Statewide Research - Freshwater Fisheries

Jim Bulak
Research Coordinator

John Crane
Assistant Project Leader

Jean Leitner
Fishery Biologist

James Long
Fishery Biologist

Jason Bettinger
Fishery Biologist

ANNUAL PROGRESS REPORT

F-63

July 1, 1999 through June 30, 2000

Submitted November 1, 2000

S.C. Department of Natural Resources
Division of Wildlife and Freshwater Fisheries
William S. McTeer, Deputy Director

CONTENTS

Contents Page(s) i

Tables Page(s) iii

Figures Page v

Relative performance of two strains of largemouth bass in farm ponds 1
Summary 1
Appendix I: A Comparison of First and Third Year Growth of Two Genetic Strains of Largemouth Bass When Stocked in Different Regions of South Carolina A-1

Relative performance of two strains of largemouth bass in state lakes 2
Introduction 2
Methods 3
Results 6
Discussion 10
Recommendations 13
References 14

A genetic survey of smallmouth bass populations in South Carolina 15
Introduction 15
Methods 16
Results 16
Discussion 22
Recommendations 23
Bibliography 24

Development of Reservoir-Specific Largemouth Bass Management Models 25
Summary 25
Introduction 25
Materials and Methods 28
Results and Discussion 29
Recommendations 32
Literature Cited 32
Appendix I: Population Dynamics and Management of Largemouth Bass in South Carolina A-1

An Inventory of the Aquatic Resources of the Broad River, with Emphasis on Fishes 33
Introduction 33
Methods and Materials 33
Results and Discussion 34

Recommendation 35
Appendix I: An inventory of the aquatic resources of the Broad River, with emphasis on fishes A-1

Inventory of the fish community of tidal freshwater wetlands of the Cooper River 37
Introduction.....37
Methods.....37
Results39
Discussion 40
References.....41

TABLES

Relative performance of two strains of largemouth bass in state lakes

Table 1. Allele frequencies (proportions) for largemouth bass used to stock study lakes, with historic data for reservoirs where stocks originated 7

Table 2. Mean growth rate at age-1, in mm/day, for Moultrie and Wateree strains of largemouth bass stocked in Lake Wallace and Sunrise Lake with corresponding T-test statistics and probabilities.....8

Table 3. Mean growth rate at age-3, in mm/day, for Moultrie and Wateree strains of largemouth bass stocked in Lake Wallace with corresponding T-test statistics and probabilities.....9

Table 4. Length frequency distributions by genetic strain for age-3 largemouth bass collected from Lake Wallace 9

A genetic survey of smallmouth bass populations in South Carolina

Table 1. Mean lengths for smallmouth bass collected from South Carolina populations in the Summer and Fall of 1999.....17

Table 2. Enzymes, loci, tissues (E=eye, L=liver, M=muscle) and buffers used for smallmouth bass genetics survey 18

Table 3. Allele frequencies for polymorphic loci in 5 populations of smallmouth bass in South Carolina. 19

Table 4. Measures of genetic variability calculated for South Carolina smallmouth bass populations. All 20 loci examined are included in this measurement 21

Development of Reservoir-Specific Largemouth Bass Management Models

Table 1a-d. Comparisons of largemouth bass population parameters in selected South Carolina reservoirs, 1999. 30

An Inventory of the Aquatic Resources of the Broad River, with Emphasis on Fishes

Table 1. Habitat unit definitions for visual assessment. 36

Table 2. Results of the habitat inventory of the Broad River. 36

Inventory of the fish community of tidal freshwater wetlands of the Cooper River

Table 1.–List of species captured by electrofishing and drop traps in Dean Hall (DH) and Bonneau Ferry (BF) wetlands in the Cooper River, South Carolina from April 1999 through January 2000.....42

Table 2.–Catch rates (mean fish per meter of electrofishing) of fish in Dean Hall and Bonneau Ferry wetlands from April 1999 - December 1999. 45

FIGURES

A genetic survey of smallmouth bass population in South Carolina

Figure 1. Genetic relationships among South Carolina smallmouth bass populations as calculated using Roger's genetic similarity (1972). 22

Inventory of the fish community of tidal freshwater wetlands of the Cooper River

Figure 1.–Map of Cooper River, South Carolina showing locations of Dean Hall and Bonneau Ferry ricefields where comparisons of fish communities were made. ...46

Figure 2.–Canonical correspondence analysis diagram of fish community data comparing Dean Hall to Bonneau Ferry based on electrofishing in April through December 1999.....47

JOB PROGRESS REPORT

STATE: South Carolina PROJECT NUMBER: F- 63

PROJECT TITLE: Fisheries Investigations in Lakes and Streams - Statewide

STUDY: Survey and Inventory STUDY TITLE: Fishery surveys - Statewide Fisheries Research

JOB NO: II JOB TITLE: Relative performance of two strains of largemouth bass in farm ponds

Summary

During the project period July 1, 1999 - June 30, 2000 final analysis for the growth portion of this study was completed. Results were compiled into a manuscript which is currently under review for publication. That manuscript is included here as Appendix 1.

In June of 2000 N=26-30 juvenile largemouth bass were collected from 12 study ponds in a continuing effort to monitor the shift in allele frequencies in these study populations. These fish were shipped to Auburn University for genetic analysis along with juveniles that were collected in 1999. Results are pending, and will be reported when available

Prepared by: Jean K. Leitner Title: Fishery Biologist

Appendix 1.

A Comparison of First and Third Year Growth of Two Genetic Strains of Largemouth Bass When Stocked in Different Regions of South Carolina

Jean Leitner and James Bulak

South Carolina Department of Natural Resources

1921 Vanboklen Road, Eastover, South Carolina 29044

Abstract

A statewide reciprocal transplant study was initiated to compare the performance of two strains of largemouth bass endemic to South Carolina. South Carolina is located in the broad hybrid zone that exists between the ranges of the northern and Florida subspecies of largemouth bass. Allozyme surveys have shown South Carolina coastal largemouth bass populations possess 98% Florida alleles, while Piedmont populations possess as few as 36% Florida alleles. Thirty seven new or renovated farm ponds were stocked in 1994 and 1995 with either coastal or Piedmont strain largemouth bass. We characterized performance differences between the two strains by evaluating growth of original stocks at one and three years. Selected water quality parameters were monitored to define differences among ponds. Region (Coastal Plain or Piedmont), strain, and the interaction of region and strain were tested as predictors of growth rate for first year and third year growth. Differences between regions were significant (P=0.05) for growth at age-1 and at age-3, with fish stocked in the Coastal Plain growing faster. Differences due to strain and the region/strain interaction were not significant.

Introduction

Two subspecies of largemouth bass *Micropterus salmoides*, the Florida *M. s. floridanus*

and the northern largemouth bass *M. s. salmoides*, exist and readily interbreed in both natural and hatchery environments (Isely et al., 1987, Gilliland and Whitaker 1989, Philipp and Witt 1991). The range of the Florida subspecies (FLMB) is restricted to peninsular Florida. The northern subspecies (NLMB) is found in the Mississippi drainage and the Atlantic Slope coastal drainage, north of Maryland (Philipp et al., 1983).

