

**Population Dynamics of the Louisiana Black Bear in the Upper Atchafalaya
River Basin**

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DEDICATION

This thesis is dedicated to:

My dad for inspiring me to find a passion in life
that would fulfill me the way law enforcement does for you,

My mom for teaching me patience and how to love life,

And my sister for teaching me perseverance and determination
in the face of adversity.

I am so blessed to call the three of you my family, my friends and my inspiration.

“Is fada an bóthar nach mbíonn casadh ann.”

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Abstract

The Louisiana black bear (*Ursus americanus luteolus*) is listed as Threatened under the Endangered Species Act as a result of habitat loss and human-related mortality. Two of the 3 sub-populations must be viable for delisting to occur. I collected hair samples from 2010 to 2012 in a DNA mark-recapture study to augment data collected from 2007 to 2009 in the Upper Atchafalaya River Basin (UARB) to estimate abundance (N), growth rate (λ), and apparent survival rates (ϕ) to ultimately be used in a population viability analysis. In addition, I evaluated the effects of the opening of the Morganza Spillway in 2011 which flooded >50% of the UARB study area. I used a Multi-state model to estimate changes in transition rates (ψ) from the flooded area to non-flooded area before (2007–2010), during (2011), and after (2012) the flooding event. Finally, I evaluated a 2-wire hair sampling system that was implemented in 2010 to increase capture probabilities (p) for males. Average N from 2010 to 2012 was 62.1 (SE = 3.6) and averaged across all years of study (2007–2012) N was 57.6 (SE = 2.2), excluding the year of the flooding event. Population growth rate indicated an increasing population, averaging $\lambda = 1.11$ across all 6 years of the study and mean ϕ was 0.83 (SE = 0.01). Estimates of ψ from the flooded to non-flooded areas increased slightly during the flood year indicating that some bears left the floodway but most did not. Apparent survival did not change for flooded or non-flooded areas during the period of flooding. Finally, p for males increased and decreased for females as predicted for a wire effect, but models with constant p were more parsimonious. The 2-wire system increased capture probabilities but the effect was not significant.

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Chapter 1: Introduction

Background and Justification

The American black bear (*Ursus americanus*) was once distributed throughout North America, from the northern parts of Canada and Alaska south to Mexico (Lowery 1974). Its range has been greatly reduced by anthropogenic actions, mostly due to deforestation and the conversion of wooded land to agriculture. There are 16 subspecies of the American black bear that exist within the continent. The Louisiana black bear (*Ursus americanus luteolus*) historically ranged throughout the bottomland hardwood forests of Louisiana and parts of Texas, Mississippi, and Arkansas (Fig. 1; Hall 1981).

The colonization of the Mississippi Alluvial Valley by Europeans resulted in agricultural development of the fertile soils and timber harvesting of the forests. From the 1950s to 1970s, high prices for soybeans increased the demand for more agricultural land which led to the clearing of bottomland hardwood forests; Federal legislation (Swampland Acts of 1849, 1850 and 1860; Flood Control Act of 1944; and Federal Watershed Protection and Flood Prevention Act of 1953) also provided financial incentives to clear bottomland hardwood forests and drain swamps (Hemlich et al. 1998, King et al. 2006). Since then, bottomland hardwood forests have been reduced by >80% within the historic range of the Louisiana black bear (Neal 1990). The remaining bottomland hardwood forests are fragmented and primarily surrounded by agricultural land (King et al. 2006).

The conversion and fragmentation of bottomland hardwood forest habitat led to population declines in original bear numbers and range by the mid-twentieth century and bears were restricted to 3 sub-populations located in the Tensas and Atchafalaya river basins. The

Tensas River Basin (TRB) population, in the northern part of the state, has the largest number of bears. The Upper Atchafalaya River Basin (UARB) population, in the south-central portion of the state, has the fewest number. The Lower Atchafalaya River Basin (LARB) population is located along the coast and is the most isolated (Fig. 2).

Because of black bear population declines, the Louisiana Department of Wildlife and Fisheries (LDWF) initiated a restocking program in 1964 to help bolster bear numbers in the state. Bears were trapped in Minnesota and released into 2 of the sub-populations; 130 individuals were released in UARB and 31 were released in TRB (Taylor 1971). Thirty of 161 released bears were known to have died shortly after release; many others scattered and were never seen again (Taylor 1971). In the 6 years following the restocking program, verified black bear sightings were reported in 37 of 64 parishes in Louisiana (Taylor 1971). Whereas many of the translocated bears died or did not stay in the reintroduction area, genetic analyses suggest that at least some animals persisted in the UARB (Miller et al. 1998, Warrillow et al. 2001, Csiki et al. 2003). The bear hunting season in Louisiana was closed in 1987 (Anderson 1997).

In 1992, the US Fish and Wildlife Service (USFWS) listed the Louisiana black bear as Threatened under the Endangered Species Act (Neal 1992). The Louisiana black bear is the only North American black bear subspecies ever to be listed as such. Habitat loss was cited as the primary reason for population decline and human-related mortality was listed as a secondary cause. In 1994, the USFWS published the Louisiana Black Bear Recovery Plan (USFWS 1995), which listed 3 recovery criteria that must be met for delisting:

1. Two of the 3 sub-populations must be viable,
2. The 2 viable sub-populations must have habitat corridors that protect gene flow, and
3. Habitat corridors must be protected to ensure use and gene flow.

Since the listing of the Louisiana black bear, many studies have been conducted to understand the ecology, habitat use and needs, genetic makeup, and population status of bears in the different sub-populations. Studies conducted in the early 1990s focused on basic bear natural history. For example, Weaver and Pelton (1994) found that bears in Louisiana denned for a shorter period than in northern or western North America. There were differences in denning duration based on reproductive status; males and females without cubs denned for a shorter time than females with cubs (Weaver and Pelton 1994, Wagner et al. 2001, and Hightower et al. 2002). Hightower et al. (2002) found that bears moved to a greater extent during winter at LARB compared with UARB. Anderson (1997) found that bears often used wooded corridors to move between habitat patches.

Beausoleil (1999) was the first to estimate bear population size in the TRB. His study was conducted on the Deltic Tracts, 1 of 2 sub-populations in the TRB, and he estimated a population of 45 (95% CI = 35–67) bears and an extremely high density of 1.43 bears/km². Following Beausoleil (1999), Boersen et al. (2003) conducted a study on the Tensas River National Wildlife Refuge and Big Lake State Game Management Area and estimated a population of 119 (95% CI = SE = 29.4) bears. In 1999, mark-recapture studies were conducted in UARB and LARB; population size was estimated at 41 (SE = 6, 95% CI = 29–53) and 77 (SE = 9, 95% CI = 59–95; Triant et al. 2004), respectively.

In addition to these studies, LDWF wanted to establish a bear population located between the TRB and UARB to create a connection between the 2 sub-populations (Fig. 3). Females with cubs from TRB were translocated during winter months to the Red River Complex which consisted of Red River and Three Rivers management areas, owned by LDWF, and Lake Ophelia National Wildlife Refuge, owned by USFWS. Females with cubs were used because

this population segment is less likely to return to the source population (Eastridge and Clark 2001). From 2001 to 2009, 48 females and 104 cubs were moved to the Red River Wildlife Complex (Benson and Chamberlain 2007; J. Laufenberg, University of Tennessee, unpublished data). Since the translocation, 35 litters of cubs were reported to have been born to 21 different females (Benson and Chamberlain 2007; J. Laufenberg, University of Tennessee, unpublished data).

The USFWS defines a viable population as one that will have 95% chance of persisting for 100 years. To estimate that rate, a Population Viability Analysis (PVA) must be performed. PVA requires accurate estimates of population vital rates such as abundance (N), survival rate (ϕ), and growth rate (λ ; Ginzburg et al. 1982, Gilpin and Soule 1986). PVAs also require adequate data to estimate inter-annual variability in population parameters because that variability can have a dramatic effect on persistence (White 2000).

In recent years, large-scale mark-recapture studies have taken place in all 3 bear sub-populations in Louisiana to update abundance estimates and to estimate other population parameters. These parameters will eventually be used in the PVA to assess sub-population viability. Hooker (2010) estimated an average of 294 bears at TRB from 2006 to 2009 (SE = 31, 95% CI = 233–355). In the LARB, Troxler (2013) used mark-recapture from 2010 to 2013 to produce a mean population estimate of 138.4 (SE = 9.9, 95% = 118.9–157.9). Finally, Lowe (2011) conducted DNA mark-recapture from 2007 to 2009 at UARB and estimated mean N to be 56 (SE = 4.5, 95% CI = 49–68).

When populations are small, as in UARB, they are more likely to be affected by genetic drift and genetic bottlenecks, and have higher probabilities of extinction. Probability of extinction is affected not only by N , but also by the fluctuations of N over time as a result of

environmental variation. Populations subject to high annual variability in N and other population parameters are more prone to extinction (White 2000). However, this annual variation can only be estimated if the study length is sufficient. Therefore, my goal was to continue the field studies initiated by Lowe (2011) so that better estimates of environmental variance on vital rates could be made. Consequently, I continued collecting data on the UARB bear population beginning in 2010 so that a PVA could eventually be performed.

The Mississippi River is well known for its historic flood regime that created fertile croplands. However, these floods have been known to cause extensive urban and agricultural damage, the most notable being the flood of 1927. Following that, the U.S. Flood Control Act was passed in Congress and the U.S. Army Corps of Engineers (USACOE) developed a plan to contain the Mississippi River within its banks and divert water from the river when necessary. The Morganza Spillway control structure, which lies within the UARB (Fig. 4), was completed in 1953 and was designed to divert water from the Mississippi River through the Atchafalaya Basin to the Gulf of Mexico during periods flooding. The control structure had only been opened once, in 1973.

The control structure was again reopened in May 2011 to prevent flood waters from overflowing levees in Baton Rouge and New Orleans after record snowfall and spring rains in the upper portion of the Mississippi Valley. Seventeen of the 125 flood gates were opened and operated at 21% capacity. USACOE estimated peak flow to be 186,000 cu ft/s (USACOE 2012). Flood waters covered approximately 60% of the occupied range of the UARB bear population. All flood gates were closed by July 7, 2011 and the water completely subsided by the end of July 2011.

The effects of such a major flooding event on wildlife were not known and had the potential to jeopardize the UARB bear population. Information on wildlife responses to extreme flooding events has been largely anecdotal; there is little quantitative data to document the population-level responses of large mammals to flooding. However, the flooding of the land below the dam (hereafter, Spillway) in 1973 was thought to have caused extensive wildlife movement and mortality (J. Broussard, LDWF, personal communication). Because Lowe (2011) collected data from 2007 to 2009 and my study began in 2010, there was a unique opportunity to evaluate the effects of the flooding on this threatened bear population. Therefore, I continued data collection into 2012 to compare bear population demographics before, during, and after the 2011 flood event to assess the effects on population growth and sustainability.

Objectives and Hypotheses

My study objectives were to:

1. Continue mark-recapture data collection from 2010 to 2012 following general methods used by Lowe (2011) to refine and supplement the long-term data set to estimate N , λ , and ϕ and their associated annual variances, and
2. Use mark-recapture to evaluate the effects of flooding on bear survival and to characterize bear movement between flooded and non-flooded areas before, during, and after the flooding event. I tested 4 hypotheses to assess population-level responses to the flooding event:
 - A. bears left the Spillway during the flood and returned prior to sampling in the following year,
 - B. bears left the Spillway during the flood and did not return,
 - C. bears did not survive the flooding event, and

D. bears stayed in the Spillway during the flood and survived.

Chapter 2: Study Area

My study area was located within the UARB and within the political boundaries of Pointe Coupee Parish. The area consisted of 270 km² of forested land bordered on the north by Louisiana Highway 1, east by the Mississippi River, south by US Highway 190, and west by the Atchafalaya River (Fig. 5). The study area was located on land privately held by either timber companies or small landowners. The study area was divided into 3 main fragments. About 150 km² of the area was within the levees of the Spillway and was comprised of relatively contiguous forest. Northwest of the Spillway, there were several small wooded areas totaling about 23 km² (hereafter, Batchelor) interspersed with agricultural fields, some of which had been recently enrolled in the Conservation Reserve Program or the Wetland Reserve Program. East of the Morganza Spillway levee was a 97-km² forested tract owned by various timber companies and small private landowners (hereafter, Fordoche; Fig. 6).

