.4610762E-04	227.00000	227.00006

Appendix 9. Using only the 2002 study area, sampling success of unique bears via DNA hair traps for 4 week sampling sessions during 2002-2004 in Hyde County, North Carolina.

Sampling period	Week 1	Week 2	Week 3	Week 4	Total
Spring 2002					
Total samples that were genotyped	67	110	105	82	364
Unique bears sampled	38	60	60	47	159
# of males (%)	26 (68.4%)	36 (60.0%)	33 (55.0%)	24 (51.1%)	91 (57.2%)
Unique corrals with hair (%)	28 (32.9%)	39 (45.9%)	32 (37.6%)	28 (32.9%)	62 (72.9%)
Range in total samples per corral	1-5	1-11	1-16	1-10	1-30
Range in unique bears per corral	1-4	1-7	1-8	1-5	1-13
Average # of samples for corrals with hair	2.4	2.8	3.3	2.9	5.9
Average # of bears for corrals with hair	1.6	1.7	1.9	1.8	3.1
Fall 2002					
Total samples that were genotyped	45	83	53	114	295
Unique bears sampled	33	42	31	45	129
# of males (%)	21 (63.6%)	25 (59.5%)	12 (38.7%)	16 (35.6%)	64 (49.6%)
Unique corrals with hair (%)	21 (24.7%)	22 (25.9%)	24 (28.2%)	23 (27.1%)	49 (57.6%)
Range in total samples per corral	1-8	1-16	1-11	1-12	1-35
Range in unique bears per corral	1-6	1-7	1-3	1-6	1-11
Average # of samples for corrals with hair	2.1	3.8	2.2	5.0	6.0
Average # of bears for corrals with hair	1.6	2.0	1.3	2.0	2.9
Spring 2003					
Total samples that were genotyped	71	69	65	60	265
Unique bears sampled	38	34	36	29	120
# of males (%)	23 (60.5%)	17 (50.0%)	18 (50.0%)	14 (48.3%)	61 (50.8%)
Unique corrals with hair (%)	27 (28.4%)	30 (31.6%)	30 (31.6%)	21 (22.1%)	62 (65.3%)
Range in total samples per corral	1-8	1-7	1-7	1-11	1-15
Range in unique bears per corral	1-5	1-3	1-3	1-4	1-6
Average # of samples for corrals with hair	2.6	2.3	2.2	2.9	4.3
Average # of bears for corrals with hair	1.5	1.2	1.3	1.4	2.2
Spring 2004					
Total samples that were genotyped	112	79	97	61	349
Unique bears sampled	50	43	42	35	133
# of males (%)	29 (58.0%)	23 (53.5%)	22 (52.4%)	16 (45.7%)	69 (51.9%)
Unique corrals with hair (%)	34 (35.4%)	31 (32.3%)	26 (27.1%)	24 (25.0%)	65 (67.7%)
Range in total samples per corral	1-20	1-12	1-12	1-8	1-39
Range in unique bears per corral	1-8	1-6	1-6	1-4	1-16
Average # of samples for corrals with hair	3.3	2.5	3.7	2.5	5.9
Average # of bears for corrals with hair	1.6	1.4	1.7	1.5	2.4

Appendix 10. Sampling history of 423 unique bears caught in DNA hair traps during 2002-2004 in Hyde County, NC, using only the 2002 study area to calculate apparent survivorship between years.

Sampling periods	# of weeks sampled in Spring 2002						# of weeks sampled in Fall 2002				# taken by hunters in 2002		# of weeks sampled in Spring 2003						# taken by hunters in 2003		# of weeks sampled in Spring 2004					# taken by hunters in 2004
	1	2	3	4	Total		0	1	2	Total			0	1	2	3	4	Total			0	1	2	3	Total	
Spring 2002 (May 10-Jun 3)	119	33	5	1	158	**From Spring 2002**	134	21	3	158	6	**From Spring 2002**	127	23	2	0	0	152	7 + 1*	**From Spring 2002**	120	18	4	2	144	5
Fall 2002 (Sep 12-Oct 6)						**New in Fall 2002**		85	19	104	1	**From Fall 2002**	94	6	3	0	0	103	0 + 1**	**From Fall 2002**	90	9	3	0	102	5 + 1***
Spring 2003 (May 16-Jun 19)												**New in Spring 2003**		76	7	0	1	84	5	**From Spring 2003**	60	14	3	2	79	3
Spring 2004 (May 30-Jul 3)																				**New in Spring 2004**		60	15	2	77	7

*Bear with tattoo # 733 was collared and could not be located after Summer 2003.
**Bear with tattoo # 766 drowned in August 2003.
*** Bear with tattoo # 775 was killed by another bear in May 2004.