South Carolina is located in the broad hybrid zone between the ranges of the two pure subspecies. A statewide allozyme study of largemouth bass confirmed that South Carolina populations were hybrids (Bulak et al., 1995). This study also showed the existence of a geographic cline within South Carolina where the relative abundance of Florida alleles decreased from southeast to northwest. The relative frequency of alleles that were diagnostic for the Florida subspecies ranged from 98% in Lake Moultrie, a Coastal Plain reservoir, to 36% in Lake Wateree, a Piedmont reservoir.

Physiological and ecological differences among FLMB, NLMB, and their hybrids have been documented. A number of studies have shown a difference in the response to various temperature regimes (Fields et al., 1987, Carmichael et al., 1988). Other studies have shown differences in timing of spawning, growth rate, reproductive success and survival of the two subspecies (Philipp and Witt 1991, Maceina et al. 1988, Gilliland and Whitaker 1989, Isely et al. 1987).

The objective of this study was to examine growth differences between Piedmont (Lake Wateree) and coastal (Lake Moultrie) strains of largemouth bass in South Carolina. Privately-owned ponds were used as study sites. Each pond was stocked with either a coastal or Piedmont strain of largemouth bass. The objective was assessed by measuring growth to age-1 and age-3.

Materials and Methods

Ponds were selected prior to stocking through a series of phone interviews and site visits. All ponds measured 0.4 to 1.2 ha and were either new or recently renovated. Ponds were located in either the Coastal Plain or Piedmont regions of South Carolina. All study sites were relatively secluded and showed little potential for invasion by wild fish. Finally, all pond owners agreed to allow site access to study personnel for data collection.

Largemouth bass for experimental stockings were produced from fish collected from Lakes Moultrie and Wateree. Lake Moultrie broodfish were collected by electrofishing in March of 1993. Lake Wateree broodfish were collected by electrofishing in March of 1994. Stocks were held in separate ponds. In 1994 and 1995 the resulting fry from each strain were collected and transferred to grow-out ponds where they were raised to a total length of approximately 25 mm. Fry were harvested from as many schools as possible to maximize the number of parents contributing to the gene pool.

Size at stocking and allele frequencies characteristic of the northern and Florida subspecies were determined for each strain. At harvest, forty fingerlings from each strain were weighed (gm), measured (TL mm) and then preserved in 100% isopropyl alcohol. Also, two sets of 100 fingerlings from each strain were placed on dry ice and stored frozen for allozyme analysis. Horizontal starch gel electrophoresis was performed according to Norgren (1986). Gels were stained for two allozymes (*sAAT-2**, *sIDHP-2**), with fixed allelic differences and two with non-fixed differences (*sMDH-B**, *sSOD-1**) between the northern and Florida subspecies. Allele frequencies of stocked fingerlings were compared to source lake populations (as defined in Bulak et al. 1995) using the G-test (Sokal and Rohlf, 1969).

One half of the ponds in each region were stocked with Moultrie and the other half with

Wateree strain bass. Ponds were chosen at random for stocking with the Lake Moultrie strain. As each pond was chosen, its closest neighbor was assigned the Wateree strain. This ensured a uniform distribution of each strain throughout each region. Only one strain was hauled per day and the truck was flushed and stocked with fresh fingerlings each morning. Largemouth bass were hand counted and stocked at the rate of 124 and 247 fingerlings per hectare for unfertilized and fertilized ponds, respectively.

To account for productivity differences among ponds, selected water quality parameters were measured. Water quality was measured three times in 1994 and twice a year in 1995-1997, during the early summer to early fall growing season. Hardness and alkalinity were measured using a standard Hach kit with digital titrator. Temperature and pH were measured using an Orion field pH meter equipped with a Ross electrode. Water samples for chlorophyll-a determination were taken from 0.3 m below the surface at three sample sites on each pond. Sample sites followed the pond's stream gradient with an upper or inflow site, a middle, and a lower or outflow site. Chlorophyll-a concentration was determined with a Turner Filter Fluorometer Model 111 using the methods outlined in Arar and Collins (1992) for calibration and sample analysis.

Mean annual water quality parameters were computed for each pond. Mean pH, hardness, and alkalinity were the simple average of measurements taken throughout the sampling season . Mean annual chlorophyll-a concentration was computed by first taking the mean of the three samples for each sampling event and then taking the average of these means for each pond.

Adult largemouth bass were collected by electrofishing or angling from each pond at one and three years post-stocking. Ponds stocked in 1994 were sampled from 6/15-7/27/95 and from 6/12-8/21/97. Ponds stocked in 1995 were sampled from 6/11-6/19/96 and from 6/1-6/26/98.

For the assessment of age-1 growth, we collected 10% of the number stocked with a minimum of 20. All fish were weighed, measured, and returned to the pond. Scales were collected from fish that were suspiciously large or small for age verification. To assess growth to age-3, we collected as many bass as possible during each site visit. All collected fish were weighed, measured and fin-clipped, to avoid re-sampling. A length-frequency histogram was constructed in the field so that apparent age classes could be visualized. Scales were taken for age estimation from some fish from each size group, and from all fish that appeared to be older than age-1. In 1998, all fish in the largest size class and several from smaller size classes were sacrificed; otoliths, as well as scales were collected from these fish. Age was estimated from scales and otoliths, where available, by two independent readers. Growth rate for each fish was computed as:

$$\text{growth rate} = \frac{\text{length at harvest - length at stocking}}{\text{days since stocking.}}$$

Mean growth rate at age-1 and age-3 of largemouth bass was computed for each study pond. Atypical ponds were identified and not included in analysis of growth. These included ponds where introductions of wild fish or poor water quality had a substantial effect on reproduction or forage availability.

A mixed linear model (SAS, 1996) was used to identify factors that were significant predictors of largemouth bass growth rate. Region (Piedmont or Coastal Plain) and strain were fixed effects while individual study sites (pond) were random effects. The effects of pond , region, strain, and the interaction of region and strain were evaluated. Each water quality variable was included in the model as a covariate. Least squares analysis (SAS, 1996) was used to test the significance of the evaluated factors to growth rate. All statistical evaluations were conducted at

P = 0.05.

Results

Thirty seven ponds were stocked in May of 1994 and 1995. In each geographic region, approximately half of the ponds were stocked with Wateree and half with Moultrie strain bass

Moultrie and Wateree strain bass were of similar size at stocking in both 1994 and 1995. In 1994, Moultrie fingerlings (N=41) averaged 26 mm TL (SD=3.3) while Wateree fingerlings (N=39) averaged 34 mm TL (SD=1.8). In 1995, Moultrie fingerlings (N=44) averaged 32 mm TL (SD=3.9) while Wateree fingerlings (N=40) averaged 25 mm TL (SD=2.7).

