LOUISIANA BLACK BEAR
MONITORING REPORT

16 JUNE 2025

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CONTENTS

INTRODUCTION

In 1992, the U.S. Fish and Wildlife Service (USFWS) granted the Louisiana black bear (*Ursus americanus luteolus*), a subspecies of the American black bear, threatened status under the U.S. Endangered Species Act (ESA), listing loss and fragmentation of habitat as the primary threats (U.S. Fish and Wildlife Service 1992). The 1995 Recovery Plan outlined recovery goals designed to meet the objective of reducing threats to the Louisiana black bear and the habitat supporting it (U.S. Fish and Wildlife Service 1995). At that time, the bear subpopulations in the state were located at Tensas River Basin (TRB), the Upper Atchafalaya River Basin (UARB), and the Lower Atchafalaya River Basin (LARB). Later, a fourth subpopulation was established at Three Rivers Complex (TRC) with bears being translocated from TRB. Laufenberg et al. (2016) performed a population viability analysis (PVA) for the Louisiana black bear based in part on capture-mark-recapture (CMR) data collected at TRB from 2006 to 2012 and UARB from 2007 to 2012. The CMR data consisted of genotyped bear hair samples collected at barbed wire sampling sites. These data were used to develop stochastic population models using hierarchical Bayesian modeling methods to estimate probability of persistence. Laufenberg et al. (2016) concluded that the probability of persistence of the TRB and UARB subpopulations over 100 years were >0.928 and >0.906, respectively, which supported the decision to remove *U. a. luteolus* from the list of threatened species in March 2016 (U.S. Fish and Wildlife Service 2016a).

Post-delisting monitoring is a requirement under the U.S. Endangered Species Act. A post-delisting monitoring plan was developed and implemented by the Louisiana Department of Wildlife and Fisheries and the USFWS (U.S. Fish and Wildlife Service 2016b). Post-delisting monitoring based on spatially explicit capture-recapture was completed in 2021 (Clark et al. 2025). Model-averaged estimates of population abundance (*N*) for primary range at TRB ranged from 135 (95% CI = 121–149) female bears in 2006 to 140 (95% CI = 123–157) in 2020 with mean λ of 1.003 (95% CI = 0.991–1.015), which suggested a stable population. An estimated 56 (95% CI = 19–92) additional female bears occurred in the secondary range at TRB in 2020. At UARB, model-averaged estimates of *N* for the primary range were from 35 (95% CI = 28–43) females in 2007 to 33 (95% CI = 28–43) in 2020, with mean λ = 0.996 (95% CI = 0.972–1.020), again suggesting a stable population. Three (95% CI = 0–6) additional female bears were estimated to occur in the secondary range at UARB during 2020. The estimate of *N* at TRC was 28 (95% CI = 18–44) females in 2014 and 42 (95% CI = 19–94) in 2021. The number of bears in the secondary ranges suggests some bears may have emigrated from the primary areas and colonized secondary areas, likely facilitated by increases in bottomland hardwood habitat adjacent to the core populations. The stable primary populations, the reintroduced population at TRC, and the number of bears in the secondary range adjacent to TRB together suggested the overall number of Louisiana black bears has increased since monitoring began in 2006 (Clark et al. 2025).

Following the completion of the post-delisting monitoring, the Louisiana Department of Wildlife and Fisheries adopted a new sampling strategy whereby each of four identified subpopulations (i.e., TRB, UARB, TRC, LARB), and a new area, the Upper Ouachita River Basin (UORB), would be sampled on a rotating schedule, with one site being surveyed each year based on CMR hair sampling. The UORB subpopulation was located along the norther border with Arkansas where bears from White River National Wildlife Refuge, Arkansas, were reintroduced to Felsenthal National Wildlife Refuge, Arkansas, in 2000- 2002 (Wear et al. 2005, *Figure 1*).

This report is an analysis of CMR hair sampling data completed at UORB in 2023 and at UARB in 2024 (*Figure 1*). Our objectives were to estimate population abundance (*N*) and density (*D*) at UORB and UARB based on spatially explicit CMR methods (Clark et al. 2025).