Forests in the UARB were bottomland hardwoods, much of which were inundated during winter; water was regulated by a series of levees and dams. Water features in the UARB included bayous, canals, rivers, and lakes. Tree species were baldcypress (*Taxodium distichum*), water tupelo (*Nyssa aquatica*), oaks (*Quercus* spp.), hickory (*Carya* spp.), sweetgum (*Liquidambar styraciflua*), and red maple (*Acer rubrum*). The climate was humid subtropical with an average annual temperature of 19.7°C and average annual rainfall of 143.5 cm (National Climate Data Center 2013).

The main use of bottomland hardwood forests in the UARB was timber extraction. The largest timber company in the area was Roy O. Martin, which conducted both uneven and even-aged stand management (Roy O. Martin Forest Management Plan 2013). Agriculture and cattle production also were prominent land uses in the UARB. Major crops in the area were soybeans

(*Glycine max*), corn (*Zea mays*), milo (*Sorghum bicolor*), and sugarcane (*Saccharum officinaru*). Levees of the Morganza Spillway were used for cattle grazing. The most common recreational activity in the UARB was hunting through leases from timber companies and private land owners. Prominent game species included white-tailed deer (*Odocoileus virginianus*), wild turkey (*Melaeagris gallopavo*), rabbit (*Sylvilagus* spp.), wild hog (*Sus scrofa*), raccoon (*Procyon lotor*), squirrel (*Sciurus* spp.), American alligator (*Alligator mississippiensis*), and several duck species. Other recreational activities included the use of ATV trails and fishing, mostly for crayfish (*Procambarus clarkii*), catfish (*Ictalurus* spp.), and gar (*Atractosteus* spp.).

Chapter 3: Materials and Methods

Study design

I used mark-recapture (MRC) methods to estimate abundance (N), growth rate (λ), and survival (ϕ). In MRC analysis, there are 2 basic types of population assumptions: closed and open. Closure must be both geographic, i.e., there are no immigrations or emigrations, and demographic, i.e., there are no births or deaths. The most basic model for closed population abundance estimation is the Lincoln-Peterson model:

$$\hat{N} = \frac{M^2}{m},$$

where M is the number of marked individuals, p is the capture probability, and N is the number of individuals in the population. Assumptions associated with the Lincoln-Peterson method are (1) all individuals have the same probability of being captured, (2) there are no additions via births or immigration and no subtractions via deaths or emigration, (3) all individuals are identified correctly, and (4) marks on the individual are not lost. Whereas the assumption of strict closure is not realistic in wild populations, a population can be considered closed if a large area is sampled during a short period when the study species is not giving birth or migrating (Otis et al. 1978). Conversely, open population estimators allow for immigration, emigration, births, or deaths. The Jolly-Seber model (Jolly 1965, Seber 1965) is the simplest method for estimating N in open populations. In addition to N , dynamic parameters such as ϕ , and λ can be estimated with open models. Because the model does not differentiate between bears that die and bears that permanently leave the study area, ϕ is referred as “apparent survival”. Assumptions associated with open models are (1) all individuals have the same probability of being captured, (2) all individuals are identified correctly, and (3) marks are not lost.

Violating these assumptions can bias population parameter estimates, particularly N (Otis et al. 1978). Capture biases are the most common violations and are classified as behavioral (when being trapped changes the subsequent capture probability of the individual), temporal (capture probability varies across the duration of the study due to things like temperature or precipitation), or individual heterogeneity (individuals have inherently different probabilities of being captured). Various methods have been developed to estimate and correct for these biases. However, those methods are valid only in a closed model design (Otis et al. 1978). Individual capture heterogeneity is the most common bias and most difficult to correct (Boulanger et al. 2002, Link 2003).

The Robust Design (Pollock 1982) is a mixture of both open and closed methods. Sampling consists of a series of sessions whereby the population is considered closed (i.e., secondary sampling sessions) and open (i.e., primary sessions). The different sampling protocols allow for more realistic assumptions associated with natural populations. The Robust Design can be used to estimate a wide array of population parameters including N , ϕ , and λ (Pollock 1982). The primary sampling occasions are used to estimate ϕ and λ , whereas the secondary sampling occasions are used to estimate N . Capture (p) and recapture (c) probabilities are nuisance parameters and are estimated with data from the secondary sampling occasions. I used each year (2007–2012) as primary sampling occasions and hair sampling weeks during June and July as the secondary sampling occasions.

In addition to the above parameters, the probability of an individual transitioning to another state can be estimated within the Robust Design using Multi-state models (Fujiwara and Caswell 2002, Kendall and Nichols 2002, Bailey et al. 2004, Schaub et al. 2004). Transitions (ψ) can be defined as animals moving from one age class to another, animals moving through

reproductive stages (e.g., from having cubs, to having yearlings, to having no young), or animals physically moving from one area to another, such as migrating waterfowl (Arnason 1972,1973; Schwarz et al.1993). The simplest Multi-state models are limited to estimating ϕ , p , and ψ . By combining the Multi-state model with the Robust Design, N can also be estimated for each state and precision is improved for ϕ and ψ . Furthermore, capture biases such as individual capture heterogeneity can be estimated with mixture models (Pledger 2000, White et al. 2006). Multi-state models are based on the assumption that there are equal movement probabilities for all animals (although these probabilities can differ among areas and time), movement probability and recapture probabilities do not depend on the past history of the animal, and there are no transitions between states during closed secondary occasions (Arnason 1972, 1973; Kendall and Nichols 2002). Parameters are estimated for each state; consequently, multi-state models can become extremely complex (Kendall and Nichols 2002, White et al. 2006).

Because transition rates are a probability, transition rates for each state must add up to 1. For example, in an area with 2 states (a and b) at time t and assuming no unobservable state, the probability of an animal moving from state A to state B is ψ_t^{ab} . It follows then that the probability of an animal remaining in state a is $1 - \psi_t^{ab}$ (or ψ_t^{aa}). This relationship is enforced by using the multinomial logit link function whereby $0 \leq \psi \leq 1$ (White et al. 2006).

Site placement and construction

Mark-recapture studies traditionally involve live-trapping and physical marking or tagging of animals. Advances in genetic analysis have allowed us to “capture” and “mark” animals using their DNA through non-invasive sampling. The use of DNA as the marker has many benefits including no loss of marks, greater capture and recapture rates, less invasiveness, and less bias (Woods et al. 1999). Because of these benefits, Lowe (2011) used DNA-based

mark-recapture by collecting hair samples which I also used in my study to supplement those data.

Lowe (2011) collected hair samples from 2007 to 2009. To optimize encounter rates, Otis et al. (1978) recommend ≥ 4 sampling sites per individual bear home range. Lowe (2011) based site densities on an estimated home range size of 15.7 km², an estimate of female spring-summer home ranges in the UARB (Wagner 1995). Using this home range size, Lowe (2011) created and used a 1.6- × 1.6-km grid for site placement, resulting in a total of 115 sites (Fig. 7). For consistency, I used the same site locations as Lowe (2011).

Barbed wire stretched between trees has been shown to be an effective mechanism for collecting bear hair samples (Woods et al. 1999). Lowe (2011) used a single strand of 4-point 15.5-gauge wire placed at 40–50 cm above the ground stretched between 3–4 corner trees. However, remote cameras recorded large bears (presumably males) stepping over or on the wire to enter hair sampling sites without leaving hair samples. Disproportionate sampling of a group of animals, such as large bears, can cause individual capture heterogeneity and can lead to population estimates that are biased low (Otis et al. 1973). In contrast to Lowe (2011), I used 2 strands of barbed wire; the bottom wire was set at 35–40 cm and the top wire at 65–70 cm above the ground (Fig. 8). In areas of uneven ground, I used debris to fill in low spots or sticks to block the wire where the ground was high. I kept the barbed wires tight throughout the sampling period by cinching the wires together at the corner trees with twine. Bait, consisting of 1–2 doughnuts or other bakery products, was hung in the center of the site. I also hung a tampon soaked in artificial candy flavoring (Mother Murphy's Laboratories, Greensboro, North Carolina) as scent lure. Caution tape and flagging were used to mark the corner trees and barbed wire as a human safety precaution.

Sample collection

I checked sites weekly for 8 weeks (i.e., weeks were the secondary sampling occasions) during June and July 2010–2012 (i.e., years were the primary sampling occasions). I collected hair samples if there were >5 guard hairs or >20 underfur hairs to ensure there was enough genetic material to identify an individual (Paetkau 2003, Tredick et al. 2007). Hair samples were collected with tweezers and placed in coin envelopes. I labeled each envelope with date, site location, sample number, and indicated if the sample came from the top or bottom wire. After each sample was collected, I sterilized the tweezers by burning with a lighter. After collection at the site was complete, I burned the barbed wire with a propane torch to ensure all hair was removed to reduce the chance of cross-contamination. After each visit, I re-baited and re-scented the sites. I sent samples to Wildlife Genetics International (WGI, Nelson, British Columbia, Canada) for analysis.

Because of the large amount of samples collected each summer, it was cost prohibitive to analyze every sample. Therefore, I sub-sampled by randomly selecting 25 sites per week, randomizing the samples collected at those sites, and then selecting the first hair sample that met our minimum threshold for genotyping. In 2012, I increased the sub-sample size from 25 to 38 with the goal of increasing p for more reliable vital rate estimates (Laufenberg et al. 2013). Sub-sample size was likewise increased for each previous year and those samples were submitted for analysis and eventually used to augment the past capture history data. The only exception to this protocol was that, because of the flooding event in 2011, I was only able to collect hair from 52 of 115 sites. To avoid inflating p in the non-flooded areas during that year (as would have been the case if 38 samples had been analyzed within only the non-flooded areas), I further sub-divided the hair samples from 2011 based on the average number typically analyzed in previous

years in the non-flooded areas (40%). Therefore, I only included 13 samples/week in my analysis in 2011. In addition to the protocol specified by Lowe (2011), I randomized the samples by top or bottom wire from 2010 to 2012.

Genetic analyses

Microsatellites are repeated segments of an individual's DNA and vary based on the number of base pairs, i.e., the length of the repeated segment that an individual exhibits at a specific locus. Because microsatellites are relatively easy to isolate, they are commonly used in analysis for identifying individuals, estimating relatedness among individuals, and assessing genetic variation (Paetkau and Strobeck 1994). Microsatellites are identified by amplifying specific loci using polymerase chain reaction (PCR) that are unique to each individual's DNA (Paetkau and Strobeck 1994, Woods et al. 1999, McKelvey and Schwartz 2004). Individuals are then identified based on the number of base pairs for all loci that were amplified (Paetkau and Strobeck 1994, McKelvey and Schwartz 2004). Lowe (2011) performed a preliminary analysis of a group of 30 samples from the UARB populations using 22 loci (A06, CPH9, CXX110, CXX20, G10B, G10H, G10U, G10X, MSUT2, MU50, MU51, PO7, G1A, G1D, G10J, G10C, G10L, G10M, G10P, MU23, MU26, and MU59). The 7 most variable markers (G10C, G10L, G10M, G10P, MU23, MU26, and MU59) were selected for the samples, plus an additional marker to identify sex. I used these same 8 markers for my study.

The third assumption of mark-recapture is that all individuals must be correctly identified. Error checking to ensure individuals are correctly identified was an important part of my genetic analysis. Two errors can occur during amplification: 1) allelic dropout, where for a heterozygous individual 1 allele fails to amplify, resulting in what appears to be a homozygous individual; and 2) false alleles, resulting in what appears to be a new individual. These errors

can bias abundance estimates (Woods et al. 1999, McKelvey and Schwartz 2004) but can be minimized by selecting markers that are highly variable and by implementing rigorous lab protocols. Paetkau (2003) developed strict lab protocols which were followed by WGI that minimize such errors. For example, samples that failed to amplify at >3 loci were eliminated and those that failed to amplify at 1–3 loci were reanalyzed. When samples mismatched at 1 or 2 loci (1MM or 2MM) they were reanalyzed at the mismatched markers; if they were still mismatched at 1 or 2 loci, then additional loci were amplified until the samples differed at >3 loci.