Allele frequencies of stocked fingerlings were generally consistent with source populations (Table 1). Lake Moultrie fingerlings were not significantly different from wild Lake Moultrie stock at any of the four loci examined in either 1994 or 1995. Lake Wateree fingerlings produced in 1994 from Lake Wateree brood stock were significantly different from the source population at *sMDH-B** and potentially at *sIDHP-2**. At *sMDH-B**, the stocked fingerlings possessed the northern allele in significantly higher numbers than the wild stock. Analysis at *sIDHP-2** indicated that stocked fingerlings possessed a rare allele, *sIDHP-2*142*, in significantly higher numbers than wild Lake Wateree stock. However, the presence of this rare allele in the 1994 stock was not confirmed; neither a survey of the wild stock or juveniles produced in 1995 and 1996 showed this rare allele. Lake Wateree fingerlings produced in 1995 were significantly different from their source population at *sAAT-2** and *sIDHP-2**. At *sAAT-2** the stocked fingerlings possessed the

Florida alleles in significantly higher numbers than the wild stock. At *sIDHP-2** the stocked

fingerlings possessed the northern allele in significantly higher numbers than the wild Lake

Wateree stock. Despite these differences from their source, Wateree strain fingerlings still possesed a significantly greater percentage of alleles typical of the northern subspecies than did Moultrie strain fingerlings.

Water quality was variable among the study ponds (Table 2). The range of water quality values detected during the study were typical of South Carolina ponds.

Age-1 largemouth bass were collected from 38 of 40 ponds sampled in 1995 and 1996. Growth of individual fish was computed 386 to 474 days post-stocking.

Largemouth bass stocked in Coastal Plain ponds grew faster to age-1 (_ = 0.61 mm/d, SD = 0.11, N = 215) than those stocked in Piedmont ponds (_ = 0.55 mm/d, SD = 0.09, N = 324) (Figure 1). Mixed model analysis showed that region and pH, as a covariate, were significant predictors of age-1 growth. Least squares means analysis indicated the difference in growth to age-1 between regions was significant; there was not a significant difference between growth rates of the two strains or between the interaction of strain and region. Data from five atypical ponds were removed from the data set prior to this analysis.

Samples to assess growth to age-3 were collected from 35 of 36 ponds in 1997 and 1998. A total of 240 fish were aged; 57 age-3 largemouth bass were identified. Agreement between scales and otoliths for 54 fish was 65%. Growth was computed 1107 to 1197 days post-stocking.

There was a significant difference in growth to age-3 between regions (Figure 2.). Largemouth bass stocked in the Coastal Plain grew more (_ = 0.31 mm /d, SD = 0.04, N = 29) than those stocked in the Piedmont (_ = 0.27 mm per day, SD=0.04, N=28). Mixed model analysis showed that region was a significant predictor of growth to age-3. Least square mean analysis confirmed a significant difference in growth between regions. Strain was not a significant

predictor of age-3 growth.

Discussion

This study documented that when evaluating largemouth bass strains endemic to South Carolina, the region where fish were stocked was the most important predictor of their growth. Largemouth bass of both strains exhibited significantly greater growth in Coastal Plain ponds than in Piedmont ponds. This is likely because fish stocked in the Coastal Plain experienced a milder climate and longer growing season than those stocked in the Piedmont. For example, Greenwood, a Piedmont town, has a mean annual temperature of 15.6°C while Moncks Corner, a town in the Coastal Plain, has a mean annual temperature of 17.6°C.

Genetic strain did not have a significant impact on growth in this study, neither whithin the two geographic regions nor statewide. In a reciprocal transplant study in Illinois, Phillip and Claussen (1995) found that largemouth bass from a northern river drainage differed significantly from fish from a southern river drainage with respect to growth, survival and reproductive success. Each strain performed best in its native region. This indicates that local adaptations can result in demonstrable differences between largemouth strains even of the same subspecies, and even when those strains are geographically close. The largemouth bass strains we evaluated in South Carolina were from close geographic regions but were quite divergent genetically. Still we did not observe any difference in growth between them.

High environmental variability among ponds, and small sample sizes of age-3 bass may have impacted our ability to detect growth differences between strains. A study design where ponds were stocked with equal numbers of fish from each strain would have minimized the effect of pond to pond variation. We have employed this strategy in an ongoing effort. Unanticipated

difficulty in collecting 3 year olds could have been avoided by total sampling (i.e. draining and rotenone renovation) of each pond. This was not considered due to the private ownership of each pond site.

The lack of growth differences between these two strains indicates that small pond owners and managers in South Carolina probably can not predictably impact, at least in the short term, the success of their fishing ponds by stocking a particular strain of largemouth bass. This should not be used to infer a lack of fitness differences between the two strains studied. Bulak et al. (1995) proposed that the largemouth bass allelic cline in South Carolina was maintained by a natural selection gradient. Other factors related to the fitness of a fish, such as disease resistance and reproductive timing, were not evaluated in this study. There may also be differences in growth that would show up in older age classes.

In a continuation of the present study, we will monitor the allele frequencies of filial generations of largemouth bass produced in the study ponds. Changes in allele frequencies over time will provide direct information as to what genotypes are most successful in each region. In recent years South Carolina has adopted a regionalized approach to stocking largemouth bass. We recommend continuing the current policy to protect the existence of potentially important local adaptations.

Acknowledgments

This study was supported by the U. S. Fish and Wildlife Service through the Sport Fish Restoration Act. Much of the allozyme analysis presented was supplied by the Southeastern Cooperative Genetics Project at Auburn University. Drew Robb's assistance with all aspects of field sampling was invaluable. John Crane, Jennifer Barwick, Allison Haddock and Jeff

Hansbarger also provided assistance with field collections. Mitch Manis, Donny Taylor, Farrel Beck, Jimmy Singleton, and their staffs provided hatchery space and care for our broodstocks and their offspring. We greatly appreciate the generosity of the thirty seven pond owners who opened their properties to us as study sites. Without their participation this study would not have been possible.

References

Arar, Elizabeth J., and Gary B. Collins. 1992. In vitro determination of chlorophyll *a* and pheophytin *a* in marine and freshwater phytoplankton by flourescence. Turner Designs. Sunnyvale, CA.

Bulak, J., J. Leitner, T. Hilbish, R. A. Dunham. 1995. Distribution of largemouth bass genotypes South Carolina: Initial Implications. American Fisheries Society Symposium

15:226-235, 1995.

Charmichael, G. J., J. H. Williamson, C. A. Woodward, and J. R. Tomasso. 1988. Responses of northern, Florida and hybrid largemouth bass to low temperature and low dissolved oxygen. Progressive Fish-Culturist 56:288-290.

Fields, R., S. L. Lowe, C. Kaminski, G. S. Whitt, and D. P. Philipp.1987. Critical and chronic thermal maxima of northern and Florida largemouth bass and their reciprocal F_1 and F_2 hybrids. Transactions of the American Fisheries Society 16:856-863.

Gilliland, E. R., and J. Whitaker. 1989. Introgression of Florida largemouth bass into northern largemouth bass populations in Oklahoma reservoirs. Proceedings of the Annual Conference Southeastern Association of Fish and Wildlife Agencies 43(1989):182-190.

Isely, J. J., R. L. Noble, J. B. Koppleman, and D. P. Philipp. 1987. Spawning period and first-year growth of northern, Florida, and intergrade stocks of largemouth bass. Transactions of the American Fisheries Society 116:757-762.