Appendix 11. Exact probability tests of Hardy-Weinberg Equilibrium produced by GENEPOP 3.4 (Rousset and Raymond 1997) for bears in Hyde County, North Carolina.

Spring 2003 NGS samples

		Fis:			
LOCUS	P-val	S.E	W&C	R&H	Matr
PRIMER_A	0.2117	0.0141	-0.002	+0.008	-
PRIMER_B	0.3629	0.0192	+0.123	+0.070	-
PRIMER_C	0.5674	0.0161	-0.010	-0.017	-
PRIMER_D	0.0462	0.0092	+0.022	+0.008	-
PRIMER_L	0.0142	0.0043	+0.016	+0.017	-

All (Fisher's method) :
chi2 : 20.9263
Df : 10
Prob: 0.0216

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Hunter harvest 2003 samples

		Fis:			
LOCUS	P-val	S.E	W&C	R&H	Matr
PRIMER_A	0.8728	0.0061	+0.035	+0.043	-
PRIMER_B	0.4394	0.0157	+0.096	+0.071	-
PRIMER_C	0.5441	0.0141	-0.005	-0.018	-
PRIMER_D	0.1195	0.0096	-0.048	-0.018	-
PRIMER_L	0.1028	0.0095	+0.035	+0.036	-

All (Fisher's method) :
chi2 : 11.9339
Df : 10
Prob: 0.2895

Appendix 11 (cont.)

Spring 2004 barb samples

	Fis:				
LOCUS	P-val	S.E	W&C	R&H	Matr
PRIMER_A	0.5581	0.0171	+0.029	+0.021	-
PRIMER_B	0.7606	0.0175	+0.013	+0.001	-
PRIMER_C	0.5218	0.0152	+0.032	+0.013	-
PRIMER_D	0.2739	0.0164	+0.064	+0.023	-
PRIMER_L	0.6208	0.0152	-0.024	-0.007	-

All (Fisher's method) :
chi2 : 6.5587
Df : 10
Prob: 0.7663

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Hunter harvest 2004 samples

	Fis:				
LOCUS	P-val	S.E	W&C	R&H	Matr
PRIMER_A	0.0010	0.0004	+0.075	+0.074	-
PRIMER_B	0.6502	0.0130	-0.008	+0.001	-
PRIMER_C	0.7446	0.0077	+0.039	-0.010	-
PRIMER_D	0.3212	0.0118	-0.024	-0.028	-
PRIMER_L	0.0730	0.0132	-0.008	-0.017	-

All (Fisher's method) :
chi2 : 22.6745
Df : 10
Prob: 0.0120

Appendix 12. Linkage disequilibrium test for each pair of loci in each population produced by GENEPOP 3.4 (Rousset and Raymond 1997) for bears in Hyde County, North Carolina.

Spring 2003 barb samples

Pop	Locus#1	Locus#2	P-Value	S.E.
001	PRIMER_A	PRIMER_B	0.25186	0.03018
001	PRIMER_A	PRIMER_C	0.55142	0.03583
001	PRIMER_B	PRIMER_C	0.35608	0.03365
001	PRIMER_A	PRIMER_D	0.67466	0.03672
001	PRIMER_B	PRIMER_D	0.11251	0.02151
001	PRIMER_C	PRIMER_D	0.00000	0.00000
001	PRIMER_A	PRIMER_L	0.90002	0.02354
001	PRIMER_B	PRIMER_L	0.01822	0.01014
001	PRIMER_C	PRIMER_L	0.05375	0.01693
001	PRIMER_D	PRIMER_L	0.31024	0.03825

P-value for each locus pair across all populations
(Fisher's method)

