Louisiana Black Bear Post-Delisting Monitoring

1st Annual Report 2016

Monitoring Team Cooperators:

Louisiana Department of Wildlife and Fisheries

U.S. Fish and Wildlife Service

U.S. Geological Survey - Southern Appalachian Research Branch
University of Tennessee

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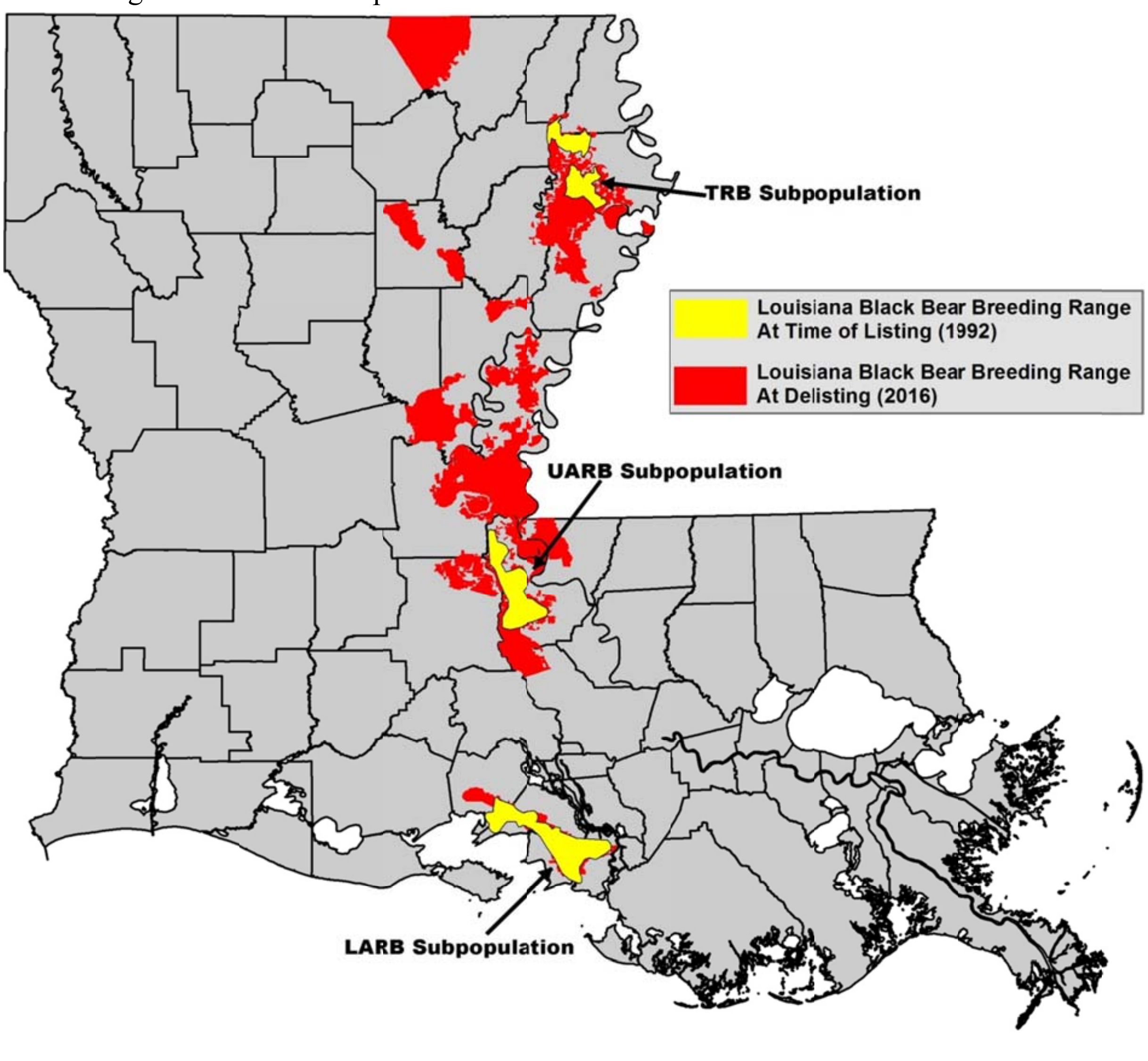
This annual report is available on the web at:
https://www.fws.gov/Lafayette/la_black_bear.html

Introduction

The Louisiana black bear is one of 16 subspecies of the American black bear. It historically inhabited the forests of Louisiana, southern Mississippi, and eastern Texas, but extensive land clearing, mainly for agricultural purposes, reduced its habitat by more than 80 percent. The Louisiana black bear was listed as threatened on January 7, 1992, primarily due to the reduction in population size resulting from extensive historic habitat loss, reduction in habitat quality due to fragmentation, and human-associated mortality (57 FR 588). Simultaneously, other free-living black bears within the historic range of the Louisiana black bear were listed as threatened due to their similarity of appearance to the Louisiana black bear. On March 10, 2009, the Service published a final rule in the Federal Register (74 FR 10350) designating 1,195,821 acres of critical habitat for the Louisiana black bear.

At the time of listing, the subspecies was restricted to core subpopulations in the Tensas River Basin (TRB subpopulation), the upper Atchafalaya River Basin (UARB subpopulation), and the lower Atchafalaya River Basin in coastal St. Mary and Iberia Parishes (LARB subpopulation). After more than two decades of management, we were able to conclude that the threats to the species had been eliminated or reduced, adequate regulatory mechanisms existed, and subpopulations were stable. Due to recovery, the Louisiana black bear was officially removed from the List of Endangered and Threatened Species on March 11, 2016 (81 FR 13124); critical habitat designation for this subspecies was also withdrawn at that time.



Methodology

The Service and state resource management agencies have latitude in determining the post-delisting monitoring activities that are necessary and appropriate. The Endangered Species Act does not require the development of a formal Post-Delisting Monitoring (PDM) Plan. However, concurrent with our delisting rule, the Service and the Louisiana Department of Wildlife and Fisheries (LDWF) published a plan to extensively monitor the status of the Louisiana black bear for 7 years following its delisting (though the Endangered Species Act only requires that such monitoring occur for a minimum of 5 years post-delisting). That monitoring, which is ongoing, is designed to detect any potential population decreases or threat increases that may warrant the implementation of measures to ensure that the Louisiana black bear remains secure from risk of extinction. The results of our first year of annual post-delisting monitoring are provided in this report.

On page 24 of the Louisiana Black Bear PDM Plan, it is stated that "A sensitivity analysis of Louisiana black bear demographic parameters is currently being conducted to better inform the decision threshold for post-delisting monitoring. Those methods, which can only improve monitoring accuracy, **will be incorporated** where appropriate once they are developed. . . ". The Louisiana Black Bear PDM Plan (page 33) states "To ensure that the most reliable population demographic measure will be used for post-delisting monitoring, a sensitivity analysis is currently being conducted by USGS (Appendix 1). **That analysis will be used** to directly calculate the relative importance of demographic rates to population growth rate and other population-level statistics (Caswell 2001) and to population persistence based on methods used in Laufenberg et al. (2013). Decision thresholds identified by that analysis could then be used in conjunction with statistical power analyses **to explore alternative study designs and data collection options for further improving or refining post-delisting monitoring protocols.**" Likewise, the PDM Plan (page 35) provides a footnote to all trigger categories which states that the triggers ". . . may be adjusted based on the results of the sensitivity analyses in order to achieve the best accuracy." A synopsis of the planned sensitivity analysis was provided in Appendix 1, Page 52, of the PDM Plan.

On January 23, 2017, we received a draft of the sensitivity analysis report from Dr. Joseph Clark. That report underwent independent peer review[1] and the final document was submitted to our office on March 13, 2017. The PDM group (U.S. Fish and Wildlife Service – Louisiana Field Office, LDWF, and USGS [Southern Appalachian Research Branch] – University of Tennessee) concurred that the results of that sensitivity analysis reflect the best available science and have, in fact, better informed the decision threshold for post-delisting monitoring. In accordance with the existing PDM Plan, we have agreed to implement alternative study designs and data collection options for the purpose of improving and refining post-delisting monitoring protocols. These PDM methodology improvements are not only consistent with the original

[1] Peer reviewers included Mark Haroldson (USGS Supervisory Wildlife Biologist for the Interagency Grizzly Bear Study Team – Northern Rocky Mountain Science Center in Bozeman, MT. Over 30 years of professional experience in bear management and research.) and Dr. Frank van Manen (Former President of the International Association for Bear Research and Management, current Team Leader of the Interagency Grizzly Bear Study Team, and current Associate Editor for the journal *Ursus*. Over 25 years of professional experience in bear management and research.)

intent and language of the PDM Plan, but are necessary to comply with the guidance provided in the original PDM Plan which states that we should make necessary improvements to continue to monitor effectively based on the results of the sensitivity analysis (i.e., that we should utilize the best available science). The final sensitivity analysis report is included in Appendix III of this document. The following are our PDM methodology improvements, based primarily on the results of that analysis.

Methodology Improvements

Response Trigger #1 (PDM Plan, Section VII, Part A, Item 1, Page 33)

ORIGINAL LANGUAGE: "***Average annual female survival (S)***, based on an average of the previous three years, and per-capita recruitment (f), observed from radio-collar data, annual den checks, and ***mark-recapture efforts, remains within the 95% confidence interval of values observed for this species during 2006 – 2012***"

REVISION (addressing bold/italic print shown above): In accordance with guidance provided in the original PDM Plan, we instituted a study to identify thresholds in demographic rates governing population dynamics that could be used to better understand demographic requirements of long-term persistence of Louisiana black bear subpopulations (i.e., the UARB and TRB). Our intent was to identify reliable indicators of long-term population persistence that could be measured over relatively short monitoring durations (e.g., 5 years). The initial phase of the study involved a sensitivity analysis that was conducted using stochastic population simulations combined with machine learning techniques to identify demographic rates most important to extinction risk for bears of the TRB and UARB subpopulations and to identify demographic thresholds that can be used to develop population monitoring plans. The second phase incorporated spatially-referenced capture-mark-recapture (CMR; hair-snare) data and a spatially-explicit open-population CMR model to estimate abundance and parameters governing the spatial detection process that could be used to simulate new data based on prospective study designs. The final phase involved a power analysis to test alternative study designs that would reduce labor and financial requirements yet produce reliable demographic rate estimates for long-term monitoring. The study team generated 2,000 random combinations of projection model parameters for the TRB and 2,000 for the UARB and used each of those combinations to simulate 500 population trajectories for 100 years resulting in 1,000,000 trajectories for each subpopulation. The goal of this analysis was to generate simulated data that would be used to identify individual population parameters most associated with extinction risk and to identify demographic thresholds indicative of long-term persistence. Of the short-term rates evaluated for the TRB and

UARB, average apparent female survival was most important for predicting extinction for both monitoring durations (5-year and 10-year) and both subpopulations. An average apparent female survival value of 0.91 or greater resulted in high probabilities of persistence (≥95%). Accordingly, rather than direct temporal comparisons of various life-history data (as initially presented in the PDM Plan), our monitoring goal is to determine whether the average apparent female survival threshold of 0.91 or greater (and, likewise, the long-term probability of persistence of the respective Louisiana black bear subpopulations) has been met. A detailed explanation of the analysis associated with this study is provided in Appendix III.

Response Trigger #1 (PDM Plan, Section VII, Part A, Item 1, Page 33)

ORIGINAL LANGUAGE: "Average annual female survival (S), ***based on an average of the previous three years***, and per-capita recruitment (f), observed from radio-collar data, annual den checks, and mark-recapture efforts, remains within the 95% confidence interval of values observed for this species during 2006 – 2012"

REVISION (addressing bold/italic print shown above): According to guidance provided from the USGS (Southern Appalachian Research Branch) – University of Tennessee, it would be preferable to use 5-year averages of apparent adult female survival to determine whether a trigger threshold has been reached because it increases the accuracy of detection over 3-year averages. In fact, the demographic modeling study and sensitivity analysis described above incorporated monitoring durations equal to, or exceeding, 5 years which is known (from that study) to provide a reliable short-term monitoring duration for estimation of long-term population persistence. Accordingly, a 5-year monitoring duration will be used in determining average apparent female survival.

Response Trigger #1 (PDM Plan, Section VII, Part A, Item 1, Page 33)

ORIGINAL LANGUAGE: "Average annual female survival (S), based on an average of the previous three years, and ***per-capita recruitment (f), observed from radio-collar data, annual den checks***, and mark-recapture efforts, remains within the 95% confidence interval of values observed for this species during 2006 – 2012"

REVISION (addressing bold/italic print shown above): According to guidance provided from the USGS (Southern Appalachian Research Branch) – University of Tennessee, the sample sizes for our telemetry data are insufficient to yield results with a level of accuracy that would be necessary to conclusively determine whether a trigger category has been reached. Accordingly, it was recommended that telemetry data not be used for that purpose. Instead, telemetry data will be used (along with other pertinent data) in determining whether there are any new or increasing threats to the continued existence of the Louisiana black bear within the foreseeable future (as described in bullet point "3" within each of the trigger categories). Telemetry data analysis will not be associated with any specific response trigger thresholds.

Annual Telemetry Monitoring Period (PDM Plan, Page 35)

ORIGINAL LANGUAGE: "Annual reports . . . will include all data collected since October 1 of the prior year (one fiscal year)."

REVISION: In order to base our monitoring periods on science, the annual monitoring period will be revised from fiscal years (October 1 – September 30) to "bear years" based on the life history of the Louisiana black bear (denning season to denning season; i.e., April 1 – March 31). The PDM group (described above) unanimously concurred with this revision.

Results/Conclusions

LDWF Bear Sighting Data

LDWF personnel recorded 140 sightings and 182 bear-related complaints during the current reporting period (April 1, 2015 – March 31, 2016). Additional information regarding LDWF's bear incident reporting data can be found in Appendix I.

Radio Telemetry

Radio telemetry analysis includes known-fate survival data and cub/yearling recruitment data gathered in the post-delisting monitoring period (2013-2016*). The annual female survival rate average ranged from 0.924 (when lost signals were assumed to be live bears) to 0.908 (when lost signals were assumed to be dead bears) for the UARB subpopulation. The annual female survival rate averaged 0.937 (regardless whether lost signals were assumed to be dead or live bears) for the TRB subpopulation. A more detailed description of the analysis and results is provided in Appendix I.

Capture-Mark-Recapture (CMR; Hair-Snare)

Capture-mark-recapture (CMR; hair-snare) data was gathered during the summers (typically during the month of June) of 2013, 2014, and 2015[2]. The apparent female survival rate was 0.936 for the TRB subpopulation and 0.969 for the UARB subpopulation, during this monitoring period. A more detailed description of the analysis and results is provided in Appendix I.

[2] Initiation of these monitoring activities immediately followed the analysis period for which data demonstrated that the Louisiana black bear population had long-term stability (2012). The first post-recovery year (or, first year following *known* long-term population persistence) is 2013, and begins our post-delisting analysis period.

Habitat Analysis

Permanently Protected Lands

From 2014 to the end of 2016, there has been an addition of over 7,800 acres of permanently protected lands (National Wildlife Refuges/Wildlife Management Areas/Wetland Reserve Program Perpetual Easements/Compensatory Wetland Mitigation Banks) within the Louisiana black bear habitat restoration planning area (HRPA). Since the Louisiana black bear five-year review was completed in 2011, over 33,000 acres of land have been permanently protected within the HRPA.

USDA National Aerial Imagery Program (NAIP)

We evaluated changes to forested habitat in three large areas that occur between the TRB and UARB subpopulations. Those areas total almost 5,000 acres and are not permanently protected. Comparing 2013 to 2015 imagery, there were virtually no detectable habitat changes noted on any of those sites.

A more detailed description of all habitat analyses is provided in Appendix II.

OVERALL CONCLUSION

Bear sighting and radio telemetry data for our analysis period appear typical and suggest that no new or increasing threats are impacting the subpopulations. CMR data indicate that there is a high probability of long-term persistence (≥95%) for the TRB and UARB subpopulations, based on apparent female survival rates that exceed 0.91 for both subpopulations. Our analysis of permanently protected lands and forested habitat in the vicinity of breeding subpopulations indicate that bear habitat is stable to increasing. Based on the analyses described above, we conclude that all Category I standards have been achieved as described in Section IV of the PDM Plan indicating that the "Louisiana black bear metapopulation remains secure without ESA protections."

Appendix I. Field Data Analysis and Results

Prepared By:

Louisiana Department of Wildlife and Fisheries

U.S. Geological Survey - Southern Appalachian Research Branch
University of Tennessee

POPULATION MONITORING FIELD ACTIVITIES

In order to collect information needed as per the Louisiana black bear Post Delisting Monitoring Plan, we collected data in accordance with section VI.C of the PDM. This report covers the first year of annual data collection and analysis activities which covers April 1, 2015 through March 31, 2016. As stated in the PDM, trends in population demographics will be based on an average of annual estimates and compared to baseline data. It has been agreed upon that we will use 5 year averages.

We live-captured bears and outfitted these individuals with VHF or VHF-GPS radio-collars, or marked bears based on sex and age class. Using monthly aerial telemetry, we monitored 58 radio-collared bears (10M; 48F) from all four subpopulations. We conducted our ninth consecutive year of non-invasive hair trapping in the Tensas River and Upper Atchafalaya River basin subpopulations during May-July 2015. Samples were collected from 209 and 116 sites in both subpopulations, respectively, resulting in 3,264 hair samples. Lab results were analyzed by USGS and that report is attached. To collect information on reproductive vital rates, we conducted 22 adult female den visits across all four subpopulations during February-March, 2016 to count and mark cubs-of-the-year, and to count yearlings. Adult female collars were changed as necessary. We continued carcass recovery and documented 48 mortalities from all causes during the reporting period. The Beartrak database was routinely updated and we logged 140 sightings and 182 complaints during this reporting period. All complaints received a response as detailed in the LDWF Louisiana black bear Management Plan.

RADIO-TELEMETRY DATA

Survival.—The radio telemetry data to be analyzed consisted of known-fate survival data from 2002 to 2016 and cub and yearling recruitment data from the same time period. Data from 2002-12 were from Laufenberg et al. (2016) and the more recent data came from the Louisiana Department of Wildlife and Fisheries (LDWF). Data from 2002–12 will be referred to as the pre-delisting monitoring period (pre-DMP) and 2013–2016 will be the post-DMP.
The objective of the survival analysis was to use known-fate analysis in Program MARK to estimate annual survival rates (White and Burnham 1999). The known-fate analysis in MARK is based on a Kaplan-Meyer staggered entry procedure that is simple and works well for radio-telemetry analyses (Pollock et al. 1989). The format that Laufenberg et al. (2016) used for estimating survival from the 2002–2012 data was based on a hazard rate survival function in a Bayesian analysis which had to be converted to a capture history format for MARK. Once reformatted, the 2002–12 data were appended with the LDWF data from 2013 to 2016. Survival rates (S) were annual rates beginning on 1 April (approximate date of den exit) to 31 March. The models were based on the assumption that every bear was radio located monthly. Entries were censored only if the bear was not detected for >4 months. Annual survival rates were estimated by censoring animals whose collars unexpectedly ceased to function (S_{AA} or assumed alive) and also estimated survival parameters assuming those animals died at the time of signal loss (S_{AD} or assumed dead). I estimated annual survival rates for the post-DMP by sex

and by study area. The study areas consisted of the Tensas River Basin (TRB), Upper Atchafalaya River Basin (UARB), and Three Rivers Complex (TRC).

Annual survival rates for 110 females at TRB (S_{AA}) averaged 0.937 (95% CI = 0.817–0.979) during the post-DMP period, and were essentially the same assuming lost signals were from dead animals (S_{AD} = 0.937, 95% CI = 0.819–0.979). Fourteen females were monitored at UARB with S_{AA} and S_{AD} averaging 0.924 (95% CI = 0.731–0.981) and 0.908 (95% CI = 0.682–0.976), respectively, during the post-DMP period. At TRC, 57 females were monitored and S_{AA} and S_{AD} were 0.846 (95% CI = 0.643–0.940) and 0.839 (95% CI = 0.627–0.936), respectively, during the post-DMP period.

Annual survival rates for 15 males at TRC during the post-DMP averaged 0.931 (95% CI = 0.607–0.990, S_{AA}) and 0.927 (95% CI = 0.588–0.989, S_{AD}). Likewise, male survival at UARB (n = 3) was 0.636 (95% CI = 0.172–0.894, S_{AA}) and 0.504 (95% CI = 0.012–0.911, S_{AD}). Only 1 male was monitored at TRB.

Fecundity.—Data compiled by Laufenberg et al. (2016) from 2002–12 and LDWF from 2013–16 were used to estimate per capita recruitment or fecundity (f_{telem}). Transition data from 2015 to 2016 are needed to estimate some 2015 parameters, so 2017 data will be needed before 2016 reproductive parameters can be estimated. Therefore fecundity rates are reported for 2013–2015. The first step was to estimate the proportion of the radiocollared females that were in 1 of 3 reproductive states: no cubs ($P_{no\ cubs}$), with cubs (P_{cubs}), and with yearlings ($P_{yearlings}$). That distribution is assuming that the collared females are representative of adult females in the population. Subadult females are not routinely collared so the per-capita recruitment based solely on adult females is likely biased high. These reproductive state proportions we based on a Bayesian formulation developed by Laufenberg et al. (2016). Cub and yearling litter sizes and cub and yearling fecundity rates were similarly estimated. I reported the modes of posterior distributions and used 2.5 and 97.5% credible intervals. Because modes are reported, the reproductive stable state proportions will not necessarily sum to 1.

On TRB, 10 female bears were monitored during the post–DMP with 14.8 (95% CI = 3.4–55.2), 47.8 (95% CI = 25.1–55.2), and 37.9% (95% CI = 18.3–46.1) without cubs, with cubs, and with yearlings, respectively. The mean number of cubs and yearlings during this time period was 2.30 (95% CI = 1.88–2.74) and 1.91 (95% CI = 1.52–2.42, respectively. Cub fecundity (f_{cub}) averaged 0.52 (95% CI = 0.29–0.68) during the post-DMP. Yearling fecundity ($f_{yearling}$) averaged 0.34 (95% CI = 0.17–0.49) female yearlings annually produced per breeding age female during the post-DMP.

On UARB, 10 female bears were monitored during the post–DMP with 21.2 (95% CI = 6.8–62.6), 48.3 (95% CI = 24.4–57.8), and 31.0% (95% CI = 10.7–42.6) without cubs, with cubs, and with yearlings, respectively. The mean number of cubs and yearlings during this time period was 2.22 (95% CI = 1.76–2.76) and 1.90 (95% CI = 1.35–2.81), respectively. Cub fecundity (f_{cub}) averaged 0.52 (95% CI = 0.27–0.70) during the post-DMP. Yearling fecundity ($f_{yearling}$) averaged

0.26 (95% CI = 0.10–0.49) female yearlings annually produced per breeding age female during the post-DMP period.

On TRC, 5 female bears were monitored during the post–DMP with 20.2 (95% CI = 4.9–88.9), 50.5 (95% CI = 7.4–70.8), and 21.7% (95% CI = 2.8–39.8) without cubs, with cubs, and with yearlings, respectively). The mean number of cubs and yearlings during this time period was 2.22 (95% CI = 1.82–2.73) and 2.28 (95% CI = 1.62–3.25), respectively. Cub fecundity (f_{cub}) averaged 0.55 (95% CI = 0.08–0.83) during the post-DMP. Yearling fecundity ($f_{yearling}$) averaged 0.27 (95% CI = 0.03–0.52) female yearlings annually produced per breeding age female during the post-DMP period.

CAPTURE-MARK-RECAPTURE DATA

The capture-mark-recapture data (CMR) to be analyzed consisted of bear captures as a result of DNA extracted from hair collected at barbed-wire sampling sites at TRB from 2006 to 2015 and at UARB from 2007 to 2015. The data were reformatted and analyzed as a Pradel robust design framework in Program Mark (White and Burnham 1999). The data were analyzed based on apparent survival (φ) and the finite rate of population increase (λ) differing by sex but constant from 2012-13 to 2014-15 (post-DMP). Models whereby capture probabilities (p) were estimated as time independent, by sex, with an additive behavioral effect, and as 2 heterogeneous mixtures (Pledger 2000) were most supported.

At TRB, φ for females post-DMP was 0.936 (95% CI = 0.868–0.970) and λ for females was 1.023 (95% CI = 0.967–1.079). At UARB, φ for females post-DMP was 0.969 (95% CI = 0.754–0.997) and λ for females was 1.054 (95% CI = 0.975–1.134).

LITERATURE CITED

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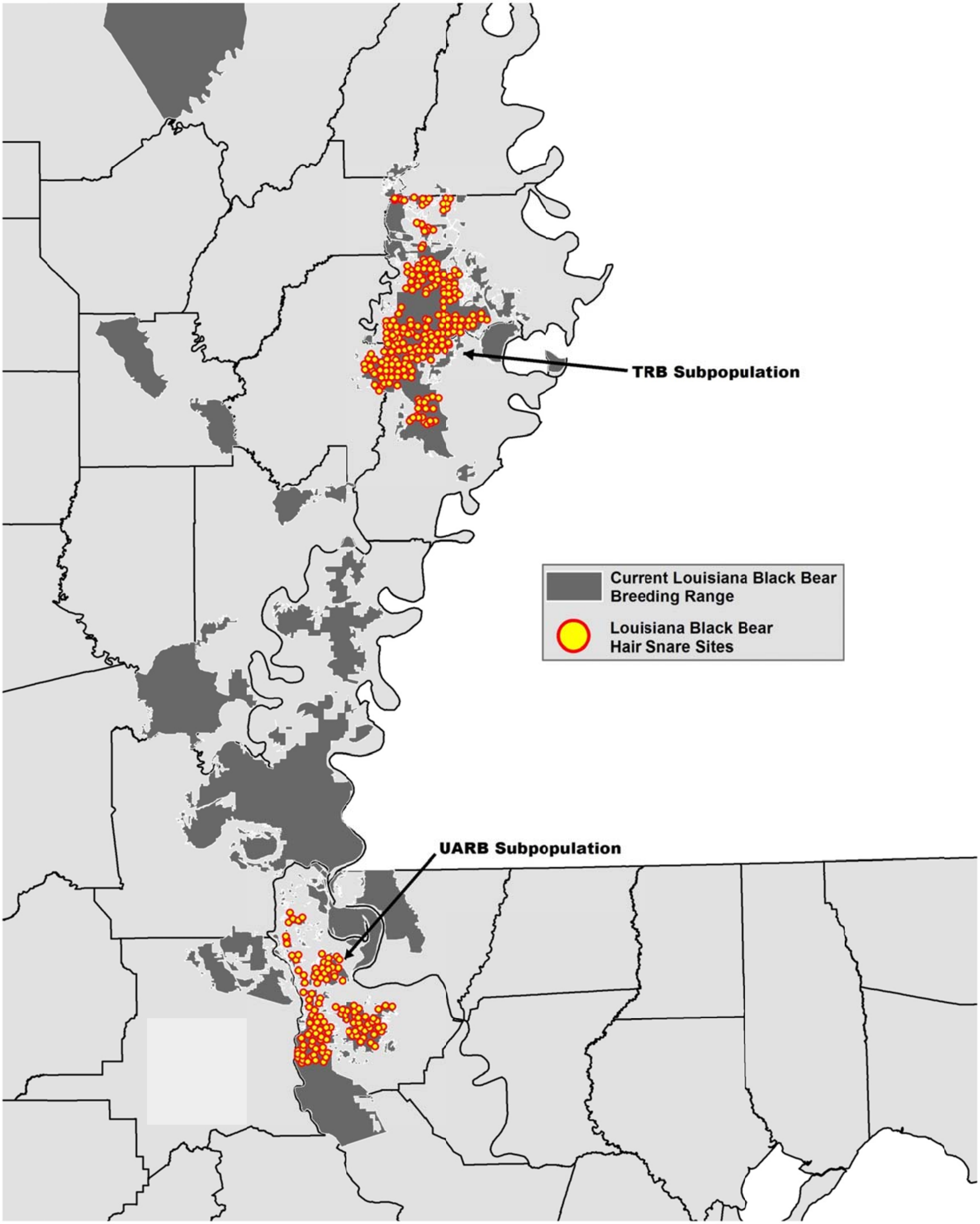
Pledger, S. 2000. Unified maximum likelihood estimates for closed capture–recapture models using mixtures. Biometrics 56:434–442.

White, G. C., and K. P. Burnham. 1999. Program MARK: survival estimation from populations of marked animals. Bird study 46:S120–S139.

Map of Louisiana black bear hair snare locations.



Appendix II. Habitat Analysis and Results

Prepared By:

U.S. Fish and Wildlife Service – Louisiana Field Office

Habitat Monitoring

Monitoring Changes in Permanently Protected Lands

Annual updates were obtained for state and federally owned wildlife managed lands, privately owned mitigation banks and USDA-NRCS Wetland Reserve Program permanent easement enrollments within the Louisiana black bear habitat restoration planning area (HRPA). These datasets were verified for accuracy, summarized acreages and depicted their spatial locations using geographic information systems (GIS) ArcGIS 10.4.1 (ESRI, Redlands, California, USA).

From 2014 to the end of 2016, there has been an addition of over 7,800 acres of permanently protected lands (NWR/WMA/WRP/MB) within the HRPA. This is a continuation of a positive trend of lands being placed in permanent conservation from when the Louisiana black bear five-year review was completed in 2011. Since 2011, there have been over 33,000 acres of land permanently protected within the HRPA.

