

Factors Related to the Genetic Composition and Fishing Quality of Largemouth Bass Fisheries in Texas Reservoirs

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Abstract: The Florida subspecies of largemouth bass (*Micropterus s. floridanus*) has been widely stocked throughout the southern United States, including Texas. Quantifying the success of these stockings has been difficult. In this study, relationships among large scale genetic, biological, physical, and limnological variables, and measures of fishing quality and trophy were examined in 89 Texas reservoirs greater than 202 hectares. No relationships among stocking measures and any genetic variable were detected. In general, oligotrophic reservoirs in South Texas had significantly higher measures of Florida introgression compared to eutrophic reservoirs in North Texas. Largemouth bass growth rates increased from west to east and as elevation decreased. Angler success variables measuring number of bass caught were negatively related to longitude, whereas angler success variables related to size of bass caught were more influenced by local reservoir-specific variables. Anglers generally caught larger fish in large, shallow, young reservoirs with higher measures of Florida introgression. The results of this study do not provide clear answers to current questions surrounding Florida largemouth bass stocking allocation in Texas reservoirs. Microsatellite analysis is a newer technique to determine genetic makeup that promises to improve our understanding of the impact of stocking and genetics on largemouth bass fisheries in Texas reservoirs.

Key words: Largemouth, stocking, genetics, fishing, trophy

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Largemouth bass (*Micropterus salmoides*) are a popular sport fish throughout North America. Two distinct subspecies, Florida largemouth bass (*M. s. floridanus* [FLMB]) and northern largemouth bass (*M. s. salmoides* [NLMB]), were initially recognized on the basis of meristics (Bailey and Hubbs 1949). These subspecies are currently differentiated by biochemical genetic variation (Philipp et al. 1983). FLMB are native to peninsular Florida, whereas NLMB occur in much of the midwestern, eastern, and southeastern United States (Philipp et al. 1983). Originally, naturally intergraded populations existed in areas of western Florida, Alabama, Georgia, and South Carolina (Bailey and Hubbs 1949).

Florida largemouth bass have been stocked throughout much of the United States and Mexico. The rationale commonly used by fisheries agencies is that FLMB grow faster and reach greater maximum size than NLMB (Maceina et al. 1992). Consequently, the range of intergrade populations has increased substantially during the past 40 years. Studies to quantify the effects of these stockings, in Texas as well as other states have provided mixed results.

Kulzer et al. (1985) examined genetic data from 19 Texas reservoirs in 1983. Intergradation rates ranged from 2% to 92% and was positively related to the number of years fish were stocked ($R^2 = 0.37$, $P < 0.01$) and water clarity ($R^2 = 0.24$, $P < 0.03$). However, these two variables were intercorrelated and the R^2 values were rather low, making inferences regarding the factors affecting intergradation limited in scope.

Norgren et al. (1986) examined the genetics of 22 largemouth

bass populations in Alabama to determine the extent of intergradation. Florida bass allelic frequency ranged from 0.0% to 11.0% in reservoirs not supplementally stocked with FLMB whereas the range was 0% to 47% in stocked reservoirs. The authors noted that expression of Florida genetics was “irregular and complex” suggesting forces other than stocking variables were at work.

Dunham et al. (1992) evaluated the effects of FLMB stocking in 11 Alabama reservoirs ranging in size from 18 to 74 ha. They found that the frequency of Florida alleles was positively correlated with the number of stockings ($r = 0.86$, $P < 0.001$), time since the first stocking ($r = 0.86$, $P < 0.001$), and total number of fish stocked per hectare ($r = 0.78$, $P < 0.01$). Unlike Kulzer et al. (1985), they found an inverse correlation between secchi disk visibility and Florida allele frequencies ($r = -0.61$, $P < 0.05$).

