

Evaluating the Genetic Response Following Introduction of Florida Largemouth Bass into Two Large Arkansas Reservoirs

Sean C. Lusk¹, Arkansas Game and Fish Commission, Fisheries Management Division, 2 Natural Resources Drive, Little Rock, AR 72205

T. Brett Hobbs, Arkansas Game and Fish Commission, Fisheries Management Division, 350 Fish Hatchery Road, Hot Springs, AR 71913

Kelly Winningham, Arkansas Game and Fish Commission, Fisheries Management Division, 350 Fish Hatchery Road, Hot Springs, AR 71913

D. Colton Dennis, Arkansas Game and Fish Commission, Fisheries Management Division, 7004 Highway 67 East, Perrytown, AR 71801

Jeffrey Buckingham, Arkansas Game and Fish Commission, Fisheries Management Division, 350 Fish Hatchery Road, Hot Springs, AR 71913

Christopher R. Middaugh, Arkansas Game and Fish Commission, Research Division, 2 Natural Resources Drive, Little Rock, AR 72205

Ronald L. Johnson, Arkansas State University, Department of Biological Sciences, State University, AR 72467

Abstract: The Florida largemouth bass (FLMB; *Micropterus salmoides floridanus*) is widely stocked throughout the southeastern United States with the intent of increasing the size potential of resident northern largemouth bass (NLMB; *M. s. salmoides*) populations. During the early 2000s the Arkansas Game and Fish Commission initiated an eight-year FLMB stocking program on selected reaches of DeGray Lake and Lake Ouachita in an effort to satisfy angler preferences. The goal of this stocking program was to achieve 40% of sampled largemouth bass in each introduction zone possessing FLMB alleles by the end of the program. To assess this, fin clips were removed from hundreds of largemouth bass collected both within the stocking area as well as three areas distant from the stocking area of each reservoir. Fin clip samples were collected before, during, and after the stocking program and microsatellite analysis was used to evaluate temporal trends in the percent contribution of FLMB and F₁ hybrids as well as the overall shift in genetic composition. Both reservoirs met the *a priori* standard of success after five years of stocking in Lake Ouachita and seven years in DeGray Lake. However, the majority of fish collected near stocking sites at the end of this study contained relatively low levels of FLMB alleles (q range = 0.649 to 0.886) and very few F₁ or FLMB were collected during the study. Therefore, we suspect that these fish contributed little to angler catch in these systems. This stocking was successful in creating high abundances of F_X-NLMB, but future work is needed to know if these individuals enhance the population size structure or improve angler satisfaction.

Key words: *Micropterus*, alleles, introgression, management

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Largemouth bass (*Micropterus salmoides*) provide highly valued recreational fisheries across North America (USFWS and USCB 2018) and are intensively managed and evaluated by natural resource agencies. Two subspecies of largemouth bass are defined: the northern largemouth bass (NLMB; *M. salmoides salmoides*) and the Florida largemouth bass (FLMB; *M. s. floridanus*; Fields et al. 1987, Isely et al. 1987, Koppleman et al. 1988, Kassler et al. 2002, Near et al. 2003). Endemic only to peninsular Florida, the native range of the FLMB is considerably smaller than that of the NLMB, which occupies much of the eastern United States (Barthel et al. 2015, Claussen 2015). The intergrade zone between the NLMB and FLMB has been thought to extend through Florida, Georgia, into South Carolina, and parts of Alabama (Bailey and Hubbs 1949) although recent research suggests this zone is much larger (Silliman et al. 2021).

Florida largemouth bass are commonly stocked outside their native range in an attempt to increase the trophy potential of largemouth bass in systems where they are stocked. Numerous studies demonstrate larger largemouth bass are associated with a greater proportion of FLMB alleles (Forshage et al. 1989, Horton and Gilliland 1993, Forshage and Fries 1995, Hughes and Wood 1995, Lutz-Carrillo et al. 2006, Tibbs 2008, Lamothe and Johnson 2013, Gowan 2015). Since the 1970s, FLMB have been stocked in Arkansas with the purpose of increasing the growth potential of resident NLMB (Dennis et al. 2017) to satisfy angler preferences for larger bass (Hunt and Westlake 2019). These stocking efforts have primarily been directed towards smaller waterbodies in southern Arkansas, but have historically occurred state-wide with mixed results in terms of the percent contribution of FLMB and their alleles to the resulting population and improvements in population size

1. E-mail: sean.lusk@agfc.ar.gov

structure (Allen et al. 2009, Lamothe et al. 2012, Lamothe et al. 2016).