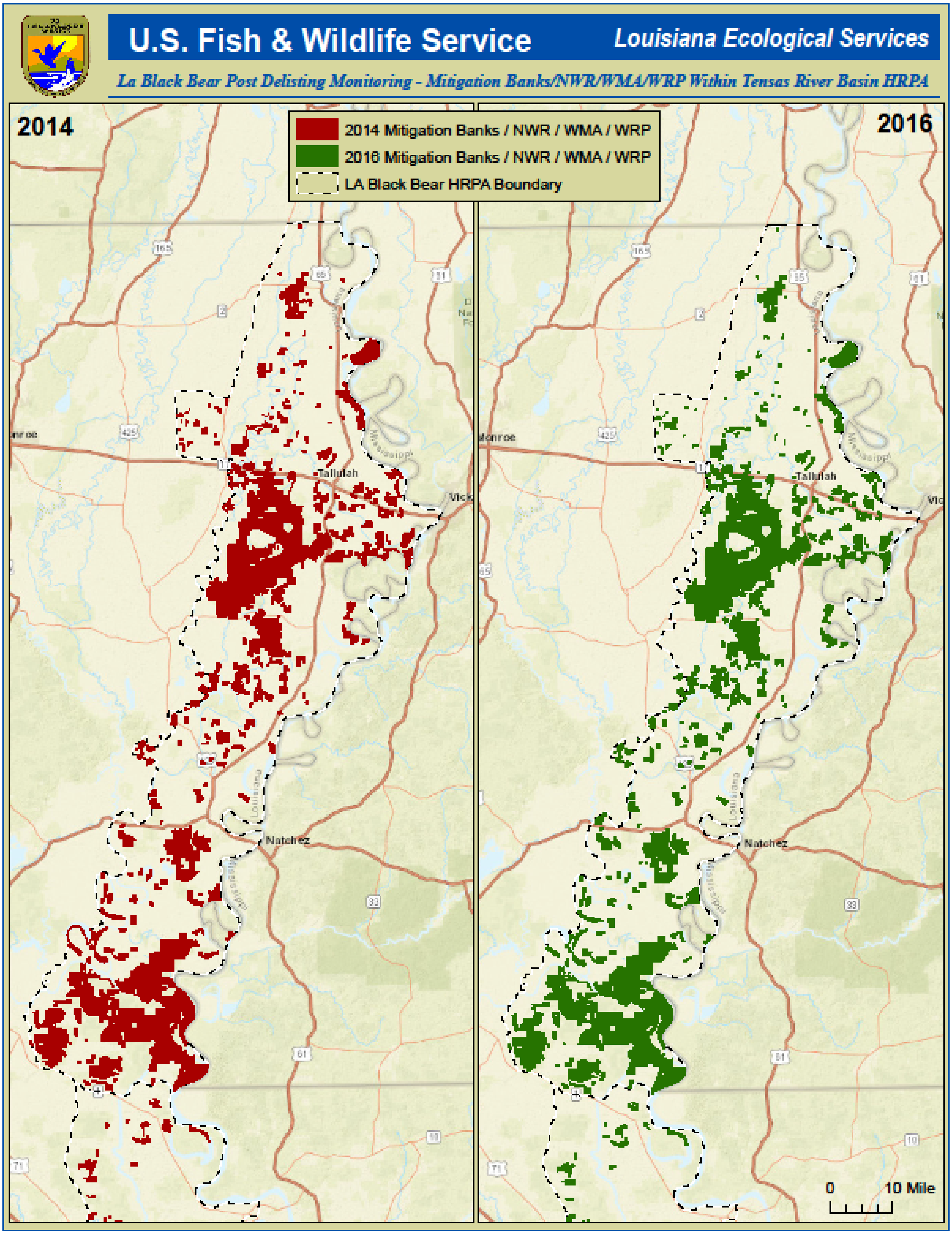
Conservation Lands Within HRPA	**HRPA Acres Change (2011 to 2014)**	**HRPA Acres Change (2014 to 2016)**	**HRPA Acres Change (2011 to 2016)**
NWR/WMA/WRP/MB	25,372.26	7,869.73	33,241.99

Tensas River Basin (TRB) of HRPA

Conservation Lands Within HRPA	**TRB Acres (2011)**	**TRB Acres (2014)**	**TRB Acres (2016)**
National Wildlife Refuge (NWR)	109,334.11	111,965.56	112,224.64
Wildlife Management Area (WMA)	143,248.78	143,933.45	143,584.53
Wetland Reserve Program (WRP)	120,668.96	136,869.81	142,188.63
Mitigation Banks (MB)	5,216.94	5,929.94	6,233.07
Totals:	**378,468.79**	**398,698.75**	**404,230.87**

Changes within Tensas River Basin (TRB) of HRPA

Conservation Lands Within HRPA	**TRB Acres Change (2011 to 2014)**	**TRB Acres Change (2014 to 2016)**	**TRB Acres Change (2011 to 2016)**
National Wildlife Refuge (NWR)	2,631.46	259.08	2,890.53
Wildlife Management Area (WMA)	684.66	-348.92	335.74
Wetland Reserve Program (WRP)	16,200.85	5,318.82	21,519.67
Mitigation Banks (MB)	712.99	303.13	1,016.13
Totals:	20,229.96	5,532.11	25,762.07


U.S. Fish & Wildlife Service
Louisiana Ecological Services
La Black Bear Post Delisting Monitoring - Mitigation Banks/NWR/WMA/WRP Within Tensas River Basin HRPA
2014
2016
2014 Mitigation Banks / NWR / WMA / WRP
2016 Mitigation Banks / NWR / WMA / WRP
LA Black Bear HRPA Boundary
Tallulah
Natchez
0
10 Mile

Upper Atchafalaya River Basin (UARB) of HRPA

Conservation Lands Within HRPA	UARB Acres (2011)	UARB Acres (2014)	UARB Acres (2016)
National Wildlife Refuge (NWR)	17,340.52	17,614.20	17,611.82
Wildlife Management Area (WMA)	58,718.25	59,422.91	61,430.82
Wetland Reserve Program (WRP)	9,722.97	11,530.24	11,064.04
Mitigation Banks (MB)	2,020.97	2,726.21	3,571.00
Totals:	**87,802.72**	**91,293.56**	**93,677.68**

Changes within Upper Atchafalaya River Basin (UARB) of HRPA

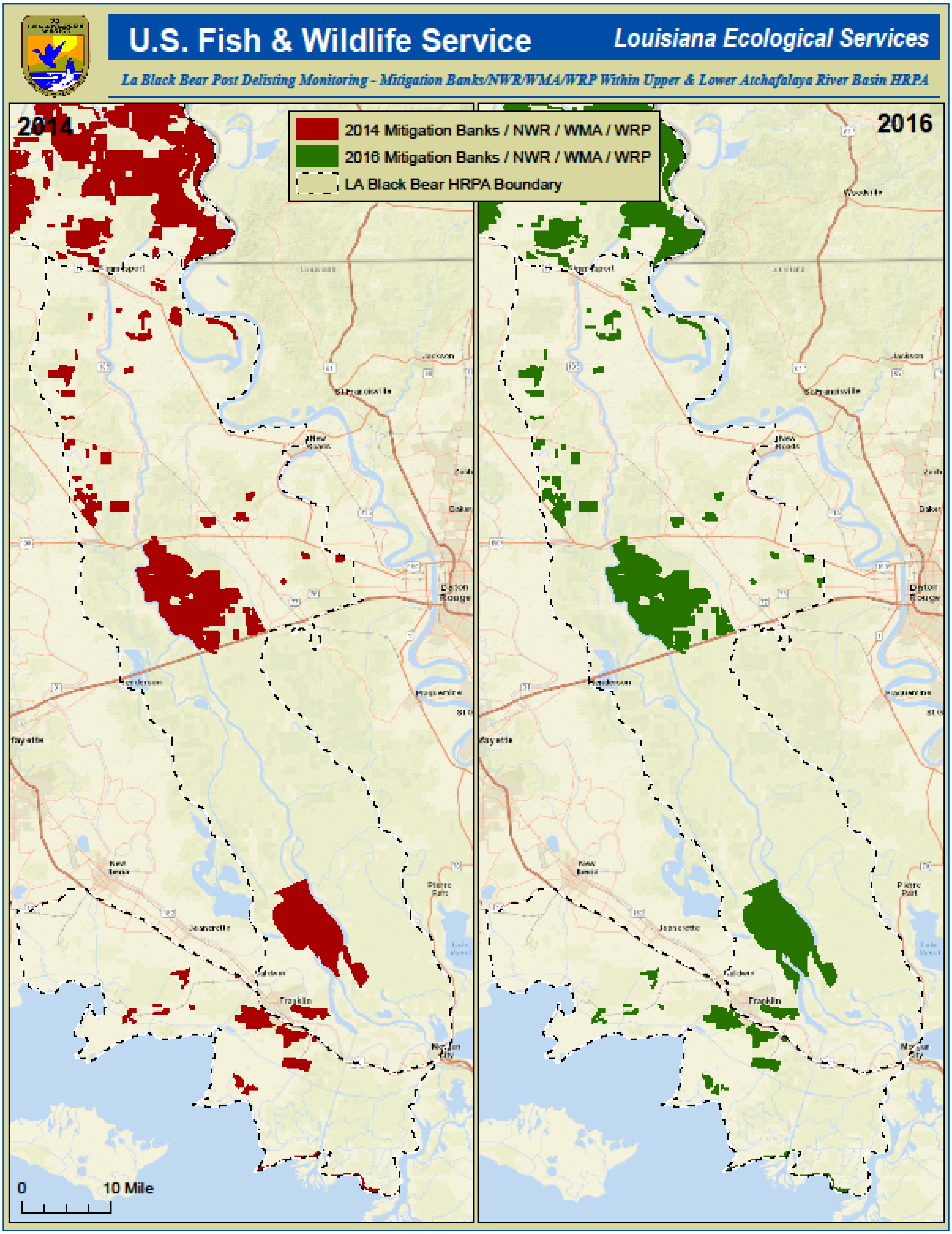
Conservation Lands Within HRPA	UARB Acres Change (2011 to 2014)	UARB Acres Change (2014 to 2016)	UARB Acres Change (2011 to 2016)
National Wildlife Refuge (NWR)	273.67	-2.38	271.30
Wildlife Management Area (WMA)	704.66	2,007.91	2,712.57
Wetland Reserve Program (WRP)	1,807.27	-466.20	1,341.07
Mitigation Banks (MB)	705.24	844.79	1,550.03
Totals:	3,490.84	2,384.12	5,874.97

Lower Atchafalaya River Basin (LARB) of HRPA

Conservation Lands Within HRPA	LARB Acres (2011)	LARB Acres (2014)	LARB Acres (2016)
National Wildlife Refuge (NWR)	7,505.31	7,426.19	7,379.68
Wildlife Management Area (WMA)	1,474.09	1,474.09	1,474.09
Wetland Reserve Program (WRP)	0.00	0.00	0.00
Mitigation Banks (MB)	941.82	2,672.41	2,672.41
Totals:	**9,921.22**	**11,572.68**	**11,526.18**

Changes within Lower Atchafalaya River Basin (LARB) of HRPA

Conservation Lands Within HRPA	LARB Acres Change (2011 to 2014)	LARB Acres Change (2014 to 2016)	LARB Acres Change (2011 to 2016)
National Wildlife Refuge (NWR)	-79.12	-46.51	-125.63
Wildlife Management Area (WMA)	0.00	0.00	0.00
Wetland Reserve Program (WRP)	0.00	0.00	0.00
Mitigation Banks (MB)	1,730.58	0.00	1,730.58
Totals:	1,651.46	-46.51	1,604.95


U.S. Fish & Wildlife Service
Louisiana Ecological Services
La Black Bear Post Delisting Monitoring - Mitigation Banks/NWR/WMA/WRP Within Upper & Lower Atchafalaya River Basin HRPA
2014
2016
2014 Mitigation Banks / NWR / WMA / WRP
2016 Mitigation Banks / NWR / WMA / WRP
LA Black Bear HRPA Boundary
St Francisville
New Roads
Baton Rouge
Henderson
Plaquemine
Jeanerette
Franklin
Baldwin
Morgan City
Pierre Part
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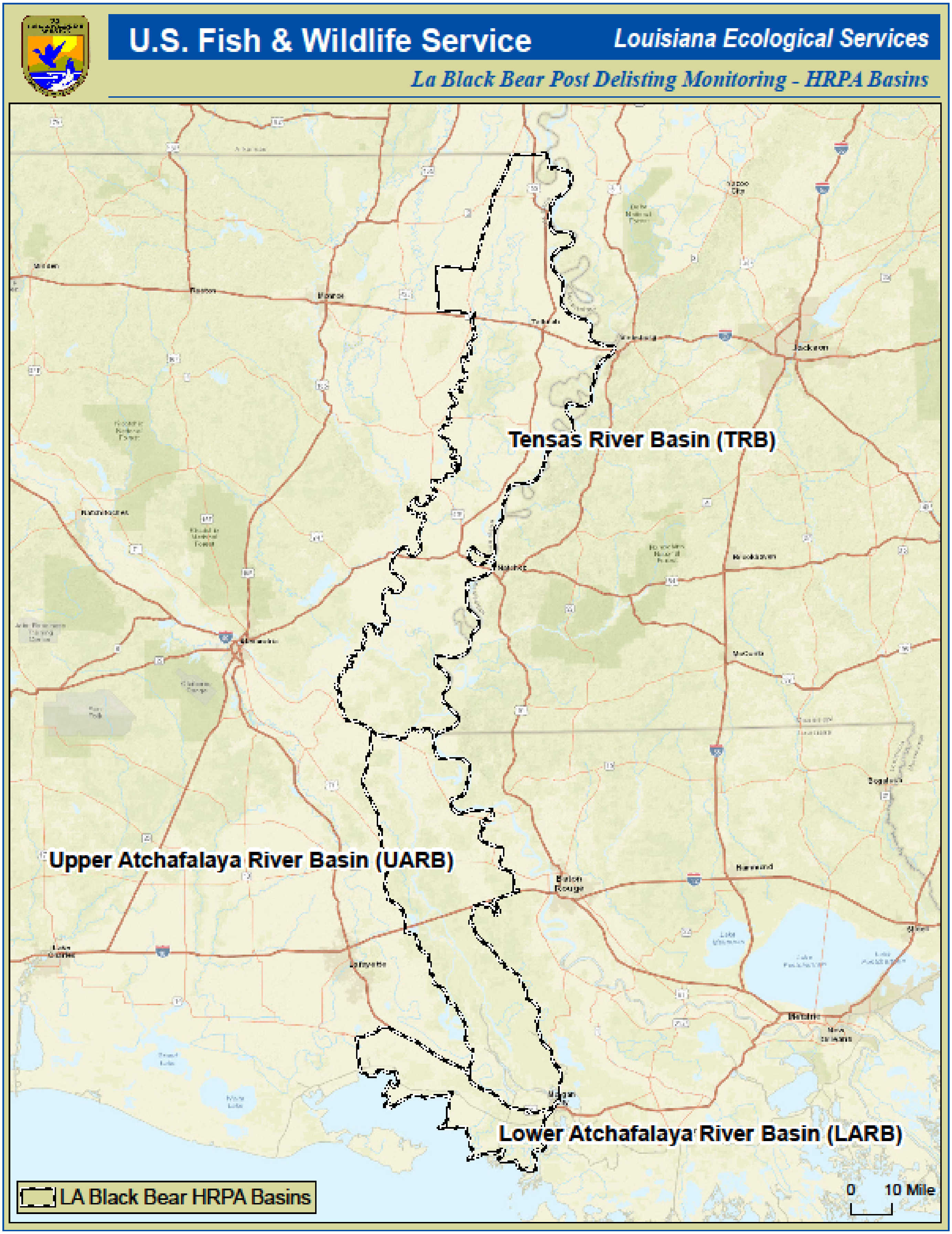
U.S. Fish & Wildlife Service
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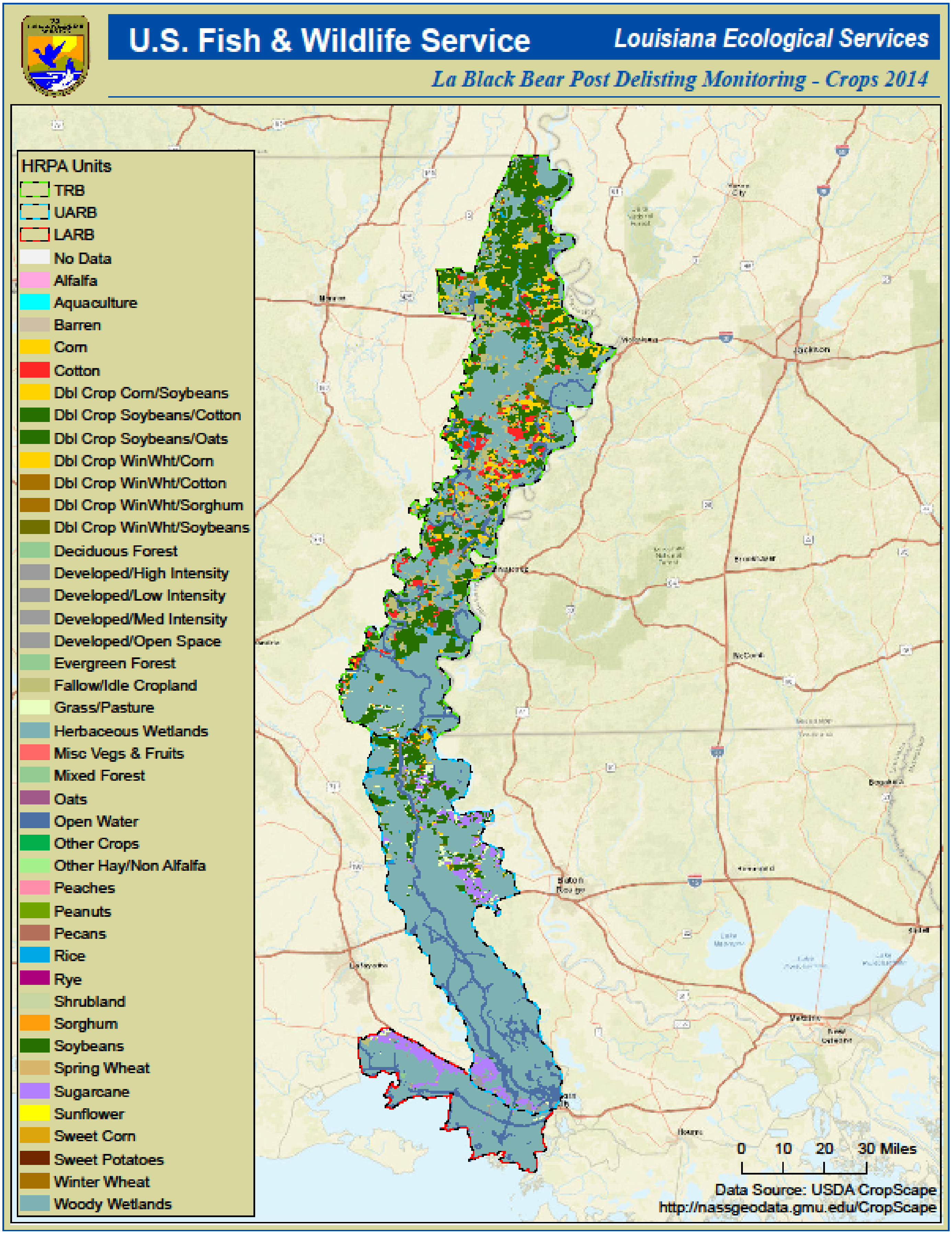
La Black Bear Post Delisting Monitoring - HRPA Basins
Tensas River Basin (TRB)
Upper Atchafalaya River Basin (UARB)
Lower Atchafalaya River Basin (LARB)
LA Black Bear HRPA Basins
0 10 Mile

Monitoring Change in Agricultural Land Uses using CropScape

2014 CropScape data for HRPA Basins

Crop	TRB 2014	UARB 2014	LARB 2014	Total Acres	Percent
Alfalfa	284.24	0.22	0.22	284.69	0.01%
Aquaculture	424.75	2,687.73	895.38	4,007.87	0.11%
No Data	0.00	0.00	2,692.46	2,692.46	0.07%
Barren	1,505.80	317.59	294.67	2,118.07	0.06%
Corn	153,114.93	14,295.35	16.23	167,426.52	4.62%
Cotton	101,275.45	2,168.62	0.67	103,444.74	2.86%
Dbl Crop Corn/Soybeans	583.05	0.00	0.00	583.05	0.02%
Dbl Crop Soybeans/Cotton	175.17	0.00	0.00	175.17	0.00%
Dbl Crop Soybeans/Oats	172.73	101.16	0.67	274.56	0.01%
Dbl Crop WinWht/Corn	0.44	9.78	0.00	10.23	0.00%
Dbl Crop WinWht/Cotton	0.00	0.00	0.00	0.00	0.00%
Dbl Crop WinWht/Sorghum	6.45	0.00	0.00	6.45	0.00%
Dbl Crop WinWht/Soybeans	25,129.37	18,225.95	81.36	43,436.68	1.20%
Deciduous Forest	2,174.69	1,019.99	1,459.13	4,653.82	0.13%
Developed/High Intensity	556.98	612.57	790.93	1,960.48	0.05%
Developed/Low Intensity	10,552.69	19,409.12	6,921.28	36,883.08	1.02%
Developed/Med Intensity	3,455.94	1,400.54	1,019.91	5,876.39	0.16%
Developed/Open Space	54,306.49	19,382.13	3,528.80	77,217.42	2.13%
Evergreen Forest	1,123.44	70.91	13.34	1,207.70	0.03%
Fallow/Idle Cropland	229,174.38	10,331.64	10,858.17	250,364.19	6.91%
Grass/Pasture	25,134.52	50,314.59	7,149.65	82,598.76	2.28%
Herbaceous Wetlands	9,589.99	18,595.86	147,506.85	175,692.70	4.85%
Herbs	141.18	0.00	0.00	141.18	0.00%
Misc Vegs & Fruits	0.44	0.00	0.00	0.44	0.00%
Mixed Forest	6,951.95	261.31	45.57	7,258.83	0.20%
Oats	1,954.18	0.89	0.00	1,955.07	0.05%
Open Water	81,609.02	80,216.93	23,183.43	185,009.38	5.11%
Other Crops	27.34	13.12	0.44	40.90	0.00%
Other Hay/Non Alfalfa	8,416.53	1,473.68	84.42	9,974.63	0.28%
Peaches	0.67	0.00	0.00	0.67	0.00%
Peanuts	1.78	0.00	0.00	1.78	0.00%
Peas	0.00	0.00	0.00	0.00	0.00%
Pecans	672.81	2.00	0.00	674.81	0.02%
Pop or Orn Corn	369.68	0.00	0.00	369.68	0.01%
Rice	30,470.31	10,556.33	240.17	41,266.81	1.14%
Rye	7.56	0.00	0.00	7.56	0.00%
Shrubland	7,987.06	4,276.82	193.62	12,457.50	0.34%
Sod/Grass Seed	32.02	13.12	2.45	47.59	0.00%
Sorghum	32,722.30	4,685.60	8.45	37,416.35	1.03%
Soybeans	522,686.17	106,326.82	2,679.08	631,692.06	17.44%
Spring Wheat	8.23	0.00	0.00	8.23	0.00%
Sugarcane	512.39	63,446.04	33,832.89	97,791.32	2.70%
Sunflower	78.26	3.78	0.00	82.04	0.00%
Sweet Potatoes	1,102.80	0.00	0.00	1,102.80	0.03%
Winter Wheat	13,569.47	955.52	58.46	14,583.46	0.40%
Woody Wetlands	726,747.27	769,668.05	122,442.69	1,618,858.02	44.70%
Total	**2,054,810.95**	**1,200,843.78**	**366,001.38**	**3,621,656.11**	**100.00%**


U.S. Fish & Wildlife Service
Louisiana Ecological Services
La Black Bear Post Delisting Monitoring - Crops 2014
HRPA Units
TRB
UARB
LARB
No Data
Alfalfa
Aquaculture
Barren
Corn
Cotton
Dbl Crop Corn/Soybeans
Dbl Crop Soybeans/Cotton
Dbl Crop Soybeans/Oats
Dbl Crop WinWht/Corn
Dbl Crop WinWht/Cotton
Dbl Crop WinWht/Sorghum
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Deciduous Forest
Developed/High Intensity
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Developed/Med Intensity
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Herbaceous Wetlands
Misc Vegs & Fruits
Mixed Forest
Oats
Open Water
Other Crops
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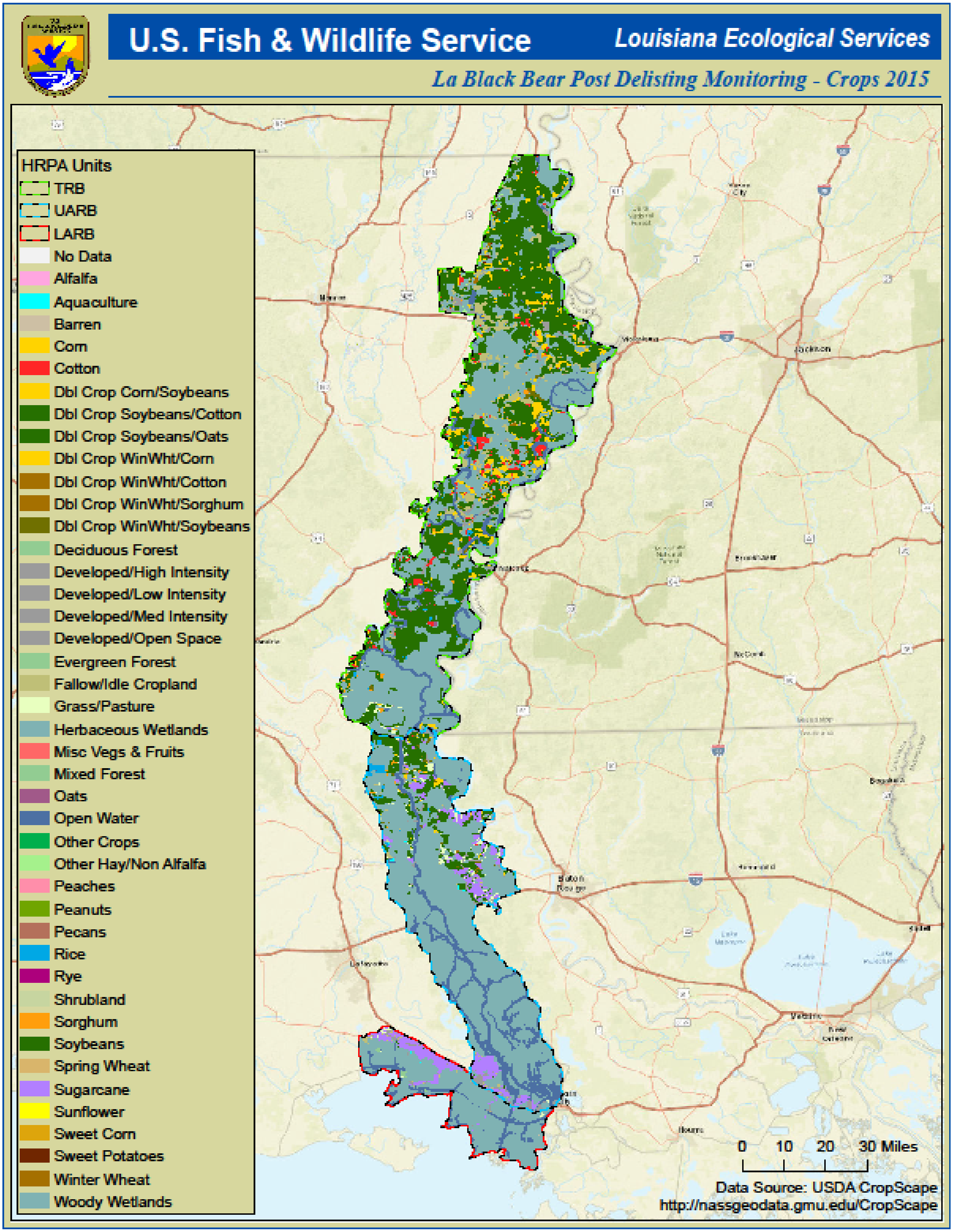
Peaches
Peanuts
Pecans
Rice
Rye
Shrubland
Sorghum
Soybeans
Spring Wheat
Sugarcane
Sunflower
Sweet Corn
Sweet Potatoes
Winter Wheat
Woody Wetlands
0 10 20 30 Miles
Data Source: USDA CropScape
http://nassgeodata.gmu.edu/CropScape

2015 CropScape data for HRPA Basins

Crop	TRB 2015	UARB 2015	LARB 2015	Total Acres	Percent
Alfalfa	102.43	0.00	0.00	102.43	0.00%
Aquaculture	855.36	3,100.82	955.65	4,911.83	0.14%
No Data	0.00	0.00	2,692.46	2,692.46	0.07%
Barren	1,281.77	374.31	839.54	2,495.63	0.07%
Corn	145,666.71	12,478.51	14.67	158,159.90	4.37%
Cotton	56,018.45	1,262.67	0.00	57,281.13	1.58%
Dbl Crop Corn/Soybeans	0.00	0.00	0.00	0.00	0.00%
Dbl Crop Soybeans/Cotton	0.00	0.00	0.00	0.00	0.00%
Dbl Crop Soybeans/Oats	12.45	23.34	0.44	36.24	0.00%
Dbl Crop WinWht/Corn	0.00	0.00	0.00	0.00	0.00%
Dbl Crop WinWht/Cotton	0.67	0.00	0.00	0.67	0.00%
Dbl Crop WinWht/Sorghum	6.23	0.00	0.00	6.23	0.00%
Dbl Crop WinWht/Soybeans	12,866.29	10,488.69	3.11	23,358.09	0.64%
Deciduous Forest	1,907.38	1,142.46	1,973.91	5,023.75	0.14%
Developed/High Intensity	537.24	577.83	785.24	1,900.31	0.05%
Developed/Low Intensity	9,871.78	19,100.67	6,754.50	35,726.95	0.99%
Developed/Med Intensity	4,113.33	1,365.97	971.18	6,450.48	0.18%
Developed/Open Space	51,831.01	18,401.01	3,337.89	73,569.92	2.03%
Evergreen Forest	1,412.49	38.24	28.23	1,478.96	0.04%
Fallow/Idle Cropland	164,651.10	14,812.71	11,490.39	190,954.19	5.27%
Grass/Pasture	16,972.84	42,320.54	6,092.54	65,385.91	1.81%
Herbaceous Wetlands	8,832.90	16,115.13	148,779.28	173,727.31	4.80%
Herbs	0.22	0.00	0.00	0.22	0.00%
Misc Vegs & Fruits	0.00	0.00	0.00	0.00	0.00%
Mixed Forest	5,559.23	233.89	46.91	5,840.02	0.16%
Oats	1,763.75	0.00	0.00	1,763.75	0.05%
Open Water	79,190.28	81,707.60	22,303.38	183,201.27	5.06%
Other Crops	0.00	0.00	0.00	0.00	0.00%
Other Hay/Non Alfalfa	12,271.23	1,402.07	6.45	13,679.75	0.38%
Peaches	0.44	0.00	0.00	0.44	0.00%
Peanuts	0.00	0.00	0.00	0.00	0.00%
Peas	4.89	0.00	0.00	4.89	0.00%
Pecans	1,597.23	8.23	0.00	1,605.45	0.04%
Pop or Orn Corn	511.07	0.00	0.00	511.07	0.01%
Rice	23,314.16	9,378.62	503.28	33,196.06	0.92%
Rye	37.13	0.00	0.00	37.13	0.00%
Shrubland	4,958.23	6,606.95	426.13	11,991.31	0.33%
Sod/Grass Seed	4.16	36.91	3.34	44.41	0.00%
Sorghum	21,821.71	5,334.74	1.33	27,157.79	0.75%
Soybeans	685,269.07	116,016.95	3,433.21	804,719.22	22.22%
Spring Wheat	0.00	0.00	0.00	0.00	0.00%
Sugarcane	235.49	63,448.67	33,132.20	96,816.36	2.67%
Sunflower	3.78	0.00	0.00	3.78	0.00%
Sweet Potatoes	2,766.91	0.00	0.00	2,766.91	0.08%
Winter Wheat	10,895.24	2,272.55	45.79	13,213.59	0.36%
Woody Wetlands	727,666.26	772,793.71	121,380.34	1,621,840.30	44.78%
Total	**2,054,810.95**	**1,200,843.78**	**366,001.38**	**3,621,656.11**	100.00%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Data Source: USDA CropScape
http://nassgeodata.gmu.edu/CropScape