Forshage and Fries (1995) found that FLMB alleles averaged 36.3% for largemouth bass populations in 126 Texas reservoirs during 1991–1993. In that study, greater FLMB influence was associated with newer and smaller reservoirs in the southern portion of Texas. However, only six independent variables were used in the analysis, and they explained only modest amounts of the variation when related to genetics data ($R^2 = 0.02$ to 0.17 , $P < 0.05$). Exclusion of other physical and limnological variables may have hampered the ability to explain greater amounts of variation in the genetic composition of largemouth bass populations in Texas.

The previous studies all used increased Florida bass allelic fre-

quencies as the variable of interest in determining whether supplementary stocking was successful. However, genetic composition is not necessarily a surrogate for measures of fishing quality. To date, no studies have directly examined the relationships among large scale genetic, biological, physical, and limnological variables and measures of fishing quality and trophy potential.

Forshage and Fries (1995) suggested a link between stocking, genetics, and measures of fishing quality in Texas reservoirs. However, the data were not statistically testable, and may merely have indicated a coincidental relationship. From 1972 through 1993, they reported that over 66 million FLMB were stocked by the Texas Parks and Wildlife Department (TPWD) into 454 public reservoirs. Coincidental with these stockings, the quality of many of Texas' largemouth bass fisheries improved significantly (Forshage and Fries 1995). The weight of the current state record largemouth bass is 26% greater than the weight of the state record before FLMB were introduced. Additionally, the mean weight of largemouth bass entered into TPWD's Big Fish Awards program, as well as the number of reservoirs producing these fish, has substantially increased since stockings commenced (Forshage and Fries 1995). Another item of note is the fact that 100% of fish submitted to the Sharelunker program contained FLMB alleles (TPWD unpublished data).

In response to these perceived successes, production of FLMB by TPWD hatcheries increased from an average of 2.1 million per year in the 1980s to an average of 7.7 million per year from 1990–1997 (TPWD unpublished data). Genetic composition was one of the primary criteria in allocating bass fingerlings in Texas reservoirs during the period this study encompassed. Criteria for FLMB stocking were as follows:

- 1) New or renovated reservoirs.
- 2) Reservoirs with limited largemouth bass recruitment.
- 3) Only reservoirs not designated as Community Fishing Lakes may be stocked with Florida largemouth bass.
- 4) Reservoirs with a history of producing trophy bass but lacking sufficient numbers of pure Florida largemouth bass (<20% pure Florida genotype in electrophoresis samples from age-0 or age-1 fish).
- 5) Reservoirs which do not have Florida largemouth bass established (<20% Florida largemouth bass alleles in electrophoresis samples from age-0 or age-1 fish).

Increased emphasis on stocking FLMB in Texas and high variability in FLMB influence among populations provided the impetus to learn more about the factors affecting the genetic composition of largemouth bass populations in Texas reservoirs. Additionally, it became obvious that an understanding of the relationships among genetic, biological, physical, and limnological variables

and a reservoir's potential for producing quality and trophy fisheries was required to develop effective stocking and management strategies for largemouth bass fisheries in Texas.

Therefore there were two major components of this study. One was to identify variables correlated with increasing measures of Florida genetics, and the other was to identify variables correlated with increasing measures of fishing quality in Texas reservoirs.

Methods

Eighty-nine reservoirs larger than 202 ha were selected for analysis based on availability of data. Variables were selected for their relevance to genetics and fishing quality measures, and were obtained from a variety of sources. Categories of variables included stocking, physicochemical, genetic, TPWD statewide monitoring, and measures of tournament angler success (Table 1). Stocking variables used data from 1980 to 1998 to encompass historical information. However, all other variables were obtained from the period 1993 to 1998 to reflect reservoir conditions current at the time of analyses.

The analyses were broken up into three separate portions. The first looked at factors influencing genetic variables similar to Gilliland and Whitaker's (1989) evaluation in Oklahoma. The independent variables tested to determine their influence on genetics included all physicochemical variables and stocking metrics. The second portion looked at the influence of physicochemical and genetic variables on monitoring data. The last portion looked at factors influencing angler success variables. The independent variables tested included physicochemical, genetic, and monitoring. Data were analyzed using SYSTAT for Windows (1992).

