

Project Title: [Establishing Largemouth Bass Strains for Rapid Growth to 1.5 Pounds in the North Central Region \[Termination Report\]](#)

Key Word(s): Largemouth Bass

Total Funds Committed: \$155,000

Initial Project Schedule: September 1, 2014 to August 31, 2016

Current Project Year: September 1, 2016 to April 30, 2018

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Reason for Termination: Completion of project objectives.

Project Objectives

1. Identify the best genetically distinct Largemouth Bass populations for fast growth in the NCR.
2. Conduct a meta-analysis using all appropriate data for Largemouth Bass from both published and non-published sources to identify at minimum three populations of LMB with the potential to exhibit rapid growth to target weight in the NCR.
3. Evaluate the identified populations at two or more latitudes in the NCR to identify the optimal source population

Deliverables

1. Publication of results in journal articles(s).
2. Extension products, including a selection matrix.

Project Summary

Largemouth Bass (LMB) is an important aquaculture species. Interest in improving commercial culture efficiency has grown due to the great demand and high value compared to other cultured species. A NCRAC Priority is to increase the efficiency of LMB growth to market size through means beyond dietary modification. One impediment beyond nutritional insufficiency is the rearing of LMB stocks with little to no domestication or selective breeding for efficient production. Therefore, strain evaluation and identification of the best Largemouth Bass populations for fast growth would result in an immediate impact on the economic return of many small aquaculture operations in the North Central Region (NCR). In this project, Genetic evaluation of eight strains of 1,045 LMB in total for selective breeding and genetic improvement was completed. The best genetically distinct LMB and the optimal source populations with the potential to exhibit rapid growth to target weight for the NCR were identified. An experiment to compare growth performance of the identified group vs. Ohio control group was conducted in indoor system and the result showed that fish from the identified group grew 80.83% faster than control group. A selection matrix is not possible due to the single source of Largemouth Bass that was identified as the best performer in the full-scale growth trial.

Technical Summary and Analysis

Objective 1.— The Ohio State University (OSU) genotyped ~1050 Largemouth Bass in total from 25 populations across the United States using eight microsatellite loci, which are standard genetic markers for population genetic analysis. Those strains were obtained from Florida, Texas, Mississippi, South Carolina, Arkansas, Ohio, Wisconsin, and Minnesota. The data are been analyzed together with previous data to confirm the major findings resulted from previous data: (1) allelic richness was lower among cultured populations than among wild populations; (2) effective population size in hatcheries could promote high levels of genetic variation among individuals and minimize loss of genetic diversity; (3) the majority of Largemouth Bass populations had a significant heterozygosity excess, which is likely to indicate a previous population bottleneck; and (4) the phylogeny based on eight microsatellites revealed a clear distinction between northern and southern populations, although samples from 25 populations were different. The information provides a valuable basis for development of aquaculture genetic breeding programs in Largemouth Bass. A manuscript has been completed based on the results.

Southern Illinois University Carbondale (SIUC) collected DNA from 30 LMB populations across the NCR in year 1. DNA from each fish was sent to the Ohio State University for analysis of genetic diversity, to be

determined in year 2 and added to the results discussed above. Analysis of putative genetic growth markers associated with the insulin-like growth factor (IGF-I and IGF-II) genes was conducted on these samples at SIUC. Unique alleles for these genes were identified in NRC fish and share some similarities to those published for increased growth in Chinese LMB populations (Li et al. 2009, 2012). Researchers also identified a unique allele for IGF-II in some of the populations. Based on project results and those of Li et al. (2009, 2012), four LMB stocks were selected for a juvenile growth study to verify predicted growth associations.

Objective 2. — Southern Illinois University Analysis of putative genetic growth markers associated with the IGF-I and IGF-II genes was conducted on these samples at SIUC. Unique alleles for these genes were identified in NRC fish and share some similarities to those published for increased growth in Chinese LMB populations (Li et al. 2009, 2012). We also identified a unique allele for IGF-II in some of the populations. Based on our results and those of Li et al. (2009, 2012), four LMB stocks were selected for a juvenile growth study to verify predicted growth associations.