METHODS

We used DNA extracted from hair collected at baited, barbed-wire enclosures (hereafter referred to as hair traps) to determine individual identities and record capture histories for CMR analysis (Woods et al. 1999). Hair traps consisted of two strands of barbed wire, one located 35-40 cm and one 65-70 cm above the ground and enclosing an area about 5 × 5 m in size. Field technicians began sampling in June and baited each site with small amounts of bakery products (e.g., sweet rolls, donuts) and a scent attractant (raspberry or honey extract; Mother Murphy's Laboratories, Greensboro, North Carolina, USA). Technicians placed hair samples collected from individual barbs in separate coin envelopes and stored them in a dry location at room temperature until DNA extraction was performed. All sites were checked for hair samples and rebaited every seven days for six weeks.

As in the previous monitoring studies, we used a clustered sampling design (Clark 2019) in the forested areas adjacent to the primary range of those populations (*Figure 1*), but we used higher trap densities in core areas. These trap clusters were intended to help us evaluate how much colonization of previously unoccupied areas had occurred.

DNA extraction and microsatellite genotyping were performed by Wildlife Genetics International, Inc. (Nelson, British Columbia, Canada) following standard protocols (Woods et al. 1999, Paetkau 2003, Roon et al. 2005). Guard hair roots were clipped and used for extraction whereas, in the case of underfur, entire clumps were used for extraction. In contrast with previous studies, we genotyped all collected bear hair samples and did not subsample.

The power of multilocus genotypes to differentiate between individuals depends on the number and variability of markers used for individual identification and the number of individuals sampled (Paetkau 2003). To assess the power of the marker systems used to differentiate individuals, we estimated the probability that two full siblings randomly drawn from a population will have the same multilocus genotype (PI_{sibs}, Taberlet and Luikart 1999). To determine whether independence of loci and random sampling assumptions were met, we tested for linkage disequilibrium (lack of allele independence between loci) and conformity to Hardy-Weinberg equilibrium (independence of alleles within loci) in Program GENEPOP version 3.4 (Raymond and Rousset 1995). We used the Dunn-Sidak method (Sokal and Rohlf 1995) to ensure an experiment-wise error rate of $\alpha = 0.05$ by restricting critical values for individual comparisons to $\alpha = 1 - (1 - 0.05)1/k$, where k is the number of individual comparisons.

Genetic marker systems for individual identification were independently developed for each study area to ensure adequate power. WGI selected marker sets consisting of 10 loci in the UORB (D123, G10B, G10M, G10P, G1D, MSUT-2, MU23, MU26, MU50, and sex marker ZFX/ZFY) and 9 loci in the UARB (G10C, G10L, G10M, G10P, MSUT-2, MU23, MU26, MU59, and sex marker ZFX/ZFY) for identification of individual bears. DNA was extracted from selected hair samples using DNeasy Tissue kits (Qiagen N.V., Venlo, Netherlands). Extracted DNA was amplified at all loci using polymerase chain reaction. Reactions contained 50 nM KCl, 0.1% Triton X-100, and 160 µM deoxyribonucleotide triphosphates in a volume of 15 µL with concentrations of $MgCl_2$, Taq polymerase, and primers optimized to permit co-amplification. Thermal cycling was performed using a Perkin Elmer 9600 (Perkin Elmer, Waltham, Massachusetts, USA). Amplified DNA samples were sequenced on a 373A automated sequencer (Applied Biosystems [ABI], Foster City, California, USA) using ABI's four-color detection system. DNA fragments were analyzed and genotype data were generated using Genescan software (ABI), and genotypes were determined using Genotyper software (ABI). Genotyping followed a three-phase approach to assign individual identities to samples and minimize genotyping errors causing misidentification of individuals (Paetkau 2003).