Maceina, M. J., B. R. Murphy, J. J. Isely. 1988. Factors regulating Florida largemouth bass stocking success and hybridization with northern largemouth bass in Aquilla Lake, Texas. Transactions of the American Fisheries Society 117:221-231.

Norgren, K. G. 1986. Biochemical genetic survey of largemouth bass populations in Alabama. Master's thesis. Auburn University, Alabama.

Philipp, D. P. and J. E. Claussen 1995 . Fitness and performance differences between two stocks of largemouth bass from different river drainages within Illinois. American Fisheries Society Symposium 115:236-243.

Philipp, D. P., and G. S. Whitt. 1991. Survival and growth of northern, Florida, and reciprocal F_1 hybrid largemouth bass in central Illinois. Transactions of the American Fisheries

Society 120:58-64.

Philipp, D. P., W. F. Childers, and G. S. Whitt. 1983. Biochemical genetic evaluation of two subspecies of largemouth bass, *Micropterus salmoides*. Transactions of the American Fisheries Society 112:1-20.

SAS Institute Inc., 1996. SAS/STAT© Software: Changes and enhancement through release 6.11, SAS Institute, Cary, NC. 1104 pp.

Sokal, R. R., and F. J. Rohlf, 1969. Biometry. W. H. Freeman, San Fransisco, California.

Table 1. Allele frequencies for Moultrie and Wateree strain largemouth bass fingerlings used to stock study ponds in 1994 and 1995, with survey data of allele frequencies for L. Moultrie and L. Wateree where stocks originated. Alleles, or allele pairs, listed first are fixed (sAAT-2*, sIDHP-2*) or dominant in the Northern subspecies. Alleles listed second are fixed or dominant in the Florida subspecies. An * indicates a significant difference (P=.05) from survey data.

	Lake Moultrie			Lake Wallace		
Locus/allele	1995 survey data	1994 fing	1995 fing	1995 survey data	1994 fing	1995 fing
	N=116	N=52	N=100	N=122	N=100	N=100
*sAAT-2**						
100, 110	0.10	0.19	0.14	0.66	0.65	0.44*
126, 139	0.90	0.81	0.86	0.34	0.35	0.54*
*sIDHP-1**						
100	0.02	0.00	0.02	0.47	0.18*	0.66*
121	0.98	1.00	0.98	0.52	0.50*	0.34*
142	0.00	0.00	0.00	0.01	0.32*	0.00*
*sMDH-B**						

100	0.00	0.00	0.00	0.60	0.73	0.60
114	1.00	1.00	1.00	0.40	0.27	0.40
*sSOD-1**						
147	0.19	0.14	0.13	0.57	0.58	0.64
100	0.81	0.86	0.87	0.43	0.42	0.36

Table 2. Water quality parameters monitored on study ponds, with mean, standard deviation and range reported for each. Mean values reported are for the three year sampling period.

	Parameter			
	chl-a (µg/l)	pH	hardness (mg/l as $CaCO_3$)	alkalinity (mg/l as $CaCO_3$)
N	42	42	42	41
Mean	5.3	7.6	38.1	34.1

Standard Dev.	2.1	0.9	32.2	27.0
Range	2.2 - 10.4	5.3 - 9.8	3.2 - 172.8	3.3 - 137.2

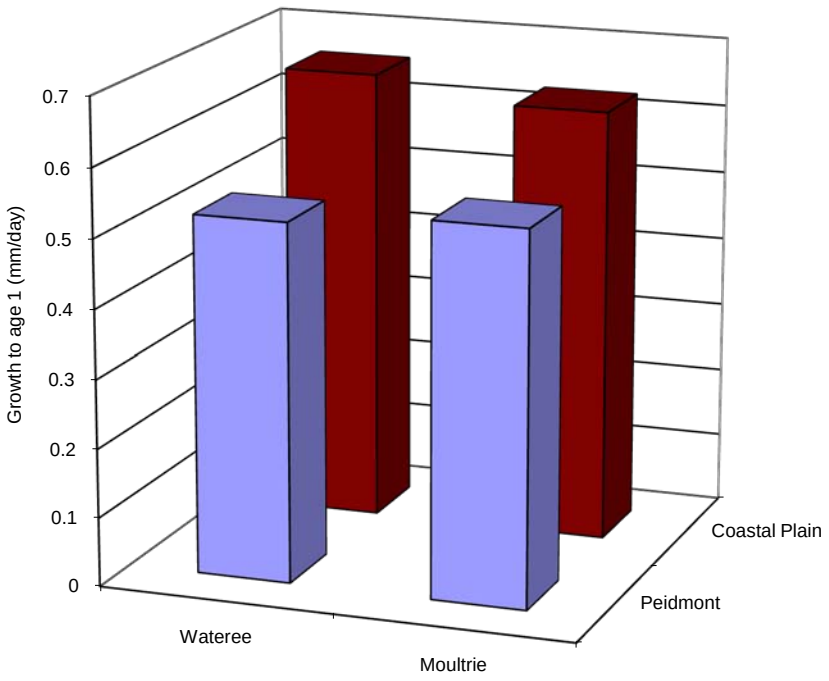

Figure 1. Growth to age 1 of largemouth bass in mm/day. Results are presented for each of four study groups defined by region (Coastal Plain or Piedmont) and strain (Moultrie or Wateree).

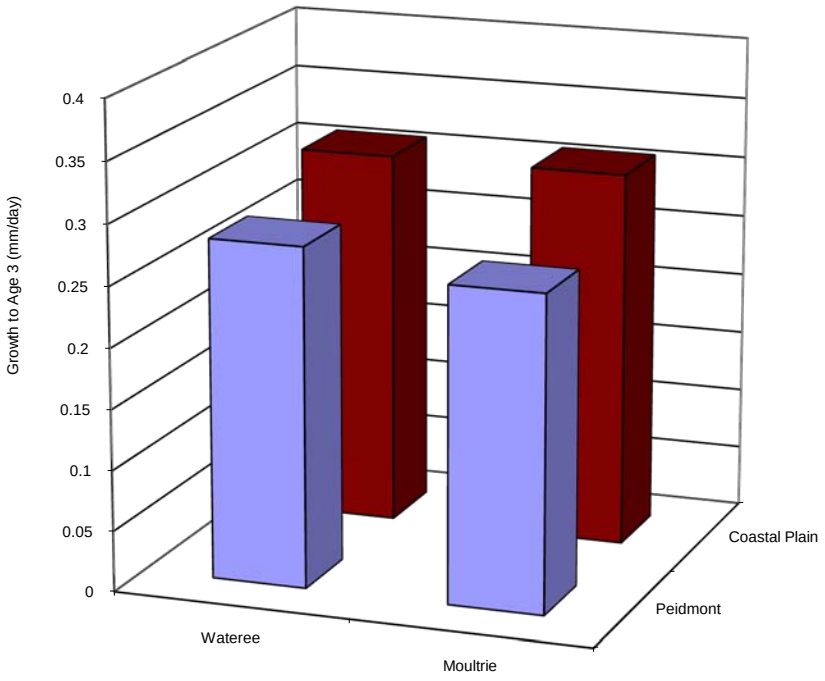

Figure 2. Growth to age 3 of largemouth bass in mm/day. Results are presented for each of four study groups defined by region (Coastal Plain or Piedmont) and strain (Moultrie or Wateree).