Despite using variable microsatellite markers, there was a chance that 2 closely related individuals have the same alleles at a particular locus and thus would be considered the same individual (Woods et al. 1999). I calculated the probability of identity for random individuals (PI_{ran}), for parent–offspring pairs ($PI_{\text{par-offs}}$), and for siblings (PI_{sib}) having the same genotype at those alleles. PI_{sib} is the most conservative of these tests and was of particular interest because bear siblings often have overlapping home ranges (Mace and Waller 1997, Woods et al. 1999). Woods et al. (1999) recommended $PI_{\text{sib}} > 0.25$.

Probability of identity analyses are based on the assumption that the population is in Hardy-Weinberg equilibrium (Taberlet and Luikart 1999). Hardy-Weinberg equilibrium (HWE) is reached when large populations randomly mate and have no mutation, migration, or selection (Connor and Hartl 2004). I tested for HWE by comparing observed heterozygosity) and expected heterozygosity at each locus. Heterozygosity is a measure of the amount of genetic variation in the population. Genetic bottlenecking or inbreeding can be consistent with < 0.05 . Small populations of large carnivores, like the UARB population, are particularly susceptible to loss of genetic diversity (Paetkau and Strobeck 1994). Therefore, I calculated

mean and for the UARB population with GenALEx 6.5 (Peakall and Smouse 2006) in Excel.

Data analyses

I used data collected from 2010 to 2012 and data collected by Lowe (2011) from 2007 to 2009 in a closed Robust Design Multi-state full-heterogeneity model in Program MARK (Version 5.1, White and Burnham 1999) to estimate population parameters. In this model formulation, primary periods (between years) are open and the secondary periods (8 weeks of collection each summer) are closed. This analytical framework allowed me to directly estimate p , c , ϕ , and ψ . This model can also directly estimate heterogeneity mixtures (π) which helped address capture bias by allowing individuals to be divided into 2 groups based on similar capture probabilities (e.g., easy- vs. difficult-to-catch individuals; Pledger 2000). N was a derived parameter and λ was calculated based on the change in N from year to year.

Parameters estimated by models in Program MARK are based on maximum likelihood estimation (MLE) methods. I used Akaike's Information Criterion with a second-order correction for small sample size (AIC_c , Burnham and Anderson 2002) to select among the different models. AIC_c values are calculated using both the likelihood function (i.e., how well the model fits the data) and the number of parameters in the model (i.e., how simple the model is). I calculated AIC_c weights as an indication of the relative support of an individual model compared with the other models. I chose the model with the lowest AIC_c value as my top model. In the case of multiple top models (i.e., models with similar AIC_c weights), I used model averaging to obtain parameter estimates (Burnham and Anderson 2002). With model averaging, models with higher weight have more influence in the calculation and the variances are adjusted for model selection error. I used the slope of the effect (β) being modeled on the parameter to

assess significance. If the 95% confidence interval did not include 0, then the effect was considered significant.

Typically males and females have different probabilities of surviving and ϕ can change over time. Therefore, I modeled ϕ with a sex effect and a year effect. Lowe (2011) found capture heterogeneity in the population; therefore, I used a mixture model, modeling π as constant and differing by sex. Because of the bait and scent lure at the site, I expected a behavioral effect, i.e., bears would have a positive response to being captured. Therefore, I separately estimated p and c and as additive effects to test if there was a behavioral response.

In previous studies in Louisiana, trail cameras revealed large bears stepping over the 1-wire system creating a possible bias in our estimates. In addition, Lowe (2011) found that p for male bears was low ($p = 0.12$, $SE = 0.03$) which can result in poor precision and possibly bias in N (Laufenberg et al. 2013). By adding a higher second wire and moving the original wire lower, I hypothesized that larger male bears would be less likely to evade capture. Therefore, I created models to compare parameter estimates with the 1-wire system (2007–2009) versus the 2-wire system (2010–2012). My hypothesis was if the 1-wire system was missing a portion of male bears, then overall p for males would increase after switching to the 2-wire system. Because my sampling intensity was consistent across years (i.e., 38 samples per week), an increase in males would result in a decrease in p for females because a lower proportion of female samples would be available for genotyping. I calculated overall p () as the sum of the product of each mixture (π) and its respective p (). I developed models whereby p and c were additive effects and differed by sex during years with and without the wire (i.e., wire). I compared that model with one whereby the sex effect was modeled as an interaction with wire,

which enabled male λ to increase and female λ to decrease after addition of the second wire, as hypothesized.

To average parameter estimates, I calculated the mean of the estimate and used the Delta method for independent variables to calculate respective variances (Seber 1982, Powell 2007). This method was used for π , ϕ , and N . I used the Delta method for non-independent variances to estimate the variance of λ :

Growth rates, λ , were calculated using $\lambda = \sqrt{N_{t+1}/N_t}$. Because the Multi-state model produces independent estimates of N for each state, I combined the estimates of N across states for each year to get an overall estimate of λ . Estimates of N for the flooded area during the flood year were not available so I estimated λ for 2010–2012 and then took the square root of that value, resulting in 2 identical estimates of λ for 2010–11 and 2011–12. Because of the missing year of data I could not calculate the variance around the over-all λ . Additionally, I compared N for 2007, 2008, and 2009 and its respective standard errors (SE) to Lowe's (2011) estimates. I hypothesized the increase in sub-sample size would increase the precision of each N and that N would be less variable from year to year.

I used a closed Robust Design Multi-state mark-recapture model to evaluate flooding effects by using estimates and changes of ψ before, during, and after the opening of the Morganza Spillway control structure. My study area consisted of 3 different sub-areas, Fordoche, Batchelor, and Spillway (Fig. 6). These areas were geographically isolated by agriculture, levees, and highways but bears were known to move between them. I considered

Fordoche and Batchelor to be “non-flooded” states and Spillway to be the “flooded” state and estimated ψ to infer movement between these states in response to the flooding event. I created models based on 4 *a priori* hypotheses of possible bear responses to the flooding event and changes in parameters:

Hypothesis A: Bears left the Spillway during the flood and returned the following year. If that was the case, the probability that bears transitioned from the flooded to the non-flooded areas (in 2010–2011 would increase compared with earlier years and the probability of transitioning back to the flooded area) in 2011–2012 would also increase. Abundance would increase in the non-flooded areas during 2011 and would then decrease in 2012 (Fig. 9).

Hypothesis B: Bears left the Spillway during the flood and did not return. In that case, would increase in 2010–2011 but would not decrease in 2011–2012 compared with 2010–2011. Abundance would increase in the non-flooded areas during 2011 but would not decrease in 2012. Post-flood estimates of N in the Spillway would decrease due to the loss of bears (Fig. 10).

Hypothesis C: Bears stayed in the Spillway and did not survive the flooding event. In that case, estimates of ϕ in the non-flooded areas would be constant across all years, but would decrease in the flooded area. Because ϕ in the flooded area was inestimable in 2011, I constrained this parameter to be equal to ϕ from 2012 and, therefore, estimated the probability of surviving from 2010 to 2012, or ϕ^2 . Transition rates would be constant across all years and states. Post-flood estimates of N in the Spillway would decrease due to the loss of bears (Fig. 11).

Hypothesis D: Bears stayed in the Spillway during the flood and survived. In this case, ψ and ϕ would be constant across time between the flooded and non-flooded areas and there would be no decrease in N in the flooded areas (Fig. 12).

Because I could not sample the flooded state in 2011, I fixed p and c for that year to zero and could not estimate for N in the Spillway in 2011. Transition rates are conditional upon the animal surviving from time i to time $i+1$ and being in a different state at time $i+1$. All ψ for a state must equal 1 so Program MARK estimates all but 1 ψ , which is derived by subtraction (e.g., for 2 states, $\psi_{21} = 1 - \psi_{11}$). The choice of which parameter to directly estimate is up to the user so I estimated ψ_{11} and calculated ψ_{21} by subtraction. I assumed that inestimable parameters were independent and that permanent emigration was equal for all states.

Nine bears were observed in multiple states during secondary periods violating the closure assumption. The Robust Design Multi-state model in Program MARK does not accommodate bears in multiple states in secondary periods. To include those bears in the analysis, I randomly selected one of the states for each of the 9 bears during the secondary periods when multiple states occurred. I did this a multiple of 5 times and obtained model averaged parameter estimates in Program MARK. I averaged the 5 randomized parameter estimates and their standard errors to obtain overall estimates.

Chapter 4: Results

Genetic analyses

Including samples from Lowe (2011), 12,088 hair samples were collected from 2007 to 2012. Based on a sub-sample of 38 per week, 2,046 samples were sub-selected of which 1,494 (73.0%) were successfully genotyped to 109 unique individuals (62F:47M), ranging from 27 to 60 unique individual bears annually (Table 1). The mean number of captures per individual was 13, with 1 female bear being caught 133 times and 20 bears being caught only once (11F:9M).

All loci were found to be in HWE (Table 2), i.e., the observed (H_o) and expected (H_e) allele frequencies did not differ ($p = 0.914$). The 7 loci had mean H_o ranging from 0.670 to 0.798, an overall mean H_o of 0.727 (SE = 0.018), and a mean of 4.14 alleles per locus (Table 3). PI_{sib} for each locus ranged from 0.39 to 0.47. PI_{ran} for all 7 loci was 1.3×10^{-6} , i.e., a 1 in 769,231 chance of having 2 random individuals with the same genotype in the UARB population. PI_{sib} for all 7 loci was 3.1×10^{-3} , i.e., 1 in 322 chance of having 2 siblings with the same genotype in the UARB population (Table 3).

Data analyses

Population parameter estimation

My candidate set for the 2007-2012 data set consisted of 17 models; 11 had ΔAIC_c values < 3 . The top 4 models had relatively equal weights and ΔAIC_c of < 1 (Table 4). Because there was no predominant model, I used AIC_c weights to model average each parameter estimate.

Sex was a significant effect for ϕ ($\beta = -1.13$, 95% CI = -2.02--0.24), with males having lower annual ϕ (0.759, SE = 0.013) than females (0.901, SE = 0.006). Constant ϕ across years for the non-flooded areas was most supported. Heterogeneity mixture models were well supported ($\pi = 0.744$, SE = 0.006, $\beta = 1.09$, 95% CI = 0.66--1.52) but a sex effect on π was not (β

= 0.13, 95% CI = -0.65–0.91). Capture probabilities differed by state ($\beta = -0.59$, 95% CI = -0.98–0.22), sex ($\beta = -0.66$, 95% CI = -1.04–0.27), and mixture ($\beta = -2.05$, 95% CI = -2.33–1.78). The Fordoche and Batchelor areas had higher p than the Spillway. Averaged across state, for males was 0.20 (SE = 0.009) and for females was 0.31 (SE = 0.009). I found a positive additive behavioral response in c in the top 4 models ($\beta = 0.52$, 95% CI = 0.25–0.79). The effect on p of changing from a 1-wire to a 2-wire system in 2010 was not well supported ($\beta = -0.04$, 95% CI = -0.34–0.42), nor was the wire-sex interaction ($\beta = -0.49$, 95% CI = -1.24–0.26). However, the direction of the effect was as predicted with male increasing (0.144 to 0.177) and female decreasing (0.272 to 0.239; Table 5).

Annual abundance estimates of males ranged from 9.9 (SE = 2.3, 95% CI = 5.4–14.5; non-flooded areas only) in 2011 to 26.6 (SE = 4.0, 95% CI = 18.7–34.4) in 2012 (Table 6). Female annual abundance estimates ranged from 15.0 (SE = 1.6, 95% CI = 11.9–18.1; non-flooded areas only) in 2011 to 43.3 (SE = 3.5, 95% CI = 36.4–50.0) in 2012 (Table 6). After additional samples were analyzed for 2007–2009, standard errors for N declined from those reported by Lowe (2011; Table 7). The Spillway had the highest average N (excluding the flood year, $N = 39.9$, 17M:23F, 95% CI = 35.9–43.9), followed by Fordoche ($N = 11.3$, 5M:6F, 95% CI = 9.9–12.7), and then Batchelor ($N = 7.6$, 2M:6F, 95% CI = 6.6–8.5). The mean N combined by sex and averaged across years and states, excluding 2011, was 57.5 (SE = 2.2, 95% CI = 55–63). Overall λ averaged across state, year, and sex was 1.11. Overall male λ was 1.11 and female λ was 1.10.