We first formatted the CMR data from UORB and UARB for analysis. We estimated *D* and *N* based on an annual closed model for each study area with the Program R package secr (R Core Team 2022, Efford 2022). We created a 5,000-m buffer around all traps in core areas and an 11,000-m buffer around all traps in secondary areas using the mask.check routine in secr. We used a 1,000-m mesh spacing to define the mask and considered only forested land cover types for density estimation. Field technicians placed all traps in forested land-cover types (i.e., National Land Cover Database 2011 classes deciduous forest, evergreen forest, mixed forest, shrub/scrub, and woody wetlands; *https://www.mrlc.gov/data/nlcd-2011-land-cover-conus*) and we excluded non-forested areas from the analysis. Consequently, our abundance estimates only apply to areas of forested land cover. Hair traps were placed in forest cover (even if it was not large enough to be present as a mask point) and, thus, we assume no bear home range centers were in non-forested areas. However, those masks sometimes included land in other states (MS and AR) so, to derive estimates of *N* exclusive to Louisiana, we excluded the out the out-of-state mask points and summed the densities for the remaining mask points. At UARB, we also excluded from the mask some areas of semi-permanently flooded wetland south of U.S. Highway 190 that were deemed to be unsuitable for bears (Clark et al. 2025).

We assumed the probability of capture if the trap was at the home range center (g_0) did not vary across occasions within each session except for possible within-year trap response effects, which we modeled as a trap-specific behavioral response (bk). We also fit 2-class finite mixture models (Pledger 2000) for individual capture heterogeneity (h2) on g_0. We modeled the spatial scaling parameter (σ) as constant across all occasions and years. We expected bear densities in the secondary range to decline with distance from primary range so we created a distance covariate (dist_core, defined as the distance from the outer perimeter of primary range), which we rescaled from 0 to 1 by dividing by the maximum distance to the core. We used this covariate as a constraint on *D* in the secondary range at UORB and UARB. We estimated expected *N* for the primary range at UORB and UARB using the region.N function in secr.

We selected the best fit models based on Akaike's information criterion scores, corrected for small sample sizes (AIC$_c$, Burnham and Anderson 1998). Arnold (2010) and Sutherland et al. (2023) demonstrated that AIC is functionally equivalent to conducting a likelihood ratio test with a significance level of 0.157; they suggested using 85% CI for determining significance of β values when AIC model selection is used. Consequently, we adopted the 85% criterion and considered effects to be supported if 85% CIs did not include zero.

RESULTS

At UORB, field technicians checked up to 169 hair traps for six weeks during 2023 and detected 59 visits by 25 individual female bears and 26 visits by 14 individual male bears (*Figure 2*). WGI successfully genotyped 330 of 357 hair samples (92% success rate). The overall PI$_{sibs}$ for UORB was 1.5×10^{-3}, corresponding to a 1 in 673 chance that a bear shared its multilocus genotype with another bear (Laufenberg et al. 2016). Three of nine microsatellite loci violated Hardy-Weinberg expectations ($\alpha = 0.006$) and 15 of the associations among 36 pairs of loci exhibited linkage disequilibrium ($\alpha = 0.001$). The top closed model for females at UORB (model weight = 0.967) was based on a distance to core covariate on *D* (β = -3.13, 85% CI = -5.56–-0.69), a site-specific behavioral response (bk; β = 4.18, 85% CI = 3.51–4.85) on g_0, and a heterogeneity mixture on g_0 (β =-2.34, 85% CI = -3.43–-1.25; *Table 1*). The top closed model for males at UORB (model weight = 0.877) was based on a distance to core covariate on *D* (β = -18.93, 85% CI =-54.93–17.08), a site-specific behavioral response (bk; β = 1.39, 85% CI = 0.59–2.19) on g_0, and a heterogeneity mixture on g_0 (β =-2.48, 85% CI = -3.75–-1.21). The dist_core covariate was strongly supported for density estimates in the secondary range for females, with densities declining with increasing distance from the primary range, but not for males as the 85% CI included zero. The estimate of *N* within the mask but excluding land in Arkansas was 70.4 females (95% CI = 25.2–196.7) and 34.3 males (95% CI = 10.3–113.5). Mean densities were 0.019 female bears/km^2 (95% CI = 0.013–0.027) and 0.014 male bears/km^2 (95% CI = 0.007–0.029). Confidence intervals were wide for both sexes. We also estimated male and female population abundances for only the primary area in UORB, which would not be affected by the dist_core covariate. Estimates in the core at UORB were 34.7 (95% CI = 10.4–115.3) for males and 45.7 (95% CI = 16.4–127.2) for females. The similarity of the male estimates with (34.3) and without the secondary range was likely because the dist_core covariate could not be estimated accurately.