Each variable was tested to ensure a normal distribution. Those that exhibited a non-normal distribution were log-transformed to best approximate a normal distribution. Relationships among all variables were initially tested using a Pearson correlation matrix. Independent variables that were significantly correlated with the dependent variable in question were tested with stepwise multiple regression. This reduced the number of independent variables to those that were significant in the overall equation, and calculated partial regression coefficients, which defined the proportion of the variance that each variable explained (Zar 1984). Those selected for inclusion in the overall equation were examined for intercorrelation and none was found. The threshold for significance was set at ($P < 0.05$) for all analyses. Regression equations with adjusted R-squared values less than 0.200 were not included.

Results

Few regression equations yielded R-squared values greater than 0.2 (Table 2). When the genetic data were analyzed, only three in-

Table 1. Stocking, physicochemical, genetic, monitoring, and angler success variables measured in selected Texas reservoirs.

Variable	Description
Stocking	
Fingerlings per acre ^a	Total fingerlings stocked per acre
Fry per acre ^a	Total fry stocked per acre
Years of fingerling stocking ^a	Number of years fingerlings were stocked
Years of fry stocking ^a	Number of years fry were stocked
Total years of stocking ^a	Number of years fingerlings or fry were stocked
Physicochemical	
Drainage area ^b	Area of the watershed surrounding the reservoir
Elevation ^b	Elevation of the reservoir at conservation pool
Latitude ^b	Latitude of the dam
Longitude ^b	Longitude of the dam
Reservoir age ^b	Years since the dam was completed as of 1999
Reservoir area ^b	Area of the reservoir at conservation pool
Reservoir depth ^b	Average depth of the reservoir at conservation pool
Annual fluctuation ^b	Range in water level fluctuation
Shoreline development index ^b	Complexity of the shoreline expressed as a ratio
Conductivity ^c	Average water conductivity
Total dissolved solids ^c	Average total dissolved solids
TSI (chlorophyll a) ^c	Trophic state index based on average chlorophyll a concentrations
Total phosphorus ^c	Average phosphorus concentrations
Secchi disk ^c	Average secchi disk measurements
Genetic	
Percent Florida alleles ^d	Number of Florida alleles divided by the total number of alleles in the sample
Percent pure Florida ^d	Number of bass that possess only Florida alleles divided by the total number of bass in the sample
Percent F ₁ genetics ^d	Number of bass with one half Florida alleles and one half northern alleles divided by the total number of bass in the sample
Percent F _x genetics ^d	Number of bass that have one quarter or three quarters Florida alleles divided by the total number of bass in the sample
Percent Florida influence ^d	Number of bass that have at least one Florida allele divided by the total number of bass in the sample
Monitoring	
Length at age-3 ^e	Length of three-year-old bass when collected in the fall
Length at age-4 ^e	Length of four-year-old bass when collected in the fall
Length at age-5 ^e	Length of five-year-old bass when collected in the fall
Electrofishing catch of bass >14" ^e	Average of electrofishing catch rate (n/hr) of bass > 14"
Vegetation coverage ^e	Percent of the reservoir covered by vegetation
Angler success	
Percent successful ^f	Percent of anglers weighing in one or more bass
Average weight ^f	Average weight of all bass weighed in
Fish per hour ^f	The number of bass weighed in divided by the total number of angling hours
Pounds per hour ^f	The weight of all bass weighed in divided by the total number of angling hours
Hours to catch a 5 pound fish ^f	The number of 5-pound bass weighed in divided by the total number of angling hours
Heaviest fish ^f	The heaviest fish weighed in for all tournaments on a particular reservoir.
Average of the heaviest fish ^f	The heaviest fish for each tournament on a particular reservoir divided by the number of tournaments.

Table 2. Results of stepwise regression. "n" refers to number of reservoirs.