Modeling effects of flooding

A flood effect for ϕ within the Spillway was not supported ($\beta = -0.08$, 95% CI = -2.31–2.16), nor was a sex effect on ψ ($\beta = -0.25$, 95% CI = -1.61–1.09). Before the flood,

(0.089; SE = 0.008) was greater than (0.032; SE = 0.003; $\beta = -5.59$, 95% CI = -8.16--3.04) and each were constant across pre-flood years (2007–2010). Model-averaged estimates indicated that increased from 0.032 (SE = 0.003) in years prior to flooding to 0.087 (SE = 0.012) during the flood year ($\beta = -4.79$, 95% CI = -6.60--2.98). I found decreased slightly from 0.087 (SE = 0.0012) during the flood to 0.049 post-flood (SE = 0.012, $\beta = -5.59$, 95% CI = -8.05--3.14; Table 9). Model averaged estimates for were 0.089 (SE = 0.008) pre-flood and 0.117 (SE = 0.025) post-flood but that effect was not significant ($\beta = 0.95$, 95% CI = -1.09--2.99; Table 9).

Chapter 5: Discussion

Genetic analyses

The addition of 13 new samples per week (from 25 to 38) increased the overall sub-sample size only marginally, from about 5% to about 7% of the total collected. Nevertheless, these additional samples increased the average number of captures per bear from 9 to 13 and resulted in the identification of 7 previously unknown individuals. For every 3 additional samples I recorded 1 new capture in time, i.e., 1 individual was found in a session where it previously had not been captured (D. Paetkau, WGI, personal communication).

My estimates of PI_{ran} and PI_{sib} for 2007–2012, and including the additional sub-samples, were identical to those estimated by Lowe (2011) for 2007–2009. The PI_{sib} for individual loci either remained the same or decreased compared with Lowe (2011). Mean H_o decreased from 0.750 (Lowe 2011) to 0.727. Even with this slight decrease, the UARB population was still the most genetically diverse population in the state (TRB: $H_o = 0.66$, Hooker 2010; LARB: $H_o = 0.66$, Troxler 2013). This high genetic diversity is most likely the result of the introduction of black bears from Minnesota in 1964 (Csiki et al. 2003).

Data analyses

Parameter estimates

From 2010–2012, ϕ for males (0.759, SE = 0.013) was lower than for females (0.901, SE = 0.006). This finding contradicts Lowe (2011) who found male and female ϕ did not differ and were higher ($\phi = 0.91$, SE = 0.06). However, Lowe (2011) did find some support in her models for a sex effect. The additional years of data and additional samples likely increased the power to detect a sex effect. Therefore, I suggest there was not a true decline in survival in my study

compared with Lowe (2011). Clark and Eastridge (2006) found similar male ϕ (0.708, SE = 0.168) for a bear population in White River National Wildlife Refuge where quota hunts took place on private lands adjacent to the refuge. Because bear hunting does not occur in Louisiana, the lower apparent survival must be due to other factors. Road and nuisance kills are one possibility but the number of reported mortalities near my study area was not high. Permanent emigration is another possibility because males from the UARB have been known to travel to the repatriation area at the Red River Complex and numerous bear sightings have been reported in nearby areas (M. Davidson, LDWF, personal communication). Studies on the 2 other populations in Louisiana have also found no differences between ϕ of males and females and were higher than in the UARB (TRB, $\phi = 0.91$ SE = 0.08, Hooker [2010]; LARB $\phi = 0.86$, SE = 0.03, Troxler [2013]). Interestingly, those 2 populations do not have as much potential habitat for emigration of males as does the UARB area.

Capture heterogeneity has been a common problem in DNA mark-recapture studies. In Louisiana, Hooker (2010), Lowe (2011), and Troxler (2013) all found capture heterogeneity in the black bear populations they studied. In my study, p for males and females was over the 0.20 threshold suggested for unbiased estimates (Boulanger et al. 2004, Laufenberg et al. 2013) and higher than Lowe (2011). Lowe (2011) sub-sampled at a rate of 25 samples/week and had a $p = 0.12$ (SE = 0.03) for males and $p = 0.25$ (SE = 0.04) for females. When the additional samples were added, p increased to 0.20 (SE = 0.012) for males and to 0.31 (SE = 0.012) for females for those years. Laufenberg et al. (2013) found through simulated data that when $p > 0.2$ estimates of N were accurate 96% of the time and precise 83% of the time.

Although p for males increased and p for females decreased slightly as hypothesized, these slight changes with the wire effect were not adequate to warrant model support. I speculate

that even though large male bears may be able to step over the wire, enough of them were caught that p was not significantly biased. The addition of the second wire raised concerns that there might be a difference in genotyping error or success rates based on the hypothesis that if bears went through the 2 wires more guard hair would be left on the top wire and more underfur would be left on the bottom. I randomized the sample order to ensure that the top and bottom wire had equal chances of being selected at each site and found there was no difference in error or success rates (D. Paetkau, WGI, personal communication). Although the wire effect appeared in many of my top models, this was not a strict control-treatment experiment. Therefore, changes in the population, e.g., a population increase, could have led to changes in p or could have confounded real wire effects on p . Regardless, the 2-wire system does not drastically increase cost or time spent at each trap; therefore, I would recommend it be employed when feasible.

I estimated population size for each state and sex except for the Spillway during the flood year. The largest numbers of bears were estimated within the Spillway and the fewest within the Batchelor area; this was expected because they are the largest and smallest of the 3 states, respectively. My estimates of N were similar to those of Lowe (2011), but my estimates were more precise (i.e., smaller confidence intervals). This was due the increase in sub-sampling intensity (Laufenberg et al. 2013) and due to the addition of more years of sampling. Even with an increase in precision, annual estimates of N for both males and females fluctuated from year to year.

The UARB population seems to be slightly increasing. To estimate λ for 2010–2011 and 2011–2012, I estimated λ for 2010–2012 and took the square root, assuming linear growth for the 2 intervals. In Multi-state models N is a derived parameter so it is not possible to constrain N as a trend. However, models with a linear trend in ϕ were not supported ($\beta = 0.004$, 95% CI = -

0.399–0.347) so there is no empirical evidence that the survival rate from 2006 to 2012. Of course, population growth rate is equal to the sum of survival and recruitment. Black bears have a 2-year breeding cycle and any decline may not be detected until 2-years post flooding when cubs from 2011 would be sub-adults in 2013 and would become large enough for capture by hair snares. Thus, I was not able to estimate the effects of the flood on recruitment.

Effects of flooding

Although my results were not unequivocal for any 1 hypothesis, the weight of evidence suggests some bears left the flooded area and survived (i.e., Hypothesis A and B). The egress from the flooded area from before to during flooding was 0.032 to 0.089, respectively, meaning that 3.2% of the bears left the Spillway to go to Fordoche or Batchelor prior to the flood and 8.9% left during the flood year, with no change in ϕ , thus supporting Hypothesis A. Further support for the hypothesis that bears left the Spillway during the flood was that p decreased in non-flooded areas. Because of my standardized sub-sampling methods across years, an increase in the number of animals would cause a decrease in p . Also, female N in Fordoche almost doubled from 2010 to 2011, 4.4 to 8.0, respectively.

However, the majority of bears remained within the Spillway during the flood, thus supporting Hypothesis D. One female, radio-collared for another study, stayed in a tree for the duration of the flood, a total of almost 2 months (M. Davidson, LDWF, personal communication). Anecdotally, only 1 documented bear mortality during the flood, a bear on a train trestle trying to escape the flood was hit by a train. That mortality occurred on a train trestle that traverses the spillway. After this bear-train collision, the rail system decreased the speed of the trains (M. Davidson, LDWF, personal communication) and no additional mortalities were reported. Five percent of the bears were found to move from the Spillway to Fordoche or

Batchelor the year after the flood. Flooding may have had extended effects on bear habitat in the region, such as loss of vegetation resulting in a food shortage in 2012.

My results were inconclusive whether the bears remained in the non-flooded habitat or moved back into the spillway after the flooding event. Although there was an increase in the post-flood year indicating bears may have moved back to the Spillway, the increase was not significant. Yet, p for the non-flooded areas returned to pre-flood levels and there was no change in N for the Spillway from 2010 to 2012.

Regardless of which hypothesis was most supported, the overall conclusions are clear; the 2011 flooding event had minimal impacts on the adult black bears in the UARB. A number of researchers have shown that small mammal species not adapted to arboreal habitats are most affected by flooding events (Blair 1939, Grinnell 1939, Williams et al. 2001, Chamberlain and Leopold 2003). Black bears are proficient climbers and, therefore according to these studies, it is logical that bears would not be greatly affected by flooding events. However, I was unable to assess how the flood impacted cub survival. At the time of the flood, there was only 1 collared female and she was without cubs (M. Davidson, LDWF, personal communication). A reduced 2011 cohort would not be evident until they were large enough to be captured in hair corrals, beginning in 2013.

Chapter 6: Conclusions and Management Implications

Male ϕ was relatively low for an un hunted population. One question that should be addressed is whether the low ϕ was due to deaths or losses to permanent emigration. While male ϕ can have an effect on population growth, Eberhardt (1990) found that female survival and recruitment were the driving forces in population growth. The UARB female ϕ was relatively high at 0.901 and consistent over time, a good indication of a stable population. The UARB has suitable habitat and reintroduced females a short distance away. Male bears have been documented traveling to this repatriation site so it is reasonable that some of the apparent mortality in males was due to emigration.

My study was the first to determine effects of a major flood on a black bear population. Because the UARB population is small, the flooding of the Morganza Spillway could have had major negative effects on the potential for recovery and delisting. Although my results do not indicate any negative effects on adult bears in UARB, I did not evaluate effects of the flood on cub survival. Additional mark-recapture data are currently being collected at UARB, which can give the managers information on cub survival through changes in λ from 2012 to 2013. Furthermore, this additional year of data could be used to supplement the 1 year of post-flood data used in my analysis to make sure there are no residual effects on ϕ and λ for adults.

Belt (1975) concluded that the 1973 Mississippi flood was man-made. The construction of levees and channelization of the river caused high stages to rise more rapidly and made the flooding higher (Belt 1975). In addition, Belt (1975) hypothesized that any further constriction of the river would cause further problems. This, in addition to the potential increase of natural disasters due to climate change, increases the likelihood that the Morganza Spillway will have to be opened again in the near future. Although I found no negative effects of the 2011 flood event,

whether black bears can successfully cope with repeated flooding of the Morganza Spillway is not known.

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Appendices

Appendix A: Tables

Table 1. Results from genetic analysis of hair samples from Louisiana black bears in the Upper Atchafalaya River Basin, Louisiana, USA, 2007–2012

Year	N^a	M_t^b	M_f^c	M_m^d
2007	192	35	22	13
2008	252	47	33	14
2009	273	60	39	21
2010	266	50	28	22
2011 ^e	259	29	17	12
2012	252	61	39	22
Total	1,494	109	62	47

^a Number of samples successfully genotyped.

^b Total number of individuals identified.

^c Number of females identified.

^d Number of males identified.

^e Part of the Upper Atchafalaya River Basin study area was flood in 2011. Results only represent non-flooded area.

Table 2. Hardy-Weinberg equilibrium chi-squared tests for microsatellites used to identify individual Louisiana black bears in the Upper Atchafalaya River Basin, Louisiana, USA, 2007–2012. P-values represent significance testing differences between observed and expected heterozygosity for each locus.

Locus	df		p-value
G10M	10	14.433	0.154
G10P	6	4.383	0.625
MU59	6	2.058	0.914
G10L	6	3.521	0.741
MU23	10	12.497	0.253
MU26	6	5.620	0.467
G10C	6	7.905	0.245

Table 3. Microsatellites used to identify individual Louisiana black bears in the Upper Atchafalaya River Basin, Louisiana, USA, 2007–2012, and their respective variability.