At UARB, technicians checked up to 237 hair traps for six weeks during 2024 and detected 95 visits by 34 individual female bears and 29 visits by 17 individual male bears (*Figure 3*). WGI successfully genotyped 408 of 550 hair samples (74% success rate). The overall PI$_{sibs}$ at UARB was 3.6×10^{-3}, corresponding to a 1 in 274 chance that two bears shared the same multilocus genotype (Laufenberg et al. 2016). None of the seven microsatellite loci violated Hardy-Weinberg expectations (α = 0.007) and 2 of 21 loci pairs exhibited linkage disequilibrium (α = 0.002). The top closed model for females at UARB (model weight = 1.000) was based on a distance to core covariate on *D* (β = -12.81, 85% CI =-18.25–-7.37), a site-specific behavioral response (bk; β = 2.42, 85% CI = 2.07–2.77) on g_0, and a heterogeneity mixture on g_0 (β =-1.67, 85% CI = -2.04–-1.29). The top closed model for males at UORB (model weight = 1.000) was based on a distance to core covariate on *D* (β = -10.66, 85% CI = -17.38–-3.94), a site-specific behavioral response (bk; β = 1.58, 85% CI = 0.74–2.42) on g_0, and a heterogeneity mixture on g_0 (β = -2.68, 85% CI = -3.45–-1.91). The dist_core covariate was strongly supported for density estimates in secondary range for both females and males, with densities declining with increasing distance from the primary range. The estimate of *N* within the mask but excluding land in Mississippi and below the spillway was 45.3 for females (95% CI = 31.6–65.0) and 33.7 for males (95% CI = 16.4–69.4). Mean densities were 0.039 female bears/km^2 (95% CI = 0.014–0.110) and 0.019 male bears/km^2 (95% CI = 0.006–0.063). In primary range only, we estimated 28.1 female bears (95% CI = 19.2–41.2) and 25.3 males (95% CI = 12.8–50.1).

CONCLUSIONS

The data from UORB suggests a substantial bear population, likely a result of range expansion by the reintroduced population just north of the border in Arkansas. Confidence intervals were wide, however, because of the small size of the area and the limited number of hair traps that could be placed there. Data may have been too sparse to adequately estimate the dist_core covariate, which can have a marked influence on estimates of *N*. We evaluated models without the covariate for males, but those models were not supported and the estimates of *N* were greatly inflated. Though the point estimate of *N* suggests a population of about 100 bears of both sexes (excluding cubs), the level of uncertainty is high. This uncertainty should be considered when making management recommendations for this population. The Arkansas Game and Fish Commission has conducted spatially explicit CMR for bears at Felsenthal National Wildlife Refuge in the past (D. White, University of Arkansas at Monticello, personal communication). Coordinating the timing of sampling efforts between Louisiana and Arkansas would increase sample sizes and may help produce more stable estimates for this population of bears in the future.

WGI conducted a principal components analysis to determine the origin of the bears at UORB based on archived samples in their database from all the Louisiana subpopulations and the White River population in Arkansas. The 38 new UORB bears clustered with TRB and White River but, whereas TRB and White River bears used to be well differentiated, the UORB bears included genotypes similar to both TRB and White River bears. This is somewhat surprising given that the reintroduced bears in Arkansas were exclusively sourced from White River and suggests that connectivity between TRB and UORB has increased in recent years.

The data from UARB suggests that the bear population has increased since our 2020 estimate of 36 females. However, the estimate in the primary range (28.1) was similar to our estimate there from 2020 (33, Clark et al. 2025). This finding suggests that most of the increase in 2024 was in secondary range. This apparent expansion is consistent with a recent genetic structure analysis whereby the increasing population in Mississippi consisted of many bears emigrating from UARB (D. Morin, Mississippi State University, personal communication). Previous research indicated that the UARB subpopulation was stable (Clark et al. 2025), but the 2024 data suggests that this population has substantially increased.