2014 to 2015 Changes in CropScape data for HRPA Basins

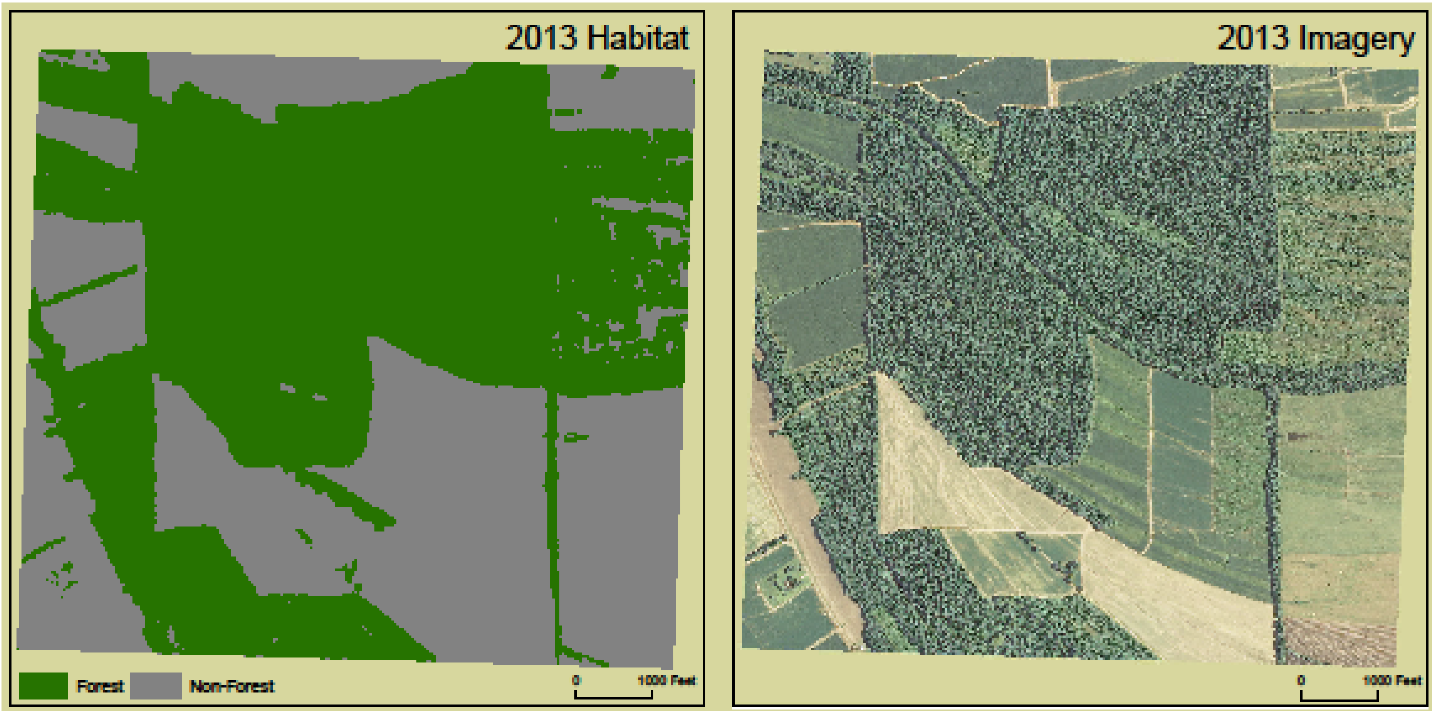
Crop	TRB 2014 to 2015	UARB 2014 to 2015	LARB 2014 to 2015	HRPA 2014 to 2015	HRPA 2014 to 2015
Alfalfa	-181.81	-0.22	-0.22	-182.25	-0.005%
Aquaculture	430.61	413.08	60.27	903.96	0.025%
No Data	0.00	0.00	0.00	0.00	0.000%
Barren	-224.03	56.72	544.87	377.56	0.010%
Corn	-7,448.22	-1,816.84	-1.56	-9,266.61	-0.256%
Cotton	-45,257.00	-905.95	-0.67	-46,163.61	-1.275%
Dbl Crop Corn/Soybns	-583.05	0.00	0.00	-583.05	-0.016%
Dbl Crop Soybns/Cotn	-175.17	0.00	0.00	-175.17	-0.005%
Dbl Crop Soybns/Oats	-160.28	-77.82	-0.22	-238.32	-0.007%
Dbl Crop WinWht/Corn	-0.44	-9.78	0.00	-10.23	0.000%
Dbl Crop WinWht/Cotn	0.67	0.00	0.00	0.67	0.000%
Dbl Crp WinWht/Sorgm	-0.22	0.00	0.00	-0.22	0.000%
Dbl Crp WinWht/Soybn	-12,263.08	-7,737.26	-78.25	-20,078.60	-0.554%
Deciduous Forest	-267.31	122.46	514.78	369.93	0.010%
Dev/High Intensity	-19.74	-34.74	-5.69	-60.18	-0.002%
Dev/Low Intensity	-680.91	-308.45	-166.78	-1,156.13	-0.032%
Dev/Med Intensity	657.40	-34.57	-48.73	574.09	0.016%
Developed/Open Space	-2,475.47	-981.12	-190.90	-3,647.50	-0.101%
Evergreen Forest	289.04	-32.68	14.89	271.26	0.007%
Fallow/Idle Cropland	-64,523.29	4,481.07	632.22	-59,410.00	-1.640%
Grass/Pasture	-8,161.68	-7,994.05	-1,057.12	-17,212.85	-0.475%
Herbaceous Wetlands	-757.09	-2,480.73	1,272.43	-1,965.39	-0.054%
Herbs	-140.96	0.00	0.00	-140.96	-0.004%
Misc Vegs & Fruits	-0.44	0.00	0.00	-0.44	0.000%
Mixed Forest	-1,392.72	-27.42	1.34	-1,418.81	-0.039%
Oats	-190.42	-0.89	0.00	-191.31	-0.005%
Open Water	-2,418.74	1,490.68	-880.05	-1,808.12	-0.050%
Other Crops	-27.34	-13.12	-0.44	-40.90	-0.001%
Other Hay/Non Alfalfa	3,854.70	-71.61	-77.97	3,705.12	0.102%
Peaches	-0.22	0.00	0.00	-0.22	0.000%
Peanuts	-1.78	0.00	0.00	-1.78	0.000%
Peas	4.89	0.00	0.00	4.89	0.000%
Pecans	924.42	6.23	0.00	930.64	0.026%
Pop or Orn Corn	141.39	0.00	0.00	141.39	0.004%
Rice	-7,156.15	-1,177.71	263.11	-8,070.75	-0.223%
Rye	29.57	0.00	0.00	29.57	0.001%
Shrubland	-3,028.83	2,330.13	232.51	-466.19	-0.013%
Sod/Grass Seed	-27.86	23.79	0.89	-3.17	0.000%
Sorghum	-10,900.59	649.14	-7.12	-10,258.57	-0.283%
Soybeans	162,582.90	9,690.13	754.13	173,027.16	4.778%
Spring Wheat	-8.23	0.00	0.00	-8.23	0.000%
Sugarcane	-276.90	2.63	-700.69	-974.96	-0.027%
Sunflower	-74.48	-3.78	0.00	-78.26	-0.002%
Sweet Potatoes	1,664.11	0.00	0.00	1,664.11	0.046%
Winter Wheat	-2,674.23	1,317.03	-12.67	-1,369.87	-0.038%
Woody Wetlands	918.98	3,125.66	-1,062.35	2,982.28	0.082%

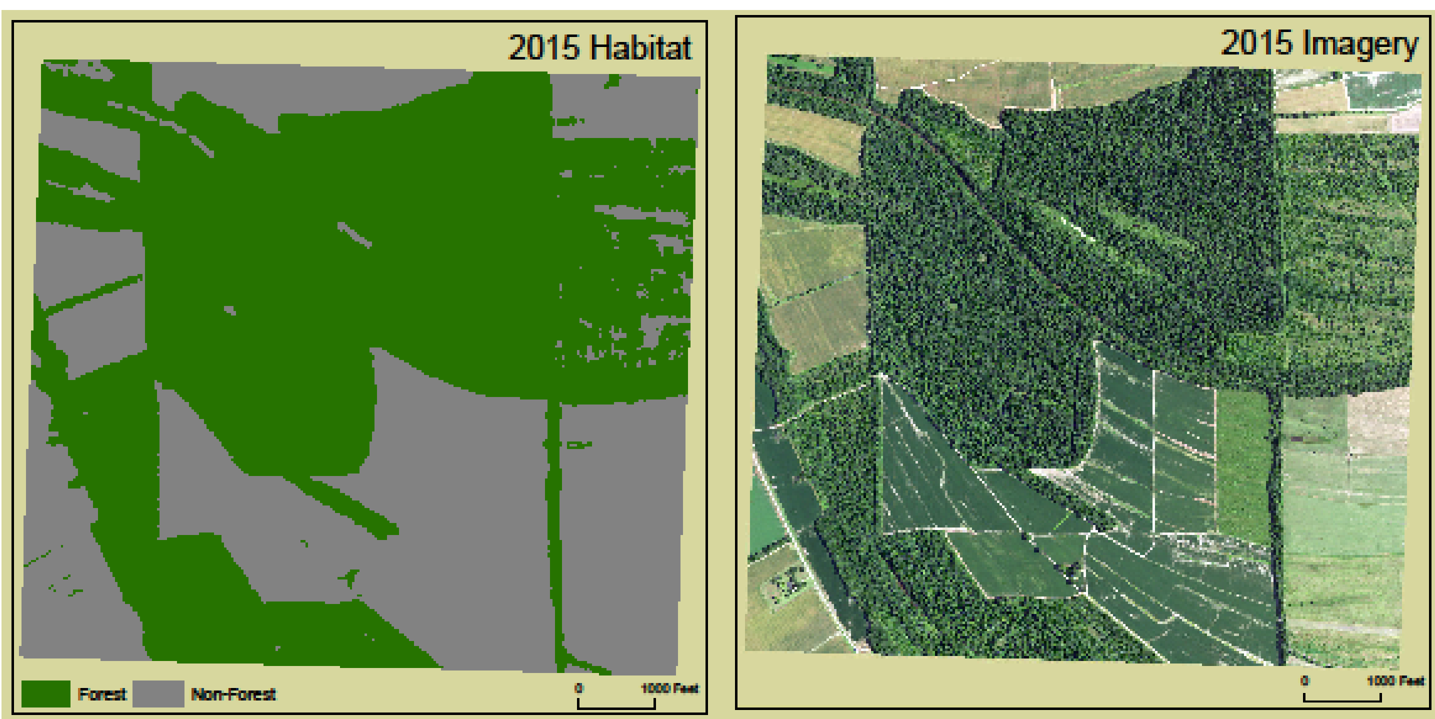
Forested Habitat Image Classification

High resolution aerial photography acquired through the USDA National Aerial Imagery Program (NAIP) was used to classify ground features into suitable (forested) and non-suitable (non-forested) habitats. ESRI's Feature Analyst GIS software provided the mechanism to conduct the habitat classification. The NAIP program acquires aerial photography of the United States, roughly fifteen states per year, normally on a three-year rotational basis. Louisiana's photography was flown in 2013, the year used for the Louisiana black bear proposed delisting habitat classification in 2014. Outside of the normal photo acquisition schedule, USDA flew Louisiana in 2015, the year used for the first Louisiana black bear post-delisting monitoring plan's image classification habitat assessment. The three sites used for analysis, north, central and south, the total acreages combined is 4,631.1 acres. Comparing the 2013 results to 2015, there was an 11.8 acre increase in forested habitat from all three sites combined. This increase was mainly from the closing in of tree canopy and the growth of existing trees since 2013. There were no large-scale habitat changes noted on any of these sites.

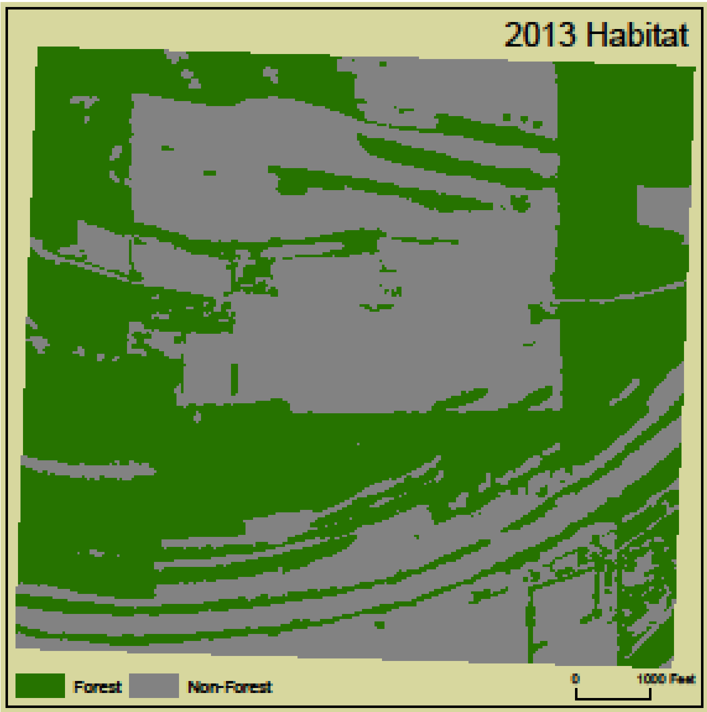
Year/Site	Forested Acres	Non-forested Acres	Total Acres
2013 North Site	831.4	712.6	1,544.0
2015 North Site	834.3	709.7	1,544.0
Change 2013 To 2015	2.9	-2.9	0.0
2013 Central Site	799.4	743.9	1,543.2
2015 Central Site	800.6	742.6	1,543.2
Change 2013 To 2015	1.3	-1.3	0.0
2013 South Site	1,389.2	154.7	1,543.9
2015 South Site	1,396.8	147.1	1,543.9
Change 2013 To 2015	7.6	-7.6	0.0