Dependent variable	R-squared	Independent variable	Coefficient
Genetic			
Percent Florida alleles	0.330 (n = 88)	Latitude	-0.505
		Trophic state index	-0.234
Percent pure Florida	0.204 (n = 52)	Latitude	-0.403
		Total dissolved solids	0.330
Percent Florida influence	0.311 (n = 85)	Latitude	-0.409
		Trophic state index	-0.284
Monitoring			
Length at age-3	0.390 (n = 81)	Elevation	-0.574
Length at age-4	0.366 (n = 81)	Elevation	-0.612
Angler success			
Percent successful	0.431 (n = 22)	Longitude	-1.015
		Total dissolved solids	-0.496
Fish per hour	0.284 (n = 40)	Longitude	-0.550
Pounds per hour	0.310 (n = 40)	Longitude	-0.573
Average weight	0.236 (n = 39)	Percent pure Florida	0.300
		Reservoir age	-0.384
Heaviest fish	0.328 (n = 70)	Percent Florida alleles	0.376
		Reservoir area	0.368
Average weight of heaviest fish	0.237 (n = 57)	Length at age-4	0.245
		Reservoir depth	-0.435

a. Data from TPWD's stocking database from 1980 to 1998.

b. Data from TPWD's Lake Categorization database.

c. Data collected by the Texas Commission on Environmental Quality from 1993 to 1997, generally near the dam, once per year. If data were available from multiple years, they were averaged to obtain a mean for each reservoir.

d. Samples collected by TPWD field crews from 1994 to 1998 and processed in TPWD laboratories at A. E. Wood and the Texas Freshwater Fishery Center using allozyme analysis of two loci. Numbers verified from data archived at A. E. Wood and from district offices when necessary. If data were available from multiple years, they were averaged to obtain a mean for each reservoir.

e. Data collected by TPWD field crews from 1993 to 1997 using standardized procedures, which was retrieved from the central database or from district offices. If data were available from multiple years, they were averaged to obtain a mean for each reservoir.

f. Data submitted by tournament directors on a voluntary basis to TPWD from 1994 to 1997. If data were available from multiple years, they were averaged to obtain a mean for each reservoir.

dependent variables yielded significant correlations. Latitude and trophic state index were negatively correlated with percent Florida alleles and percent Florida influence. Latitude was also negatively correlated with percent pure Florida, whereas total dissolved solids was positively correlated with that genetic measure.

Analysis of the monitoring data resulted in two regression equations for growth with R-squared values greater than 0.2. Elevation was the sole significant independent variable, and it was negatively correlated.

Analysis of angler success data resulted in six dependent variables with regression equations. Three dependent variables measuring quantity of fish caught by anglers were negatively correlated with longitude. They were percent successful, fish per hour, and pounds per hour. In addition, total dissolved solids was negatively correlated with percent successful. The relationships between the three dependent variables measuring size of fish caught by anglers and their significant independent variables were more complex. Average weight was positively correlated to percent pure Florida and negatively correlated to reservoir age. Heaviest fish was positively correlated to percent Florida alleles and reservoir area. Average weight of heaviest fish was positively correlated to length at age-4 and negatively correlated to reservoir depth.

Discussion

The amount of variance explained by the analyses was less than desired. The largest R^2 calculated was 0.431. The large number of cooperators involved in data acquisition is a possible cause. Additionally, tournament angler success data was voluntarily submitted to TPWD with no means of independently determining its veracity. Despite this, many useful inferences can be drawn.

Perhaps the most interesting finding was the lack of any relationship between stocking and genetic composition. Over 95% of the study reservoirs were stocked at least once in the period 1980–1998, and 64% were stocked three or more times. Unfortunately, no standardized data were available to evaluate the effects of this tremendous effort from its inception in 1972 and through the 1980s. The genetic data for this report were collected from 1994 through 1998, perhaps long after Florida genetics were well-established in many Texas reservoirs. For example, Maceina and DiCenzo (1995) evaluated long-term genetic changes in Alabama reservoirs. They presented evidence that suggested once FLMB alleles were established in a reservoir, that level of introgression would be maintained whether stocking continued or not.