During the late 1990s, anglers began asking the Arkansas Game and Fish Commission (AGFC) to introduce FLMB into two large highland reservoirs in west-central Arkansas, DeGray Lake (5423 ha) and Lake Ouachita (16,200 ha), to mitigate perceived poor production of trophy black bass (>3.6 kg) production in those systems. Roughly two-thirds of the directed fishing effort on both reservoirs targets black bass, with much of this effort associated with local, regional, and national tournament angling. After carefully considering reservoir habitat, forage base, and largemouth bass population characteristics, AGFC initiated an eight-year FLMB stocking program during 2006 on DeGray Lake and 2007 on Lake Ouachita. Although FLMB is not native to this region, both reservoirs contained trace amounts of FLMB alleles prior to this study (Philipp et al. 1983, Allen et al. 2009). Although there are no records of FLMB being stocked into either reservoir by the AGFC, the presence of these alleles could be attributed to angler mediated translocations of fish (Hargrove et al. 2017, 2019a, 2019b) or the natural intergrade zone being much larger than once believed (Sililiman et al. 2021).

The goal of this stocking program was to incorporate FLMB genes into the resident NLMB population, with a target objective of 40% of largemouth bass in each stocking area containing FLMB alleles by the conclusion of the program (Lamothe et al. 2012). Under the assumption of relatively low movement by fishes (Copeland and Noble 1994, Buckmeier and Betsill 2002), the AGFC concentrated all FLMB stocking efforts in relatively small areas (~400 ha) within both reservoirs to create a localized influence on the genetic structure of the largemouth bass population in these large reservoirs rather than influencing the genetic composition across the reservoir (Buckmeier et al. 2003). Lamothe et al. (2012) assessed the success of this program at its midpoint and found the percent of largemouth bass with FLMB alleles had increased within the stocking areas of both reservoirs but had not yet met the 40% agency goal. Our study expanded on the work of Lamothe et al. (2012) by evaluating largemouth bass genetics in both reservoirs before, during, and after the stocking program. Our specific objectives were to 1) quantify introgression of FLMB alleles into the resident NLMB populations, 2) estimate the percent contributions of FLMB and F₁ individuals, and 3) assess genetic effects at locations distant from the area stocked.