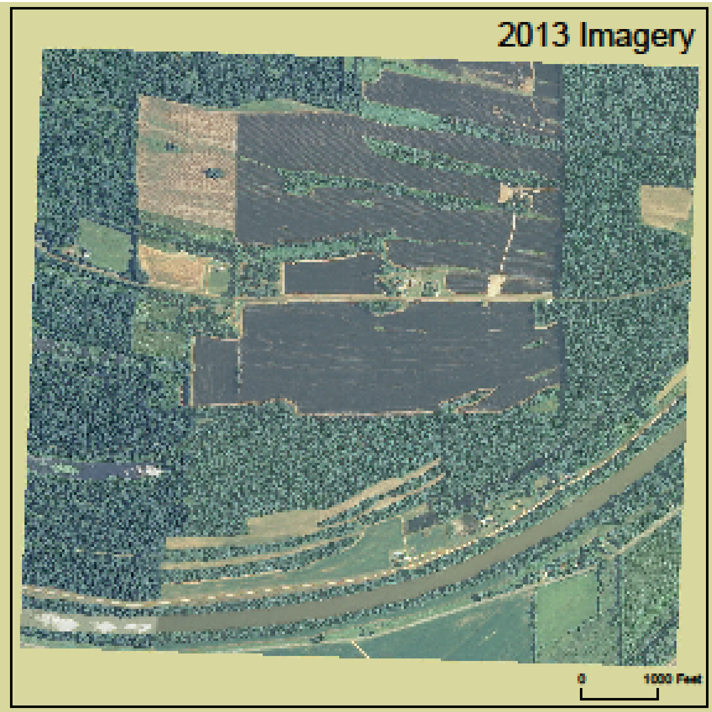
Northern Site

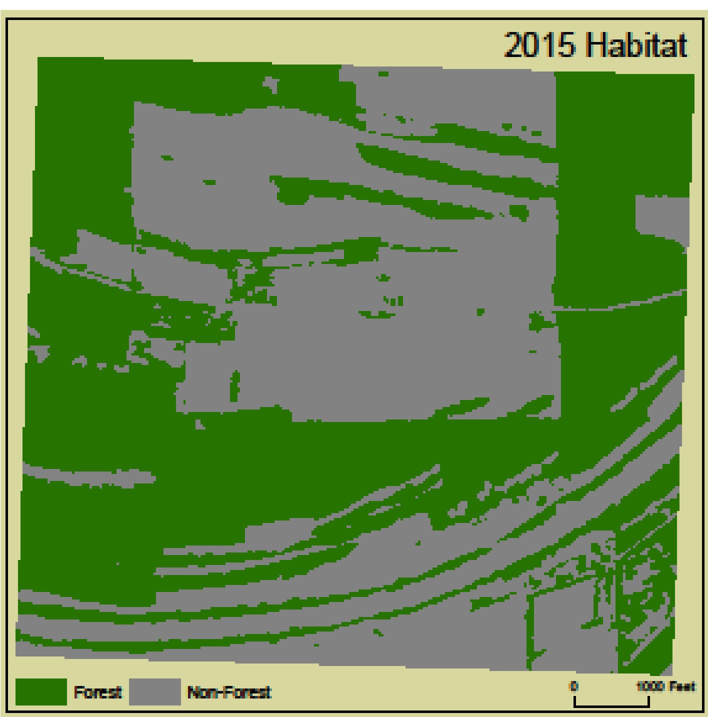


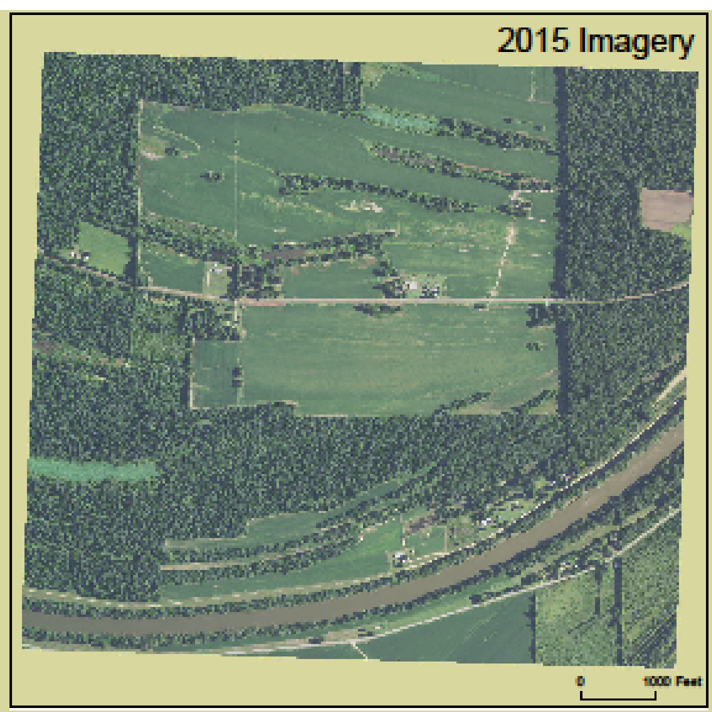


Central Site

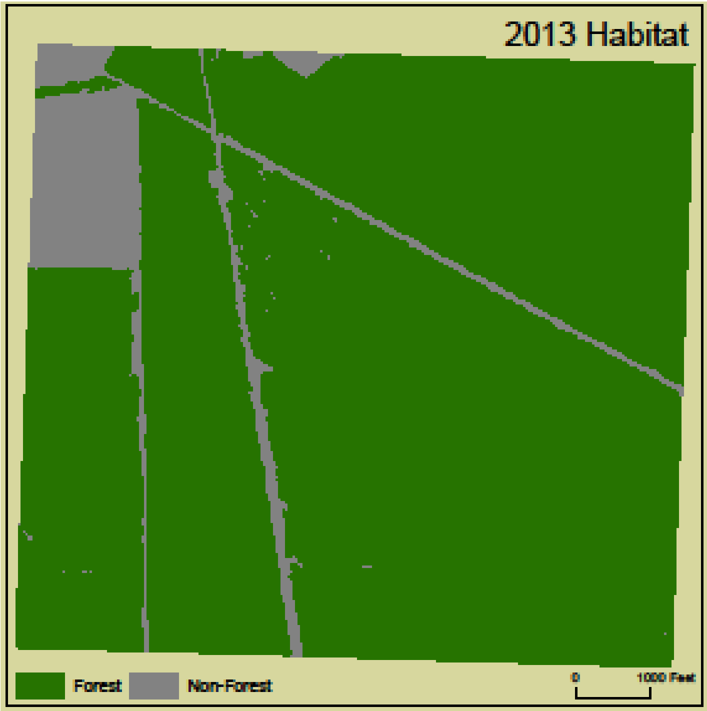


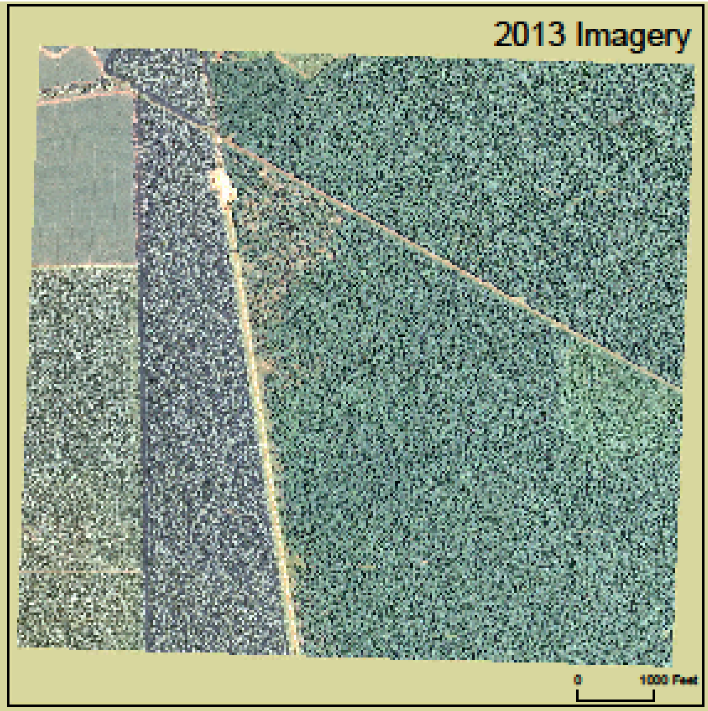


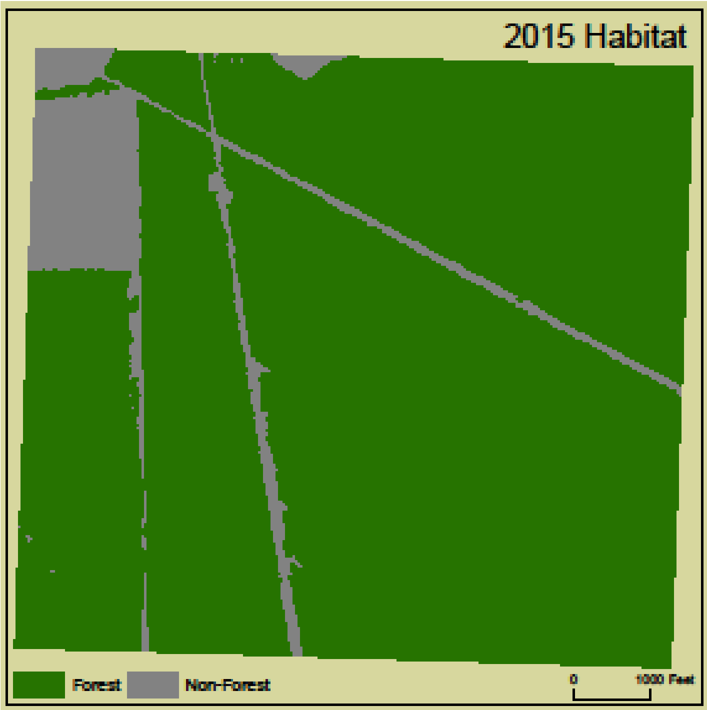


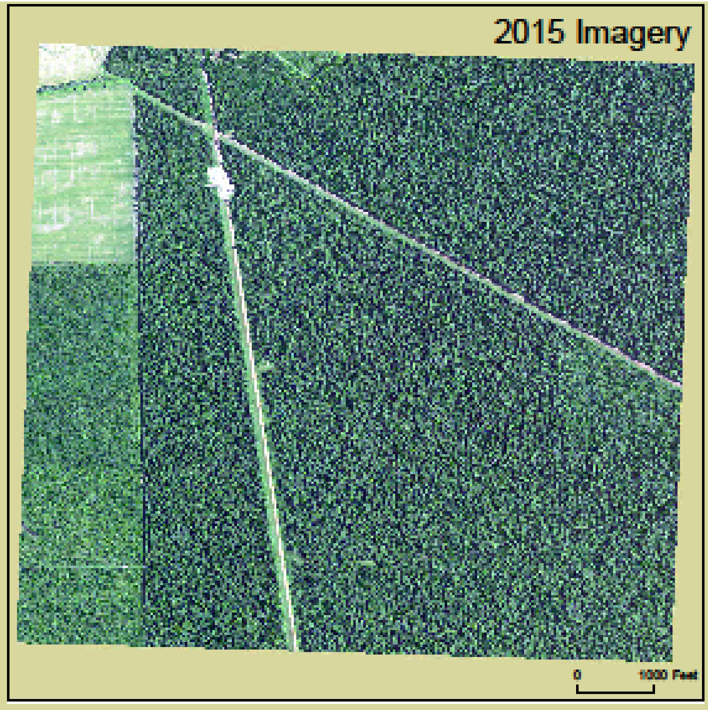


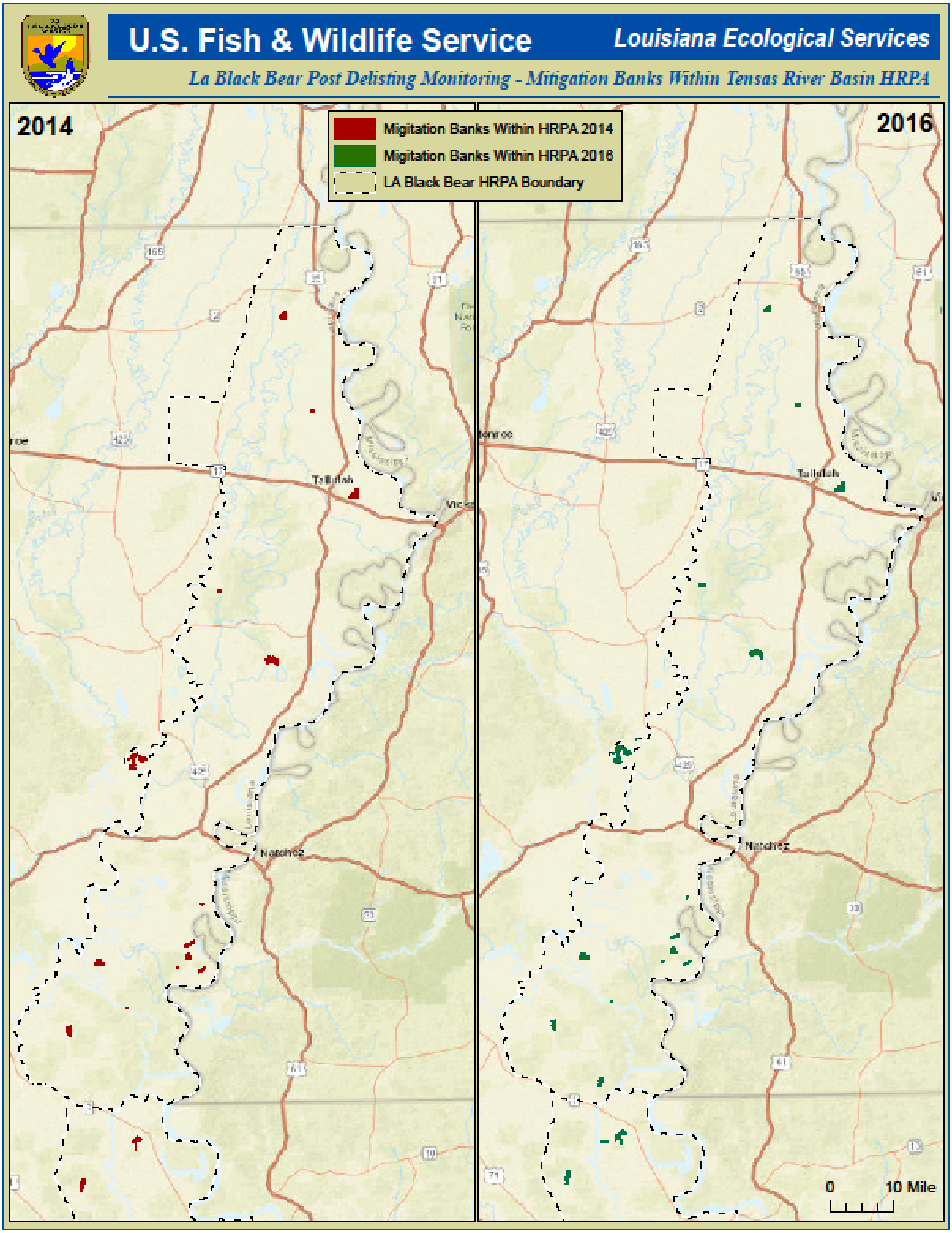
Southern Site

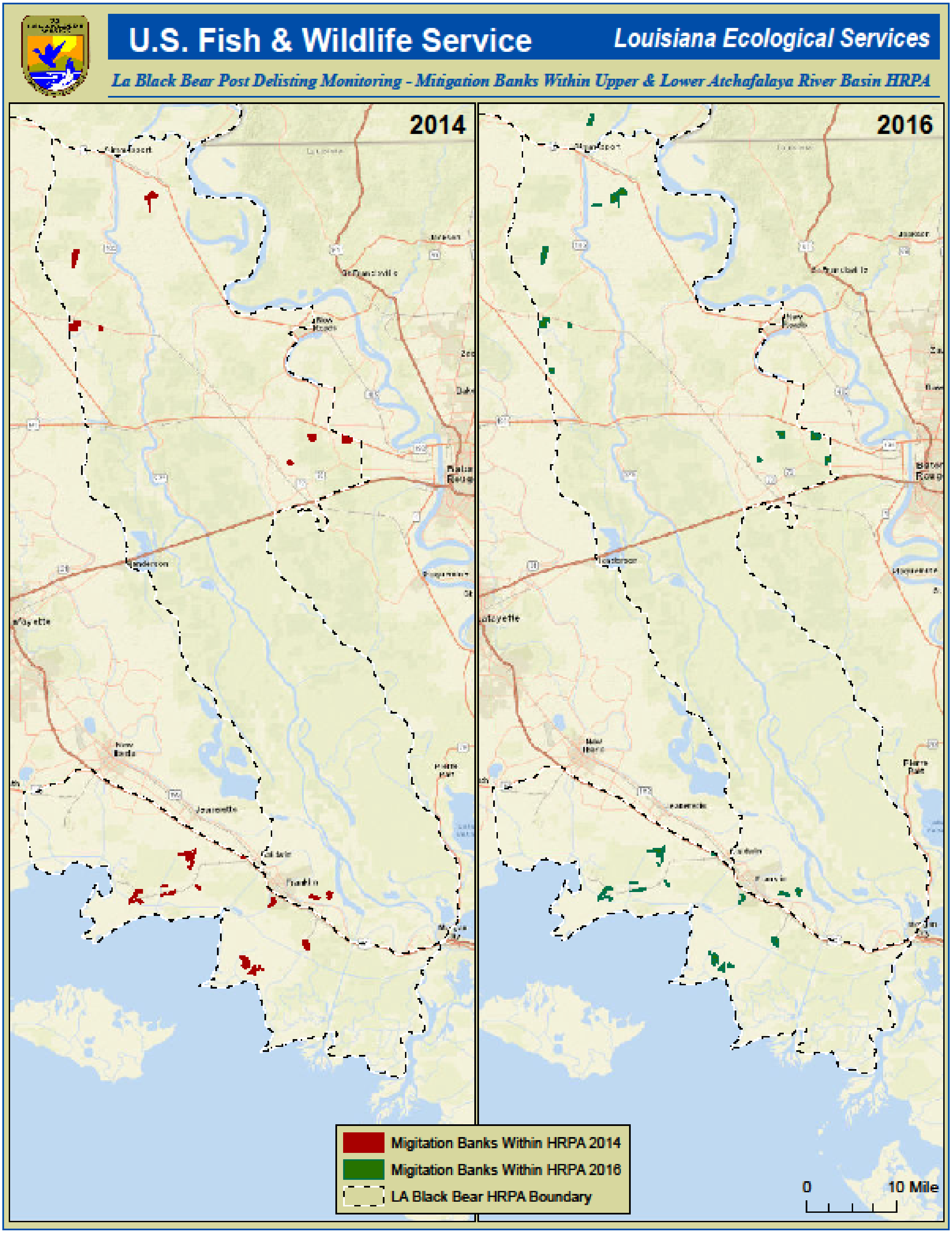









U.S. Fish & Wildlife Service
Louisiana Ecological Services
La Black Bear Post Delisting Monitoring - Mitigation Banks Within Tensas River Basin HRPA
2014
2016
Migitation Banks Within HRPA 2014
Migitation Banks Within HRPA 2016
LA Black Bear HRPA Boundary
Tallulah
Natchez
0
10 Mile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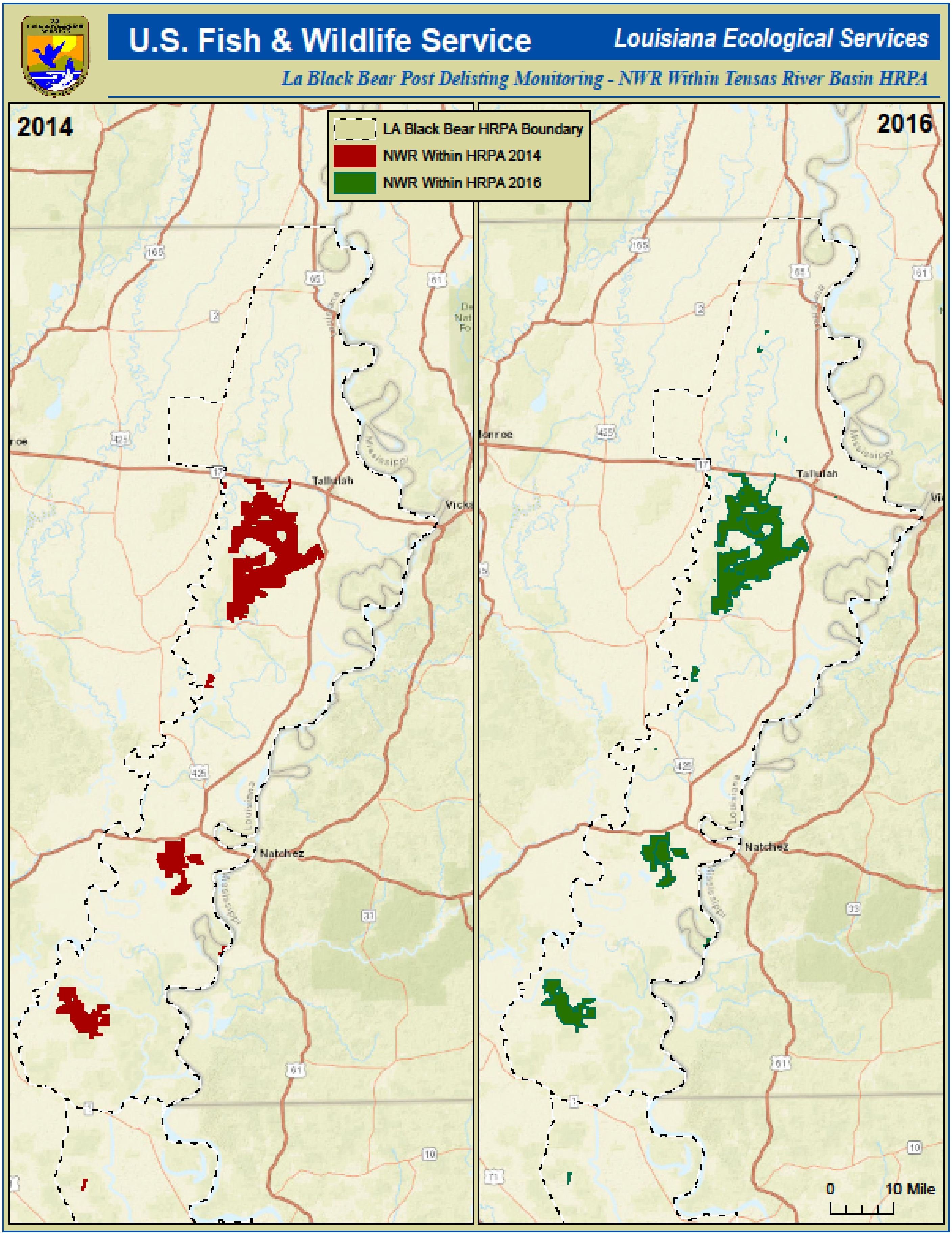
La Black Bear Post Delisting Monitoring - Mitigation Banks Within Upper & Lower Atchafalaya River Basin HRPA
2014
2016
Migitation Banks Within HRPA 2014
Migitation Banks Within HRPA 2016
LA Black Bear HRPA Boundary
0
10 Mile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2014
2016
LA Black Bear HRPA Boundary
NWR Within HRPA 2014
NWR Within HRPA 2016
Tallulah
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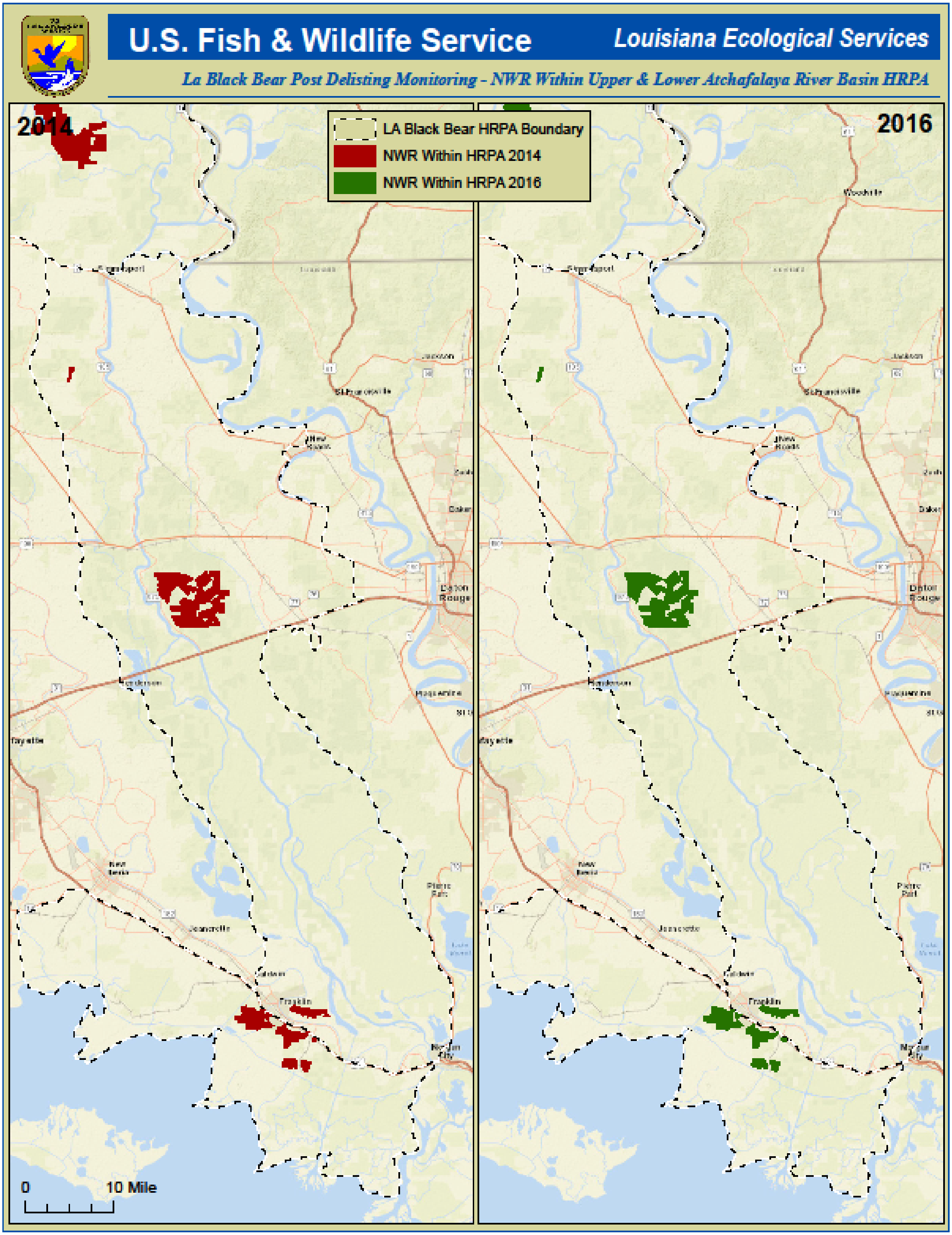
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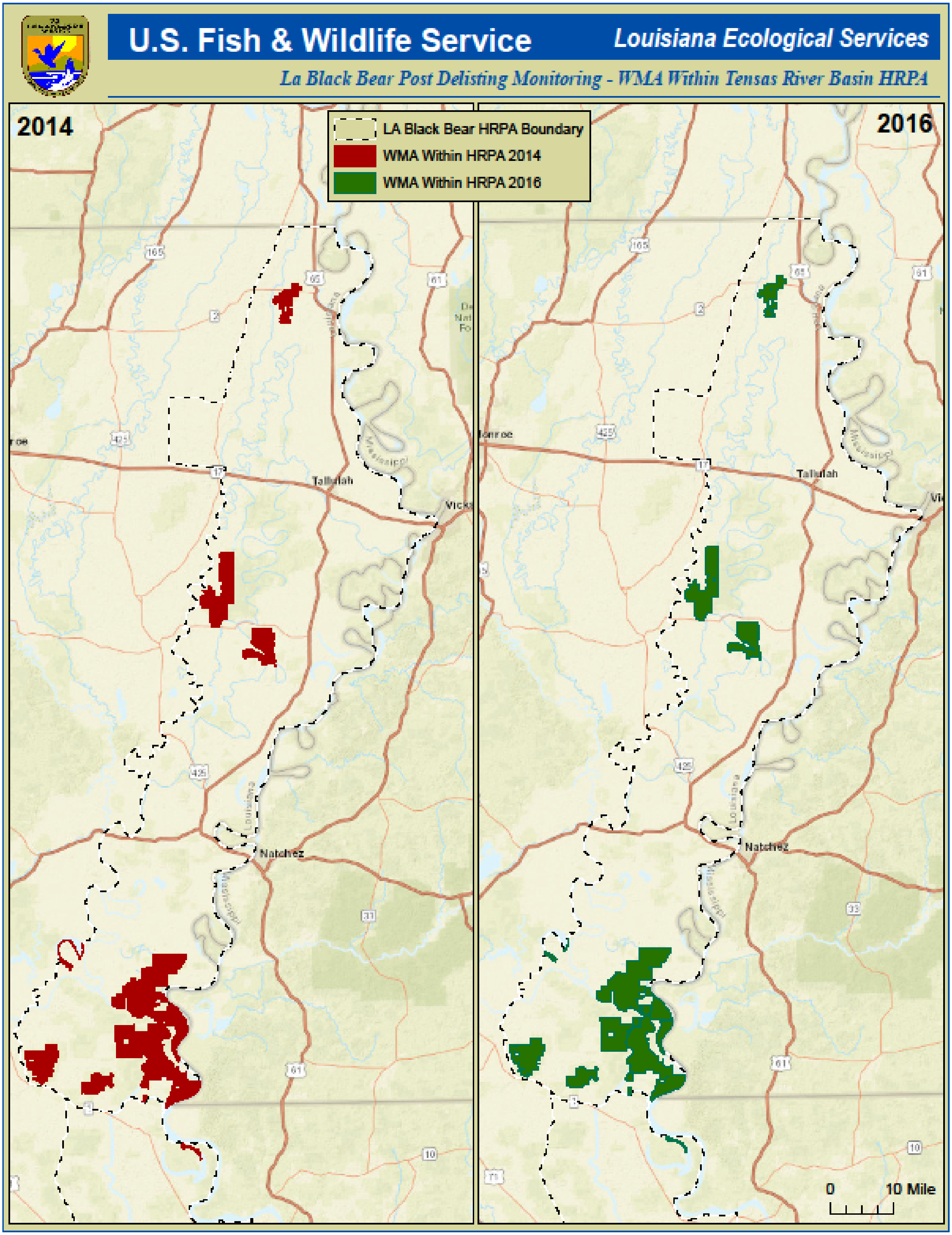
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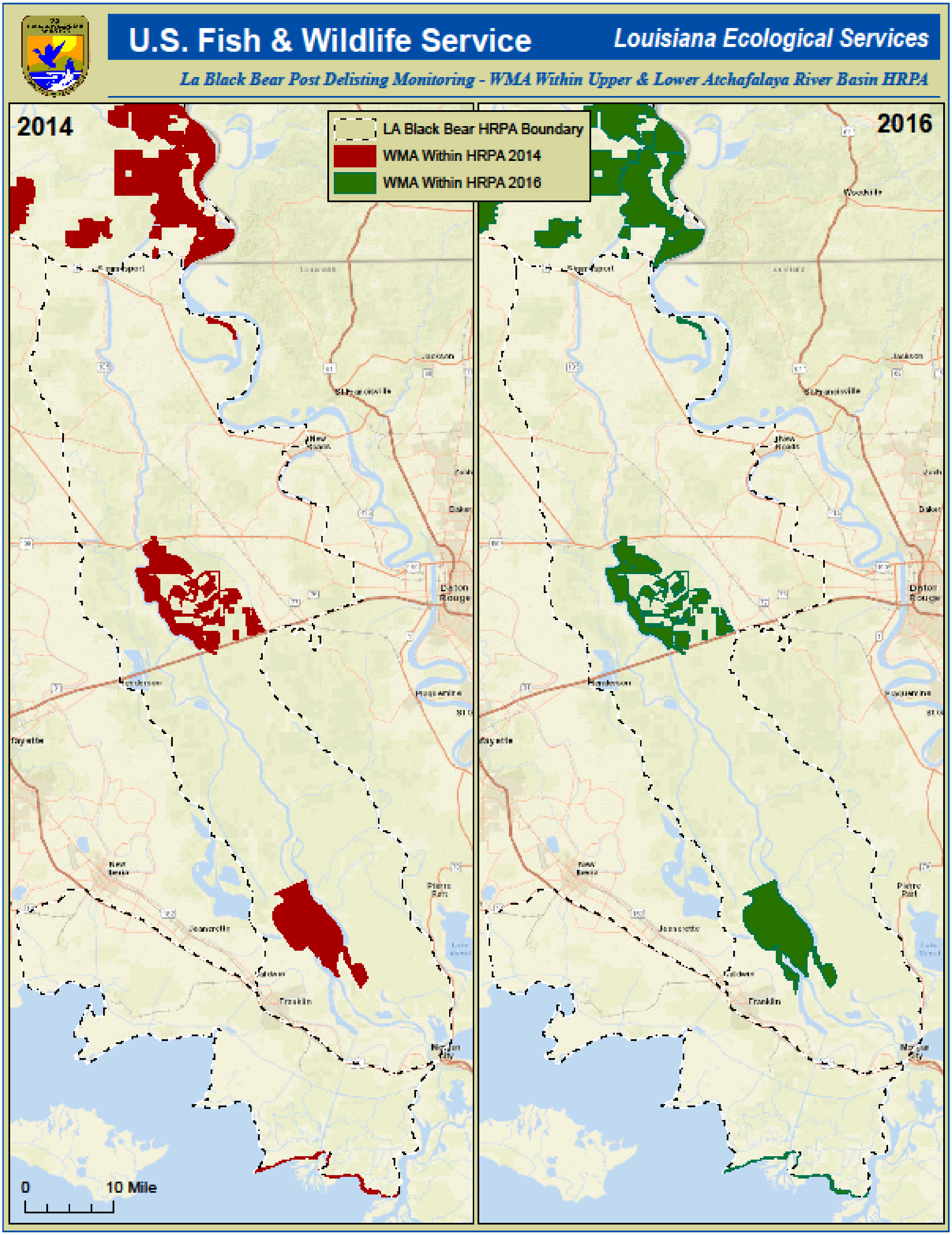

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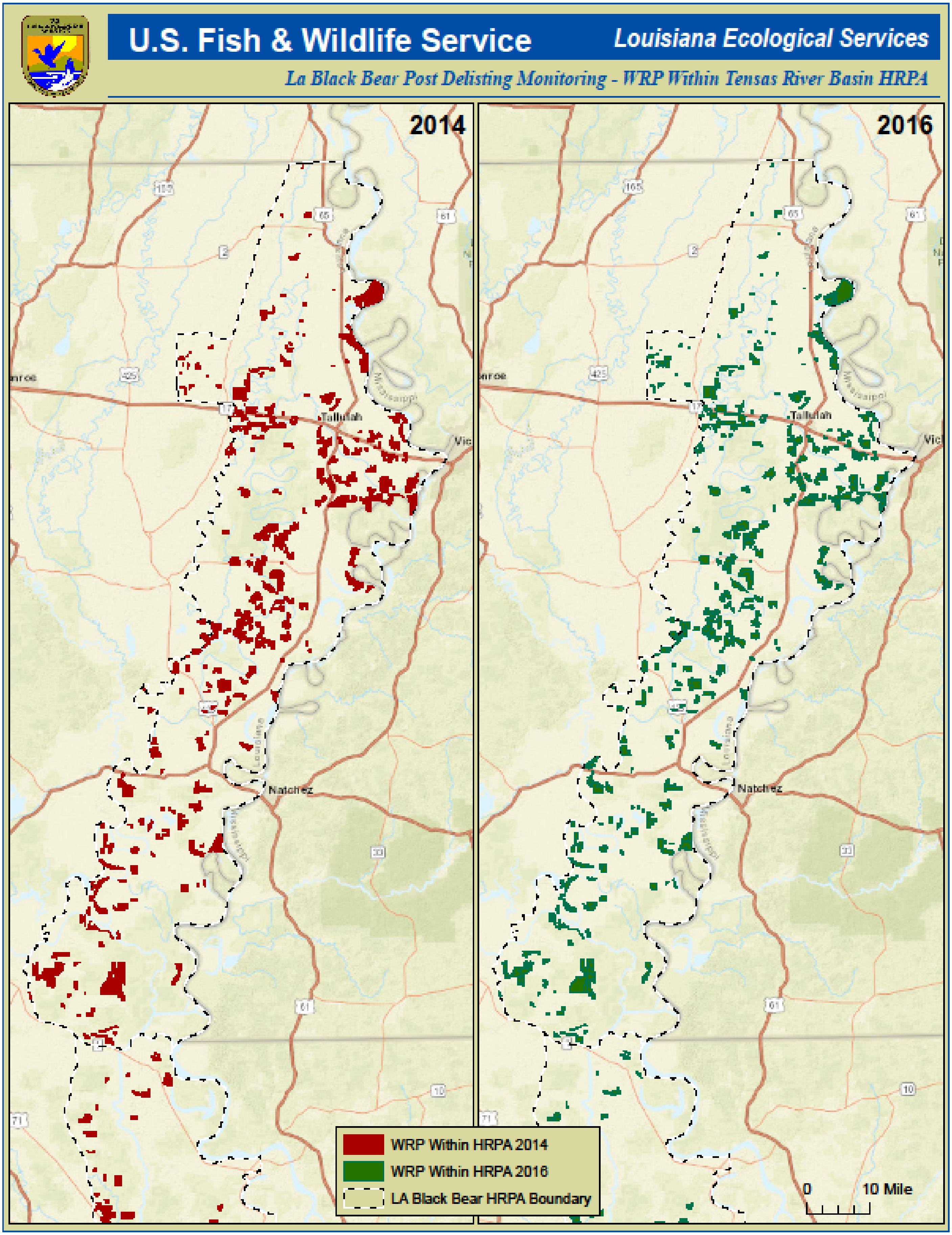
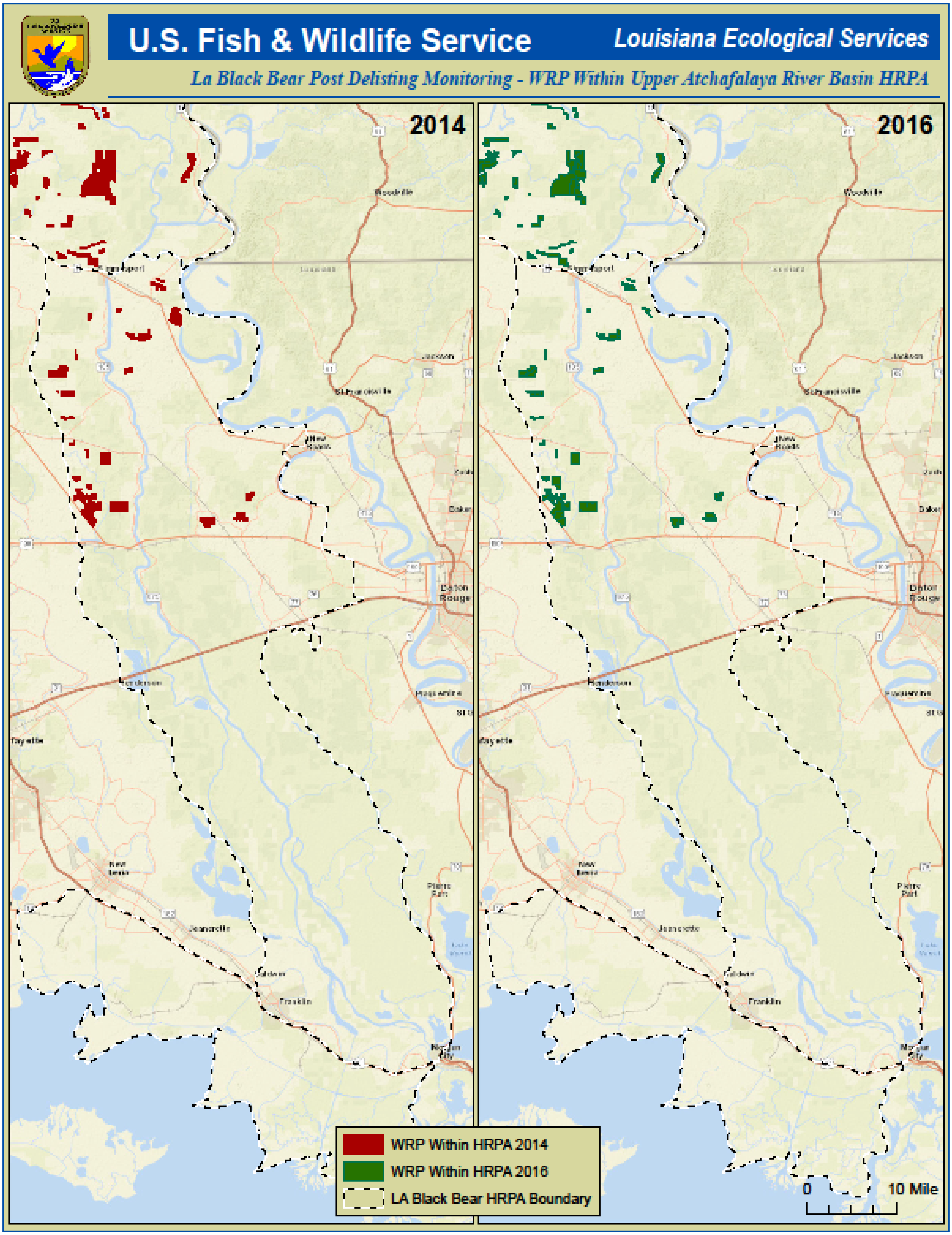
2014
2016
LA Black Bear HRPA Boundary
WMA Within HRPA 2014
WMA Within HRPA 2016
0
10 Mile


U.S. Fish & Wildlife Service
Louisiana Ecological Services
La Black Bear Post Delisting Monitoring - WRP Within Tensas River Basin HRPA
2014
2016
Tallulah
Natchez
WRP Within HRPA 2014
WRP Within HRPA 2016
LA Black Bear HRPA Boundary
0
10 Mile


U.S. Fish & Wildlife Service
Louisiana Ecological Services
La Black Bear Post Delisting Monitoring - WRP Within Upper Atchafalaya River Basin HRPA
2014
2016
WRP Within HRPA 2014
WRP Within HRPA 2016
LA Black Bear HRPA Boundary
0
10 Mile

Appendix III. Sensitivity Analysis and Results

Prepared By:

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THE UNIVERSITY OF TENNESSEE

U.S. Geological Survey - Southern Appalachian Research Branch
University of Tennessee

USGS

University of Georgia – Warnell School of Forestry and Natural Resources

The University of Georgia

FINAL REPORT

to

Louisiana Department of Wildlife and Fisheries

Project Title:

Refinements in Monitoring Methods for the Louisiana Black Bear (IP-084791)

13 March, 2017

Investigators:

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BACKGROUND AND JUSTIFICATION

In 1992, the U.S. Fish and Wildlife Service (USFWS) granted the Louisiana black bear (*Ursus americanus luteolus*) threatened status under the U.S. Endangered Species Act (ESA), listing loss and fragmentation of habitat as the primary threats (USFWS 1992). The 1995 Recovery Plan outlines recovery goals designed to meet the objective of reducing threats to the Louisiana black bear metapopulation and the habitat supporting it (USFWS 1995). To meet that objective, the Recovery Plan required 1) at least 2 viable subpopulations, 1 each in the Tensas and Atchafalaya River Basins, 2) movement corridors between the 2 viable subpopulations, and 3) long-term protection of the habitat supporting each viable subpopulation and interconnecting corridors.

Laufenberg et al. (2016) performed a population viability analysis (PVA) for the Tensas River Basin (TRB), the Upper Atchafalaya River Basin (UARB), and the Three Rivers Complex (TRC) bear subpopulation in Louisiana and, based on capture-mark-recapture (CMR) and radio-telemetry data, concluded that the probability of persistence of $\geq$1 subpopulation over the next 100 years, assuming current habitat conditions do not change, was >0.999. Based on these and other data, the USFWS removed *U. a. luteolus* from the list of threatened species in March 2016 (USFWS 2016*a*).

Section 4(g)(1) of the Endangered Species Act (16 United States Code 1431 *et seq*.) requires the Secretary of the Interior to implement a system in cooperation with the States to monitor, for no less than 5 years, the status of all delisted species. A post-delisting monitoring (PDM) plan was developed by the Louisiana Department of Wildlife and Fisheries (LDWF) and USFWS (USFWS 2016*b*). That plan was based on monitoring both population demographics and habitat. This report is focused on the population demographics component of the PDM plan.