Locus	H_o^a	H_e^b	A^c	PI_{ran}^d	PI_{sib}^e
G10M	0.80	0.73	5	0.12	0.41
G10P	0.72	0.67	4	0.17	0.46
MU59	0.67	0.65	4	0.18	0.47
G10L	0.67	0.66	4	0.19	0.47
MU23	0.78	0.77	4	0.93	0.39
MU26	0.71	0.70	4	0.15	0.44
G10C	0.74	0.72	4	0.14	0.43
	0.73	0.70	4.14	0.27	0.44
Overall PI				1.3×10^{-06}	3.1×10^{-03}

^a Observed heterozygosity.

^b Expected heterozygosity.

^c Number of alleles.

^d Probability of identity of random individuals.

^e Probability of sibling identity.

Table 4. Program MARK model results from Robust Design Multi-state with full heterogeneity DNA mark-recapture analysis of Louisiana black bears in the Upper Atchafalaya River Basin, Louisiana, USA, 2007–2012. Due to the 2011 release of the Morganza Spillway that flooded half of the Upper Atchafalaya River Basin study area, I separated my study area into 2 states, flooded and non-flooded. I modeled apparent survival (ϕ) as a function of sex, probability of transition to another state (ψ) as a function of state and sex, proportion of the population belonging to 1 of 2 heterogeneity mixtures (π) as a function of sex, probability of capture (p) as a function of state, sex, and mixture, and probability of recapture (c) as a behavioral response (*add*) or as independent (p , c). I tested for effects of the 2011 release of Morganza Spillway by modeling ϕ , ψ , p and c with a flood effect differing before (2007–2010), during (2011), and after the flood (2012). In 2010, I switched from a 1-wire sampling system (2007–2009) to a 2-wire sampling system (2010–2012). I tested for an additive wire effect and a sex*wire interaction in p and c .

Model	AICc	Δ AICc	w_i	K	Dev
ϕ (sex), ψ (state+flood), π (.), p (state+flood+sex+mix)= c (add)	4116.261	0.000	0.169	14	4087.655
ϕ (sex), ψ (state+flood), π (.), p (state+sex+mix)= c (add)	4116.503	0.242	0.150	13	4089.979
ϕ (sex+flood), ψ (state+flood), π (.), p (state+flood+sex+mix)= c (add)	4116.732	0.471	0.134	15	4086.039
ϕ (sex+flood), ψ (state+flood), π (.), p (state+sex+mix)= c (add)	4116.917	0.656	0.122	14	4088.311
ϕ (sex), ψ (state+flood), π (.), p (state+sex+mix), c (state+sex+mix)	4118.205	1.944	0.064	16	4085.418
ϕ (sex+flood), ψ (state+flood), π (sex), p (state+flood+sex+mix)= c (add)	4118.716	2.455	0.050	16	4085.929
ϕ (sex+flood), ψ (state+flood), π (.), p (state+sex+mix), c (state+sex+mix)	4118.729	2.468	0.049	17	4083.842
ϕ (sex+flood), ψ (state+flood), π (.), p (state+flood+sex+mix+wire)= c (add)	4118.778	2.517	0.048	16	4085.991
ϕ (sex+flood), ψ (state+flood), π (.), p (state+sex+mix), c (state+sex+mix)	4118.876	2.615	0.046	15	4088.182
ϕ (sex+flood), ψ (state+flood+sex), π (.), p (state+sex+mix)= c (add)	4118.903	2.642	0.045	17	4084.016
ϕ (sex+flood), ψ (state+flood), π (sex), p (state+sex+mix)= c (add)	4118.914	2.653	0.045	15	4088.220
ϕ (sex+flood), ψ (state+flood), π (.), p (state+flood+sex+mix+wire*sex)= c (add)	4119.265	3.004	0.038	17	4084.378
ϕ (sex+flood), ψ (state+flood), π (.), p (state+flood+sex+mix), c (state+flood+sex+mix)	4120.306	4.045	0.022	19	4081.201
ϕ (sex+flood), ψ (state+flood), π (.), p (sex+mix)= c (add)	4122.141	5.880	0.009	13	4095.616
ϕ (sex+flood), ψ (state+flood), π (sex), p (sex+mix)= c (add)	4123.681	7.420	0.004	14	4095.075
ϕ (sex+flood), ψ (state+flood+sex), π (.), p (sex+mix)= c (add)	4124.135	7.874	0.003	14	4095.529
ϕ (sex+flood), ψ (state+flood+sex), π (sex), p (sex+mix)= c (add)	4125.681	9.420	0.002	15	4094.988

Table 5. Comparison of capture probabilities (p) based on an additive effect (wire+sex) and an interaction effect (wire*sex) in a mark-recapture model for 2 different hair sampling systems, a 1-wire system implemented from 2007–2009 and a 2-wire system implemented from 2010–2012, for Louisiana black bears in the Upper Atchafalaya River Basin, Louisiana, USA.

Effect	Sex	Wire system	p_1^a	p_2^b	π^c	d
wire+sex						
	Males	1-wire	0.082	0.412	0.750	0.165
	Males	2-wire	0.079	0.402	0.750	0.160
	Females	1-wire	0.147	0.574	0.750	0.254
	Females	2-wire	0.142	0.564	0.750	0.248
wire*sex						
	Males	1-wire	0.069	0.367	0.747	0.145
	Males	2-wire	0.090	0.434	0.747	0.177
	Females	1-wire	0.161	0.599	0.747	0.272
	Females	2-wire	0.135	0.547	0.747	0.239

^a Capture probability for 1st proportion of the population.

^b Capture probability for 2nd proportion of the population.

^c Proportion of the population with p_1 .

^d Overall capture probability ($p_1 * \pi_1 + p_2 * \pi_2$).

Table 6. Number of individuals captured and annual abundance estimates for robust design multi-state mark-recapture model for Louisiana black bears in the Upper Atchafalaya River Basin, Louisiana, USA, 2007–2012.

Sex and Year	M_t^a	N_t^b	SE N_t	95% CI
Male				
2007	12	17.0	3.3	10.4–23.5
2008	9	18.9	3.7	11.6–26.2
2009	17	26.7	4.6	17.8–35.8
2010	20	25.6	4.1	17.6–33.5
2011 ^c	11	9.9	2.3	5.4–14.5
2012	22	26.6	4.0	18.7–34.4
Female				
2007	20	23.9	2.4	19.2–28.6
2008	27	34.9	3.1	28.9–40.9
2009	36	42.3	3.5	35.4–49.2
2010	22	28.8	2.7	23.5–34.0
2011 ^c	16	15.0	1.6	11.9–18.1
2012	39	43.3	3.5	36.4–50.0
Total				
2007	32	40.9	5.7	32.8–48.9
2008	36	53.8	6.8	44.4–63.2
2009	53	69.0	8.1	57.8–80.3
2010	42	54.3	6.7	44.4–63.2
2011 ^c	27	24.9	3.9	19.4–30.1
2012	61	69.8	7.5	59.5–80.2

^a Number of individuals captured.

^b Annual abundance estimate.

^c Part of the Upper Atchafalaya River Basin study area was flood in 2011. Results only represent non-flooded area.

Table 7. Annual abundance estimates comparison between Lowe (2011), using a sub-sample criterion of 25 samples/week, and the current study, using a sub-sample criterion of 38 samples/week

This study	N_t^a	N_t SE	95% CI	Lowe (2011)	N_t^a	N_t SE	95% CI
Male				Male			
2007	17.0	3.3	10.4–23.5	2007	22.3	6.2	15.4–42.0
2008	18.9	3.7	11.6–26.2	2008	16.4	4.8	11.3–32.8
2009	26.7	4.6	17.8–35.8	2009	31.2	7.8	22.1–56.1
Female				Female			
2007	23.9	2.4	19.2–28.6	2007	24.0	3.0	21.1–34.9
2008	34.9	3.1	28.9–40.9	2008	31.7	3.2	28.4–42.6
2009	42.3	3.5	35.4–49.2	2009	42.1	3.8	38.0–54.8
Total				Total			
2007	40.9	5.7	32.8–48.9	2007	46.3	7.5	37.4–69.9
2008	53.8	6.8	44.4–63.2	2008	48.1	6.2	40.7–67.3
2009	69.0	8.1	57.8–80.3	2009	73.3	9.4	61.5–101.2

^a Annual abundance estimate for each respective year.

Table 8. Transition rate (ψ) estimates of Louisiana black bear movement moving from flooded areas to non-flooded areas ($\psi^{F \rightarrow NF}$) and non-flooded to flooded areas ($\psi^{NF \rightarrow F}$) before (2007–2010), during (2011), and after (2012) the 2011 release of water through the Morganza Spillway in the Upper Atchafalaya River Basin, Louisiana, USA.

Transition	Time ^a	Sex	ψ	SE ψ	95% CI
$\psi^{F \rightarrow NF}$	Before	Males	0.032	0.004	0.025–0.040
	Before	Females	0.031	0.007	0.018–0.044
	During	Males	0.089	0.018	0.053–0.124
	During	Females	0.086	0.018	0.052–0.121
	After	Males	0.050	0.018	0.015–0.085
	After	Females	0.048	0.017	0.015–0.081
$\psi^{NF \rightarrow F}$	Before	Males	0.089	0.012	0.066–0.111
	Before	Females	0.091	0.011	0.069–0.113
	After	Males	0.115	0.035	0.047–0.184
	After	Females	0.118	0.035	0.050–0.186

^a Transition rates were not calculated for bears moving from the non-flooded area to the flooded area in 2011.

Appendix B: Figures

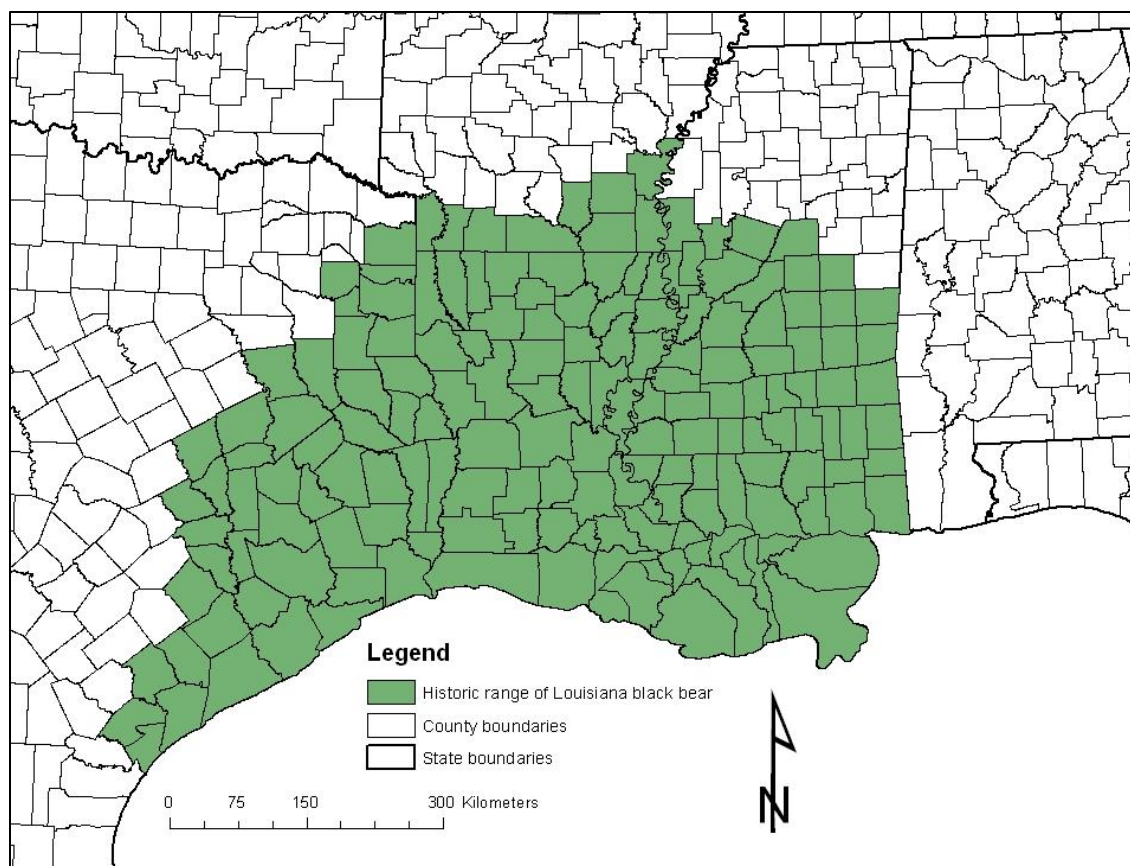


Figure 1. Historic range of the Louisiana black bear (*Ursus americanus luteolus*).