JOB PROGRESS REPORT

STATE: South Carolina PROJECT NUMBER: F- 63

PROJECT TITLE: Fisheries Investigations in Lakes and Streams - Statewide

STUDY: Survey and Inventory STUDY TITLE: Fishery surveys - Statewide Fisheries Research

JOB NO: II JOB TITLE: Relative performance of two strains of largemouth bass in state lakes

Introduction

Two subspecies of largemouth bass *Micropterus salmoides*, the Florida largemouth bass *M. s. floridanus* and the northern largemouth bass *M. s. salmoides*, exist and readily interbreed in both hatchery and reservoir environments (Isely et al., 1987, Gilliland and Whitaker 1989, Philipp and Witt 1991). The native range of the Florida subspecies (FLMB) is restricted to peninsular Florida. The northern subspecies (NLMB) is native to waters north along the Atlantic coast states from Maryland and west to the Mississippi (Philipp et al., 1983).

South Carolina is located in the broad hybrid zone between the ranges of the two subspecies. A statewide allozyme study of largemouth bass confirmed that South Carolina populations were hybrids (Bulak et al., 1995). This study also showed the existence of a geographic cline within South Carolina where the relative abundance of alleles typical of the Florida subspecies decreased from southeast to northwest. The relative frequency of alleles that are fixed for the Florida subspecies ranged from 98% in Lake Moultrie, a Coastal Plain reservoir, to 36% in Lake Wateree, a Piedmont reservoir. It was suggested that natural selection played a role in maintaining this allelic cline.

Physiological and ecological differences among FLMB, NLMB, and their hybrids have been documented. A number of studies have shown a difference in the response of the FLMB, NLMB, and their hybrids to various temperature regimes (Fields et al., 1987, Charmichael et al.,

1988). Other studies have shown differences in timing of spawning, growth rate, reproductive success and survival of the two subspecies (Philipp and Witt 1991, Maceina et al. 1988, Gilliland and Whitaker 1989, Isely et al. 1987).

The objective of this study was to examine performance differences between Lake Wateree and Lake Moultrie genetic strains of largemouth bass found in South Carolina. Two newly renovated state owned lakes, Wallace and Sunrise, were stocked with largemouth bass fingerlings from each strain. Strains were produced on separate hatcheries from broodfish collected from Lakes Wateree and Moultrie. Each strain received either a single or double oxytetracycline mark prior to stocking. Lakes Wallace and Sunrise were stocked with equal proportions of each strain. The objective will be achieved by measuring growth of stocked bass at age-1 and age-3 and by monitoring the long term temporal change in juvenile genotypes.

Methods

Sunrise Lake, a 20 acre lake in Lancaster County, and Lake Richard B. Wallace, a 280 acre lake in Marlboro County, were renovated during the summer of 1996. Largemouth bass for experimental stockings were produced from adult bass collected from Lakes Moultrie and Wateree. Lake Moultrie broodfish were collected by electrofishing in March of 1993 and were housed separately from other stocks at Cheraw State Fish Hatchery. Lake Wateree broodfish were collected in early Spring of 1997 and transported to Cohen Campbell Fisheries Center where they were stocked directly into a spawning pond separate from other stocks. Each group of broodfish was allowed to spawn. Resulting fry were harvested from as many schools as possible to maximize the number of parents contributing to the gene pool, and were grown out to fingerlings.

Prior to stocking fingerlings from each strain were marked by immersion for 6 hours in a 500 ppm solution of oxytetracycline. Moultrie strain largemouth bass were double marked, first

on 4/16/97 as fry, and then on 5/5/97 as fingerlings. Wateree strain largemouth bass were single marked as fingerlings on 4/25/97.

Each lake was stocked with equal numbers of each strain at the rate of 100 fish per acre in April and May of 1997. Lake Wallace was stocked with 28,000 and Sunrise Lake with 2000 largemouth bass. (Lakes were stocked in October 1996 with a combination of bluegill *Lepomis macrochirus* and redear *L. microlophus* fingerlings at the rate of 1000 per acre.) Wateree strain fingerlings were stocked on 4/25/97. Moultrie strain fingerlings were stocked on 5/5/97. Total lengths were recorded for a sample of 100 fingerlings from each strain at time of stocking. One hundred additional fingerlings from each strain were transported to the Berry's Mill Hatchery near Traveler's Rest and held in separate ponds for use in mark evaluation and genetic analysis.

Ponds at Berry's Mill were harvested on 11/6/97 and sagittal otoliths, liver, and muscle tissue were collected from each individual. Known single and double marked otoliths were randomly coded and given to an experienced reader for evaluation. Otoliths were mounted, sectioned and polished to the core. Presence or absence of a mark on the otolith was determined with a flourescent compound microscope.

Liver and muscle tissues were stored at -80°C for genetic analysis. Horizontal starch gel electrophoresis was performed according to Norgren (1986). Gels were stained for four enzymes which are diagnostic for the Florida and northern subspecies of largemouth bass. These are aspartate aminotransferase (*sAAT-2**), isocitrate dehydrogenase (*sIDHP-1**) and superoxide dismutase (*sSOD-1**) from liver tissue, and malate dehydrogenase (*sMDH-B**) from muscle tissue. Alleles typical of the northern subspecies are *sAAT-2*100* and *sAAT-2*110*, *sIDHP-1*100*, *sMDH-B*100*, and *sSOD-*147*. Alleles typical of the Florida subspecies are *sAAT-2*126* and *sAAT-2*139*, *sIDHP-1*121*, *sMDH-B*114*, and *sSOD-1*100*. A genetic baseline was determined for Lakes Moultrie and Wateree using data from an initial statewide

survey (Bulak et al., 1995) and data collected from large and small fish for a related performance study. Allele frequencies of each stock was compared to baseline genetic data for source populations using the G-test (Sokal and Rohlf, 1969).

Lakes were sampled in the Spring and Summer of 1998 for collection of juveniles and age-1 adults, in Summer of 1999 for collection of juveniles, and in Summer of 2000 for collection of juveniles and age-3 adults. Adults were collected by electrofishing from Lake Wallace on March 31 and April 4, 1998, and on May 25, 2000. Adults were collected from Sunrise Lake on May 22, 1998, June 1, and August 3, 2000. Total length and weight were recorded for each individual. Sagittal otoliths were collected from each largemouth bass and stored in the dark until processed for mark determination. Liver and muscle tissues were collected from age-1 fish and stored at -80°C for genetic analysis.

Seining for juveniles was conducted on both lakes in the early summer of 1998, 1999 and 2000. A variety of areas and habitats were sampled. An attempt was also made to collect young of the year from Lake Wallace in the fall of 2000 by electrofishing.

Otoliths collected from adult largemouth bass were mounted, sectioned, and polished to the core for mark determination. Marks were evaluated by two independent readers using a flourescent compound microscope. Otoliths were determined to be single marked, double marked or unmarked by each reader. Those otoliths that were not agreed on after consultation were thrown out. Growth at age-1 and age-3, in mm/day, was compared for Moultrie strain and Wateree strain fingerlings in each lake using the T-test. Length frequency distributions were generated for each strain and were compared using the Kolmogorov-Smirnov 2-sample test.