The PDM plan stated that population demographics and vital rate monitoring could consist of regular live-capture, radio-collaring, winter den checks, and radio-telemetry monitoring to estimate litter sizes, cub recruitment, and survival. The plan also called for continued non-invasive mark-recapture to estimate change in population size (λ), apparent survival (φ), and per-capita recruitment including immigrants (f). The plan also states that should better methods for population monitoring become available during the post-delisting monitoring period, those methods would be explored.

The current PDM plan calls for a 3-week data collection period (compared with an 8-week period for the PVA) for non-invasive mark-recapture analyses on the UARB and TRB subpopulations. That protocol was based on some preliminary analyses of 2006–2012 non-invasive capture-mark-recapture (CMR) data for the TRB and UARB subpopulations (J. Clark, USGS, unpublished report). Pradel robust design CMR (Pradel 1996) was used to evaluate the sensitivity and accuracy of a variety of monitoring scenarios to detect changes in abundance (λ). USFWS and LDWF were interested in refining the protocols to optimize the robustness and cost effectiveness of monitoring. Such refinement is not only desirable but essential for adaptive resource management (Walters 1986). In addition, the recent advent of spatially explicit methods (Efford et al. 2004, Borchers and Efford 2008, Royle et al. 2014) has resulted in opportunities to improve the robustness of population estimation. Finally, Chandler and Clark (2014) reported on a method that combines the CMR data with presence/absence data to estimate these same vital rates. They found that hair samples need not be genotyped every year for DNA-based CMR monitoring to be effective if presence/absence data are collected in the intervening years. That could result in a substantial cost savings over time. Furthermore, presence/absence data could also be used to predict and monitor bear range expansion. However, their analysis was based on some simplified assumptions regarding subsampling biases, capture heterogeneity, etc. Thus, more cost-efficient and robust methods may exist that can provide better insight into Louisiana black bear population dynamics but a more thorough evaluation is needed.

OBJECTIVES

Our objective was to use existing Louisiana black bear mark-recapture data and recently developed spatially explicit integrated population models to refine and develop cost-efficient long-term protocols for monitoring the vital rates and demographics of the Louisiana black bear.

METHODS

General approach

Our overall goal was to use CMR-based information on population demographics and spatial detection processes collected during the Louisiana black bear recovery monitoring period (2006–2012) to develop alternative study designs for monitoring. Our general approach was comprised of 3 separate stages of analysis (Fig. 1). First, we conducted a sensitivity analysis using stochastic population simulations combined with machine learning techniques to identify demographic rates most important to extinction risk for bears of the TRB and UARB subpopulations and to identify demographic thresholds that can be used to develop population monitoring plans. The second stage was to use spatially referenced CMR data and a spatially explicit open-population CMR model (SCRO) to estimate abundance and parameters governing the spatial detection process that could be used to simulate new data based on prospective study designs. The final stage was to conduct a power analysis to test alternative study designs that would reduce labor and financial requirements yet produce reliable demographic rate estimates for long term monitoring. We focused the final stage on the UARB because it was the smallest of the subpopulations identified at time of listing and, as such, levels of sampling effort required would also be sufficient to obtain reliable estimates for the larger subpopulations. Unless otherwise noted, all analyses were focused on the female portion of each subpopulation consistent with approaches used in the PVA.

Population simulations

To perform a sensitivity analysis, it was first necessary to develop a population projection model for calculating extinction rates. Population simulations were conducted using CMR-based demographic rate estimates for the TRB and UARB reported in Laufenberg et al. (2016). Our projection model was similar to models used by Laufenberg et al. (2016) to conduct population viability analyses because ours also included demographic and environmental (i.e., temporal) stochasticity. Demographic rates used in the projection model included mean annual apparent survival on the logit scale (μ_{φ}), temporal process variance for φ expressed as standard deviation (σ_{φ}), an intercept (β_0) and slope (β_1) for a log-linear model describing density dependence in annual per-capita recruitment (f), and temporal process variance for f expressed as standard deviation (σ_f). Apparent survival is defined as the probability that an animal survives and remains a member of the subpopulation (i.e., does not permanently emigrate). Per-capita recruitment is the ratio of the number of new recruits (i.e., in situ births or permanent immigrants available for detection) to the total number of current residents (i.e., breeding or non-breeding age) in the subpopulation. Survival and recruitment are combined to derive λ which represents the annual realized rate of change in abundance as a function of births, deaths, permanent immigration, and permanent emigration. We made 2 modifications to the original projection model that enabled us to explore a greater diversity of demographic rate combinations compared with that observed in the original analysis. The first modification was to randomly sample individual parameter values for each trajectory from uniform distributions defined by the minimum and maximum of respective parameter posterior distributions reported in Laufenberg et al. (2016, Table 1). This produced a more varied combination of values than sampling the posterior distribution. The second modification was to independently sample each parameter value in contrast to sampling from the joint posterior distribution as was done in Laufenberg et al. (2016).

We generated 2,000 random combinations of projection model parameters from the above uniform distributions for the TRB and 2,000 for the UARB. We then used each of those combinations to assess stochasticity by simulating 500 population trajectories for 100 years resulting in 1,000,000 trajectories for each subpopulation. For each trajectory, we recorded the model parameter values used in the projection and annual abundance (*N*), λ, φ, and *f*. The goal of this analysis was to generate simulated data that would be used to identify individual population parameters most associated with extinction risk and identify demographic thresholds indicative of long-term persistence.

Variable importance

We first created a binary response variable (EXTANT) by assigning a value of 1 to each simulated trajectory with the number of bears in the population after 100 years (N_{100}) ≥ 1 and assigned a value of 0, otherwise. We then randomly selected 500,000 of the 1,000,000 simulated trajectories as a training data set for which we constructed a random forest of conditional classification trees for the TRB and the UARB using the `cforest` function in the R package `party` (Hothorn et al. 2006*a*, Strobl et al. 2007, Strobl et al. 2008). Explanatory variables included all 5 data-generating parameter values (μ_{φ}, σ_{φ}, β_0, β_1, and σ_f). We restricted the size of individual trees by limiting tree depth to 4 levels to ensure interpretability of individual trees and to reduce suboptimal performance associated with overfitting when sample size is large and the number of explanatory variables is small (Lin and Jeon 2006). We set the number of explanatory variables randomly selected for determining individual splits at 3 and the number of trees in the forest to 100. All other function arguments were left at default values. Variable importance scores were calculated using the `varimp` function in the `party` package. We assessed model fit and predictive performance of the random forest by calculating the overall classification error rate and Type II error rate (i.e., incorrectly classifying a trajectory that went extinct as extant) for a holdout sample independent of the training data set that was comprised of 10,000 trajectories randomly selected from those trajectories not selected for the training data set. We considered Type II error to be the most relevant from a management standpoint.

In addition to factors influencing long-term extinction rates, we wanted to also evaluate shorter-term rates which would be more appropriate for a typical post-delisting monitoring period (e.g., 5 years). To evaluate importance of short-term rates to extinction risk, we derived new predictor variables based on values for N, φ, and λ extracted from the training data set. We calculated the mean value for each variable observed during first 5 ($\bar{N}_5$, $\bar{\varphi}_5$, and $\bar{\lambda}_5$) and first 10 ($\bar{N}_{10}$, $\bar{\varphi}_{10}$, and $\bar{\lambda}_{10}$) years of each population projection resulting in 2 sets of predictor variables that reflected population monitoring durations that could be implemented post delisting and meet ESA monitoring requirements. We then used those 2 sets of explanatory variables in separate random forest analyses each for the TRB and UARB using the same function settings as the long-term analysis. We assessed model fit and predictive performance as we did for the long-term analysis.

Demographic thresholds

Demographic thresholds or triggers are effective components of population monitoring plans when relationships between demographic rate values and some measure of population vigor can be reliably determined. For example, survival might serve as a useful index of population persistence probability for which some minimum tipping point could be established. Traditional statistical analysis methods (e.g., generalized linear models or analyses of variance) often are inadequate for revealing complex relationships in high-dimensional ecological data, whereas machine-learning methods such as classification trees are well suited to such situations (De'ath and Fabricius 2000, Strobl et al. 2009). Therefore, we used single conditional-inference classification tree analysis to explore relationships and identify robust predictive thresholds between demographic rates and the likelihood of population extinction.

We were primarily interested in identifying demographic rate thresholds that would be reliable indicators of long-term population persistence (i.e., persistence probability $\geq$95%) that could be measured over relatively short monitoring durations (e.g., 5 years) consistent with post-delisting monitoring requirements of the ESA. Additionally, we were interested in identifying thresholds in demographic rates governing population dynamics that could be used to gain a broader understanding of the underlying demographic requirements for long-term persistence of the TRB and UARB subpopulations. Therefore, we constructed 3 separate conditional classification trees for the TRB and UARB based on demographic rates consistent with our variable importance analysis: 1 for a 5-year monitoring duration, 1 for a 10-year monitoring duration, and 1 for long-term demographic rates. The first 2 classification trees were focused on duration-specific average values derived from annual demographic rates generated by our population simulations. Those averages were defined based on rate-specific numeric scales where N and λ could range from 0 to ∞ and φ could range from 0 to 1. The third classification tree was based on the long-term data-generating demographic rates used in our population simulations. Those values were defined on numeric scales related to link functions used to model and estimate those rates. Specifically, values that corresponded to survival (μ_φ and σ_φ) were on the logit scale and values that corresponded to the log-linear model describing density dependence in per-capita recruitment (β_0, β_1, and σ_f) were on the natural log scale.

For the short-term and long-term threshold analyses, we used the same training data sets and explanatory variables as our variable importance analysis except that the EXTANT variable was converted from a binary variable to a factor variable with 2 levels: EXTINCT when N_{100} <1 and EXTANT otherwise. We used the `ctree` function in the R package `party` (Hothorn et al. 2006*b*) to separately grow classification trees for each set of predictor variables (5-year, 10-year, and long-term) for the TRB and UARB resulting in 6 conditional classification trees. Again, we restricted the size of the trees to 4 levels; all other function arguments were left at default values. We assessed model fit and predictive performance based on a hold-out sample of 10,000 trajectories independent of the training data set as we did for random forests used to evaluate variable importance. For the purpose of monitoring long-term persistence, we defined reliable demographic rate thresholds as scenarios (i.e., classification tree branches) from our classification trees that resulted in persistence probabilities $\geq$95% for 100 years.

Given the findings from our power analysis of prospective monitoring designs that suggested λ could be reliably monitored (see Results), we conducted post hoc classification tree analyses solely based on 5-year ($\bar{\lambda}_5$) and 10-year ($\bar{\lambda}_{10}$) averages of λ to identify thresholds for the TRB and UARB that would predict population persistence. All procedures were the same except that these analyses only incorporated either $\bar{\lambda}_5$ or $\bar{\lambda}_{10}$ rather than multiple demographic rates as in the previous classification tree analyses.

Spatial capture-recapture

We used a spatially explicit open-population capture-mark-recapture (SCRO) modeling approach to analyzing DNA-based CMR data collected in the UARB from 2007 to 2012. This approach enabled us to obtain estimates of sex-specific N, φ, f, λ, weekly detection probabilities (p), and spatial scale parameter (σ_{SCR}) on which we could base our simulations for population trajectories and design-specific data collection. Although our power analysis only considered the UARB, we also fit SCRO models to the CMR data collected in the TRB from 2006 to 2012 to provide demographic and detection rate estimates that could be used in future sampling designs for that subpopulation.

Spatially explicit capture-recapture (SCR) methods differ from traditional non-spatial CMR modeling approaches in that they explicitly model the detection process as a function of the juxtaposition of animal activity centers to sampling devices and as a function of animal space use conditional on activity center location. The basic model used for space use represents use as a bivariate normal kernel defined by a mean location (i.e., activity or home range center) and a scale parameter σ_{SCR} that regulates use as a declining function of distance from the mean location. In practice, this basic space-use model scales p by the distance between a detection device (e.g., hair snare, camera, etc.) and an activity center which translates to the detection of an animal by a device being greatest when that device is placed at the activity center of that animal. The baseline detection probability (p_0) is defined as the probability of detection at a trap placed at the activity center and the detection probability for individual i at a trap j is defined as $p_{i,j} = p_0 \times exp\left(-\left\|\boldsymbol{x}_j - \mathbf{s}_i\right\|^2 / 2\sigma_{SCR}^2\right)$ where $\boldsymbol{x}_j$ is a coordinate vector for trap j and $\boldsymbol{s}_i$ is the coordinate vector of the activity center for individual i (Borchers and Efford 2008, Royle et al. 2014). Note that when distance is zero (i.e., trap j is located at activity center i), the detection function reduces to $p_{i,j} = p_0$. Although this model can be extended to account for heterogeneity in space use caused by resource selection (Royle et al. 2013), we chose to use the basic formulation in analyzing our empirical data to reduced complexities in simulating data for our power analysis.

A second difference between SCR models and non-spatial methods is that the SCR approach includes an explicit model for the distribution of animal activity centers across the landscape (i.e., spatial point process model) which requires a prior delineation of the area that the population of interest occupies. This area is commonly referred to as the state space or area of integration and must, at a minimum, include an area sufficiently large to include the sampled population, but should exclude areas (e.g., urban areas, water bodies, large agricultural areas) where animals are highly unlikely to locate their activity centers (Royle et al. 2014). Because the UARB is primarily comprised of a matrix of patches of bear habitat (e.g., bottomland hardwood forests) and non-habitat (e.g., large expanses of row-crop agricultural lands), we defined our state-space to only include forested areas identified as quality bear habitat. To identify those areas, we used a statewide habitat model (Murrow et al. 2013) based on the Mahalanobis distance statistic to identify suitable bear habitat in the TRB and UARB. The Mahalanobis statistic (D^2) quantifies habitat quality as a continuous non-negative value whereby habitat quality is inversely related to D^2 values (Clark et al. 1993). We used a threshold D^2 value of 80 to derive a binary raster layer from the fitted D^2 model that differentiated between bear habitat and non-habitat (Murrow et al. 2013). We then converted that raster to an ArcGIS (ArcGIS 10.2.2 for Desktop, c 1999-2013 ESRI Inc., www.esri.com) shapefile (D2HAB) containing polygons of bear habitat; we excluded all polygons <2 km^2 as areas unlikely to contain activity centers given their relatively small size (Fig. 2).

To maintain consistency between empirical data analysis, population simulations, and power analyses, we derived a common state space for all analyses. To do so, we based our derivation on the combined set of original trap locations during recovery monitoring and trap configurations (see below) considered for our power analysis. We first buffered the combined set of locations by 5 km to define the furthest extent of our state space. Next, we clipped the extent buffer by our D2HAB shapefile to derive a final state space that contained only areas defined as bear habitat in which potential activity centers for all bears with access to trapping arrays could occur. The resulting state spaces were 924.8 km^2 and 356.3 km^2 in size for the TRB and the UARB, respectively.

The complete CMR data sets for the TRB and UARB consisted of DNA-based detection records of individual bears obtained from hair-collection surveys conducted each year from 2006 to 2012 in the TRB and from 2007 to 2012 in the UARB (Laufenberg et al. 2016). In contrast to analysis of this data set by Laufenberg et al. (2016), we included capture data from both sexes whereas the former only used data from females. The final data set used for analysis consisted of count records ($y_{i,j,t}$) indicating the number of occasions out of a maximum of K occasions that individual i $(i = 1,...,n)$ was detected at trap j (j = 1,…,J) of year t (t = 1,…,T), where n is the total number of individuals ever detected, J is the number of traps operated each year, and T is the number of years.

We assumed constant density across space (i.e., homogeneous point process model) for areas defined by our state space. Because the state spaces to which our SCRO-based estimates of N encompassed areas well beyond the extent of trap arrays used during the recovery period and likely encompassed larger populations, direct comparisons between estimates of our current analysis and those from Laufenberg et al. (2016) are not appropriate. We also note that we did not account for changes in field methods or effects of the 2011 flooding event in the UARB (O'Connell et al. 2014) in this analysis as was done in Laufenberg et al. (2016), which may also contribute to differences between the 2 studies. We allowed annual values of φ, f, and λ to vary independently by year, which differed from the random effects modeling approach for annual demographic rates used in Laufenberg et al. (2016). We also allowed p_0 to differ across years independently for each sex. Although SCR methods explicitly account for detection heterogeneity caused by individual-level differences in exposure to traps and differences between sexes, we also accounted for additional latent sources of heterogeneity by assuming a sex-specific finite-mixture distribution for p_0 (Pledger 2000).

We used Markov chain Monte Carlo (MCMC) sampling methods within a Bayesian inference framework implemented in JAGS (https://sourceforge.net/projects/mcmc-jags) accessed through Program R (Version 3.0.2, http://cran.us.r-project.org/, accessed 30 Jan 2014) via the package `rjags` (Plummer 2011) for model fitting and parameter estimation. We ran a single MCMC sampling chain of 10,000 steps after 2,000 burn-in samples were discarded. We report posterior modes and 95% credible intervals for all parameter point estimates unless specified otherwise. We chose the posterior mode as the point estimator instead of the posterior mean to avoid potential influence of skewed posterior distributions on parameter estimates. We conducted all analyses using vague prior distributions.

Power analysis

Our goal was to develop study designs that would reduce the logistical costs (e.g., personnel, materials, time) compared with those used during the recovery period yet still produce reliable estimates of important demographic rates required for population monitoring. Based on the estimate of female σ_{SCR} from our SCRO analysis for the UARB, we considered 2 different levels for trap spacing (i.e., $1 \times \sigma_{SCR}$ and $2 \times \sigma_{SCR}$) that would result in a lower total number of traps compared with the study design used during recovery monitoring (Figs. 2 and 3). For each spacing, we laid a grid of points over a predefined sampling area within the GIS environment and extracted all points that fell within 100 m of the boundary of that area. The sampling area was defined by first adding a 2-km buffer to a polygon shapefile provided by LDWF that outlined an area of primary interest for population monitoring in the UARB. We then extracted areas that were classified as bear habitat by our D2HAB shapefile and used the resulting shapefile as our sampling area as previously described.

We considered designs with the original number of 1-week occasions (K = 8) and also tested designs with 4 occasions. We chose 4 because it represented a substantial reduction in cost and number of personnel yet still met minimum sampling requirements for fitting CMR models that account for detection heterogeneity based on finite-mixture models with 2 mixtures. In total, we tested designs based on all possible combinations of the 2 levels of trap spacing and 2 study durations which resulted in the following 4 study designs: 1) traps spaced at 1 × σ_{SCR} and operated for 4 weeks (Design 1-4), 2) traps spaced at 1 × σ_{SCR} and operated for 8 weeks (Design 1-8), 3) traps spaced at 2 × σ_{SCR} and operated for 4 weeks (Design 2-4), and 4) traps spaced at 2 × σ_{SCR} and operated for 8 weeks (Design 2-8).

We simulated 100 population trajectories for the UARB using a stochastic population model parameterized, in part, by demographic rates set at threshold values for those identified as important from our variable importance analysis. Because mean female φ was identified as the most important short-term demographic rate for predicting persistence of the UARB subpopulation over 5-year ($\bar{\varphi}_5$) and 10-year ($\bar{\varphi}_{10}$) periods (see Results), we chose annual values of φ that would result in a mean of 0.91. We chose that value because it met the threshold value from demographic scenarios in our 5-year and 10-year duration classification trees for the UARB that resulted in high probabilities of persistence ($\geq$95%). We set annual f for females to values that, when summed with corresponding φ, would result in annual λ, 5-year mean λ ($\bar{\lambda}_5$), and 10-year mean λ ($\bar{\lambda}_{10}$) equal to 1.0. We set annual φ for males to values that would result in a 5-year mean of 0.85 and set annual male f to values that summed to 1.0 as we did for females. For all simulated trajectories, we used the mean estimated density in the UARB from 2007 to 2012 multiplied by the area of our state space as the starting population size (N = 127) pooled across sexes and assumed an average sex ratio of 0.25M:0.75F estimated from our empirical data. For each trajectory, we then simulated spatially referenced CMR data for 5 years based on the trap configuration and sampling duration for each prospective study design, resulting in a total of 400 data sets.

For each data set, we evaluated the following 3 open population modeling approaches each of which provide estimates of different sets of demographic rates: 1) open population spatial-explicit capture-recapture models (SCRO, Royle et al. 2014), 2) spatially explicit Cormack-Jolly-Seber models (SCJS, Brownie and Robson 1983), and 3) open population non-spatial Pradel models (PRADEL, Pradel 1996). For the SCRO models, we assumed the same model structure as that used in our analysis of empirical data collected in the UARB. Apparent survival is the only structural demographic parameter in SCJS models which we modeled as sex and year specific. The SCJS model essentially is a spatial version of the CJS model whereby only φ and p are estimated. The SCJS version has the added advantage of being able to use >1 capture per occasion in estimating p whereas multiple captures must be discarded for typical CJS analysis. We modeled detection-related parameters for the SCJS analysis same as we did for the SCRO analyses. For our PRADEL analysis, we modeled φ, f, and λ as year and sex specific. Pradel models enable the estimation of λ, φ, and f but are not spatially explicit. Because the Pradel models we used were not spatially explicit, we could not account for detection heterogeneity caused by proximity of animals to the trap array. Therefore, we accounted for heterogeneity only by modeling *p* as sex specific and by using-finite mixture models.

We again used MCMC and Bayesian inference for model fitting and parameter estimation for the SCRO and SCJS power analyses. For the SCRO analysis, we ran a single MCMC sampling chain of 10,000 steps after 2,000 burn-in samples were discarded whereas we ran a chain of 15,000 steps with 5,000 burn-in samples for the SCJS analysis. We summarized posterior samples using the mode and 95% credible intervals and used vague priors as before. For the PRADEL analysis, we used robust design Pradel recruitment full likelihood data type and MLE methods available in Program MARK (White and Burnham 1999) accessed through the R package RMark (Laake 2013) for model fitting and to obtain estimates of φ, *f*, and λ. For each modeling approach, we derived applicable estimates of 5-year averages of *N*, φ, and λ depending on model type that corresponded to short-term demographic rates ($\bar{N}_5$, $\bar{\varphi}_5$, and $\bar{\lambda}_5$) from our sensitivity analyses. We evaluated the performance of each modeling approach for each design by summarizing derived parameter estimates across all 100 replicates in terms of overall bias, root mean squared error (RMSE), and confidence interval coverage.

RESULTS

Variable Importance

Mean annual female φ on the logit scale (μ_φ) was identified as the long-term rate with the greatest relative importance for predicting extinction of the TRB subpopulation (Fig. 4A). Annual variation of φ (σ_φ) was also a strong predictor for the TRB. Conversely, σ_φ had the greatest relative importance to extinction risk and $\mu_\varphi$was only moderately important in the UARB (Fig. 4B). The overall classification error rate for the random forest model predicting extinction in the TRB was 12.4% and the Type II error rate (i.e., predicted outcome is EXTANT when true outcome is EXTINCT) was 7.5% indicating reasonable predictive power. The random forest model for the UARB performed better than for the TRB with an overall error rate of 5.9% and Type II error rate of 3.2%.

Of the 3 short-term rates evaluated for the TRB and UARB, average apparent female survival ($\bar{\varphi}_5$ and $\bar{\varphi}_{10}$) was most important for predicting extinction for both monitoring durations and both subpopulations (Fig. 4C–F). Overall and Type II error rates for the TRB random forest based a 5-year duration were 8.5% and 3.2% whereas those rates for the 10-year duration were slightly lower at 6.7% and 2.7%. For the UARB, overall and Type II error rates were 8.6% and 3.7% based on a 5-year duration and were 6.4% and 2.0% for the 10-year duration.

Demographic thresholds

The overall error rate of the conditional classification tree for long-term demographic rate thresholds in the TRB was 13.6% and the Type II error rate was 4.9%. Based on the default rule implemented in the `party` package that classifies a terminal node with $\geq$50% of its samples having true values of 0 as extant, 8 combinations of demographic threshold values (hereafter scenarios) were classified as extant (Fig. 5). Only 1 scenario met our criterion as a reliable demographic rate threshold with a likelihood of the TRB subpopulation remaining extant for 100 years $\geq$95%, although a second scenario nearly met that criterion (94%; Fig. 5). Despite those scenarios differing in complexity (i.e., 3 different demographic rates vs 1 demographic rate), both occurred when μ_{φ} was relatively high (>2.01 on the logit scale, Fig. 5).

Overall error rates of the classification tree for 5-year and 10-year durations in the TRB were 8.5% and 6.8% and Type II error rates were 3.2% and 3.0% indicating strong predictive power. Based on the default rule implemented in the `party` package, the same 8 combinations of demographic threshold values were classified as extant for both monitoring durations (Fig. 6

and Fig. 7). Based on a 5-year monitoring duration, scenarios for which $\bar{\varphi}_5$ was >0.91 resulted in likelihoods of ≥95% that the TRB subpopulation would remain extant for 100 years (Fig. 6), whereas similar likelihoods for the 10-year duration required values of $\bar{\varphi}_{10}$ >0.90 (Fig. 7).

The overall error rate of 6.3% for long-term demographic thresholds in the UARB was much lower than that of the TRB and the Type II error rate was slightly lower at 4.6%. Six demographic rate scenarios resulted in terminal nodes being classified as extant (Fig. 8). The 2 scenarios that resulted in likelihoods ≥95% of the UARB subpopulation remaining extant were solely based on thresholds for μ_{φ} and σ_{φ} indicating a strong interaction between those variables (Fig. 78).

Performance of the conditional classification trees for short-term rates in the UARB was similar to the TRB tree with overall and Type II error rates of 8.7% and 3.8% for the 5-year duration and 6.4% and 2.1% for the 10-year duration. Similar to the TRB, the same 8 demographic scenarios resulted in probabilities of persistence >0.5 for both monitoring durations (Fig. 9 and Fig. 10). Of the 3 scenarios with high likelihoods of persistence (i.e., ≥95%) for the 5-year duration, 2 were solely based on thresholds for $\bar{\varphi}_5$ and the remaining scenario included thresholds for $\bar{\varphi}_5$ and $\bar{\lambda}_5$. The same was true for the 10-year duration. The minimum threshold for scenarios involving only apparent survival was 0.90 ($\bar{\varphi}_5$) and 0.91 ($\bar{\varphi}_{10}$) for the 5- and 10-year durations, respectively, which were identical to the values for the TRB subpopulation.

We conducted a post hoc evaluation of $\bar{\lambda}_5$ and $\bar{\lambda}_{10}$ to identify thresholds that would lead to reliable predictions of population persistence. Compared with classification trees including all 3 short-term demographic rates, our post-hoc classification tree analyses generally produced much higher overall error rates for the TRB (5-year = 18.3%, 10-year = 18.0%) and for the UARB (5-year = 17.1%, 10-year = 16.7%). However, Type II error rates were only slightly greater for the TRB (5-year = 4.8%, 10-year = 4.4%) and the UARB (5-year = 3.7%, 10-year = 4.8%). Based on a slightly lower definition of persistence ($\geq$0.94), persistence was predicted for the TRB subpopulation when $\bar{\lambda}_5$ or $\bar{\lambda}_{10}$ were >1.03 and >1.02, respectively, and for the UARB subpopulation when $\bar{\lambda}_5$ or $\bar{\lambda}_{10}$ were >1.08 (Figs. 11–14).

Spatial capture-recapture

We detected 392 individual bears (191M:201F) 3,222 times over 7 years in the TRB and 109 bears (47M:62F) 1,399 times over 6 years in the UARB. Depending on the year, annual estimates of male and female abundance for the TRB study area ranged from 280 (95% CI = 238–349) and 182 (95% CI = 141–338) to 480 (95% CI = 405–557) and 280 (95% CI = 234–349), respectively (Fig.15A). The realized annual population growth rates (λ) fluctuated between 0.90 (95% CI = 0.75–1.15) and 1.21 (95% CI = 0.70–1.67) for males and between 0.70 (95% CI = 0.54–1.04) and 1.23 (95% CI = 1.01–1.53) for females (Fig. 15B). Annual φ varied between 0.66 (95% CI = 0.47–0.87) and 0.95 (95% CI = 0.54–0.99) for males and between 0.68 (95% CI = 0.52–0.95) and 0.99 (95% CI = 0.91–1.00) for females (Fig. 15C). Estimates of baseline weekly detection probabilities (p_0) were relatively low (range = 0.035–0.069) for a majority of females (π_A = 0.72, 95% CI = 0.65–0.82; Fig. 16A) and males (p_0 range = 0.005–0.012, π_A = 0.90, 95% CI = 0.80–0.95; Fig. 16B). Estimated σ_{SCR} for detection was 3.87 km (95% CI = 3.70–4.07) for males and 1.75 km (95% CI = 1.71–1.81) for females.

In the UARB, annual point estimates of female *N* ranged from 62.4 (95% CI = 44–100) to 106.0 (95% CI = 82–148) and estimates for males ranged from 23.1 (95% CI = 16–39) to 45.1 (95% CI = 35–63) during the study period (Fig. 17A). Annual estimates of male λ varied between 1.00 (95% CI = 0.58–1.60) to 1.32 (95% CI = 0.85–1.85) and female estimates varied between 0.84 (95% CI = 0.67–1.05) to 1.25 (95% CI = 0.92–1.85; Fig. 17B). Apparent survival rates (φ) were variable for males and females ranging from 0.64 (95% CI = 0.39–0.94) to 0.93 (95% CI = 0.59–0.99) for males and from 0.77 (95% CI = 0.60–0.90) to 0.98 (95% CI = 0.76–1.00) for females (Fig. 17C). Again, estimates of baseline detection probabilities (p_0) were relatively low (range = 0.017–0.108) for a majority of females (π_A = 0.65, 95% CI = 0.57–0.73; Fig. 18A) and males (range = 0.005–0.011, π_A = 0.81; 95% CI = 0.69–0.90; Fig. 18B). Estimated σ_{SCR} for detection was 6.17 km (95% CI = 5.66–7.23) for males and 2.37 km (95% CI = 2.26–2.47) for females.