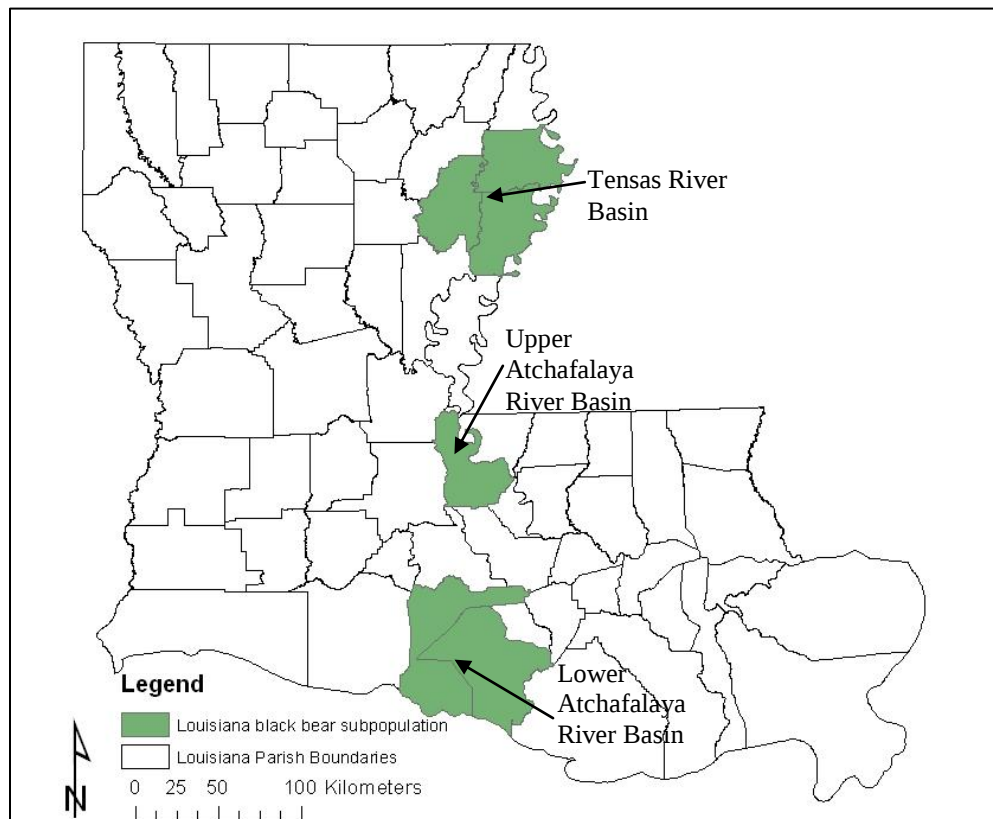


Figure 2. Current breeding sub-populations of the Louisiana black bear (*Ursus americanus luteolus*).

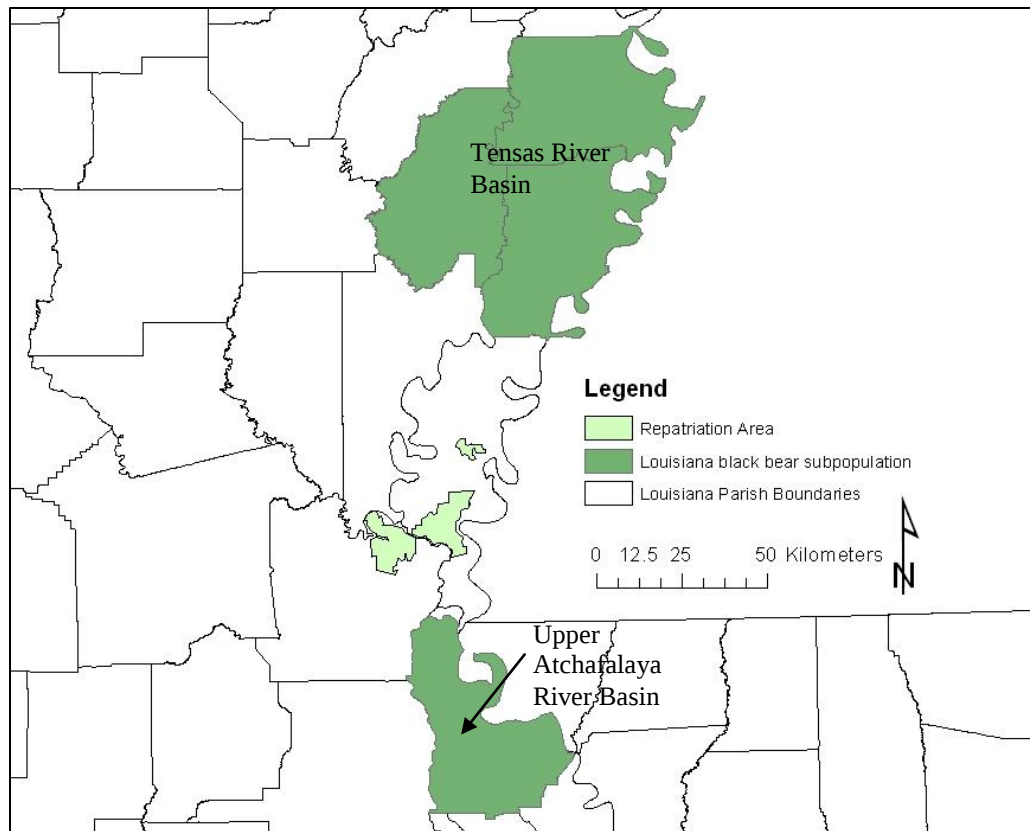


Figure 3. Location of the repatriation area where Louisiana black bears (*Ursus americanus luteolus*) were translocated.

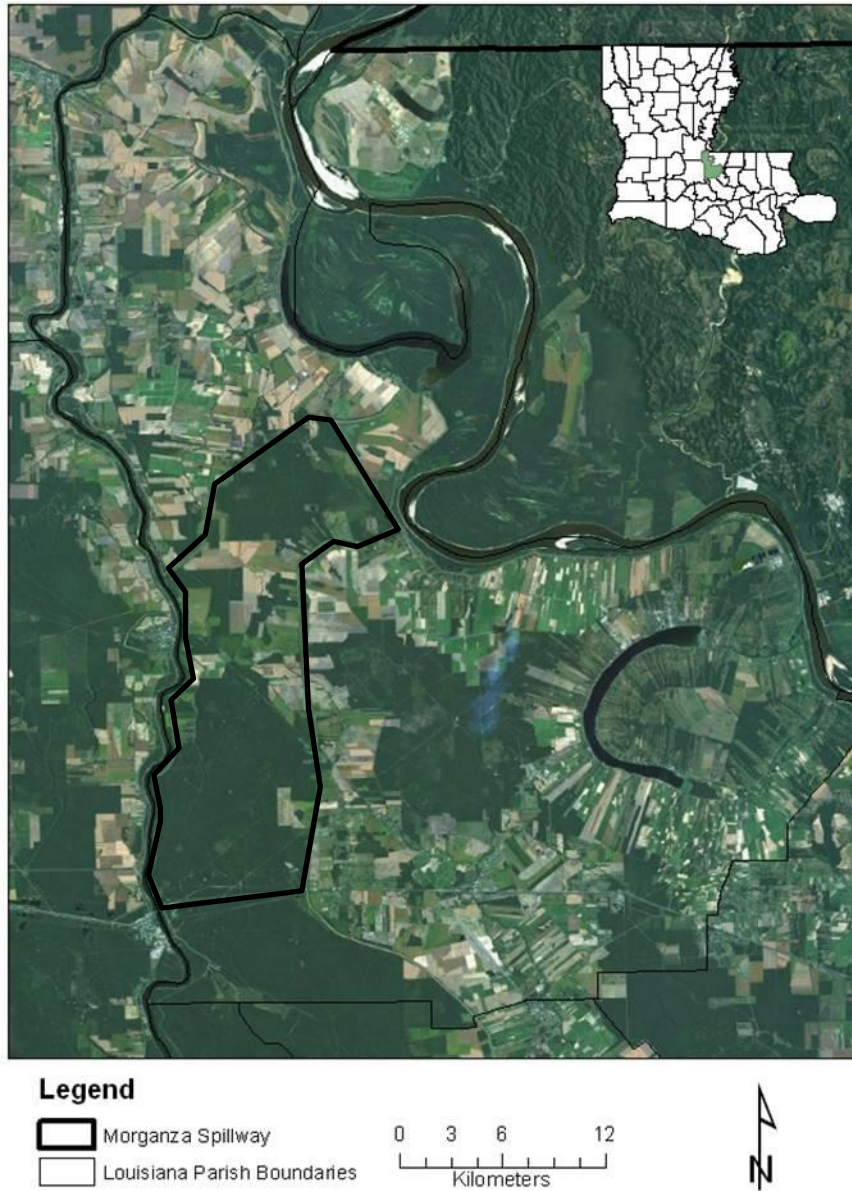


Figure 4. Morganza Spillway outlined within the Upper Atchafalaya River Basin.

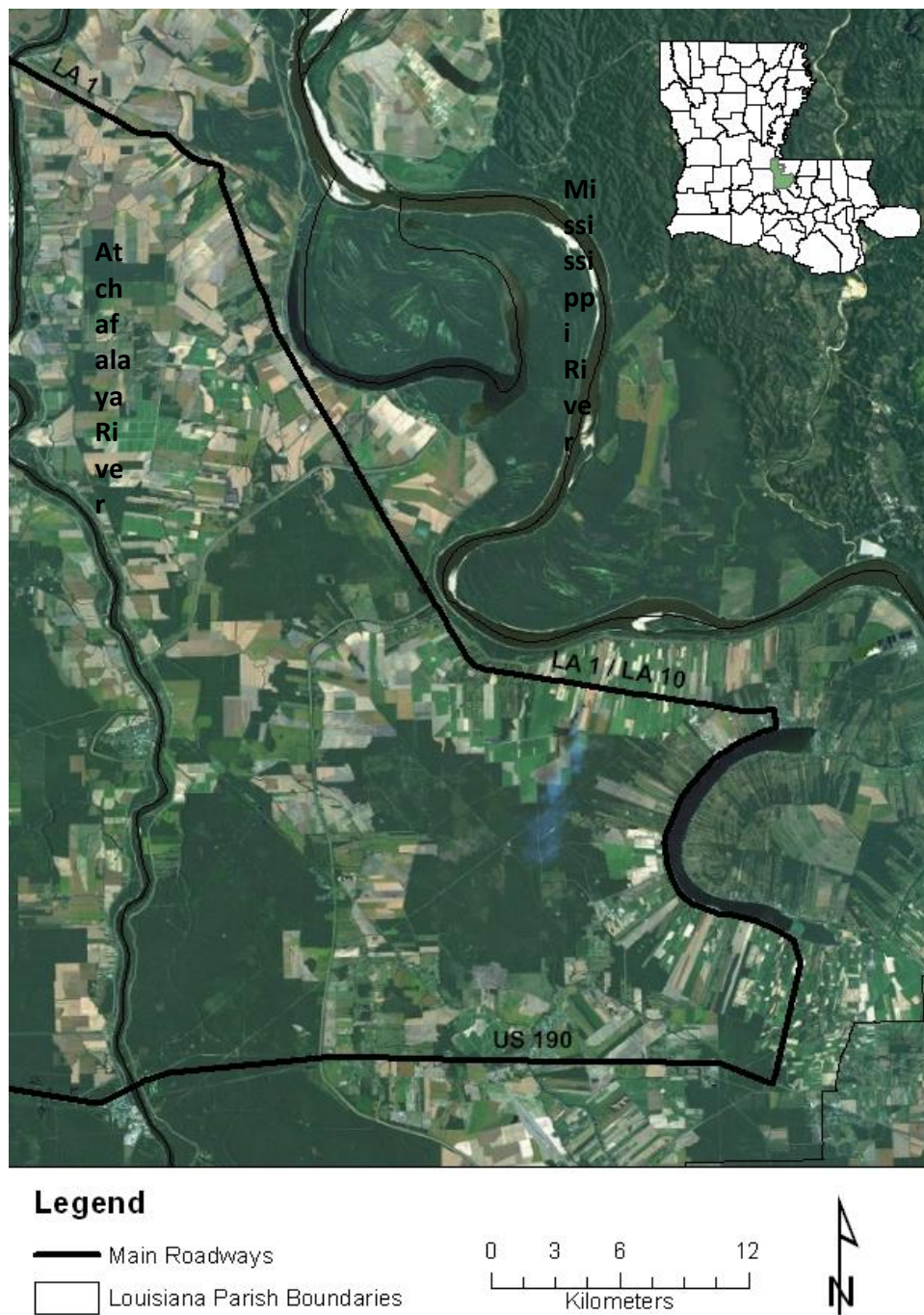


Figure 5. The Upper Atchafalaya River Basin study area borders.