Results

Size at stocking was similar for the Moultrie and Wateree strains. Moultrie strain fingerlings averaged 24.4 mm total length (n = 102, std = 2.6). Wateree strain fingerlings

averaged 23.3 mm total length (n = 92, std = 6.2).

Mark evaluations were completed on a set of 68 otoliths. Because of questionable origin made evident by genetic analysis, 8 sets of otoliths were thrown out. Of 27 Wateree strain fish 100% were correctly identified. Of 33 Moultrie strain fish 91% were correctly identified.

Genetic analysis was completed for hatchery fingerlings of each strain, and comparisons made with historic data from wild stocks (Table 1.). Fingerlings of the Wateree strain were similar to the wild Wateree stock at three of four loci. However, at the *sIDHP-1** locus the Wateree strain fingerlings possessed significantly (p=0.05) more of the *sIDHP-1*100* allele which is typical of the northern subspecies. Fingerlings of the Moultrie strain differed markedly from wild lake Moultrie stock at three of the four loci examined. They possessed significantly more of the *sAAT-2*100,110* alleles, the *sIDHP-1*100* allele, and the *sMDH-B*100* allele, all typical of the northern subspecies.. Fingerlings of the Moultrie strain possessed *sMDH-B*100* at a frequency of 20% although broodstock from Lake Moultrie were known to be fixed for *sMDH-B*114.*

Those fish possessing the *sMDH-B*100* allele were also found to be single rather than double marked. This poses a problem, as they are undistinguishable, both genetically and by mark, from the Wateree strain fish. For the purposes of this report, all single marked fish are considered to be of the Wateree strain.

Age-1 largemouth bass were collected by electrofishing from Lake Wallace on 4/31/98 and 5/22/98. Fish averaged 274.1 mm total length (n = 104, std = 28.2) and weighed an average

Table 1. Allele frequencies (proportions) for largemouth bass used to stock study lakes, with historic data for reservoirs where stocks originated. A + indicates allele frequencies significantly different from survey data.

	Lake Wateree	Lake Moultrie

Locus/Allele	Historic Data	1997 Fing.	Historic Data	1997 Fing.
sAAT-2*				
100, 110	146 (0.66)	26 (0.69)	47 (0.10)	16 (0.23) +
126, 139	74 (0.34)	12 (0.31)	443 (0.90)	54 (0.77) +
sIDHP-1*				
100	116 (0.48)	37 (0.69) +	11 (0.02)	12 (0.16) +
121	124 (0.52)	17 (0.31) +	455 (0.98)	64 (0.84) +
sMDH-B*				
100	141 (0.61)	39 (0.70)	0 (0.00)	16 (0.20) +
114	91 (0.39)	17 (0.30)	494 (1.00)	64 (0.80) +
sSOD-1*				
147	143 (0.57)	29 (0.54)	82 (0.19)	17 (0.24)
100	107 (0.43)	25 (0.46)	344 (0.81)	55 (0.76)

of 359.3 g (n = 104, std = 123.5) Age-1 largemouth bass were collected from Sunrise Lake on 5/22/98. These fish averaged 235.7 mm total length (n = 92, std = 17.3) and weighed an average of 171.7 g (n = 92, std = 49.8).

Clear marks were detected on 49 of 104 otoliths sampled from Lake Wallace, and on 44 of 92 otoliths sampled from Sunrise Lake. Twenty-one percent of otoliths from Lake Wallace were determined to be unmarked, and 32% were not readable due to cracks or occlusions. From Sunrise Lake 22% of otoliths were read as unmarked and 29% were not readable.

Marked fish were identified to strain (1 mark = Wateree, 2 marks = Moultrie), and growth rate by strain was computed for each lake (Table 2). Differences in growth to age-1 between the two genetic strains were tested for each lake using the T-test and were not significant.

Age-3 largemouth bass were collected from Lake Wallace on May 25, 2000. Fish

averaged 414.8 mm total length (n=40, std=17.1) and weighed an average of 1249.9 g (n=40, std=213.1). Mark evaluations were completed. Of 40 age-3 largemouth bass collected 11 (27%) were of the Wateree strain, 28 (70%) were of the Moultrie strain, and 1 was not readable. Growth to age-3 was computed for each strain. Differences in growth between the two strains were tested using the T-test and were not significant (Table3). Length frequency distributions for each strain were generated (Table 4). Differences between the two distributions were tested using the Kolmogorov-Smirnov 2-sample test and were not significant, although the 8 largest fish collected were of the Lake Moultrie strain.

Table 2. Mean growth rate at age-1, in mm/day, for Moultrie and Wateree strains of largemouth bass stocked in Lake Wallace and Sunrise Lake with corresponding T-test statistics and probabilities.

	Lake Wallace				Sunrise Lake			
Strain (N)	Rate (mm/d)(N)		T	Prob>|T	Rate (mm/d)		T	Prob>|T|
Moultrie	0.75	(13)	1.29	0.2038	0.54	(19)	-0.64	0.5245
Wateree	0.72	(31)			0.55	(30)		

Table 3. Mean growth rate at age-3, in mm/day, for Moultrie and Wateree strains of largemouth bass stocked in Lake Wallace with corresponding T-test statistics and probabilities.

		Lake Wallace		
Strain	N	Rate (mm/day)(std)	T	Prob>T
Moultrie	28	0.34 (0.01)	-0.97	0.3342
Wateree	11	0.35 (0.02)		

Table 4. Length frequency distributions by genetic strain for age-3 largemouth bass collected from Lake Wallace.

	Frequency by strain	
length group (mm)	Moultrie	Wateree
380	1	1
390	3	1
400	7	3
410	8	2
420	1	3
430	3	1
440	4	0
450	1	0

Largemouth bass were collected in 2000 from Sunrise Lake June 1 during the day and August 3 at night. Eight age-3 fish were collected. They averaged 437.9 mm total length (std=34.7) and weighed an average of 1148.5 g (std=319.9). Because of the small sample size these fish have not been evaluated yet for marks. This lake is scheduled for a major drawdown for repairs to the dam. Plans are to make another attempt at collecting age-3 largemouth bass this winter while the lake is low.

Despite efforts to sample a variety of areas and habitats, no juvenile largemouth bass were collected from either lake in 1998, nor from Lake Wallace in 1999 and 2000. Thirty juvenile largemouth bass were collected from Sunrise Lake in 1999 and 2000. These fish have been sent to the South Eastern Fisheries Genetics Cooperative at Auburn University for genetic analysis.

Discussion

The marked genetic difference between Moultrie strain fingerlings and Lake Moultrie broodfish is a concern, especially at the *sMDH-B** locus. It indicates that not all of the fingerlings stocked as Moultrie strain were produced from Lake Moultrie broodfish.

When they were collected in 1993 all Lake Moultrie broodfish underwent liver and muscle biopsies. Tissues were analyzed so that the alleles expressed at each loci for every fish was known. None of 112 fish biopsied possessed the *sMDH-B*100* allele. Eight out of 40 Moultrie strain fingerlings were homozygous for *sMDH-B*100* meaning they inherited that allele from both parents. All other fingerlings were homozygous for *sMDH-B*114*. The presence of the northern allele and lack of heterozygotes indicate that the fish possessing the northern allele were spawned in a different pond and from a group of parents other than the Lake Moultrie broodfish.