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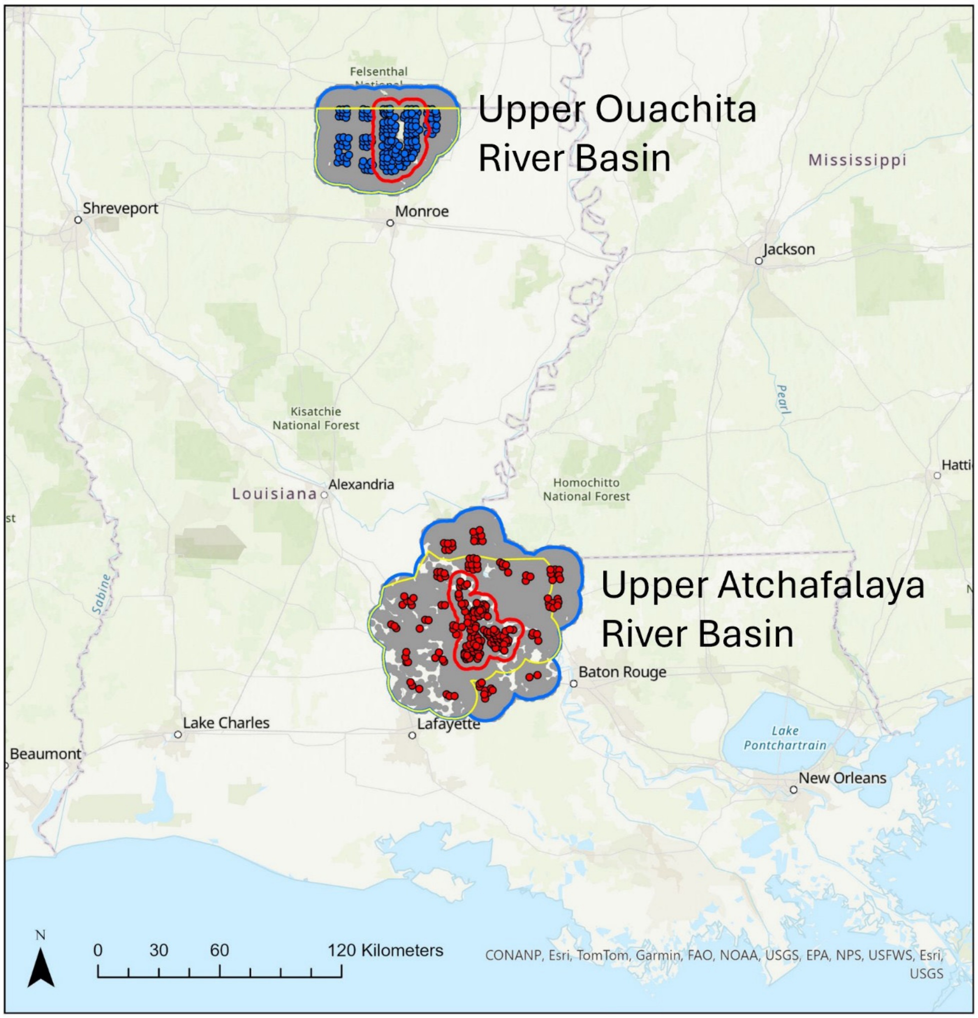
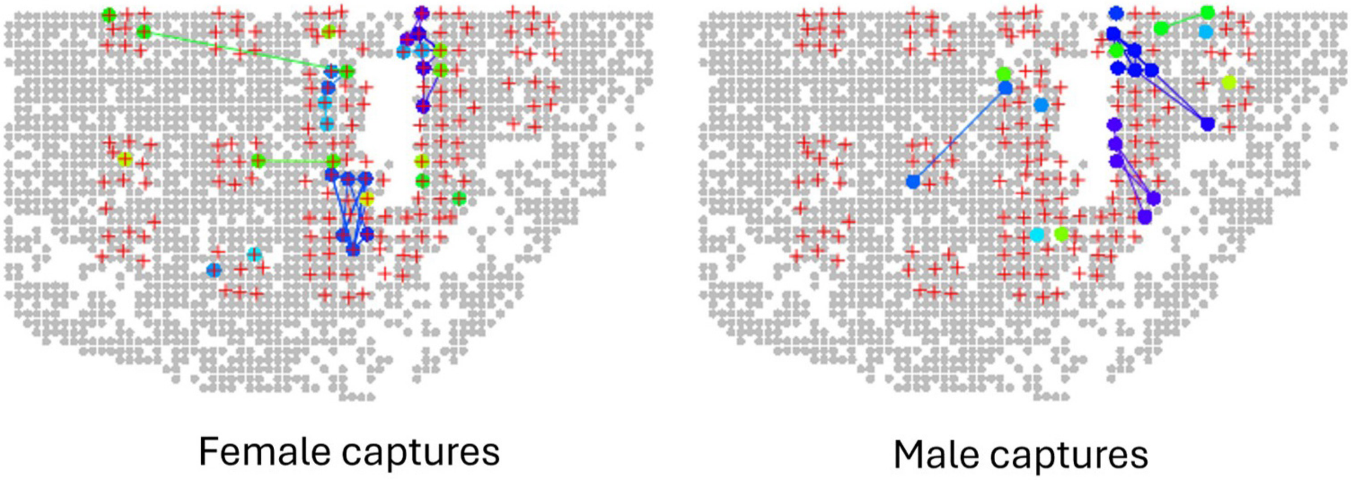
TABLE 1. Model selection results for the Upper Ouachita River basin (2023) and the Upper Atchafalaya River basin (2024) black bear populations for spatially explicit capture-mark-recapture estimation models based on Akaike information criterion adjusted for small sample size statistics (AIC_c). Density is *D*, the detection probability at animal activity centers is g_0, the scaling parameter is σ, a site-specific behavioral response persisting within years is bk, and dist_core is distance to the core population. We considered only models with ΔAIC_c <2 to be supported.