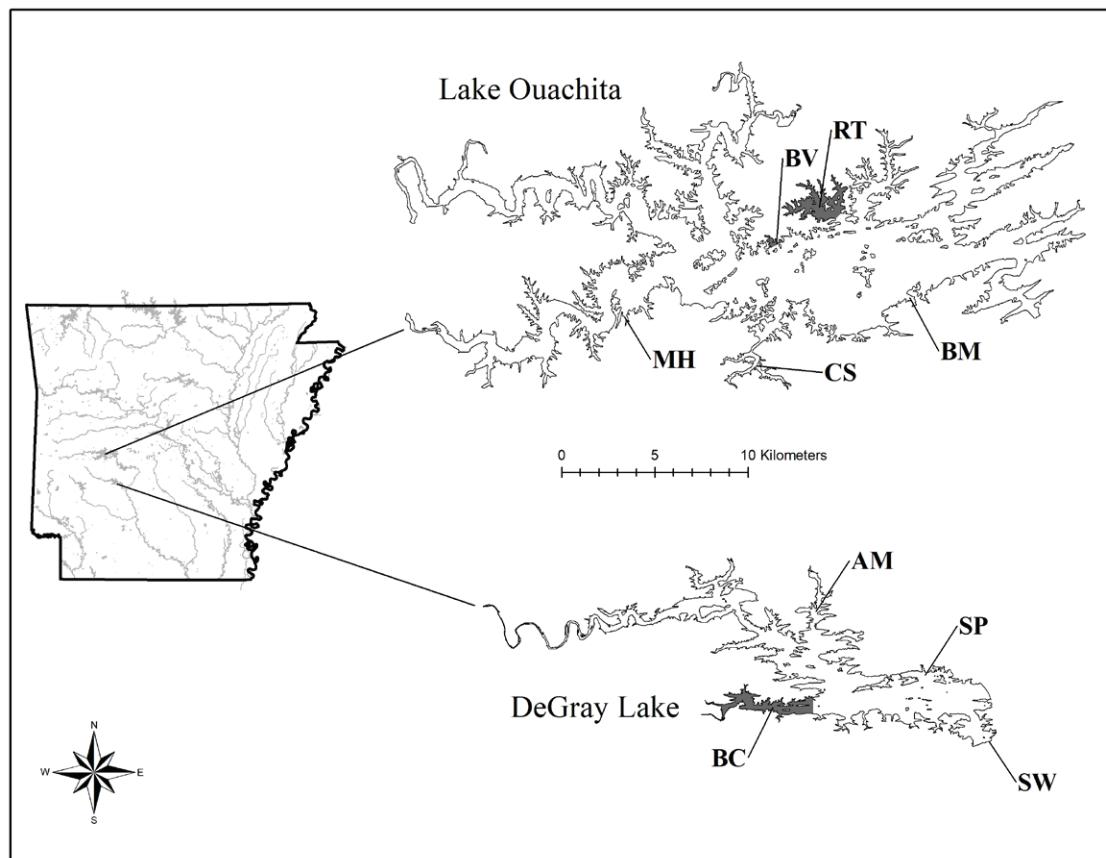


Figure 1. DeGray and Ouachita lakes, Arkansas, showing Florida largemouth bass stocking sites [DeGray: Brushy Creek (BC); Ouachita: Rabbittail (RT) and Buckville (BV)] and non-stocked sampling areas [DeGray: Arlie Moore (AM), State Park (SP), and Spillway (SW); Ouachita: Brady Mountain (BM), Crystal Springs (CS), and Mountain Harbor (MH)].

Study Area

DeGray Lake and Lake Ouachita are highland U.S. Army Corps of Engineers reservoirs located in the Ouachita Mountain ecoregion of Arkansas (Figure 1). Both reservoirs support a diverse fish community, including walleye (*Sander vitreus*), black crappie (*Pomoxis nigromaculatus*), and channel catfish (*Ictalurus punctatus*), and had high coverages (~25%) of hydrilla (*Hydrilla verticillata*) up to 2010. Widely fluctuating water levels prior to 2010 are believed to have led to a near depletion of all submersed vegetation, and vegetation levels remained low throughout the study. This region of Arkansas receives less than 3400 heating degree days, which makes it near the northern limit where successful stocking of FLMB would be expected (Gilliland 1992, Dennis et al. 2017).

Methods

Stocking Protocols

Brood FLMB were genetically tested to confirm purity and housed at the Andrew Hulsey State Fish Hatchery in Hot Springs, Arkansas. Between 2006 and 2013, FLMB fingerlings approximately 50 mm TL were stocked annually into the Brushy Creek embayment of DeGray Lake (349 ha; Figure 1). Similarly, between 2007 and 2014 FLMB fingerlings were stocked annually into two separate but proximal areas of Lake Ouachita (Buckville, 91 ha; and Rabbittail, 340 ha; Figure 1). Brushy Creek in DeGray Lake and Rabbittail are largely enclosed creek arms; in contrast, Buckville is not enclosed and is open to the main reservoir. All FLMB were boat stocked in each embayment at a rate of approximately 250 fingerlings ha⁻¹ along gently sloping banks of the reservoirs in

areas providing immediate nursery cover (e.g., flooded terrestrial and submersed aquatic vegetation).

Fish Sampling

To obtain baseline genetic data prior to stocking, largemouth bass were collected at the eventual stocking sites as well as three non-stocked sites between 2006 and 2007 on DeGray Lake and in 2007 on Lake Ouachita (Figure 1; Table 1). The non-stocked sites were selected based on their proximity to boat ramps most heavily used by bass tournament events on each reservoir, where any potential angler-mediated translocations of stocked FLMB may have been most likely to occur (Moyer et al. 2013, Hargrove et al. 2017). Every other year after initial stocking (DeGray: 2009, 2011, 2013, 2015; Ouachita: 2010, 2012, 2014, 2016; hereafter years 3, 5, 7, and 9 [post-stocking], respectively, for both lakes), sampling of largemouth bass occurred within stocking areas of both reservoirs (Table 1, 2). During year 9 of the study, sampling also occurred from all non-stocked sites.