Fish possessing the *sMDH-B*100* allele also possessed a different oxytetracycline mark from other Moultrie fingerlings. Moultrie fingerlings were marked twice, first as fry when harvested from the spawning pond, and then as fingerlings when taken from the hatchery for stocking. All eight of the fish homozygous for *sMDH-B*100* had only the later mark.

There are a number of possible explanations for the presence of the fish homozygous for *sMDH-B*100*. The first is that the Moultrie strain fingerlings were contaminated on the hatchery. This would have occurred sometime after the marking of fry but prior to the second marking, with the source of contamination either in the grow out pond or the fish house.

A second explanation is that the Moultrie strain fish were contaminated in the holding pond at Berry's Mill with fish of the single marked Wateree strain. The two strains were housed in adjacent ponds separated by an earthen dike. A third explanation is that the samples collected from Berry's Mill were mishandled and some Wateree strain fish were improperly coded as Moultrie strain. The probability that 8 fish chosen at random from the Wateree strain will all be

homozygous for *sMDH-B*100* is P = 0.002.

There is also the possibility that genetic and/or otolith interpretations of the known stocks were incorrect. This will be further investigated by reviewing those otolith samples and genetic records.

If the Moultrie strain fingerlings were in fact contaminated prior to stocking, the effects on the experiment can be assessed. Our experimental design called for the lakes to be stocked with equal proportions of each strain. Performance would be assessed by measuring growth of stocked fish at age-1 and age-3, and by the long term monitoring of allele frequencies of subsequent year classes.

In fact, the lakes were stocked with 50% Wateree strain fingerlings, 40% Moultrie strain fingerlings, and 10% fingerlings of unknown origin. Because the fingerlings of unknown origin are single marked they are indistinguishable from fish of the Wateree strain. Of the marked fish collected from lakes Wallace and Sunrise, 61% and 70% respectively were single marked. Growth assessments of the Wateree strain include those fish of unknown origin. Assessment of reproductive success of the Moultrie and Wateree strains by following changes in allele frequencies of subsequent generations will be difficult because of the unbalanced stocking, and the inability to quantify the contribution of the unknowns.

While these factors negatively impact our ability to draw conclusions regarding the performance of the Moultrie and Wateree strains, valuable information can still be obtained. Genetically the 8 unknown fish are similar to the Wateree strain. Though as a group they possess more northern alleles, individually they are not distinguishable from a Wateree strain fish. Growth can still be compared between the Moultrie strain and the more northern, single marked fish.

Comparison of growth at age-1 do not show significant differences between the strains for

either lake. Larger sample sizes would increase our ability to detect differences. Although about 100 fish were collected from each lake, only about half of these are included in analysis. A number of otoliths examined were either unmarked, or marked but too difficult to read because the core was occluded by cracks. Those samples that were too difficult to read should be reexamined using the other otolith.

Comparison of growth at age-3 did not show any significant difference between strains in Lake Wallace. However, a look at the length frequency distribution showed us that the 8 largest fish collected were all of the Moultrie strain. Though the length frequencies also are not significantly different, we are concerned that our small sample size especially for the Wateree strain (N=11) has hindered our ability to detect differences. When this data set is tripled to include 117 fish differences in growth and length frequencies are significant.

Largemouth bass in Sunrise Lake grew much slower in their first year than those in Lake Wallace. While no water quality measurements were taken a visual inspection of the two lakes indicated they were managed quite differently. Lake Wallace appeared to have received more than adequate fertilizer applications; it was deep green with no visibility below the surface in some areas. Sunrise Lake was very clear throughout. If fertilizer applications were made at Sunrise Lake they were not effective. Both of these lakes were stocked at the fertilized rate of 1000 bream/100 bass per acre.

Recommendations

Continue study. Place emphasis on increasing sample size. Process otoliths from selected samples of age-1 fish and repeat analysis with larger sample size. Collect 100 largemouth bass from Lake Wallace in Spring/Summer of 2001 for growth comparison. Perform genetic analysis on year classes collected from Sunrise Lake. Continue to collect juveniles from Sunrise Lake every other year for long term evaluation of shifts in allele frequencies. Ensure that

all state lakes are managed optimally with regard to liming and fertilization regimes.

References

Bulak, J., J. Leitner, T. Hilbish, and R. A. Dunham. 1995. Distribution of largemouth bass genotypes South Carolina: Initial Implications. American Fisheries Society Symposium 15:226-235.

Charmichael, G. J., J. H. Williamson, C. A. Woodward, and J. R. Tomasso. 1988. Responses of northern, Florida and hybrid largemouth bass to low temperature and low dissolved oxygen. Progressive Fish-Culturist 56:288-290.

Crochet, D. W. 1992. Fish Pond Management Guide for South Carolina. South Carolina Wildlife and Marine Resources Department, Columbia, South Carolina.

Fields, R., S. L. Lowe, C. Kaminski, G. S. Whitt, and D. P. Philipp.1987. Critical and chronic thermal maxima of northern and Florida largemouth bass and their reciprocal F_1 and F_2 hybrids. Transactions of the American Fisheries Society 16:856-863.

Gilliland, E. R., and J. Whitaker. 1989. Introgression of Florida largemouth bass into northern largemouth bass populations in Oklahoma reservoirs. Proceedings of the Annual Conference Southeastern Association of Fish and Wildlife Agencies 43(1989):182-190.

Isely, J. J., R. L. Noble, J. B. Koppleman, and D. P. Philipp. 1987. Spawning period and first-year growth of northern, Florida, and intergrade stocks of largemouth bass. Transactions of the American Fisheries Society 116:757-762.

Leitner, J. K., and J. J. Isely. 1994. A liver and muscle biopsy technique for electrophoretic evaluation of largemouth bass. Progressive Fish-Culturist 56:288-290.

Maceina, M. J., B. R. Murphy, J. J. Isely. 1988. Factors regulating Florida largemouth bass stocking success and hybridization with northern largemouth bass in Aquilla Lake, Texas. Transactions of the American Fisheries Society 117:221-231.

Norgren, K. G. 1986. Biochemical genetic survey of largemouth bass populations in Alabama. Master's thesis. Auburn University, Alabama.

Philipp, D. P., and G. S. Whitt. 1991. Survival and growth of northern, Florida, and reciprocal F_1 hybrid largemouth bass in central Illinois. Transactions of the American Fisheries Society 120:58-64.

Philipp, D. P., W. F. Childers, and G. S. Whitt. 1983. Biochemical genetic evaluation of two subspecies of largemouth bass, *Micropterus salmoides*. Transactions of the American Fisheries Society 112:1-20.

Sokal, R. R., and F. J. Rohlf, 1969. Biometry. W. H. Freeman, San Francisco, California.