Power analysis

Our SCRO analysis based on Design 2-4 and Design 2-8 resulted in high bias (-0.113–-0.077) and RMSE (0.087–0.136) and poor credible interval coverage (51–61%) for all demographic rates considered. We concluded that those designs were insufficient for reliable population monitoring given the modeling approach used and did not pursue those designs further with SCRO modeling. The absolute average bias of estimates for female $\bar{\varphi}_5$ (true $\bar{\varphi}_5$ = 0.91) was -0.060 (95% CI = -0.133–-0.009) for Design 1-4 (Table 4) and was slightly lower at -0.046 (95% CI = -0.102–0.019) for Design 1-8 (Table 5). However, credible interval coverage generally was poor for both designs (68 and 77%, respectively). Absolute average bias of female $\bar{\lambda}_5$ (true $\bar{\lambda}_5$ = 1.0) for Design 1-4 was similar to that of $\bar{\varphi}_5$ at -0.067 (95% CI = -0.181–0.050), whereas average bias for Design 1-4 was lower -0.038 (95% CI = -0.115–0.034). Credible interval coverage was also considerably less than nominal for Design 1-4 (54%) and for Design 1-8 (81%).

For the SCJS analysis, average bias in $\bar{\varphi}_5$ steadily decreased across study designs as sampling effort increased in terms of number of traps and occasions (Tables 2–5). Design 1-4 and Design 1-8 both resulted in average bias $\leq$0.01 and achieved near to better than nominal credible interval coverage.

Our non-spatial Pradel modeling approach resulted in bias of $\bar{\varphi}_5$ ranging from -0.092 (95% CI = -0.201–0.010) for Design 2-8 to -0.046 (95% CI = -0.113–0.023) for Design 1-8 (Tables 2–5). Credible interval coverage was substantially lower than nominal ranging from 62 to 77%. Estimates of $\bar{\lambda}_5$ (true $\bar{\lambda}_5$ = 1.0) were nearly unbiased for all designs (i.e., absolute average bias <0.007), although estimates were highly variable across simulations for all designs with the narrowest percentile range (CI = -0.089–0.097) for bias in $\bar{\lambda}_5$ corresponding to Design 1-8 (Table 5). Credible interval coverage was near to better than nominal (i.e., >92%) for all study designs.

DISCUSSION

A better understanding of which demographic rates drive population dynamics is vital to long-term planning, especially for monitoring persistence, and our sensitivity analysis for long-term demographic rates provided that. For example, viability of the UARB subpopulation was most sensitive to variation in annual female φ, whereas the TRB subpopulation was most affected by the long-term mean of annual female φ. Indeed, greater importance of temporal variation to persistence of the UARB is to be expected given its relatively small size which makes it more susceptible to environmental stochasticity even when long-term average female λ is positive (Shaffer 1987, Mills 2007).

Another benefit of the sensitivity analysis was that our classification trees also allowed us to place long-term demographic rate estimates from Laufenberg et al. (2016) into a broader context. By simulating population trajectories across a much wider range of conditions (i.e., different combinations of survival and recruitment parameters) than did Laufenberg et al. (2016), we were able to identify demographic scenarios, other than those observed during the PVA period, which could also result in high persistence probabilities. Those results relax the assumption made in the original PVA that the population dynamics (i.e., means and variances) observed during that study must persist for the determination of long-term viability to hold. We believe this is especially important because it acknowledges that long-term viability can occur under a wider range of demographic conditions which may provide greater flexibility to managers.

Our variable importance analysis for short-term demographic rates indicated that average annual female φ over 5-year ($\bar{\varphi}_5$) or 10-year ($\bar{\varphi}_{10}$) periods were good predictors of extinction risk for both subpopulations. The importance of female φ also was evident in our short-term demographic rate classification trees as it was included in every scenario that resulted population persistence ($\geq$95%). Although we identified scenarios whereby a single demographic rate corresponded to high persistence probabilities (e.g., $\bar{\varphi}_5 > 0.91$), all parameters should be evaluated. For example, if at TRB $\bar{\varphi}_5 = 0.89$ and $\bar{N}_5 = 120$, the probability of population persistence would still be high ($p = 0.94$) based on scenario S14 in Fig. 6.

Our power analysis revealed a negative bias in $\bar{\varphi}_5$ estimated with SCJS models for designs with the greatest trap spacing (Designs 2-4 and 2-8). Although capture biases can result in biases in φ if not accounted for, they are typically low (Carothers 1973) though more recent work has suggested that negative biases in φ associated with ignoring individual capture heterogeneity can be significant, especially if φ is used to estimate λ for long-lived species for which growth rates are highly sensitive to variation in survival (Fletcher et al. 2012). Our Pradel analysis results also indicated negative bias in $\bar{\varphi}_5$ but not in λ_5 despite explicitly accounting for capture heterogeneity with finite-mixture models. This is in agreement with Marescot et al.

(2011) who reported that estimates of φ were biased low and estimates of λ were unaffected by individual capture heterogeneity, although bias was greater when heterogeneity was more extreme. We contend that difficulties associated with obtaining unbiased estimates of φ are prevalent when strong heterogeneity is present because capture data are dominated by individuals that are more detectable which artificially inflates detection probability estimates resulting in negatively biased estimates of φ. Such effects are even more pronounced for sparse data sets, such as those produced by our Design 2-4 and Design 2-8, because detecting and reliably estimating capture biases can be difficult when data are limited (Laufenberg et al. 2013, Augustine et al. 2014). Our estimates from the SCRO analysis indicated that both $\bar{\varphi}_5$ and $\bar{\lambda}_5$ were negatively biased, though credible intervals for $\bar{\lambda}_5$ were wide. We suspect that the additional parameters associated with SCRO models require more data to obtain reliable estimates than Design 2-4 and Design 2-8 could produce.

Our post-hoc evaluation suggested that $\lambda > 1.03$ at TRB and >1.08 at UARB would predict population persistence with probability $\geq$0.94. Small populations are at greater risk than larger populations due to greater susceptibility to stochastic processes such as environmental variation in demographic rates over time or demographic stochasticity even when average growth rates are stable (White 2000, Mills 2007). Therefore, small populations such as the UARB would be expected to require long-term average growth rates greater than larger populations such as the TRB to ensure viability as our post-hoc analysis indicated. Although overall error rates were much higher for λ-only trees, Type II error rates were <5% for all durations and subpopulations indicating trigger points based on thresholds identified from those trees would be conservative. One of the assumptions of the Pradel model is that the study area size does not change, so the ability to monitor range expansion with the method is limited (Hines and Nichols 2002) unless adjustments for changing study area size is accommodated (Clark and Eastridge 2006). Again, different combinations of parameter values can produce viable population predictions so no one parameter should be relied on exclusively.

The overall poor performance of the SCRO models across all prospective sampling designs can probably be explained by the additional parameters that had to be estimated with spatially explicit models that included finite mixtures. The analysis by Chandler and Clark (2014) did not account for capture heterogeneity beyond spatial aspects of the sampling process and used a sampling design that was more intensive than the designs we tested. The sparse data coupled with the additional parameters resulted in poor model fits and biased estimates. Spatially explicit designs for estimating population trend are undoubtedly possible, but the sampling effort would be greater than what is currently planned. Spatially explicit models have an advantage over non-spatial models in that spatial capture heterogeneity is explicit in the modeling process. However, given our finding that λ can be reliably estimated with non-spatial Pradel models, there is little motivation for the SCRO estimate other than to perhaps obtain a more rigorous estimate of N. That analysis could always be done on an ad hoc basis or intensive sampling required to estimate N can be implemented at more affordable intervals (e.g., every 5 years) which could better ensure population sizes do not decline to precarious levels. Radio telemetry data to independently estimate survival and recruitment are also being collected; those data could be used to construct a projection matrix similar to that used in the PVA for TRB and TRC (Laufenberg et al. 2016) from which asymptotic growth rate could be derived. Alternatively, those data could be combined with the noninvasive capture-recapture data set to produce an integrated population analysis (Powell et al. 2000, Schaub and Abadi 2011, Dudgeon et al. 2015) or to improve the performance of SCRO models (Sollmann et al. 2013) but that is beyond the scope of this study.

MANAGEMENT IMPLICATIONS

Estimating long-term demographic rates similar to those used in Laufenberg et al. (2016) to assess population viability requires substantial effort and financial resources. Therefore, identifying alternative short-term demographic parameters capable of predicting long-term persistence yet requiring fewer resources to collect is critical for long-term monitoring initiatives. Our simulations suggest that a threshold of $\bar{\varphi}_5$ = 0.91 can reliably predict a 95% probability of persistence for both study areas. All of the sampling designs we evaluated indicated negative bias in φ, meaning that the real parameters are probably higher than those estimated. Consequently, it is possible that $\bar{\varphi}_5$ slightly <0.91 will also be indicative of population persistence over the long term. Regardless, non-invasive capture-recapture data planned to be collected during the post-delisting monitoring period can easily be used to estimate of λ and f in addition to φ based on Pradel robust design models. Our research and that of others suggests that λ is unbiased using a variety of methods, even for Design 2-4, which represents a much wider spacing of traps than what is currently being employed. Although the current protocol is 3 weeks of hair sampling, we simulated 4 weeks because it was possible to evaluate mixture models for individual capture heterogeneity (Pledger 2000), which is not possible with only 3 weeks of sampling. Therefore, Design 2-4 may represent a reasonable compromise between reliability and efficiency for estimating both φ and λ.

We emphasized tipping points or triggers in our analysis, and such concepts are useful for endangered species management. Other tipping points are possible depending on different probabilities of persistence or levels of uncertainty that managers are comfortable with.

Regardless, we suggest that managers should look at the entirety of the data available for species monitoring, rather than rely on a single go, no-go tipping point for any one subpopulation. The planned monitoring protocols allow for the calculation of a variety of important population parameters based on the CMR data, and other parameters can be estimated with the telemetry data. We suggest that the totality of the data should be considered across all the subpopulations in a broad context when evaluating post-delisting trends and prospects for re-listing under the ESA.

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Table 1. Minimums and maximums of posterior distributions for demographic rates estimated by Laufenberg et al. (2016) from DNA-based capture-mark-recapture data collected from Louisiana black bears in the Tensas River Basin (TRB; 2006–2012) and in the Upper Atchafalaya River Basin (UARB; 2007–2012), Louisiana, USA.

	TRB		UARB	
	Minimum	Maximum	Minimum	Maximum
Recruitment intercept (β_0)[1]	-3.6321600	42.5942900	-3.9625500	43.2671000
Recruitment slope (β_1)	-0.3268900	-0.0000340	-1.3392500	-0.0000017
Recruitment standard deviation (σ_f)	0.0000633	1.9998470	0.0000106	1.9999760
Survival mean (μ_φ)[2]	0.8456470	3.6779160	0.3466130	4.0957950
Survival standard deviation(σ_φ)	0.0001330	0.9997030	0.0000859	0.9999690

[1] Recruitment parameters estimated on the natural log scale

[2] Survival parameters estimated on the logit scale

Table 2. Estimates of absolute average bias, root mean squared error (RMSE), and credible interval coverage for demographic rates in the Upper Atchafalaya River Basin estimated from simulated data using open population spatially explicit Cormack-Jolly-Seber (SCJS) and non-spatial Pradel modeling approaches. Population simulations were based on annual survival rates that averaged 0.91 and population growth rates that averaged 1.0 over a 5 year period. Spatially referenced detection data were simulated based on a sampling design with a 5-km trap spacing and 4 occasions (Design 2-4).

	Bias[1]	Bias LCL[2]	Bias UCL	RMSE	RMSE LCL	RMSE UCL	Coverage[3]
SCJS							
Mean φ ($\bar{\varphi}_5$)[4]	-0.065	-0.151	0.004	0.078	0.001	0.149	0.95
Pradel							
Mean φ ($\bar{\varphi}_5$)	-0.079	-0.207	0.090	0.114	0.001	0.207	0.77
Mean λ (λ_5)	0.007	-0.192	0.198	0.099	0.000	0.198	0.93

[1] Average over values from 100 simulated data sets.
[2] 2.5% (LCL) and 97.5% (UCL) percentiles of values from 100 simulated data sets.
[3] Proportion of confidence intervals containing the true value from 100 simulated data sets.
[4] Means of annual demographic rates over 5-year period.

Table 3. Estimates of absolute average bias, root mean squared error (RMSE), and credible interval coverage for demographic rates in the Upper Atchafalaya River Basin estimated from simulated data using open population spatially explicit Cormack-Jolly-Seber (SCJS) and non-spatial Pradel modeling approaches. Population simulations were based on annual survival rates that averaged 0.91 and population growth rates that averaged 1.0 over a 5 year period. Spatially referenced detection data were simulated based on a sampling design with a 5-km trap spacing and 8 occasions (Design 2-8).

	Bias[1]	Bias LCL[2]	Bias UCL	RMSE	RMSE LCL	RMSE UCL	Coverage[3]
SCJS							
Mean φ ($\bar{\varphi}_5$)[4]	-0.027	-0.103	0.024	0.042	0.001	0.098	0.95
Pradel							
Mean φ ($\bar{\varphi}_5$)	-0.092	-0.201	0.011	0.109	0.006	0.187	0.66
Mean λ (λ_5)	0.005	-0.117	0.152	0.071	0.000	0.152	0.96

[1] Average over values from 100 simulated data sets.
[2] 2.5% (LCL) and 97.5% (UCL) percentiles of values from 100 simulated data sets.
[3] Proportion of confidence intervals containing the true value from 100 simulated data sets.
[4] Means of annual demographic rates over 5-year period.

Table 4. Estimates of absolute average bias, root mean squared error (RMSE), and credible interval coverage for demographic rates in the Upper Atchafalaya River Basin estimated from simulated data using open population spatially explicit capture-mark-recapture (SCRO), spatially explicit Cormack-Jolly-Seber (SCJS), and non-spatial Pradel modeling approaches. Population simulations were based on annual survival rates that averaged 0.91 and population growth rates that averaged 1.0 over a 5 year period. Spatially referenced detection data were simulated based on a sampling design with a 2.5-km trap spacing and 4 occasions (Design 1-4).

	Bias[1]	Bias LCL[2]	Bias UCL	RMSE	RMSE LCL	RMSE UCL	Coverage[3]
SCRO							
Mean φ ($\bar{\varphi}_5$)[4]	-0.060	-0.133	-0.009	0.069	0.001	0.120	0.68
Mean λ (λ_5)	-0.067	-0.181	0.050	0.091	0.001	0.167	0.54
SCJS							
Mean φ ($\bar{\varphi}_5$)	-0.005	-0.060	0.035	0.038	0.027	0.000	0.99
Pradel							
Mean φ ($\bar{\varphi}_5$)	-0.073	-0.166	0.011	0.087	0.001	0.149	0.62
Mean λ (λ_5)	0.006	-0.092	0.123	0.060	0.000	0.123	0.96

[1] Average over values from 100 simulated data sets.
[2] 2.5% (LCL) and 97.5% (UCL) percentiles of values from 100 simulated data sets.
[3] Proportion of confidence intervals containing the true value from 100 simulated data sets.
[4] Means of annual demographic rates over 5-year period.

Table 5. Estimates of absolute average bias, root mean squared error (RMSE), and credible interval coverage for demographic rates in the Upper Atchafalaya River Basin estimated from simulated data using open population spatially explicit capture-mark-recapture (SCRO), spatially explicit Cormack-Jolly-Seber (SCJS), and non-spatial Pradel modeling approaches. Population simulations were based on annual survival rates that averaged 0.91 and population growth rates that averaged 1.0 over a 5 year period. Spatially referenced detection data were simulated based on a sampling design with a 2.5-km trap spacing and 8 occasions (Design 1-8).

	Bias[1]	Bias LCL[2]	Bias UCL	RMSE	RMSE LCL	RMSE UCL	Coverage[3]
SCRO							
Mean φ ($\bar{\varphi}_5$)[4]	-0.046	-0.102	0.019	0.056	0.002	0.102	0.77
Mean λ (λ_5)	-0.038	-0.115	0.034	0.054	0.000	0.106	0.81
SCJS							
Mean φ ($\bar{\varphi}_5$)	0.010	-0.031	0.052	0.024	0.000	0.044	0.93
Pradel							
Mean φ ($\bar{\varphi}_5$)	-0.046	-0.113	0.023	0.058	0.002	0.107	0.72
Mean λ (λ_5)	-0.002	-0.089	0.097	0.047	0.001	0.097	0.92

[1] Average over values from 100 simulated data sets.
[2] 2.5% (LCL) and 97.5% (UCL) percentiles of values from 100 simulated data sets.
[3] Proportion of confidence intervals containing the true value from 100 simulated data sets.
[4] Means of annual demographic rates over 5-year period.

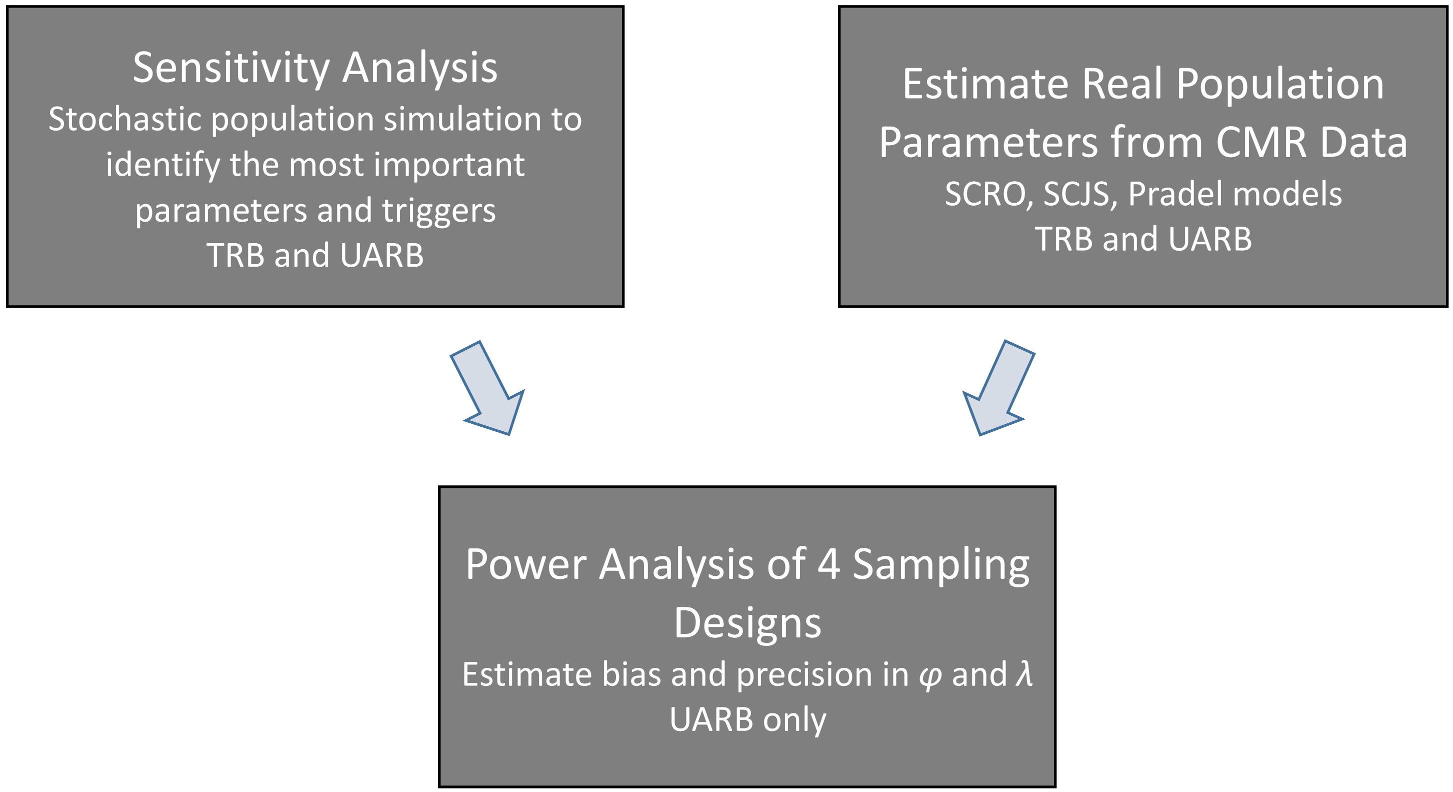

Figure 1. Conceptual relationships among the 3 stages of analysis to evaluate performance of sampling for predicting probability of persistence of Louisiana black bears.

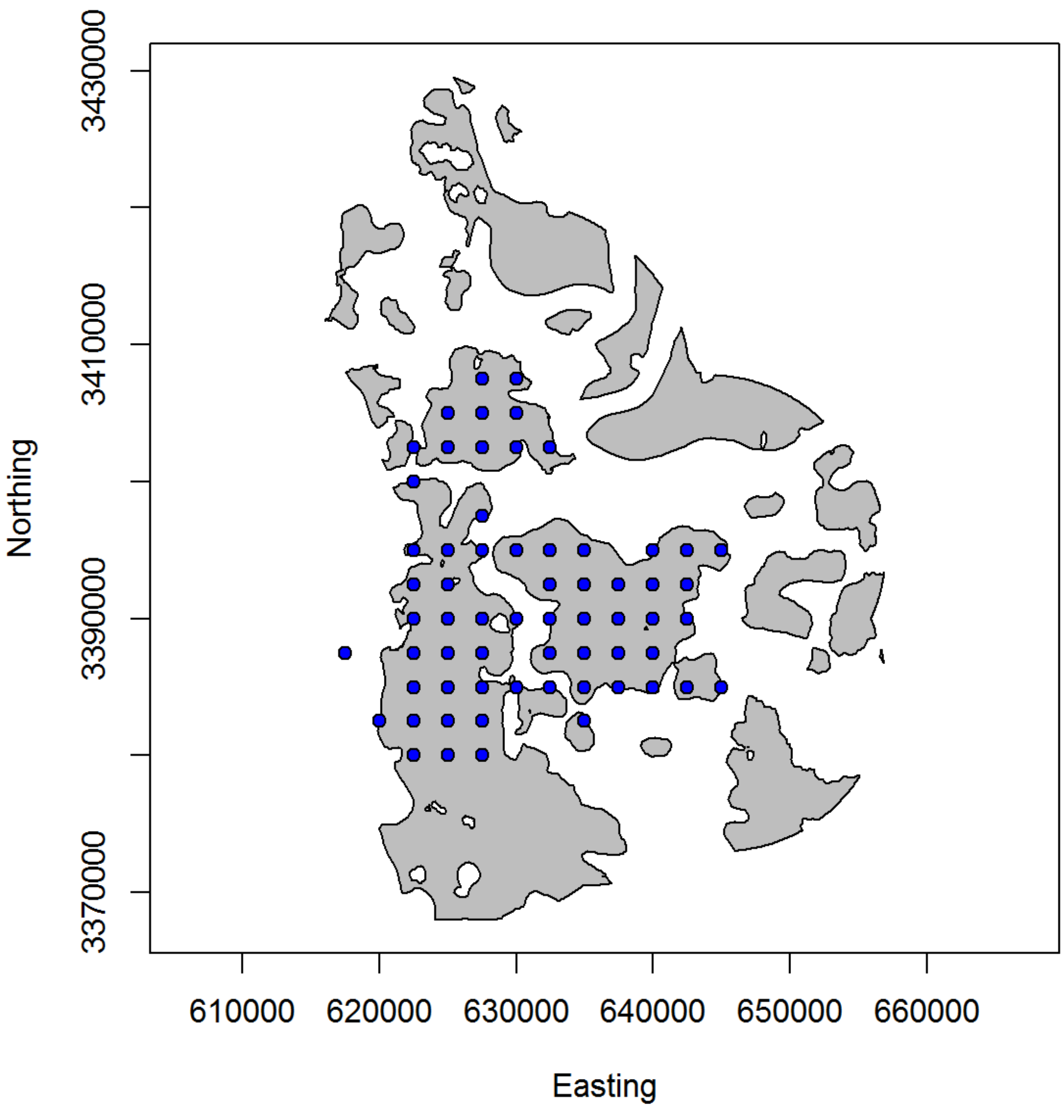

Figure 2. Trap configuration for the Upper Atchafalaya Louisiana black bear subpopulation based on a trap spacing of 2.5 km approximately equivalent to 1 × σ_{SCR} (σ_{SCR} = 2.4 km). Traps depicted by blue circles and gray areas define the state space used for all spatially explicit analyses.

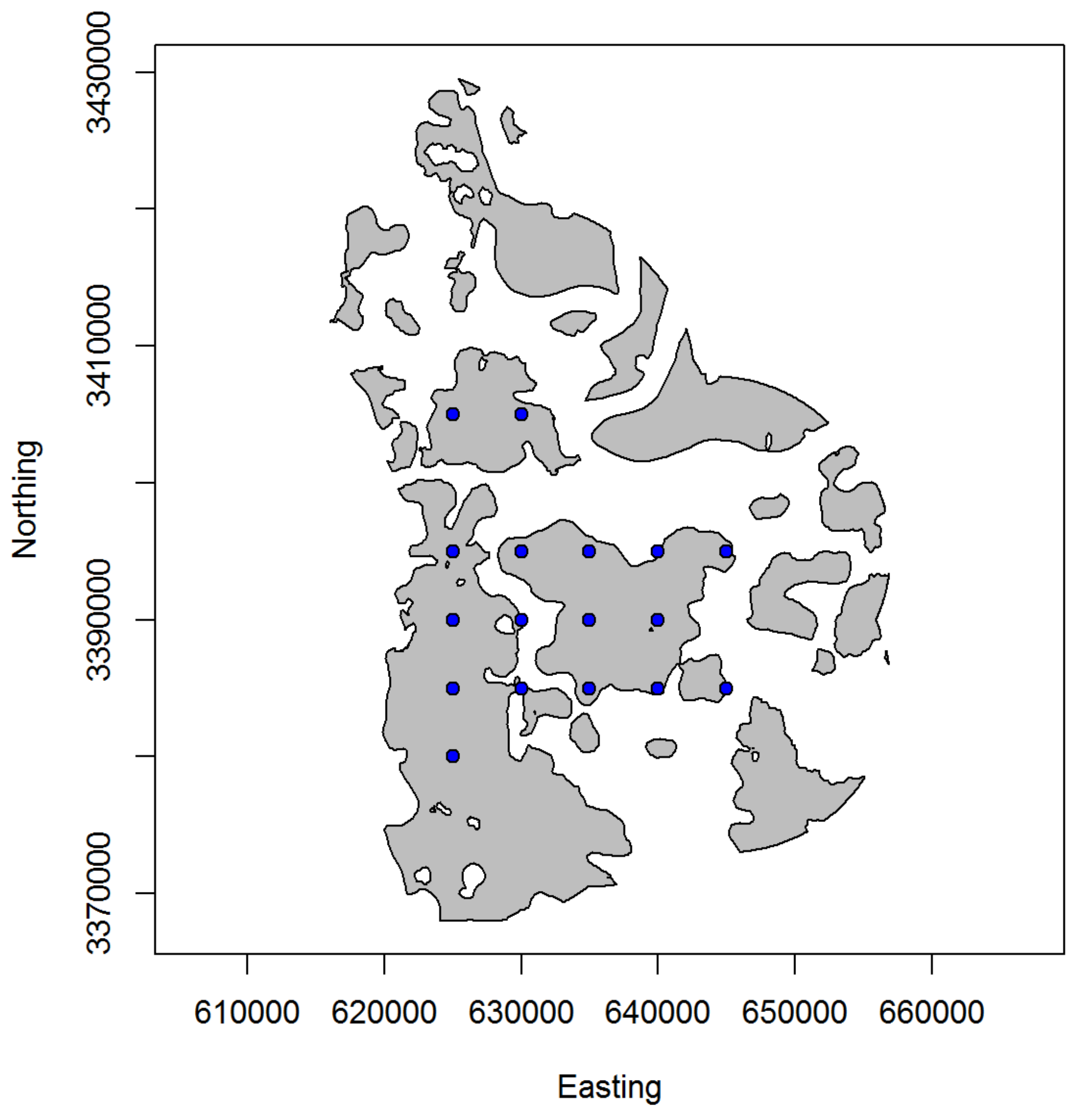

Figure 3. Trap configuration for the Upper Atchafalaya Louisiana black bear subpopulation based on a trap spacing of 5 km approximately equivalent to $2 \times \sigma_{SCR}$ (σ_{SCR} = 2.4 km). Traps depicted by blue circles and gray areas define the state space used for all spatially explicit analyses.