All sampling was conducted via boat-mounted pulsed DC electrofishing (Type 7.5 GPP, Smith-Root Inc., Vancouver, Washington). Each year 75–100 fish were sampled at each site. Sampled fish were measured (mm, TL) and weighed (g), and a fin clip was removed and stored in 95% non-denatured alcohol for genetic evaluation. During year 3, fin clips were only collected from size-appropriate fish (DeGray, <450mm; Ouachita, <380mm) to exclude cohorts hatched prior to the stocking efforts based on pre-existing age and growth data collected by the AGFC on both reservoirs (AGFC unpublished data).

Table 1. Sample size and temporal changes in largemouth bass *q*-values for the Florida largemouth bass stocking (*) and non-stocked sampling sites of DeGray and Ouachita lakes, Arkansas.

Reservoir	Site	Pre-stocking		Year 3		Year 5		Year 7		Post-stocking	
		<i>n</i>	<i>q</i> -value	<i>n</i>	<i>q</i> -value	<i>n</i>	<i>q</i> -value	<i>n</i>	<i>q</i> -value	<i>n</i>	<i>q</i> -value
DeGray	Brushy Creek*	90	0.992	376	0.942	450	0.885	450	0.604	100	0.649
	Spillway	75	0.888	—	—	—	—	—	—	100	0.714
	State Park	109	0.860	—	—	—	—	—	—	100	0.754
	Arlie Moore	75	0.981	—	—	—	—	—	—	100	0.806
	Lakewide	349	0.922							400	0.731
Ouachita	Rabbittail*	100	0.967	400	0.916	393	0.724	400	0.566	100	0.699
	Buckville*	100	0.950	75	0.910	72	0.881	75	0.640	75	0.886
	Brady Mountain	75	0.919	—	—	—	—	—	—	100	0.932
	Crystal Springs	75	0.931	—	—	—	—	—	—	100	0.960
	Mountain Harbor	75	0.929	—	—	—	—	—	—	99	0.890
	Lakewide	425	0.938							474	0.873

Table 2. Temporal changes in the percent composition of largemouth bass genotypes in areas of DeGray Lake and Lake Ouachita in locations where Florida largemouth bass (FLMB) were stocked. Pre-stocking represents 2006–2007 for DeGray and 2007 for Ouachita. Post-stocking represents 2015 and 2016 for DeGray and Ouachita, respectively. All other years represent during-stocking samples.

Reservoir	Site	Sample	Genotype					
			FX-		FX-		NLMB	FLMB
			NLMB	NLMB	F1	FX		
DeGray	Brushy Creek	Pre-stocking	96	4	—	—	—	—
	Brushy Creek	Year 3	90	4	3	—	1	3
	Brushy Creek	Year 5	74	12	10	—	3	2
	Brushy Creek	Year 7	40	37	15	1	3	4
	Brushy Creek	Post-stocking	41	41	14	1	2	1
Ouachita	Buckville	Pre-stocking	86	14	—	—	—	—
	Buckville	Year 3	75	20	1	—	1	3
	Buckville	Year 5	46	51	—	—	3	—
	Buckville	Year 7	19	69	4	3	3	3
	Buckville	Post-stocking	40	55	3	1	1	—
Ouachita	Rabbittail	Pre-stocking	77	22	1	—	—	—
	Rabbittail	Year 3	80	15	0	—	2	4
	Rabbittail	Year 5	29	43	10	—	11	7
	Rabbittail	Year 7	9	66	6	4	9	7
	Rabbittail	Post-stocking	15	66	6	4	9	—

Genetic Evaluation

DNA was extracted from fin clips collected between 2006 and 2011 using the chloroform tris-acetate borate extraction method (Allen et al. 2009). Genotypes were amplified using seven microsatellite loci: *Mdo003*, *Mdo006*, *Msa021*, *Lma007*, *Lma12*, *Msa13*, and *Msa29* (Colbourne et al. 1996, DeWoody et al. 2000, Malloy et al. 2000), with PCR specifications outlined by Lutz-Carrillo et al. (2006). Beginning in 2012, genomic DNA was extracted from each fin clip following a salting-out procedure as outlined in Dumont and Lutz-Carrillo (2011). Individual fish DNAs were amplified using three of the same initial loci (*Mdo006*, *Msa021*, *Msa029*), with a replacement of the initial four remaining loci by three new loci recommended by Lutz-Carrillo et al. (2008) (*TPW169*, *TPW111*, *TPW112*). The four microsatellite loci that subsequently were replaced had initially resulted in a low number of shared alleles between subspecies (mixed alleles represented 6–7% of the initial samples), whereas the six loci ultimately used had no shared alleles. The PCR was performed as per specifications outlined by Lutz-Carrillo et al. (2006).