Prepared by: Jean K. Leitner Title: Fishery Biologist

JOB PROGRESS REPORT

STATE: South Carolina PROJECT NUMBER: F- 63

PROJECT TITLE: Fisheries Investigations in Lakes and Streams - Statewide

STUDY: Survey and Inventory STUDY TITLE: Fishery surveys - Statewide Fisheries Research

JOB TITLE: A genetic survey of smallmouth bass populations in South Carolina

Introduction

The smallmouth bass, *Micropterus dolomieu*, is native to the middle and upper Mississippi River basin. It has been widely introduced outside of its native range. It's North American distribution now includes the mountainous and Piedmont portions of the mid-Atlantic states and even the Coastal Plain where adequate habitat exists (Rohde et al, 1994). Smallmouth bass require clear running or deep water.

Two subspecies of smallmouth bass are recognized. *M. d. dolomieu* is the northern form. It is native to the area from the Missouri and Meramec river basins northward and east of the Mississippi River. *M. d. velox*, also called the Neosho subspecies, occupies a range restricted to direct tributaries of the middle Arkansas River in the far western and southern Ozarks.

Smallmouth bass are not native to South Carolina. They have been stocked fairly regularly in the state since the early 1980's. Fish are produced on two state hatcheries from stocks that we expect originated from the Ozark genetic strain. A number of introduced populations have been established. They include the upper Broad River and its tributaries in Cherokee county, Lake Jocassee in Oconee county, and Lake Keowee in Oconee and Pickens counties.

The objective of this study was to genetically survey several of our reproducing populations and our hatcheries, to see how they compare to each other, and to determine the level of genetic diversity present. We also wanted to see how closely related our hatchery stocks are to the Ozark strain of smallmouth bass from which they reportedly originated.

Methods

Smallmouth bass were collected from each of five populations by electrofishing, angling and gillnetting in the summer and fall of 1999. Fish were collected from Broad River and Kings Creek in Cherokee County, from Lake Jocassee in Oconee County, and from the Dennis Center and Cheraw state fish hatcheries. Total lengths were recorded for each fish. Liver, muscle and eye tissues were extracted from each fish and immediately placed on dry ice. Carcasses of fish from Broad River and Kings Creek were saved for future otolith extraction and analysis.

Tissue samples were shipped to Auburn University for genetic analysis at 20 enzyme loci. Samples were analyzed using horizontal starch gel electrophoresis according to the procedures of Steiner and Joslyn (1979), Philipp et al. (1982) and Norgren et al. (1986). Allele frequencies were computed and measures of genetic diversity were calculated for each population. These included mean number of alleles per locus, percentage of polymorphic loci and mean heterozygosity. Genetic relationships among all five South Carolina populations were calculated using Rogers' (1972) genetic similarity. A dendogram of these relationships was generated.

Results

Smallmouth bass (N=116) were collected from all populations sampled. Table 1 lists the number collected and mean lengths by population. Fish were examined electrophoretically at the 20 enzyme loci listed in Table 2. Allele frequencies were computed for the 10 loci found to be polymorphic (Table 3).

Table 1. Mean lengths for smallmouth bass collected from South Carolina populations in the

Summer and Fall of 1999. Length data for Lake Jocassee is unavailable.

Population	N	Length (mm) range	Length (mm) mean	Length (mm) sd
Broad River	32	72-391	184.3	83.4
Kings Creek	21	70-303	120.8	63.2
Lake Jocassee	8	-	-	-
Dennis Center	25	112-177	140.1	18.7
Cheraw	30	43-179	125.0	36.8

Table 2. Enzymes, loci, tissues (E=eye, L=liver, M=muscle) and buffers used for smallmouth bass genetics survey.

Enzyme	Number of loci	Enzyme number	Locus	Tissue	Buffer
Aspartate aminotransferase	1	2.6.1.1	AAT-1	L	EDTA
Alcohol dehydrogenase	1	1.1.1.1	ADH	L	EDTA
Glucose dehydrogenase	1	1.1.1.47	GDH	L	TC
Glucose-6-phosphate isomerase	2	5.3.1.9	GPI-A,B	M	EDTA
Lactate dehydrogenase	2	1.1.1.27	LDH-A,B	E	EDTA
Malate dehydrogenase	2	1.1.1.37	MDH-A,B	M	EDTA
Malic enzyme	1	1.1.1.40	MEP-1	M	TC
Tripeptide aminopeptidase	1	3.4.-.-	PEPB	E	TC
Pepdidase-C	1	3.4.-.-	PEPC	L	EDTA
Dipepdidase	1	3.4.-.-	PEPA	E	TC
Pepdidase-S	1	3.4.-.-	PEPS	L	TC
Phosphogluconate dehydrogenase	1	1.1.1.44	PGDH	L	TC
Phosphogluctomutase	1	5.4.2.2	PGM	M	EDTA
General protein	2	--	PROT-1,2	M	EDTA
Superoxide dismutase	1	1.15.1.1	SOD	L	EDTA
Triosephosphate isomerase	1	5.3.1.1	TPI	M	-------

Table 3. Allele frequencies for polymorphic loci in 5 populations of smallmouth bass in South Carolina.

	Populations				
Locus	Broad River	Cheraw	Dennis Center	Kings Creek	Lake Jocassee
AAT-1					
100	.475	.650	.140	.595	1.000
90	.525	.350	.860	.405	.000
ADH-1					
100	.333	.900	.760	.476	.625
53	.000	.000	.000	.024	.375
104	.667	.100	.240	.500	.000
GDH-1					
100	.405	.552	.480	.429	.375
86	.000	.086	.000	.048	.625
105	.595	.362	.520	.524	.000
GPI-A					
100	.976	1.000	1.000	.929	.167

76	.000	.000	.000	.000	.250
83	.000	.000	.000	.000	.167
216	.024	.000	.000	.071	.417
GPI-B					
100	1.000	.914	1.000	1.000	1.000
97	.000	.086	.000	.000	.000
MDH-A					
100	.976	1.000	1.000	.929	.438
80	.024	.000	.000	.071	.563

Table 3. (Cont'd)

	Populations				
Locus	Broad River	Cheraw	Dennis Center	Kings Creek	Lake Jocassee
MEP-2					
100	.143	.483	.540	.429	.750
92	.000	.069	.180	.190	.000
107	.476	.241	.200	.190	.000

111	.381	.155	.080	.143	.250
115	.000	.052	.000	.048	.000
PGM-1					
100	1.000	1.000	1.000	.881	.688
80	.000	.000	.000	.119	.250
60	.000	.000	.000	.000	.063
SOD-1					
100	.619	.650	.292	.548	.917
145	.357	.333	.708	.405	.000
210	.024	.017	.000	.048	.083
TPI-1					
100	.952	.828	1.000	.810	.438
86	.000	.000	.000	.095	.438
140	.048	.172	.000	.095	.063
194	.000	.000	.000	.000	.063

There was a large amount of genetic variation among and within these populations (Table

4). This is partly due to the examination of loci that we expected to be polymorphic. The hatcheries showed less variability than the wild populations, with the Dennis Center population much more homozygous than the others. Broad River, Kings Creek and Cheraw all had normal to high levels of variability. Lake Jocassee had extremely high levels of mean heterozygosity.

Table 4. Measures of genetic variability calculated for South Carolina smallmouth bass populations. All 20 loci examined are included in this measurement.