MODEL	NO. PARAMETERS	AIC_c	ΔAIC_c	AIC_c WEIGHT	LOG LIKELIHOOD
Upper Ouachita River Basin - Females					
- *D*~dist_core, g_0~bk+h2, σ~1	7	704.616	0.000	0.967	-342.014
- *D*~dist_core, g_0~bk, σ~1	5	707.918	6.732	0.034	-347.380
- *D*~1, g_0~bk+h2, σ~1	6	704.616	0.000	0.967	-342.014
- *D*~1, g_0~bk, σ~1	5	707.918	6.732	0.034	-347.380
Upper Ouachita River Basin - Males					
- *D*~dist_core, g_0~bk+h2, σ~1	7	376.580	0.000	0.877	-171.957
- *D*~dist_core, g_0~bk, σ~1	5	369.642	4.228	0.106	-176.071
- *D*~1, g_0~bk+h2, σ~1	6	377.777	7.863	0.017	-176.889
- *D*~1, g_0~bk, σ~1	4	374.418	12.060	0.000	-180.987
Upper Atchafalaya River Basin - Females					
- *D*~dist_core, g_0~bk+h2, σ~1	7	1452.453	0.000	1.000	-717.073
- *D*~dist_core, g_0~bk, σ~1	5	1452.453	26.563	0.000	-732.354
Upper Atchafalaya River Basin - Males					
- *D*~dist_core, g_0~bk+h2, σ~1	7	457.166	0.000	1.000	-215.361
- *D*~dist_core, g_0~bk, σ~1	5	466.370	16.194	0.000	-225.458
- *D*~1, g_0~bk+h2, σ~1	6	471.857	18.736	0.000	-225.728
- *D*~1, g_0~bk, σ~1	4	484.179	36.125	0.000	-236.423