Microsatellite alleles were determined to be FLMB or NLMB using hatchery broodstock samples as controls (Allen et al. 2009). The software program STRUCTURE 2.3 (Hubisz et al. 2009) was used as described in Allen et al. (2009). Their previous work resulted in identifying two clusters (*k*) which corresponded with the two subspecies of largemouth bass, with all hatchery broodstock consistently genotyping as predicted. Settings included 500,000

MC/MC iterations with 50,000 burn-in steps. The *q*-values of admixture analysis ranged from 0 (FLMB) to 1 (NLMB), with a 0.05 threshold to limit Type I errors (Schwartz and Beheregaray 2008). Individuals with *q* ≥ 0.95 were classified as pure NLMB, whereas individuals with *q* ≤ 0.05 were classified as pure FLMB. Fish that were heterozygous at each locus with *q* values of 0.45 and 0.55 were considered F₁ whereas fish that had a *q* value within this range but were not heterozygous at each locus were classified as F_X. F_X-NLMB were defined as fish with *q* values between 0.55 and 0.95 and fish with *q* values between 0.05 and 0.45 were classified as F_X-FLMB. Percent contributions of FLMB and F₁ fish were determined by dividing the number of sampled FLMB and F₁ by the total number of fish in the samples.

Results

Genetic Evaluation Prior to Stocking

Pre-stocking genetic samples taken from both reservoirs contained few FLMB alleles (Tables 1–3). Despite the presence of FLMB alleles at all sample sites in both reservoirs, variation was observed among sites, with *q*-values ranging from 0.919 to 0.967 for Lake Ouachita fish and 0.860 to 0.999 for DeGray Lake fish. For example, in DeGray Lake, 4% of individuals sampled in Brushy Creek contained FLMB alleles compared to 55% of individuals having FLMB alleles near State Park (Table 2, 3). In both reservoirs prior to the study, the stocking locations had the highest *q*-values (Table 1) and lowest percentages of individuals with FLMB alleles (Table 2). Although no pure FLMB were detected in either reservoir prior to stocking, both reservoirs contained first- and later-generation backcrosses (i.e., F_X-NLMB).

Table 3. Temporal changes in the percent composition of largemouth bass genotypes in areas of DeGray Lake and Lake Ouachita not stocked with Florida largemouth bass (FLMB). Pre-stocking samples were collected during 2006–2007 in DeGray and 2007 in Ouachita. Post-stocking samples were collected during 2015 in DeGray and 2016 in Ouachita.

Reservoir	Site	Sample	Genotype					
			NLMB	FX-NLMB	F1	FX	FX-FLMB	FLMB
DeGray	Arlie Moore	Pre-stocking	92	8	—	—	—	—
		Post-stocking	64	31	4	—	1	—
	State Park	Pre-stocking	45	51	1	—	3	—
		Post-stocking	42	55	1	1	1	—
Ouachita	Spillway	Pre-stocking	57	40	3	—	—	—
		Post-stocking	38	56	3	—	3	—
	Brady Mountain	Pre-stocking	67	32	—	—	1	—
		Post-stocking	39	60	—	1	—	—
	Crystal Springs	Pre-stocking	68	32	—	—	—	—
		Post-stocking	26	74	—	—	—	—
	Mountain Harbor	Pre-stocking	64	36	—	—	—	—
		Post-stocking	32	62	2	—	3	1

Genetic Evaluation During and Following Stocking Program

The *q*-values at the stocking site in DeGray Lake declined (i.e., FLMB alleles increased) approximately 2.5% per year over the first five years of stocking, then sharply decreased between years 5 and 7 (Table 1), indicative of FLMB contributing high levels of alleles to the gene pool. By year 7 in Brushy Creek more than 40% of the sampled fish possessed FLMB alleles (Table 2). Surprisingly, the *q*-value of Brushy Creek fish had increased slightly by the end of the study, and the percent of sampled fish with FLMB genes leveled off. At the non-stocked sites of DeGray Lake, *q*-values decreased by an average of 15% between the pre-stocking and post-stocking samples. The percent of individuals with Florida bass alleles increased by over 30% in two of the non-stocked sites (Arlie Moore and Spillway); conversely, the number of Florida bass alleles increased by less than 7% at the third non-stocked site (State Park).