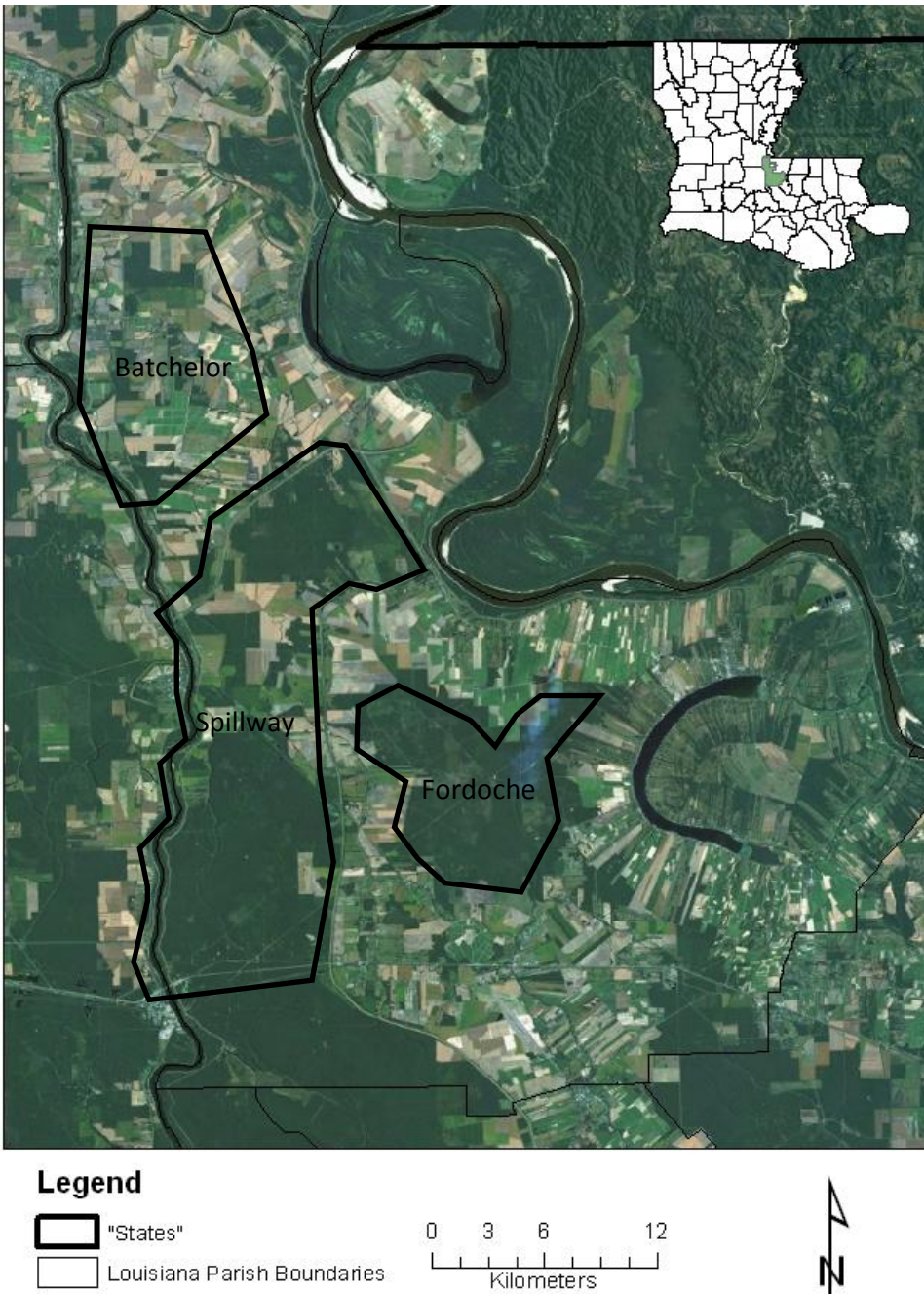


Figure 6. Batchelor and Fordoche were the “Non-Flooded” state and the Spillway was the “Flooded” state in the Multi-state mark-recapture model.

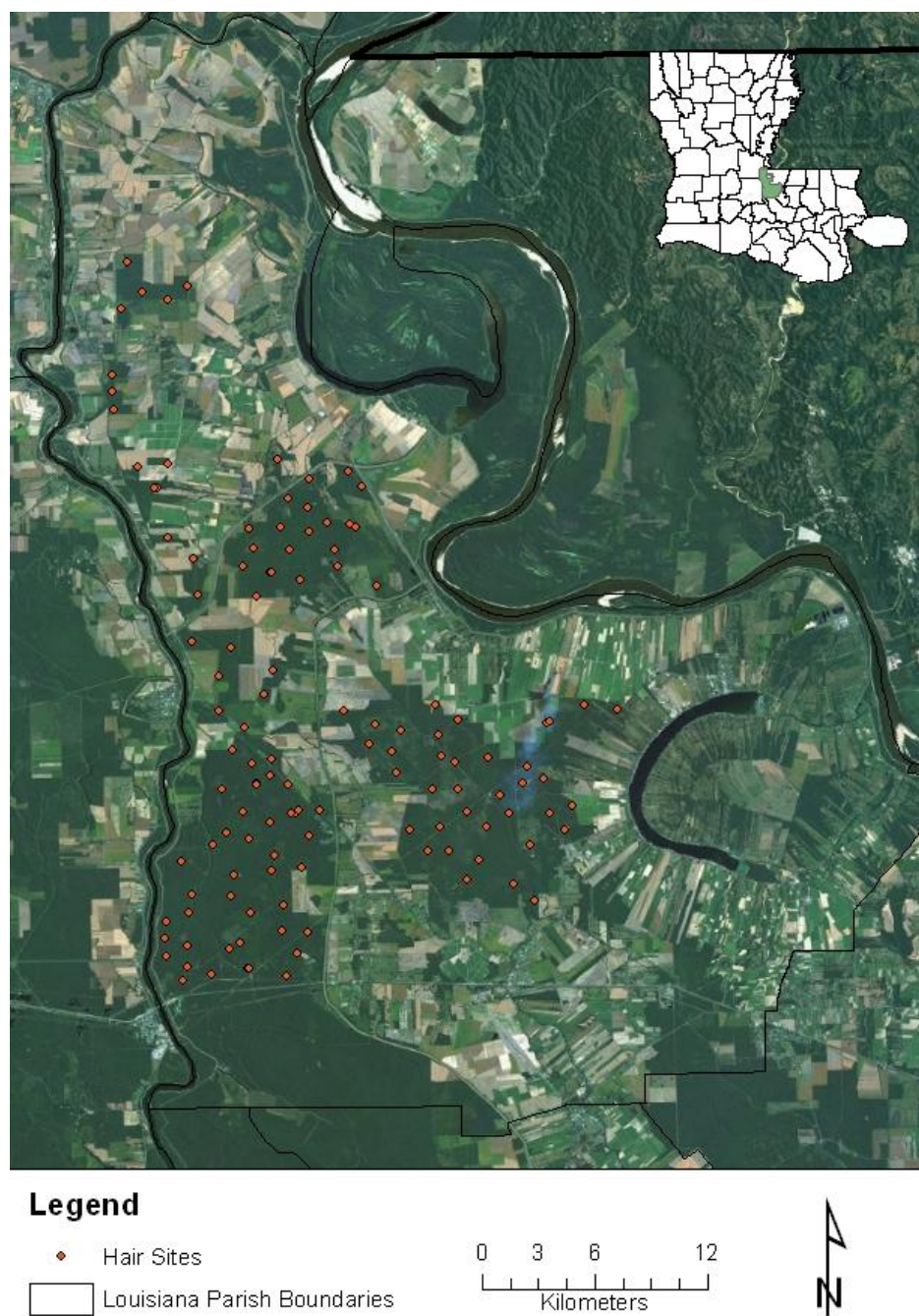


Figure 7. Sampling site locations within the Upper Atchafalaya River Basin. Sites were placed in the center of the grid cell based on 1.6- x 1.6- km² grid.

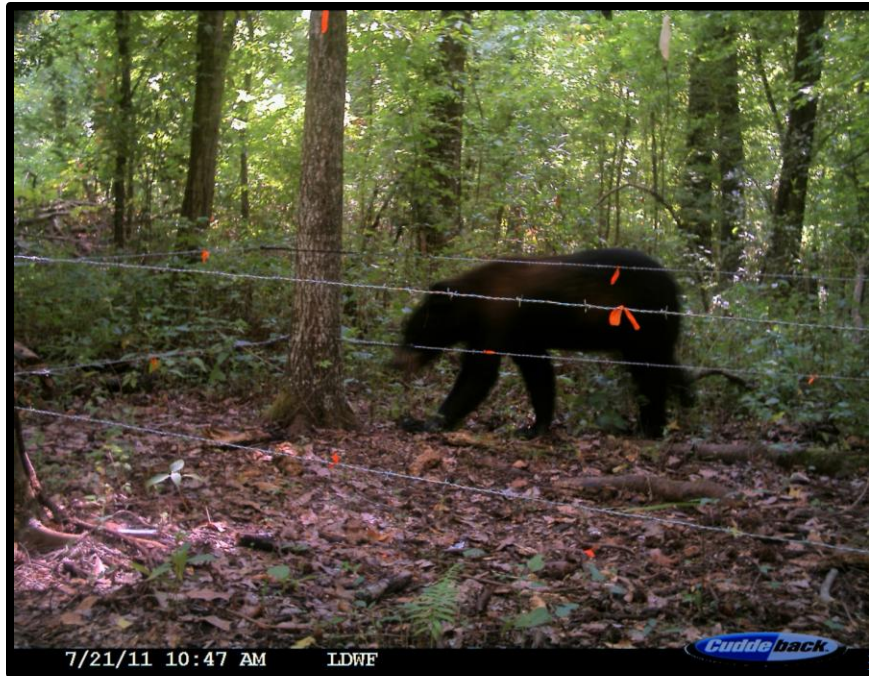


Figure 8. Two-wire hair collection system with the top wire at 65–70 cm and bottom wire at 35–40 cm above the ground.