Southern, oligotrophic reservoirs had significantly higher measures of Florida introgression as compared to northern, eutrophic reservoirs. This is consistent with the findings of Forshage and Fries (1995). One possible explanation is that, given the state-

wide uniform stocking rates currently employed by TPWD, bass stocked in reservoirs with low productivity would comprise a greater percentage of the total numbers of age-0 bass recruiting into the population. With fewer naturally spawned bass to dilute the genetic pool, stocked pure FLMB could have a greater impact on reservoir genetics. Terre et al. (1993) previously observed this phenomenon using genetically marked bass in three Texas reservoirs. They concluded that recruitment of stocked bass may be influenced by density and recruitment characteristics of the native population but cautioned against a strict interpretation of the results.

Growth was influenced almost exclusively by elevation, exhibiting a negative correlation that explained 39% and 37% of the variation in data for length at age-3 and length at age-4, respectively. Elevation in Texas generally increases from east to west. Genetics did not appear to play a role in growth rates at a statewide level.

When looking at the angler success variables that resulted in regression equations, it was useful to divide them into two groups. The first group of variables measured quantity of bass caught by anglers, and all were negatively influenced by longitude. This meant that more anglers fishing in east Texas reservoirs caught bass, and they caught more of them, compared to anglers fishing in west Texas. This is consistent with the findings of Dolman (1990), who analyzed cove rotenone data collected from 132 Texas reservoirs. He found increased densities of largemouth bass in east Texas reservoirs as compared to west Texas.

The second group of angler success variables measured size of bass caught by anglers. Genetic measures played an important supporting role in two of the three regression equations. This parallels the findings of Forshage et al. (1989) who found a significant positive correlation between the number of bass larger than 4.5 kg submitted to the Texas Big Fish Awards program and the percent of fish in the population containing Florida alleles. Variables related to reservoir age and morphometry were present in all three regression equations. This indicated that larger fish were generally caught in large, shallow, young reservoirs with higher measures of Florida introgression. Therefore, measures related to bass size were affected more by localized reservoir conditions as compared to measures related to abundance, which were affected on a large geographic scale.

It is commonly thought among management biologists that FLMB stocked into a reservoir become the lunkers reported a decade later. Unfortunately, this study was unable to directly compare stocking variables and measures of angler success. The reason for this can be found in the current TPWD stocking criteria. Trophy reservoirs can be stocked if less than 20% pure FLMB are documented in age-0 fish from that population. Texas reservoirs

not considered to have trophy potential are subject to the criteria that states only reservoirs with less than 20% Florida alleles in the population can be stocked. During the period examined, only 17% of the reservoirs selected for this study were eligible for stocking under the second, more restrictive criteria. However, fully 80% had less than 20% pure FLMB, making them eligible for stocking as long as a case could be made for including them as a trophy reservoir.

This two-tiered approach may result in a positive feedback loop, where trophy reservoirs are stocked more frequently than other Texas reservoirs. While this approach has merit for other reasons, it does not allow one to determine whether stocking is maintaining the trophy fishery or the trophy status of the reservoir is maintaining the stocking.

It is likely that since stocking frequency and density are not reflected in current allelic frequencies on a statewide basis, the use of genetic measures as criteria on which to base stocking decisions has limited applicability. That is not to say that genetic information is unnecessary, just that it may not be the single best tool for determining where and when to stock.

However, improvements in the procedures to obtain genetic information point to new avenues of research. The allozyme analyses used to determine genetic makeup during the study did not yield as much information as a newer technique using microsatellites (Lutz-Carrillo et al. 2006). Microsatellites can be resolved from any collected tissue and stored at room temperature, whereas tissue obtained for allozyme analyses need to be stored at -80°C . Microsatellite techniques currently used also provide better coverage of the genome using a total of six subspecies specific diagnostic markers as opposed to two allozyme loci and are more versatile in their applications (Lutz-Carrillo et al. 2007). The ability to collect genetic material using a non-lethal technique holds promise for new studies that will vastly improve our understanding of the role stocking and genetics plays in the maintenance of trophy bass fisheries in Texas. Additional applications for this improved technique should yield much improved information about the genetics of Texas largemouth bass populations. This is vital, as the data in this report do not provide clear answers to current questions surrounding Florida largemouth bass stocking allocation in Texas reservoirs.