Prior to stocking, FLMB influence in largemouth bass at the Lake Ouachita stocking sites was much greater than that observed at the DeGray Lake stocking site. By year 3 stocking site *q*-values of Lake Ouachita LMB had declined 4–5% compared to pre-stocking. By year 5, *q*-values had declined 24% at the Rabbittail site, yet only 7% at the Buckville site (Table 1). During this same year, the F_x -NLMB class surpassed NLMB as the most prevalent genotype in both Lake Ouachita stocking sites, with over 40% of sampled individuals containing FLMB alleles (Table 2). The *q*-values in both stocking sites continued to decrease through year 7 but increased during the post-stocking year of this study similar to DeGray Lake. At the non-stocked sites of Lake Ouachita, there were only minor changes ($\pm 3\%$) in bass *q*-values over the eight-year period. Similar to DeGray Lake, the percent of individuals with Florida alleles increased by an average of 51% despite modest changes in *q*-values observed at non-stocked sites (Table 3).

FLMB and F_1 Contribution

During year 3, FLMB were detected at all stocking sites of both reservoirs. The percent of FLMB in the stocking locations of both reservoirs increased through the duration of this study but remained less than 7% of the total sample. In both reservoirs, a single FLMB was collected from sites located outside of the stocking areas. During the post-stocking evaluation, F_1 individuals were detected at all sampling locations on DeGray Lake but composed an average of less than 3% of samples collected from locations outside the stocking site. At the DeGray Lake stocking site, the percent of F_1 individuals steadily increased through the duration of this study and peaked at 15% in year 7 (Table 2). Conversely, in Lake Ouachita, F_1 individuals were only detected at the stocking locations and one non-stocked site. There was a positive trend in the

percent of F_1 individuals within the stocking sites of Lake Ouachita that peaked at 10% in year 5 (Table 2).

Discussion

The stocking of both DeGray Lake and Lake Ouachita met the *a priori* requirement for success after seven and five years, respectively. At the approximate midpoint of our study, there was little indication that stocking efforts were successful (Lamothe et al. 2012), but shortly after that evaluation, both reservoirs met the goal of 40% of bass having FLMB alleles. This delay in response indicates the importance of multiple stocking events over a long period of time and assessment taking place after stocked fish have introgressed into the native population and begin reproducing.

Despite similar stocking rates used at both reservoirs, we found a greater system-wide effect of FLMB stocking on the fish of DeGray Lake compared to Lake Ouachita. This could be attributed to the smaller size of DeGray Lake relative to Ouachita ($\sim \frac{1}{3}$ the size), which would make it more conducive to both angler-mediated translocations and/or diffusion of introduced fish and their progeny. Angler-mediated translocations of black bass have been identified in several systems in the United States and abroad (Vander Zanden and Olden 2008, Moyer et al. 2013, Ellender and Weyl 2014, Hargrove et al. 2017), and we anticipate that it occurred in our study systems as well. However, additional work in Lake Ouachita (Middaugh et al. 2022) found that natural dispersal was a better explanation for the spread of FLMB genes in that system. We cannot determine the relative importance of angler translocations versus natural dispersal based on the present study.

In Arkansas, as well as much of the southeastern United States, the goal of stocking FLMB is to enhance size structure and increase production of trophy largemouth bass (> 630 mm) for anglers. It can be difficult both to accomplish these outcomes and then to demonstrate success when they are accomplished. Stocking density, time since stocking, and number of stocking events have all been related to success of FLMB introgression into southern U.S. reservoirs (Dunham et al. 1992, Hargrove et al. 2019a, but see Lamothe et al. 2016). Stocking densities (250 fish ha^{-1}) were relatively high in this study compared to others (e.g., 24–32 fish ha^{-1} , Buynak and Mitchell 1999; 10–41 fish ha^{-1} , Buckmeier and Betsill 2002; 10 fish ha^{-1} , Hargrove et al. 2019a), and fish were stocked continuously over an eight-year period, likely contributing to successful introgression of FLMB alleles into the local population. Stocking location also may have affected introgression levels. Both Brushy Creek and Rabbittail were largely enclosed systems in large coves; in contrast, Buckville was exposed to the main reservoir body. This open exposure to the main reservoir may be one contributing fac-

tor for the lowered introgression rate of Buckville stocking relative to the other two sites.