Locus pair	Chi2	df	P-value
PRIMER_A & PRIMER_B	2.758	2	0.252
PRIMER_A & PRIMER_C	1.191	2	0.551
PRIMER_B & PRIMER_C	2.065	2	0.356
PRIMER_A & PRIMER_D	0.787	2	0.675
PRIMER_B & PRIMER_D	4.369	2	0.113
PRIMER_C & PRIMER_D	Infinity	2	Highly sign.
PRIMER_A & PRIMER_L	0.211	2	0.900
PRIMER_B & PRIMER_L	8.010	2	0.018
PRIMER_C & PRIMER_L	5.847	2	0.054
PRIMER_D & PRIMER_L	2.341	2	0.310

Appendix 12 (cont.)

Hunter harvest 2003 samples

Pop	Locus#1	Locus#2	P-Value	S.E.
006	PRIMER_A	PRIMER_B	0.06179	0.01218
006	PRIMER_A	PRIMER_C	0.44359	0.03019
006	PRIMER_B	PRIMER_C	0.44676	0.03169
006	PRIMER_A	PRIMER_D	0.97319	0.00702
006	PRIMER_B	PRIMER_D	0.80159	0.02880
006	PRIMER_C	PRIMER_D	0.23508	0.03117
006	PRIMER_A	PRIMER_L	0.17853	0.03210
006	PRIMER_B	PRIMER_L	0.00997	0.00492
006	PRIMER_C	PRIMER_L	0.25314	0.03399
006	PRIMER_D	PRIMER_L	0.37535	0.04244

P-value for each locus pair across all populations
(Fisher's method)

Locus pair	Chi2	df	P-value
PRIMER_A & PRIMER_B	5.568	2	0.062
PRIMER_A & PRIMER_C	1.626	2	0.444
PRIMER_B & PRIMER_C	1.611	2	0.447
PRIMER_A & PRIMER_D	0.054	2	0.973
PRIMER_B & PRIMER_D	0.442	2	0.802
PRIMER_C & PRIMER_D	2.896	2	0.235
PRIMER_A & PRIMER_L	3.446	2	0.179
PRIMER_B & PRIMER_L	9.216	2	0.010
PRIMER_C & PRIMER_L	2.748	2	0.253
PRIMER_D & PRIMER_L	1.960	2	0.375

Appendix 12 (cont.)

Spring 2004 barb samples

Pop	Locus#1	Locus#2	P-Value	S.E.
002	PRIMER_A	PRIMER_B	0.14458	0.02327
002	PRIMER_A	PRIMER_C	0.74893	0.02873
002	PRIMER_B	PRIMER_C	0.25680	0.03254
002	PRIMER_A	PRIMER_D	0.87989	0.02158
002	PRIMER_B	PRIMER_D	0.00996	0.00664
002	PRIMER_C	PRIMER_D	0.00989	0.00684
002	PRIMER_A	PRIMER_L	0.87449	0.02811
002	PRIMER_B	PRIMER_L	0.75062	0.03306
002	PRIMER_C	PRIMER_L	0.02561	0.01348
002	PRIMER_D	PRIMER_L	0.30471	0.03952

P-value for each locus pair across all populations
(Fisher's method)

Locus pair	Chi2	df	P-value
PRIMER_A & PRIMER_B	3.868	2	0.145
PRIMER_A & PRIMER_C	0.578	2	0.749
PRIMER_B & PRIMER_C	2.719	2	0.257
PRIMER_A & PRIMER_D	0.256	2	0.880
PRIMER_B & PRIMER_D	9.218	2	0.010
PRIMER_C & PRIMER_D	9.232	2	0.010
PRIMER_A & PRIMER_L	0.268	2	0.874
PRIMER_B & PRIMER_L	0.574	2	0.751
PRIMER_C & PRIMER_L	7.330	2	0.026
PRIMER_D & PRIMER_L	2.377	2	0.305

Appendix 12 (cont.)