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Literature Cited

- Bailey, R. M. and C. L. Hubbs. 1949. The black basses (*Micropterus*) of Florida with a description of a new species. University of Michigan Museum of Zoology Occasional Papers 516.
- Dolman, W. B. 1990. Classification of Texas reservoirs in relation to limnology and fish community associations. Transactions of the American Fisheries Society 119:511–520.
- Dunham, R. A., C. J. Turner, and W. C. Reeves. 1992. Introgression of the Florida largemouth bass genome into native populations in Alabama public lakes. North American Journal of Fisheries Management 12:494–498.
- Forshage, A. A., P. P. Durocher, M. A. Webb, and D. G. Lewis. 1989. Management application of angler recognition program data. Proceedings of the Annual Conference of the Southeastern Association of Fish and Wildlife Agencies 43:36–40.
- , and L. T. Fries. 1995. Evaluation of the Florida largemouth bass in Texas, 1972–1993. American Fisheries Society Symposium 15:484–491.
- Gilliland, E. R. and J. Whitaker. 1989. Introgression of Florida largemouth bass introduced into northern largemouth bass populations in Oklahoma reservoirs. Proceedings of the Annual Conference of the Southeastern Association of Fish and Wildlife Agencies 43:182–190.
- Kulzer, K. E., R. L. Noble, and A. A. Forshage. 1985. Genetic effects of Florida largemouth bass introductions into selected Texas reservoirs. Proceedings of the Annual Conference of the Southeastern Association of Fish and Wildlife Agencies 39:56–64.
- Lutz-Carrillo, Dijar J., C. Hagen, L. A. Dueck, and T. C. Glen. 2007. Isolation and characterization of microsatellite loci for Florida largemouth bass, *Micropterus salmoides floridanus*, and other micropteryids. Molecular Ecology Notes. Blackwell Publishing Ltd.
- , ———, C. C. Nice, T. H. Bonner, M. R. J. Forstner, and L. T. Fries. 2006. Admixture analysis of Florida largemouth bass and northern largemouth bass using microsatellite loci. Transactions of the American Fisheries Society 135:779–791.
- Maceina, M. J., B. R. Murphy, and D. P. Philipp. 1992. Stocking Florida largemouth bass outside its native range. Transactions of the American Fisheries Society 121:686–691.
- and V. J. DiCenzo 1995. Long-term genetic changes and growth of largemouth bass populations in Alabama public reservoirs. Alabama Department of Conservation and Natural Resources, Final Report Project F-40.
- Norgren, K. G., R. A. Dunham, R. O. Smitherman, and W. C. Reeves. 1986. Biochemical genetics of largemouth bass populations in Alabama. Proceedings of the Annual Conference of the Southeastern Association of Fish and Wildlife Agencies 40:194–205.
- Philipp, D. P., W. F. Childers, and G. S. Whitt. 1983. A biochemical evaluation of the northern and Florida subspecies of largemouth bass. Transactions of the American Fisheries Society 112:1–20.
- SYSTAT for Windows: Statistics, Version 5 Edition. Evanston, IL: SYSTAT, Inc., 1992.
- Terre, D. R., S. J. Magnelia, and M. J. Ryan. 1993. Year class contribution of genetically-marked Florida \times northern largemouth bass stocked in three Texas reservoirs. Proceedings of the Annual Conference of the Southeastern Association of Fish and Wildlife Agencies 47:622–632.
- Zar, J. H. 1984. Biostatistical *Analysis*. Prentice-Hall, Inc. Englewood Cliffs, New Jersey.