Numerous studies have shown that the survival of stocked fingerling largemouth bass is generally very low (Buckmeier and Betsill 2002, Porak et al. 2002, Jackson et al. 2002, Hoffman and Bettoli 2005, Pouder et al. 2010, Hargrove et al. 2019a). Stocking of advanced fingerlings or adults can result in better survival (Wahl et al. 1995, Buynak and Mitchell 1999, Mesing et al. 2008), but raising hatchery fish to larger sizes can be cost prohibitive. Though we did not attempt to assess the annual survival and recruitment of stocked fish, reservoir-wide change in FLMB allele frequencies over time confirms that enough stocked fish were surviving to maturity to contribute to succeeding generations.

Over the course of this stocking program, F_x -NLMB increased in prevalence at a more rapid rate than any other genotypes. By the conclusion of this study, F_x -NLMB had surpassed the NLMB as the most common genotype not only in stocking areas but also in the majority of the non-stocked sampling areas of both reservoirs. Prevalence of F_x -NLMB has also been observed in other southeastern U.S. systems where FLMB have been introduced (Dunham et al. 1992, Brown and Murphy 1994, Lutz-Carrillo and Dumont 2012, Hargrove et al. 2019a). Unfortunately, little is known about the fitness of F_x -NLMB. Most historical comparisons between largemouth bass genealogical classes focus on differences among FLMB, NLMB, and their F_1 hybrids in population characteristics such as growth, mortality, and catchability (Rieger and Summerfelt 1976, Zolczynski and Davies 1976, Inman et al. 1977, Smith and Wilson 1980, Wright and Wigtil 1982, Isely et al. 1987, Maceina and Murphy 1988, Koppelman et al. 1988, Kleinsasser et al. 1990, Philipp and Whitt 1991). There is an apparent paucity of research dedicated to evaluating the fitness of F_x -NLMB, which is concerning considering their apparent prevalence following the introduction of FLMB.

We found a relatively low contribution of stocked FLMB or their F_1 hybrids to the population both within the stocking locations and the non-stocked sites of both reservoirs, similar to findings from other studies (Gilliland and Whitaker 1989, Allen et al. 2009, Lutz-Carrillo and Dumont 2012, Lamothe et al. 2016, Hargrove et al. 2019a). In contrast, many years of stocking at high densities appears capable of resulting in substantial contribution of F_1 and FLMB to the population in some circumstances (Hargrove et al. 2019b). Due to the low number of F_1 and FLMB bass observed in our study, we conclude that F_1 or FLMB were not likely a substantial proportion of angler capture beyond the local scale or in years post-stocking.

Management Implications

Although an earlier evaluation concluded that stocking success was low (Lamothe et al. 2012), our study demonstrated that the stocking program achieved the *a priori* measure of success (40% of individuals at least F_x -NLMB) five years and seven years into the stocking program in Lake Ouachita and Lake DeGray, respectively. Percent of individuals with FLMB alleles remained above this benchmark throughout the remainder of the study. We can conclude that this stocking successfully shifted the genetic composition of the local largemouth bass population in both reservoirs, but contribution of stocked FLMB and later F_1 hybrids to the overall population was low. Some factors that likely contributed to successful genetic integration were the use of pure FLMB, continuous stocking over an eight-year period, and high stocking densities in a localized area. If other managers desire to shift the genetics of fish of large reservoir systems, we recommend a similar approach of stocking focal areas repeatedly over a long period. Additionally, we recommend allowing adequate time to pass before evaluating and drawing conclusions on stocking success.

Though we met and maintained our criteria of success, the high proportion of F_x -NLMB fish resulting from this program was surprising. Additional research should be conducted to explore differences in population characteristics between F_x -NLMB fish created through a stocking program and resident, native NLMB. Given the theoretical potential for outbreeding depression (Philipp 1991, Philipp et al. 2002) and the value of maintaining genetic integrity of fish populations (Philipp 1991, Philipp et al. 2002, Barthel et al. 2010, Porak et al. 2015) the future of stocking FLMB in Lakes DeGray and Ouachita is uncertain. With any stocking program involving the introduction of FLMB, management agencies must strike a balance between the short-term potential of increasing trophy production and maintaining the long-term viability of those populations. We recommend that future evaluations of stocking success consider life-history characteristics in conjunction with genetic population shifts and that stocking goals be considered accordingly.

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