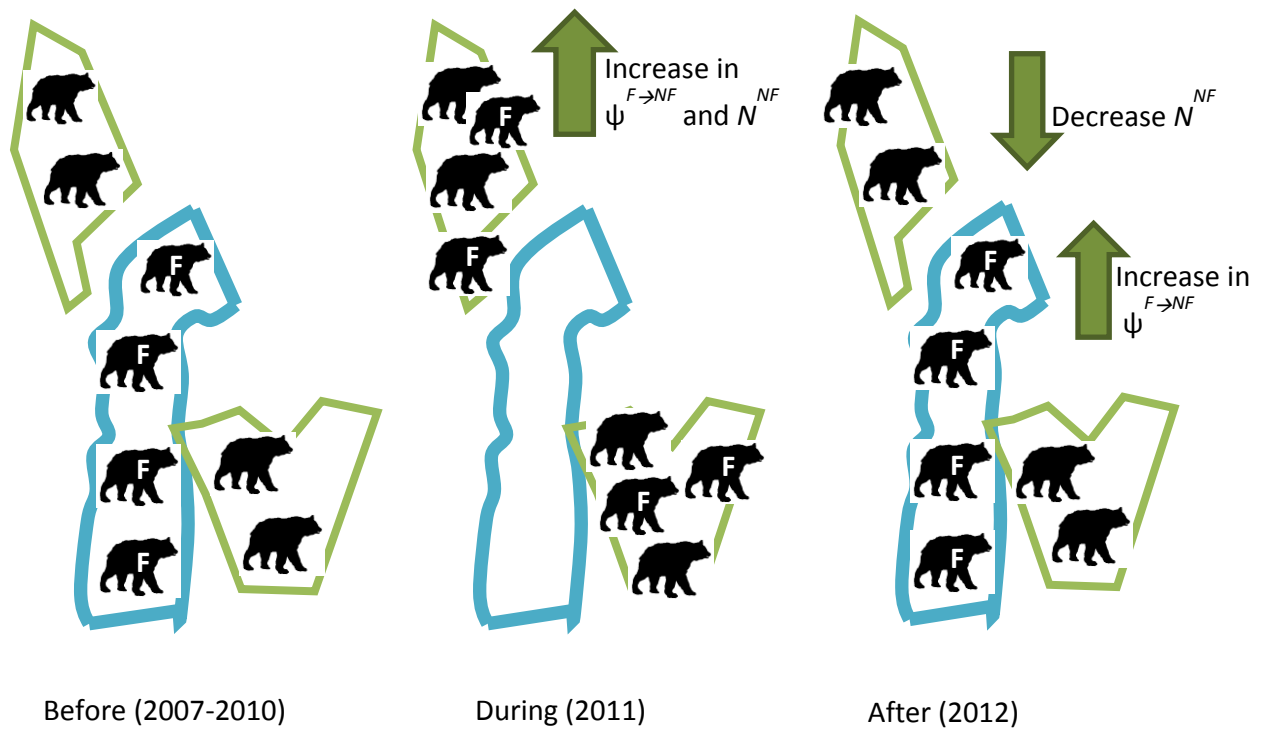


Figure 9. Hypothesis A: bears moved from flooded (blue) to non-flooded (green) areas during the flooding event in 2011 and returned to the flooded area in 2012 and the expected changes in transitions rates (ψ) and abundance (N) associated with this movement were estimated using Multi-state mark-recapture model.

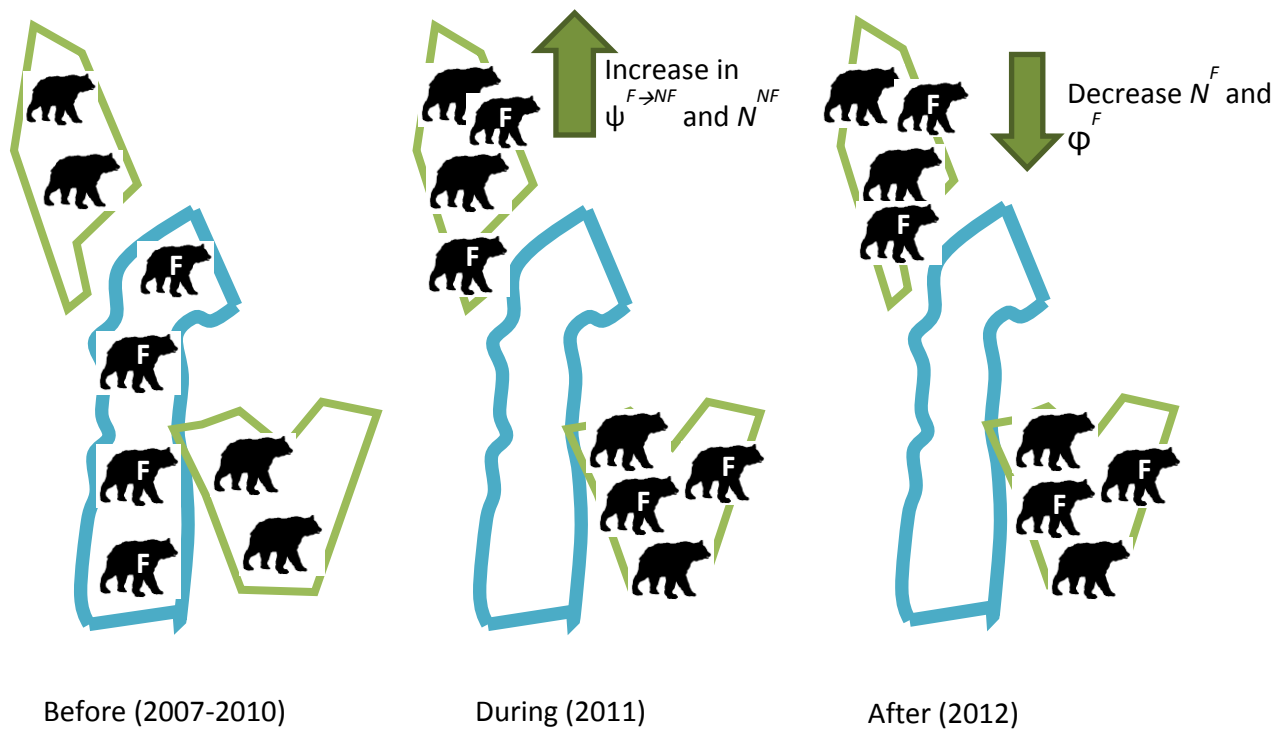


Figure 10. Hypothesis B: bears moved from flooded state (blue) to non-flooded (green) state during the flooding event in 2011 and did not return to the flooded state in 2012 and the expected changes in transitions rates (ψ), apparent survival (ϕ), and abundance (N) associated with this response were estimated using Multi-state mark-recapture model.

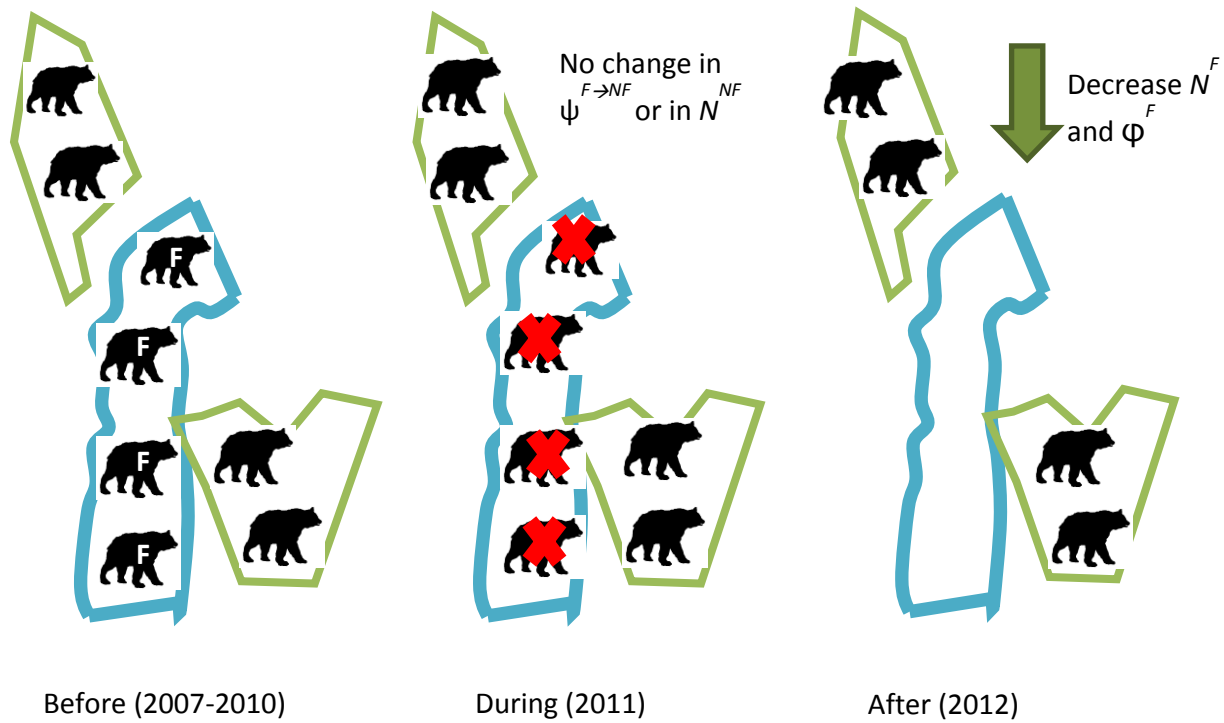


Figure 11. Hypothesis C: bears stayed in the flooded state (blue) in 2011 and did not survive the flooding event and the expected changes in transitions rates (ψ), apparent survival (ϕ), and abundance (N) associated with this response were estimated using Multi-state mark-recapture model

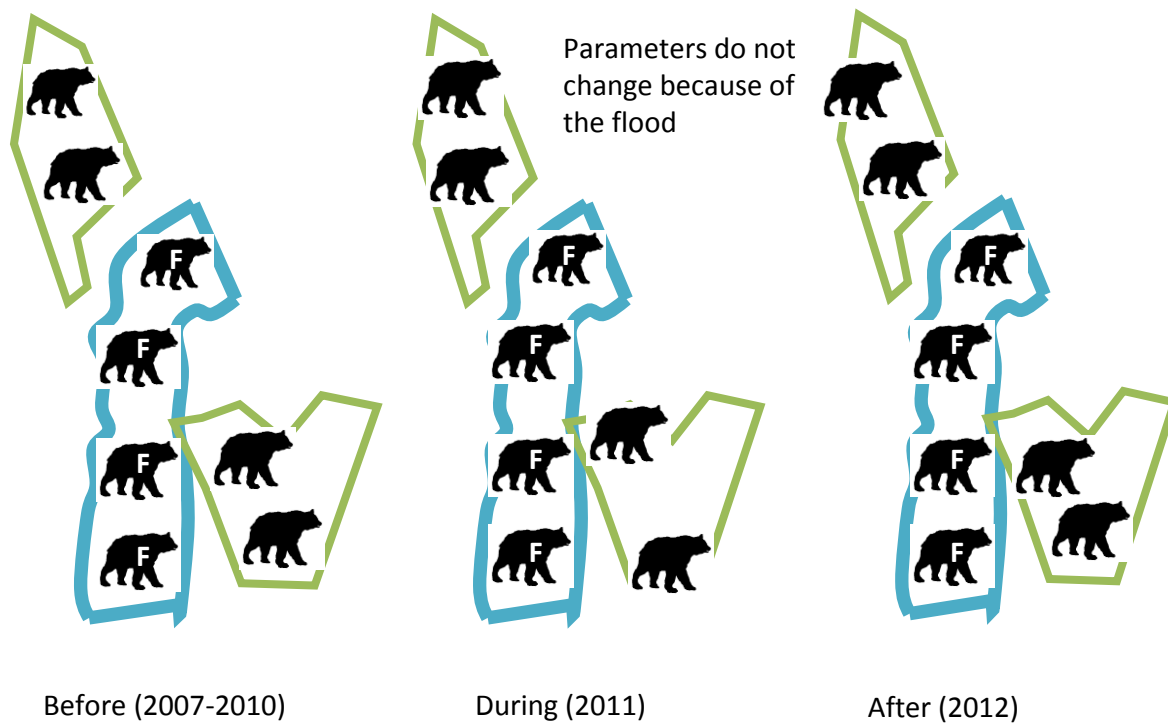


Figure 12. Hypothesis D: bears stayed in the flooded area during the 2011 flooding event and survived. There would have been no expected changes in transitions rates (ψ), apparent survival (ϕ), or abundance (N) estimates using Multi-state mark-recapture model

VITA

Kaitlin Christine O'Connell was born and raised in Lighthouse Point, Fl. She received her bachelor's degree in Environmental Studies from the Florida State University in 2010. While an undergraduate at Florida State University, she worked as an intern and office manager for the Florida Fish and Wildlife Conservation Commission's Bear Management Program where she developed aversive conditioning training materials for wildlife officers. She worked as a technician for the University of Tennessee on a black bear hair sampling study in Pointe Coupee, Louisiana. After graduation, she started her Master's degree research project with the University of Tennessee studying population dynamics of the Louisiana black bear in the Upper Atchafalaya River Basin. She received her Master's degree in Wildlife Science from the University of Tennessee in December 2013.