Hunter harvest 2004 samples

Pop	Locus#1	Locus#2	P-Value	S.E.
014	PRIMER_A	PRIMER_B	0.78361	0.02330
014	PRIMER_A	PRIMER_C	0.76323	0.02005
014	PRIMER_B	PRIMER_C	0.86657	0.01387
014	PRIMER_A	PRIMER_D	0.17364	0.02531
014	PRIMER_B	PRIMER_D	0.04507	0.01138
014	PRIMER_C	PRIMER_D	0.03927	0.00849
014	PRIMER_A	PRIMER_L	0.99163	0.00681
014	PRIMER_B	PRIMER_L	0.28128	0.03556
014	PRIMER_C	PRIMER_L	0.71081	0.03126
014	PRIMER_D	PRIMER_L	0.94980	0.01766

P-value for each locus pair across all populations
(Fisher's method)

Locus pair	Chi2	df	P-value
PRIMER_A & PRIMER_B	0.488	2	0.784
PRIMER_A & PRIMER_C	0.540	2	0.763
PRIMER_B & PRIMER_C	0.286	2	0.867
PRIMER_A & PRIMER_D	3.502	2	0.174
PRIMER_B & PRIMER_D	6.199	2	0.045
PRIMER_C & PRIMER_D	6.475	2	0.039
PRIMER_A & PRIMER_L	0.017	2	0.992
PRIMER_B & PRIMER_L	2.537	2	0.281
PRIMER_C & PRIMER_L	0.683	2	0.711
PRIMER_D & PRIMER_L	0.103	2	0.950

Appendix 13. Population differentiation test using allele frequencies produced by GENEPOP 3.4 (Rousset and Raymond 1997) for bears in Hyde County, North Carolina.

Locus: PRIMER_A

Sub-Pop.	Alleles	1	2	3	4	5	6	7	Total
Spring NGS 2003		2	51	120	60	58	95	0	386
Hunter harvest 2003		0	35	76	55	28	48	0	242
Spring NGS 2004		1	64	161	65	61	102	0	454
Hunter harvest 2004		0	27	56	39	28	35	1	186
Total		3	177	413	219	175	280	1	1268

P-Value = 0.2416 S.E. = 0.02560

Locus: PRIMER_B

Sub-Pop.	Alleles	1	2	3	4	5	6	7	Total
Spring NGS 2003		9	0	164	147	29	36	1	386
Hunter harvest 2003		6	0	117	79	16	22	2	242
Spring NGS 2004		15	1	147	190	46	53	2	454
Hunter harvest 2004		2	0	77	65	28	13	1	186
Total		32	1	505	481	119	124	6	1268

P-Value = 0.0027 S.E. = 0.00118

Locus: PRIMER_C

Sub-Pop.	Alleles	1	2	3	4	5	Total
Spring NGS 2003		3	79	27	265	12	386
Hunter harvest 2003		1	76	13	148	4	242
Spring NGS 2004		2	99	30	313	10	454
Hunter harvest 2004		0	41	15	127	3	186
Total		6	295	85	853	29	1268

P-Value = 0.2808 S.E. = 0.01935

Appendix 13 (cont.)

Locus: PRIMER_D

Sub-Pop.	Alleles	1	2	3	4	5	6	7	8	Total
Spring NGS 2003		37	143	34	1	115	40	15	1	386
Hunter harvest 2003		24	76	27	3	75	25	12	0	242
Spring NGS 2004		58	182	50	0	105	45	13	1	454
Hunter harvest 2004		19	73	24	0	49	15	6	0	186
Total		138	474	135	4	344	125	46	2	1268

P-Value = 0.3015 S.E. = 0.02537

Locus: PRIMER_L

Sub-Pop.	Alleles	1	2	3	4	5	6	7	8	9	10	11	Total
Spring NGS 2003		13	30	32	1	30	58	47	80	34	61	0	386
Hunter harvest 2003		5	25	12	0	22	30	24	49	28	47	0	242
Spring NGS 2004		16	37	27	0	29	61	57	101	33	93	0	454
Hunter harvest 2004		7	15	4	1	14	30	21	44	13	36	1	186
Total		41	107	75	2	95	179	149	274	108	237	1	1268

P-Value = 0.4068 S.E. = 0.02679

Locus	P-Value	S.E.
PRIMER_A	0.24155	0.02560
PRIMER_B	0.00271	0.00118
PRIMER_C	0.28078	0.01935
PRIMER_D	0.30147	0.02537
PRIMER_L	0.40684	0.02679

Tests combination (Fisher's method:
CHI2: 21.40018
Df: 10
Prob.: 0.01847