CONANP, Esri, TomTom, Garmin, FAO, NOAA, USGS, EPA, NPS, USFWS, Esri, USGS

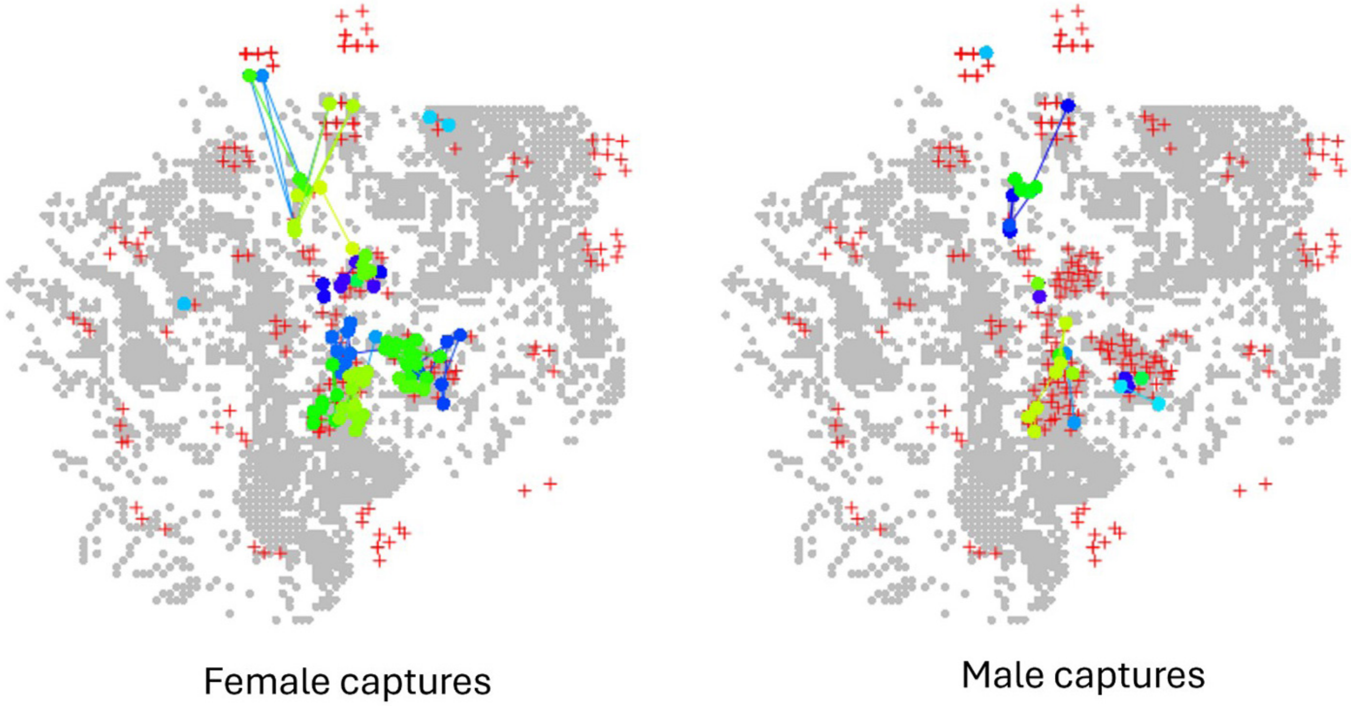
FIGURE 1. Location of hair traps and study area boundaries for the Upper Ouachita River Basin and Upper Atchafalaya River Basin bear subpopulations, Louisiana, 2023-2024. The Upper Ouachita traps are in blue and the Upper Atchafalaya hair traps are in red. The primary study area boundaries are red and the secondary boundaries are blue. The study area boundaries used to estimate population abundance are in yellow and the mask is gray.



Female captures

Male captures

FIGURE 2. Location of hair traps and capture histories for the Upper Ouachita River Basin, Louisiana, 2023. Captures and tracks of individual bears are in blue or green.



Female captures

Male captures

FIGURE 3. Location of hair traps and capture histories for the Upper Atchafalaya River Basin, Louisiana, 2023. Captures and tracks of individual bears are in blue or green.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