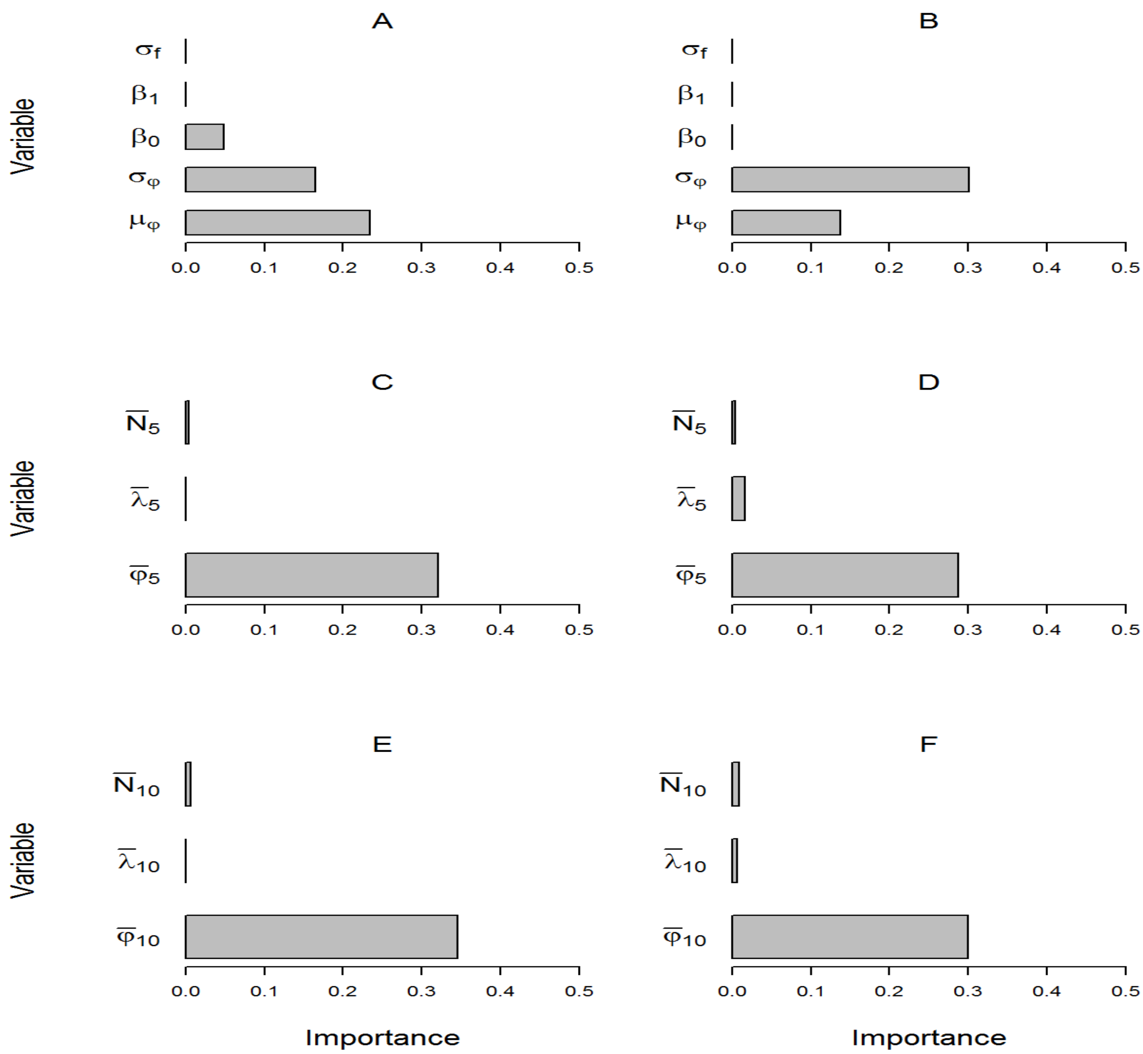

Figure 4. Variable importance values estimated from random forests of conditional classification trees based on stochastic population simulations for females in the Tensas River Basin (panels A, C, and E) and Upper Atchafalaya River Basin (panels B, D, and F) subpopulations. Explanatory variables corresponded to long-term demographic rates used to generate population trajectories (panels A and B) or averages derived from the first 5 years (panels C and D) or the first 10 years (panels E and F) of population trajectories. Explanatory variable definitions were as follows: σ_f was temporal variation in per-capita recruitment, β_0 and β_1 were the intercept and slope coefficients describing log-linear density-dependence in per-capita recruitment, σ_φ was temporal variation in apparent survival, μ_φ was temporal mean in apparent survival, $\bar{N}_5$ and $\bar{N}_{10}$were average abundance over 5 and 10 year periods, $\bar{\lambda}_5$ and $\bar{\lambda}_{10}$ were average population growth rates over 5 and 10 year periods, and $\bar{\varphi}_5$ and $\bar{\varphi}_5$ were average apparent survival probabilities over 5 and 10 year periods. The response for all random forests was a binary variable that coded for population extinction. All demographic rates are for females only.

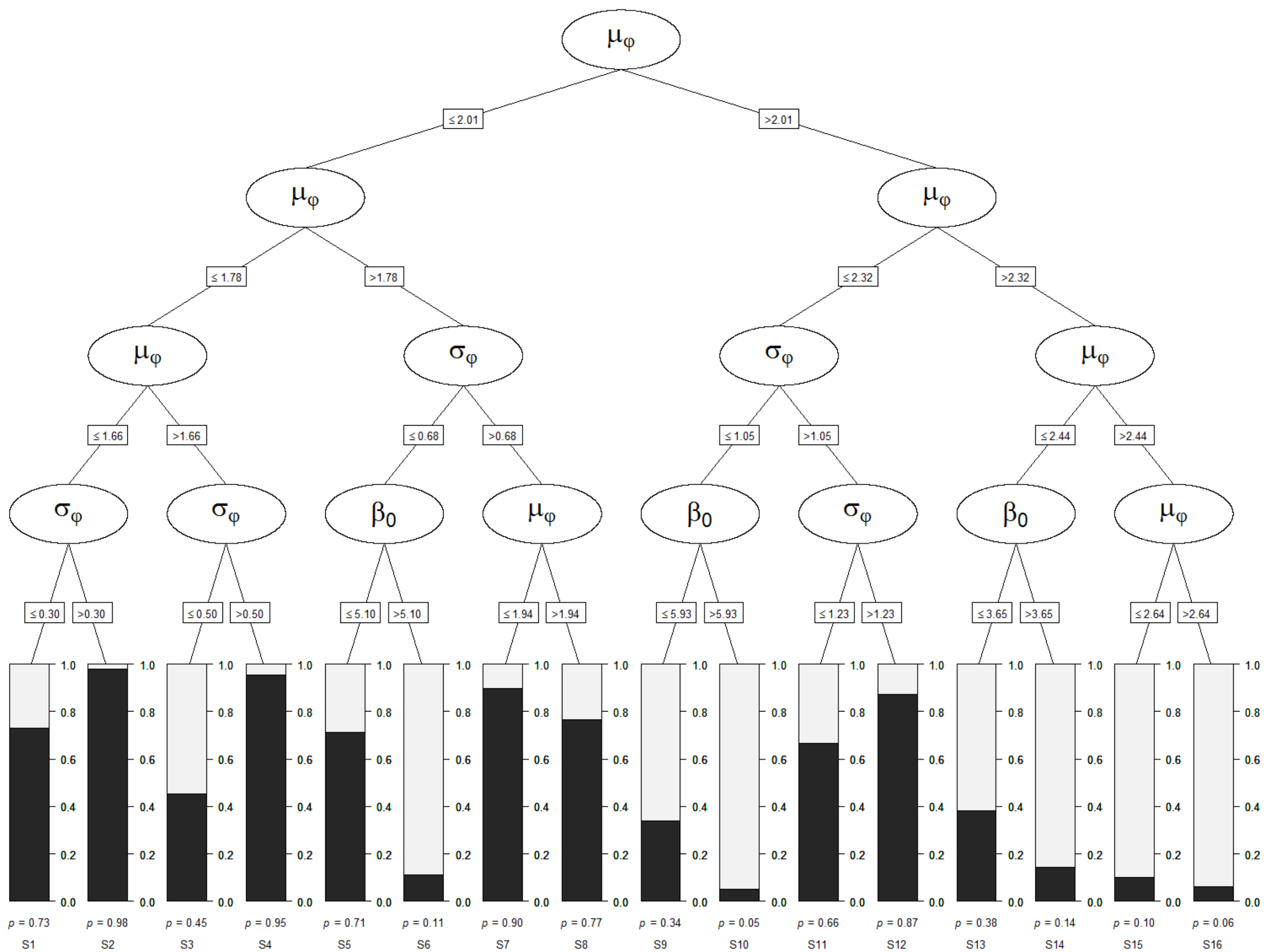

Figure 5. Conditional classification tree for long-term female demographic thresholds for the Tensas River Basin subpopulation. Proportions of bars in dark gray and values below bars (e.g., p = 0.73) represent extinction probability. Values for mean apparent survival (μ_φ) and temporal variation of μ_φ (σ_φ) are on the logit scale and values for the intercept (β_0), slope (β_1), and temporal variation (σ_f) for a log-linear model describing density dependence in annual per-capita recruitment (f) are on the natural log scale.

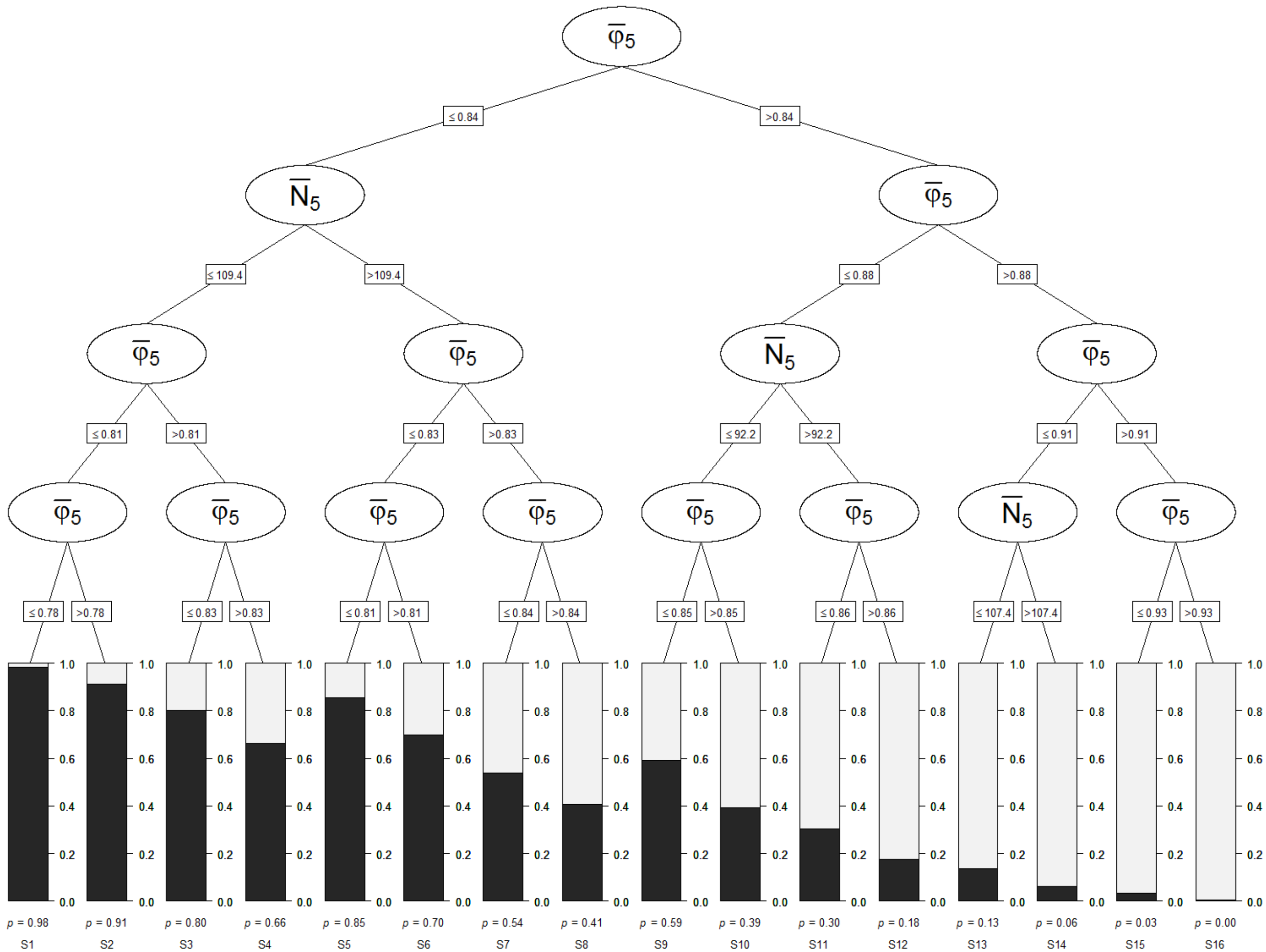

Figure 6. Conditional classification tree for short-term female demographic thresholds for the for the Tensas River Basin subpopulation based on 5-year monitoring duration. Proportions of bars in dark gray and values below bars (e.g., p = 0.98) represent extinction probability. Values for 5-year averages of abundance ($\bar{N}_5$) and apparent survival ($\bar{\varphi}_5$) are on the real scale.

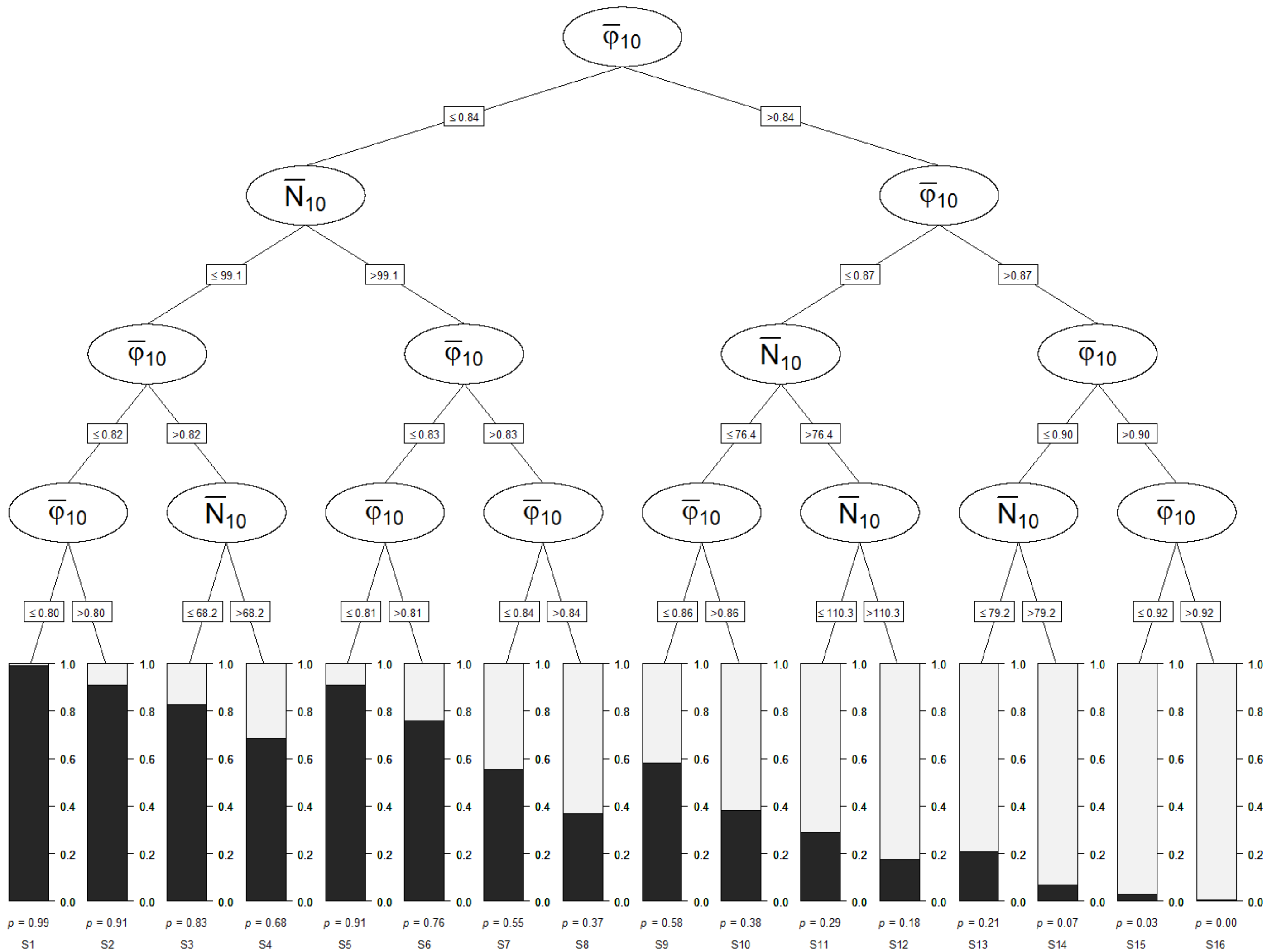

Figure 7. Conditional classification tree for short-term female demographic thresholds for the Tensas River Basin subpopulation based on 10-year monitoring duration. Proportions of bars in dark gray and values below bars (e.g., *p* = 0.99) represent extinction probability. Values for 10-year averages of abundance ($\bar{N}_5$) and apparent survival ($\bar{\varphi}_5$) are on the real scale.

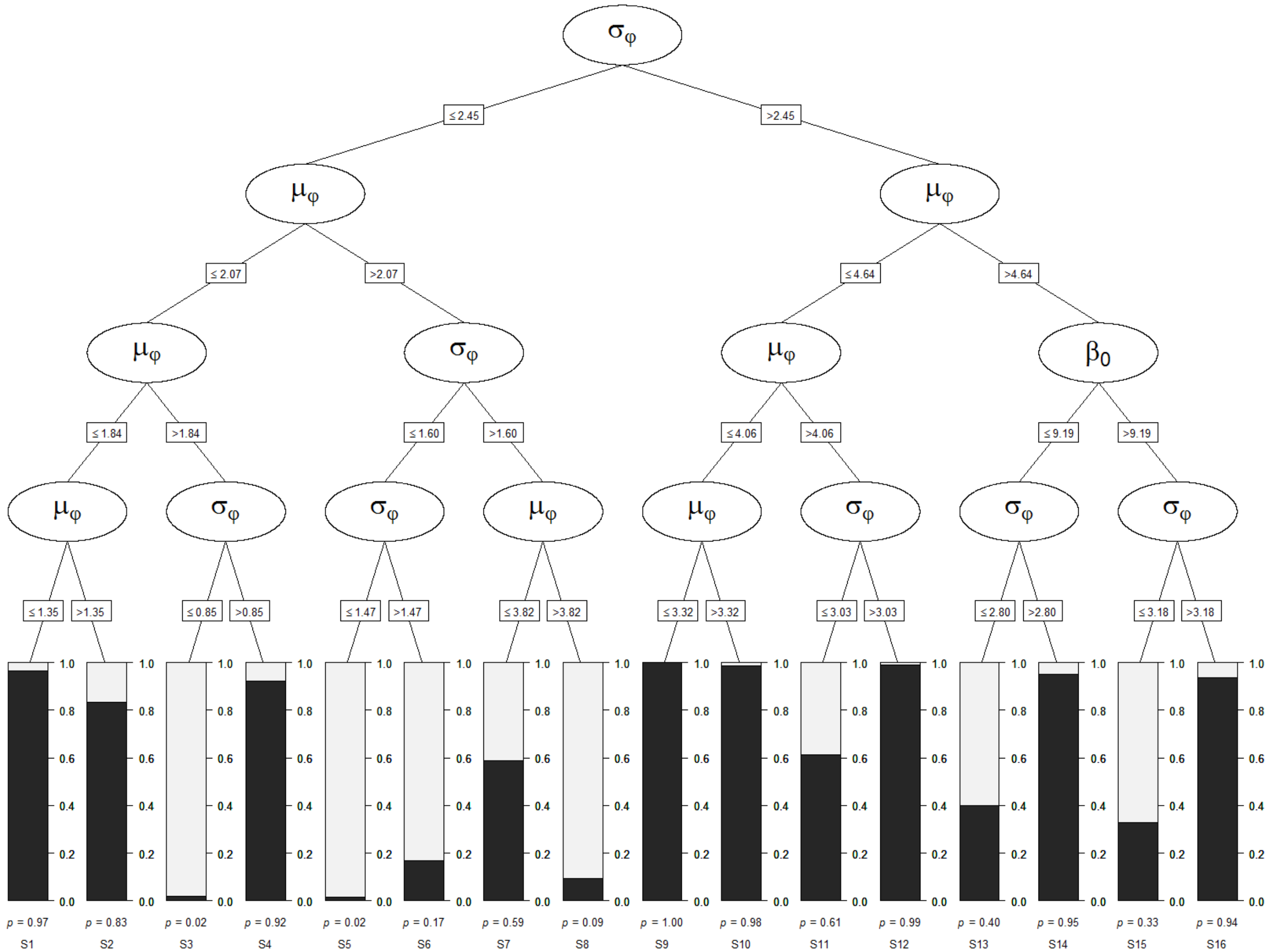

Figure 8. Conditional classification tree for long-term female demographic thresholds for the Upper Atchafalaya River Basin subpopulation. Proportions of bars in dark gray and values below bars (e.g., p = 0.97) represent extinction probability. Values for mean apparent survival (μ_φ) and temporal variation of μ_φ (σ_φ) are on the logit scale and values for the intercept (β_0), slope (β_1), and temporal variation (σ_f) for a log-linear model describing density dependence in annual per-capita recruitment (f) are on the natural log scale.

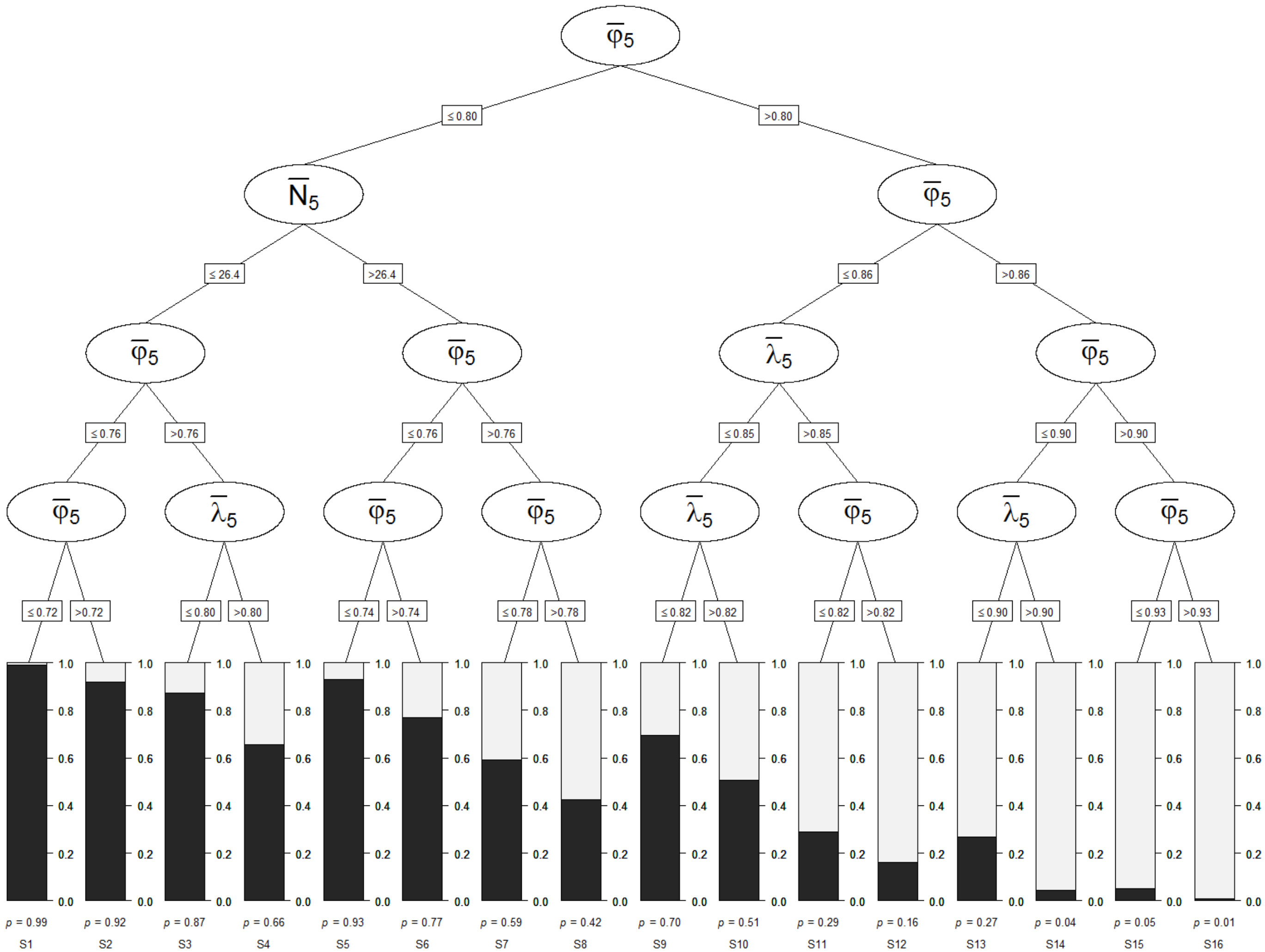

Figure 9. Conditional classification tree for short-term female demographic thresholds for the Upper Atchafalaya River Basin subpopulation based on 5-year monitoring duration. Proportions of bars in dark gray and values below bars (e.g., p = 0.99) represent extinction probability. Values for 5-year averages of abundance ($\bar{N}_5$), apparent survival ($\bar{\varphi}_5$), and population growth rate ($\bar{\lambda}_5$) are on the real scale.

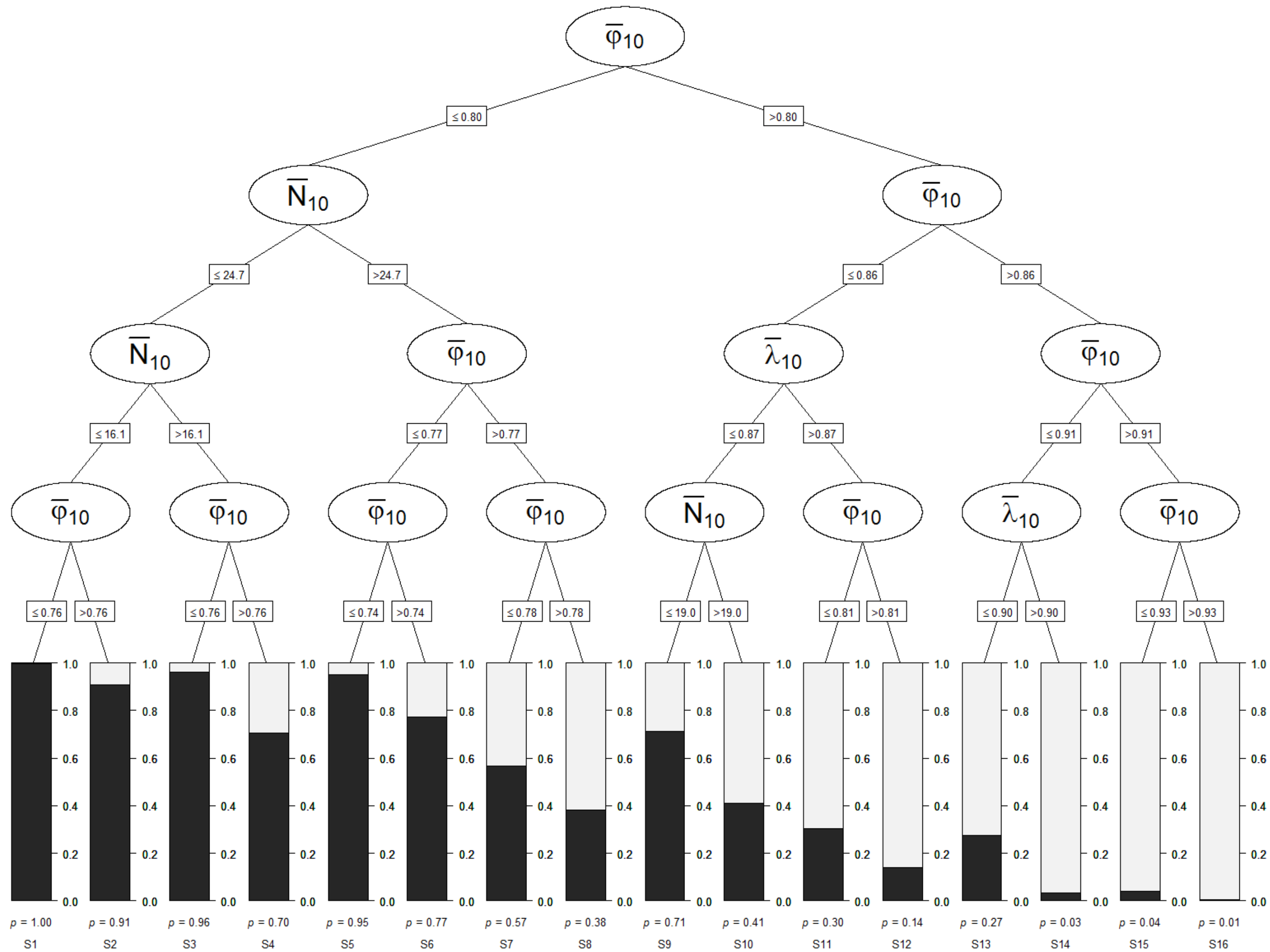

Figure 10. Conditional classification tree for short-term demographic thresholds for the Upper Atchafalaya River Basin subpopulation based on 10-year monitoring duration. Proportions of bars in dark gray and values below bars (e.g., p = 1.0) represent extinction probability. Values for 10-year averages of abundance ($\bar{N}_{10}$), apparent survival ($\bar{\varphi}_{10}$), and population growth rate ($\bar{\lambda}_{10}$) are on the real scale.

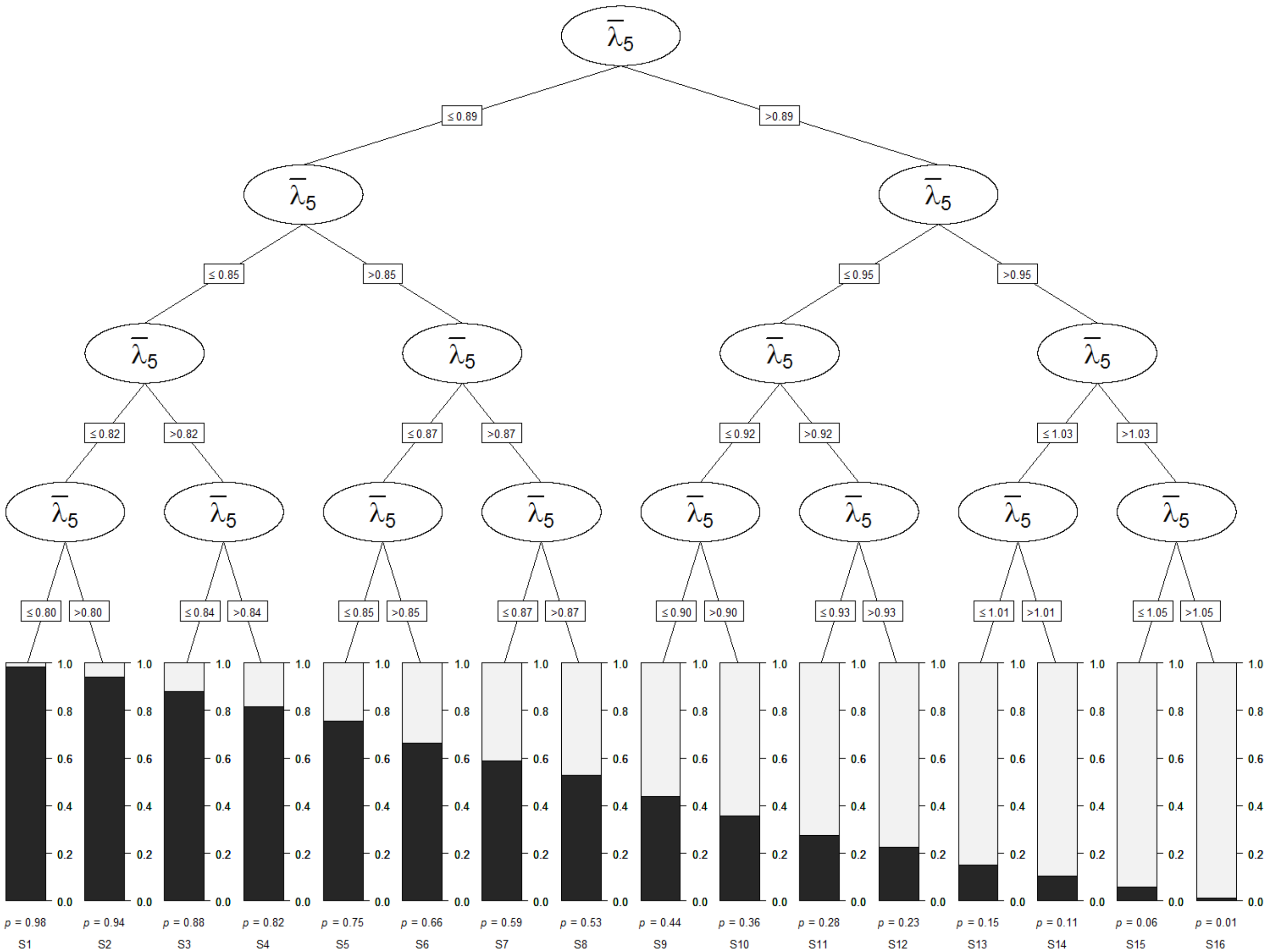

Figure 11. Conditional classification tree for short-term growth rate thresholds for the Tensas River Basin subpopulation based on 5-year monitoring duration. Proportions of bars in dark gray and values below bars (e.g., p = 0.98) represent extinction probability. All population growth rate ($\bar{\lambda}_5$) values are on the real scale.

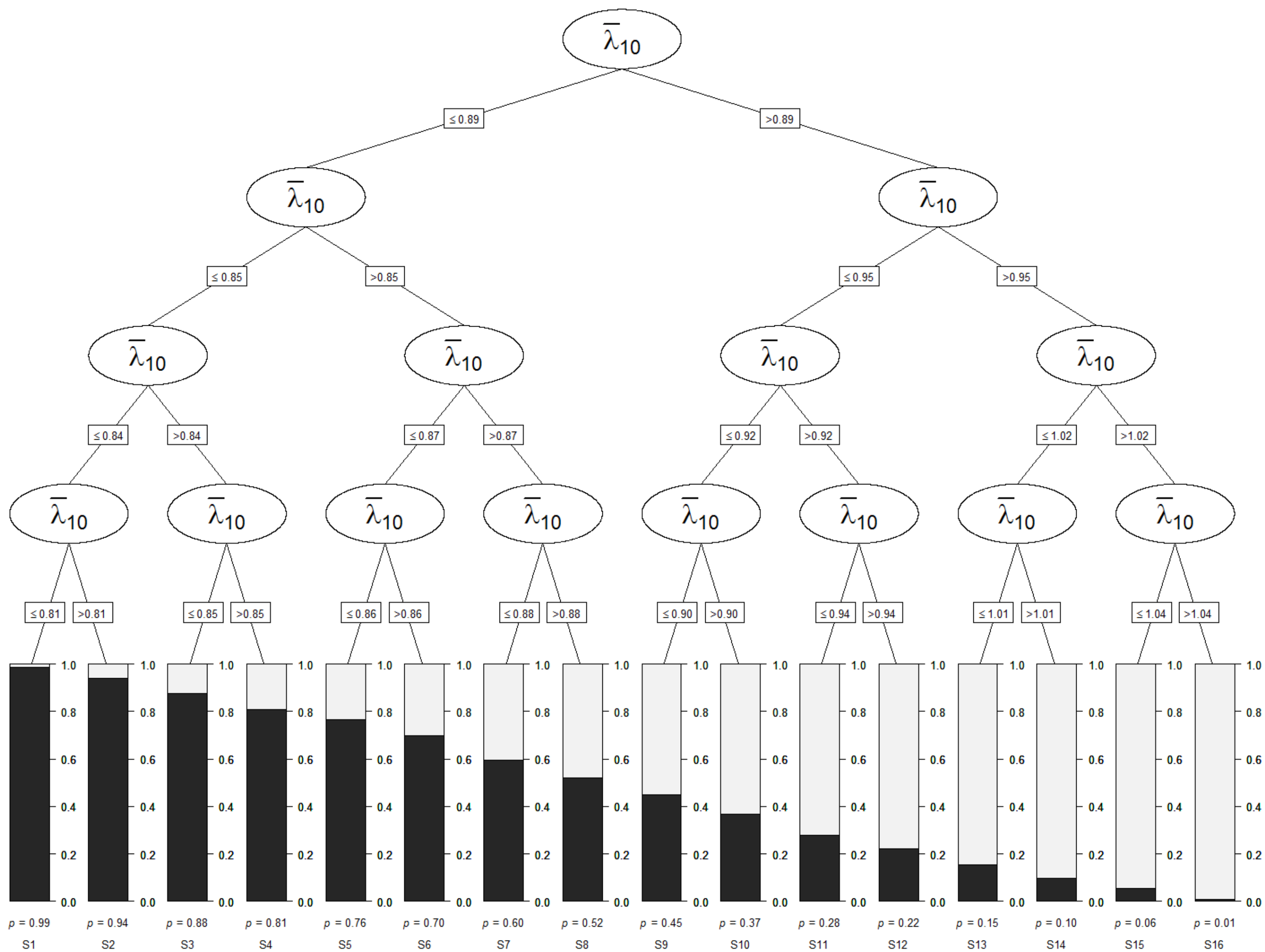

Figure 12. Conditional classification tree for short-term growth rate thresholds for the Tensas River Basin subpopulation based on 10-year monitoring duration. Proportions of bars in dark gray and values below bars (e.g., p = 0.99) represent extinction probability. All population growth rate ($\bar{\lambda}_{10}$) values are on the real scale.

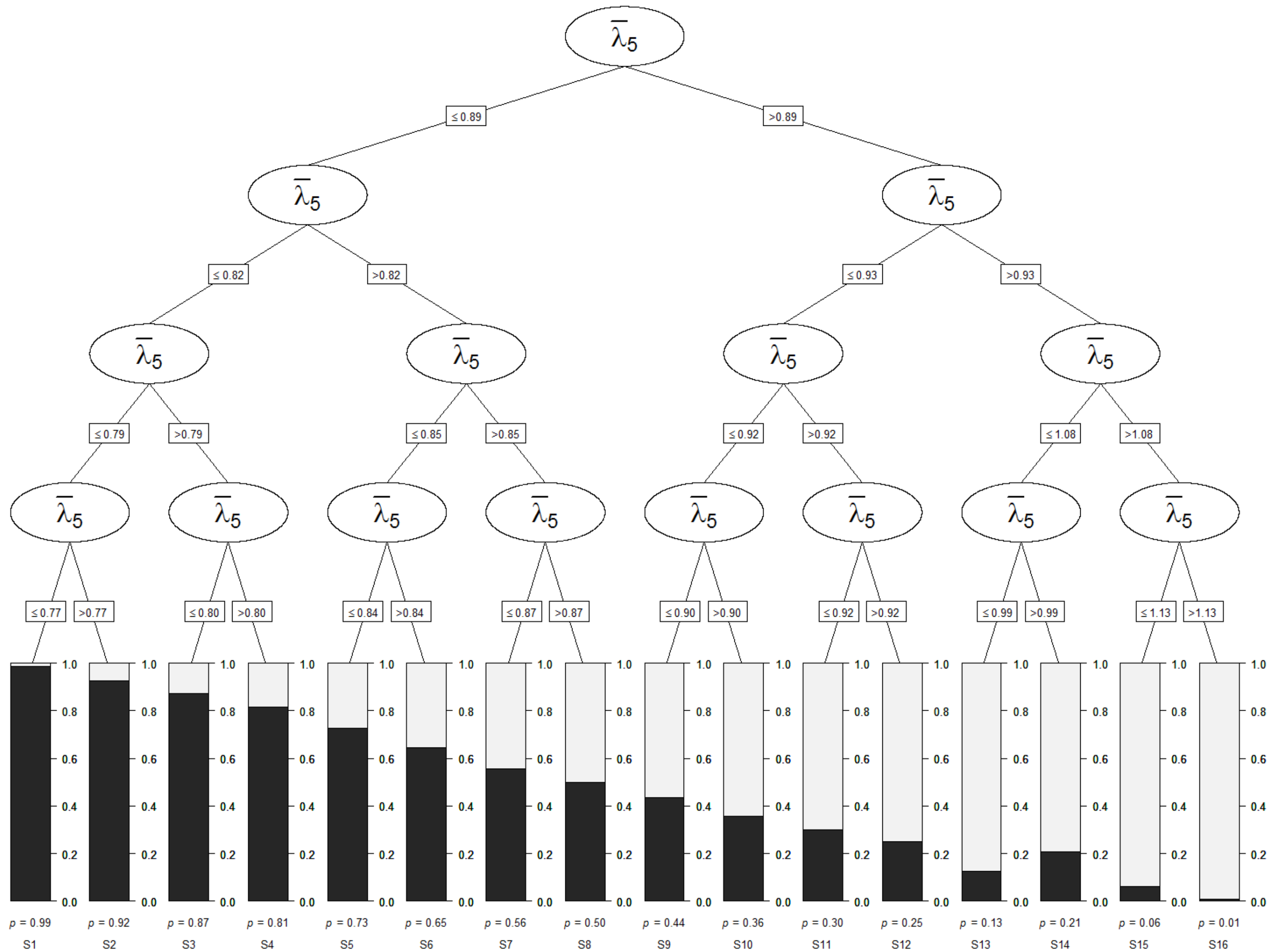

Figure 13. Conditional classification tree for short-term growth rate thresholds for the Upper Atchafalaya River Basin subpopulation based on 5-year monitoring duration. Proportions of bars in dark gray and values below bars (e.g., p = 0.99) represent extinction probability. All population growth rate ($\bar{\lambda}_5$) values are on the real scale.

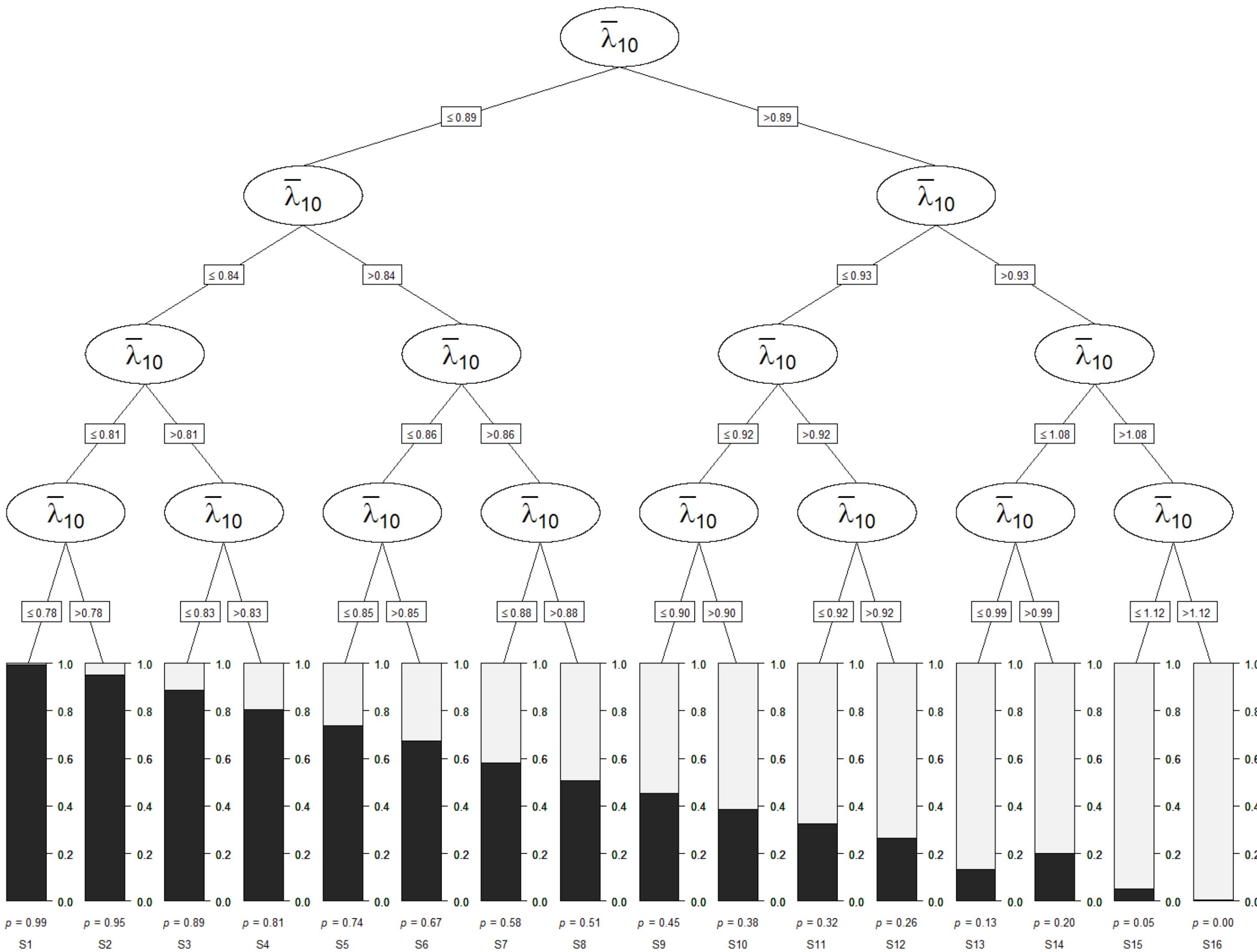

Figure 14. Conditional classification tree for short-term growth rate thresholds for the Upper Atchafalaya River Basin subpopulation based on 10-year monitoring duration. Proportions of bars in dark gray and values below bars (e.g., p = 0.99) represent extinction probability. All population growth rate ($\bar{\lambda}_{10}$) values are on the real scale.

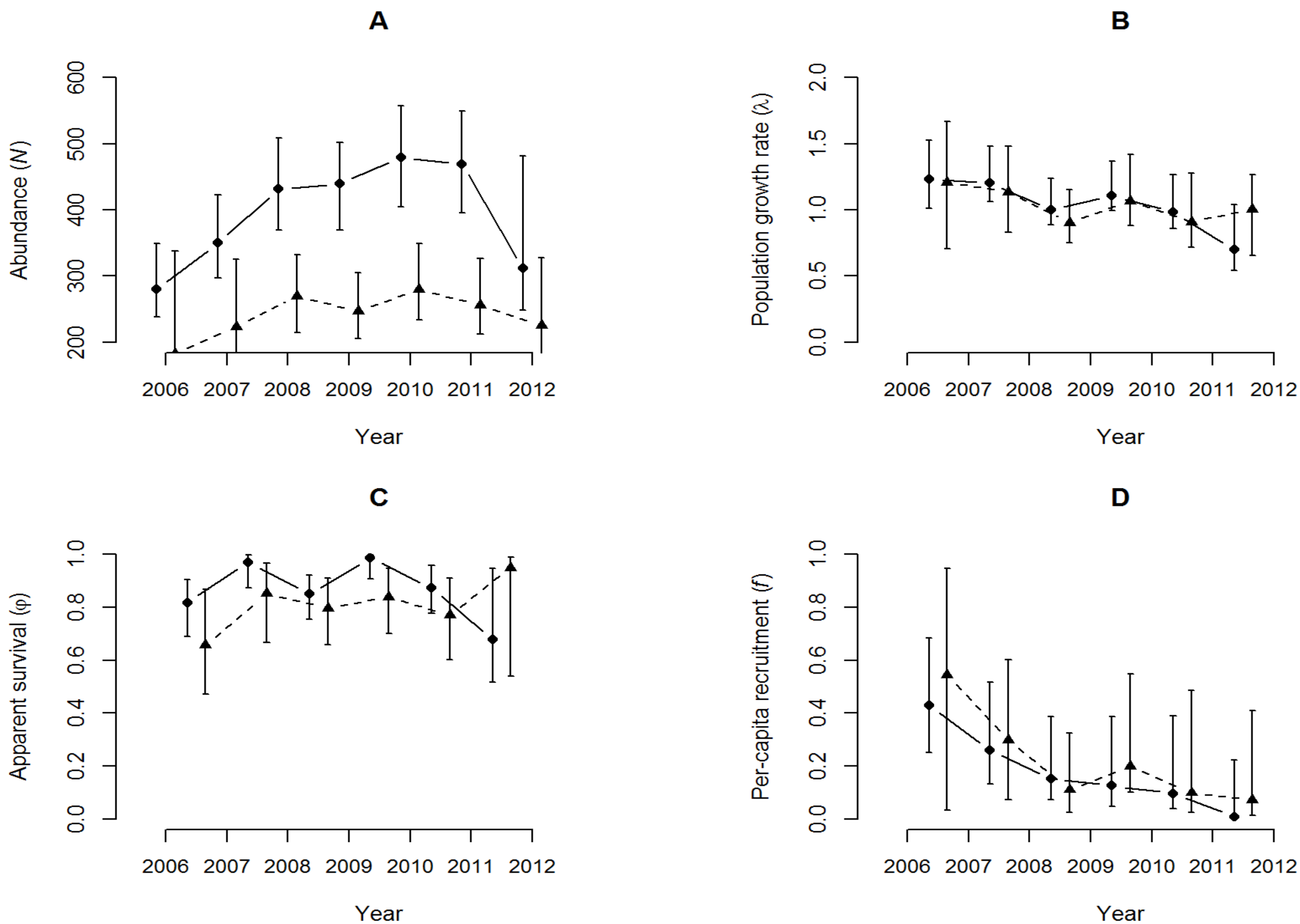

Figure 15. Male (triangles) and female (circles) demographic rate estimates and 95% credible intervals (error bars) for Louisiana black bears based on open-population spatially explicit capture-mark-recapture analysis of DNA-based detection data collected in the Tensas River Basin, Louisiana, USA from 2006 to 2012.

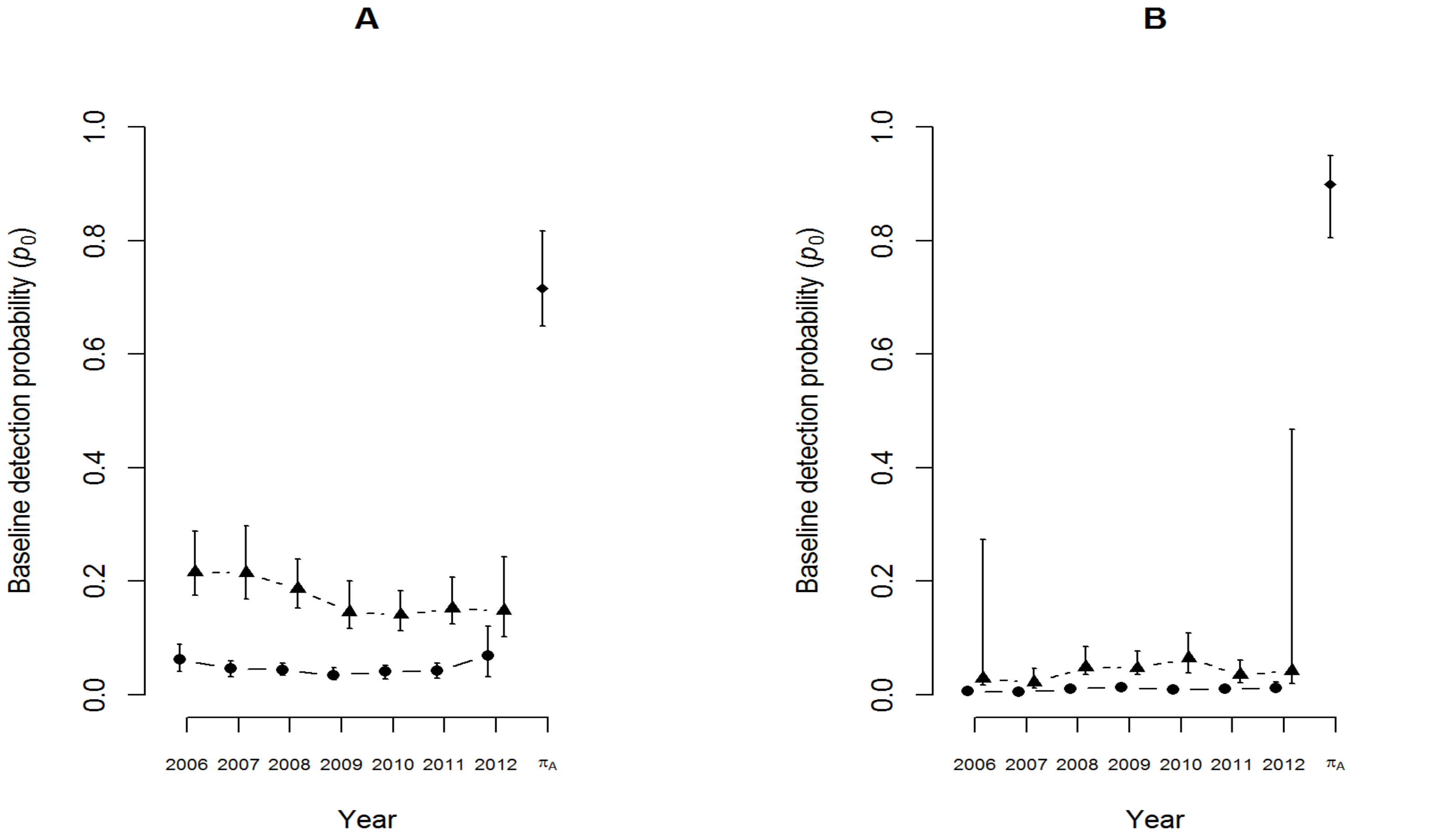

Figure 16. Male (panel A) and female (panel B) detection rate estimates and 95% credible intervals (error bars) for Louisiana black bears based on open-population spatially explicit capture-mark-recapture analysis of DNA-based detection data collected in the Tensas River Basin, Louisiana, USA from 2006 to 2012. Circles are estimates for mixture A, triangles are estimates for mixture B, and diamonds are estimates for the proportion of the population in mixture A.

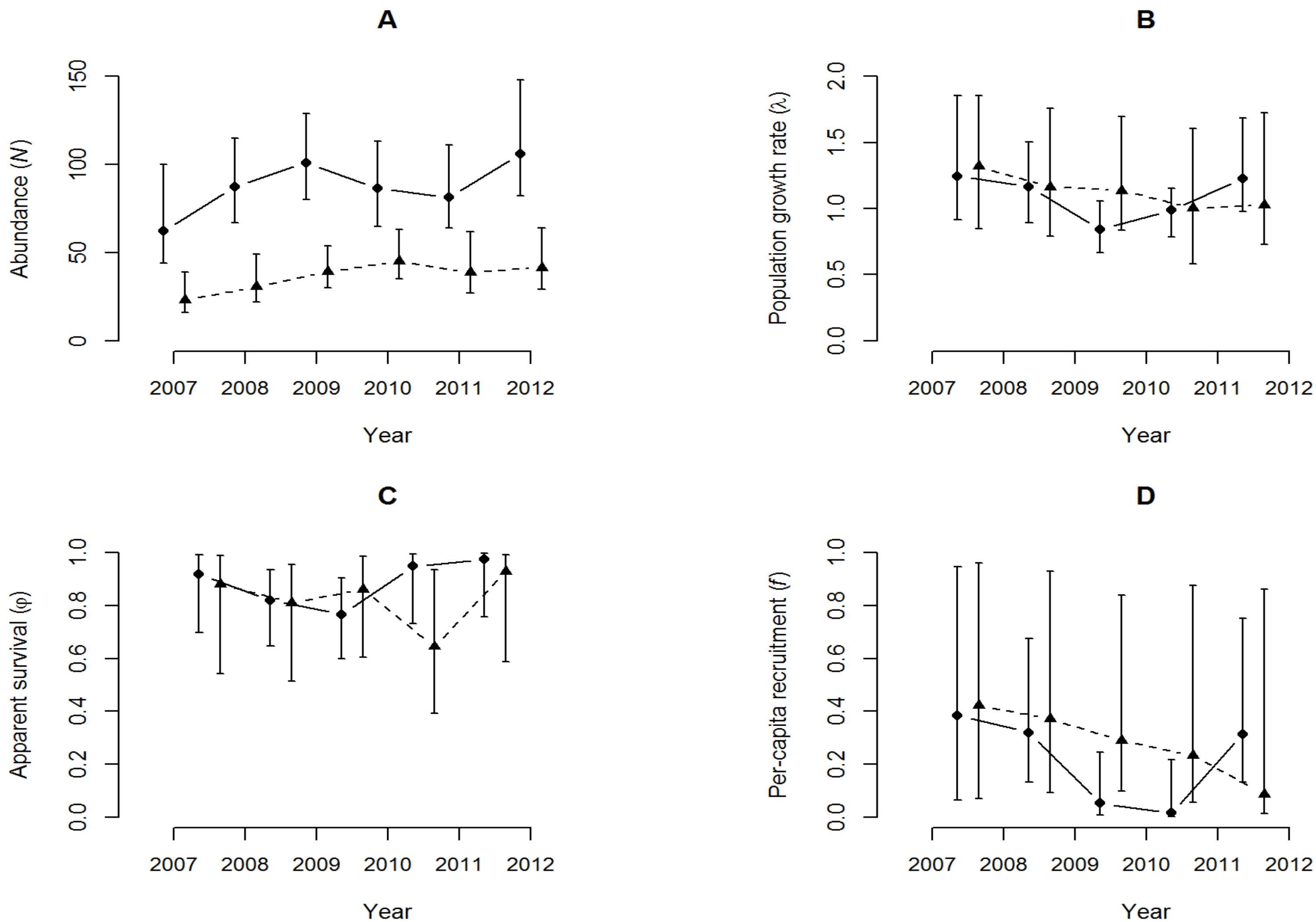

Figure 17. Male (triangles) and female (circles) demographic rate estimates and 95% credible intervals (error bars) for Louisiana black bears based on open-population spatially explicit capture-mark-recapture analysis of DNA-based detection data collected in the Upper Atchafalaya River Basin, Louisiana, USA from 2007 to 2012.

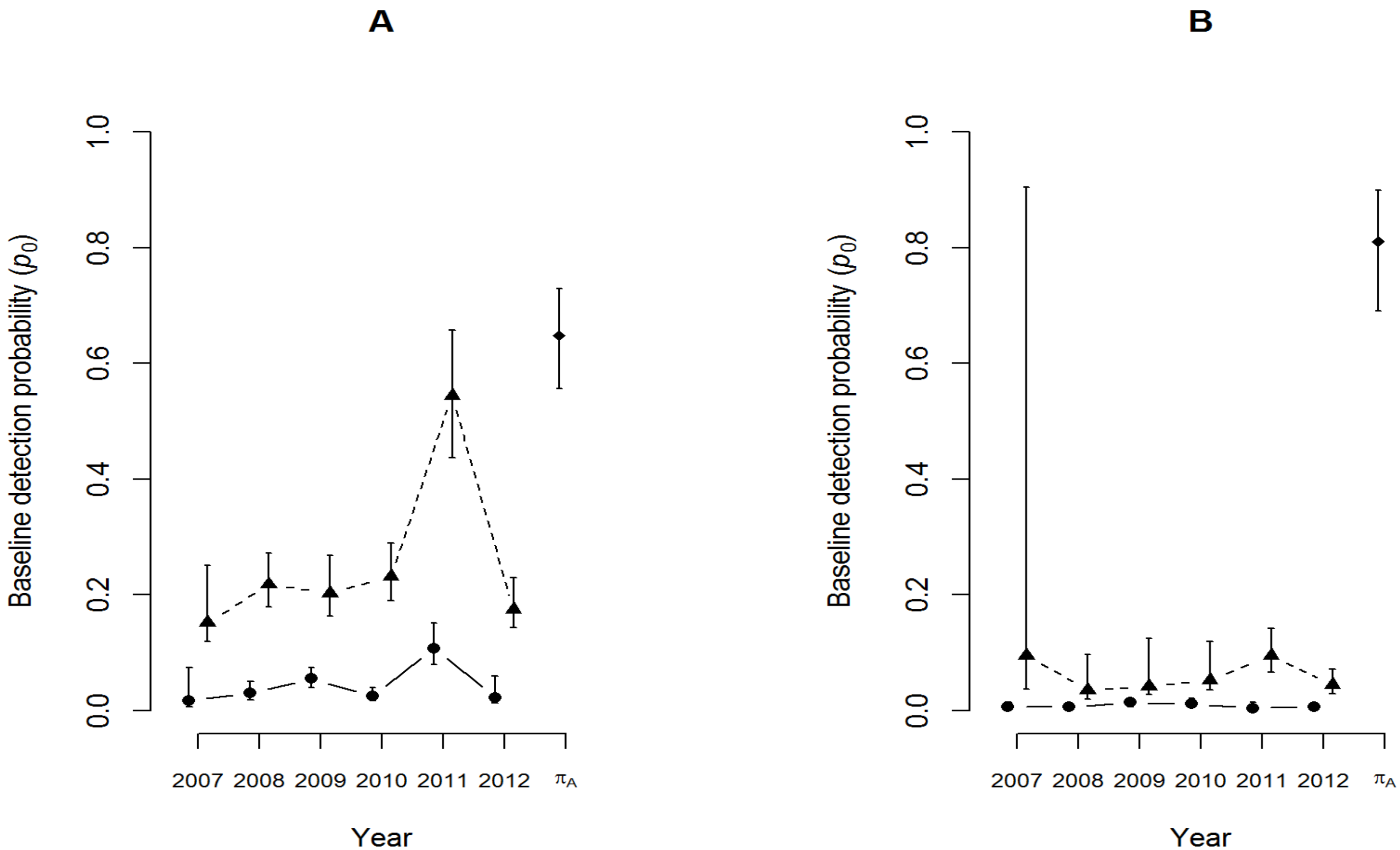

Figure 18. Male (panel A) and female (panel B) detection rate estimates and 95% credible intervals (error bars) for Louisiana black bears based on open-population spatially explicit capture-mark-recapture analysis of DNA-based detection data collected in the Upper Atchafalaya River Basin, Louisiana, USA from 2007 to 2012. Circles are estimates for mixture A, triangles are estimates for mixture B, and diamonds are estimates for the proportion of the population in mixture A.