Largemouth Bass weight- and length-at-age data from LMB populations throughout the NCR were collected.

Meta-analysis results by state suggested Kansas had the fastest growing LMB with an estimated time to market size of 1.05 years. However, Kansas had data from only one reservoir. States with large data sets ranked as follows: Illinois (1.38 years), Iowa (1.56), South Dakota (1.81), Wisconsin (2.22), Minnesota (2.40), Ohio (2.53), and Nebraska (4.19). Remaining NCR states either did not send data or it was insufficient for use with the statistical model, as many hatcheries and fish farms do not collect and keep records of data or were unwilling to share information.

A 12-week growth trial was performed at SIUC using Largemouth Bass fingerlings from four different LMB stocks picked based on results from genetic analysis. The growth trial showed no definitive correlation between growth rate and IGF I or II alleles. The growth trial did show that Largemouth Bass that came from JM Malone & Sons farm showed faster growth by weight and length as well as showing better body condition than fish from the other three sources. Malone's fingerlings finished with the most weight (68.18g) followed by Farm Cat Inc. (60.25), Logan Hollow Fish Farm (57.44), and Arkansas Pond Stockers (45.24). Based on these results Malone's fish were used for a full-scale growth trial to complete objective 3. The Malone fish were considered as the best growers in all growth parameters other than feed conversion and body condition. Although this group was viewed as vigorous eaters, there was no correlation between growth and genotype in the SIUC study.

Objective 3. — Based on results from Objectives 1 and 2, a 12-week growth trial was performed at SIUC using Largemouth Bass fingerlings from four different LMB stocks picked based on results from genetic analysis. The growth trial showed no definitive correlation between growth rate and IGF I or II alleles. The growth trial did show that Largemouth Bass that came from JM Malone & Sons farm showed faster growth by weight and length as well as showing better body condition than fish from the other three sources. Malone's fingerlings finished with the most weight (68.18g) followed by Farm Cat Inc. (60.25), Logan Hollow Fish Farm (57.44), and Arkansas Pond Stockers (45.24). Based on these results it was suggested that Malone's fish be used for a full-scale growth trial to complete objective 3. SIUC delivered ~120 identified (Malone's) LMB broodfish to Piketon aquaculture facility in June 2016. Around 60 females and 60 males from the identified group were stocked in 0.10-ha (0.25-acre) pond at Piketon, and a similar number of fish from Ohio control group were stocked in another 0.25-acre pond. In 2017, due to cannibalism in ponds only around 2,000 fingerlings from control group and 1,000 fingerlings from the identified (Malone source) group were obtained. Using these fish, OSU researchers conducted experiment to compare growth performance of the identified group vs. Ohio control group in indoor system. The fish were stocked and cultured communally in two replicate tanks. The result showed that fish from the identified group grew 80.83% faster than control group.

Principal Accomplishments

Genetic evaluation of eight strains of ~1,050 LMB in total for selective breeding and genetic improvement was completed by OSU. Genetic variation of those strains were quantified and identified the best candidate strains for the LMB aquaculture industry. Project findings strongly suggest the genetic improvement of hatchery LMB broodstock is necessary and feasible. Eight microsatellite markers have been optimized and tested as a best marker panel for identification of genetically distinct LMB populations. These results then were used to develop an experiment to compare growth performance of the identified (Malone source) group vs. Ohio control group in the indoor culture system at OSU. The fish were stocked and cultured communally in two replicate tanks. The results from this experiment showed that fish from the identified group grew 80.83% faster than control group.

Impacts

The great demand for Largemouth Bass and their high selling price and growth rate (compared to other cultured species) have raised interest in their commercial culture. Differential performance of genetic strains of Largemouth Bass is an important management consideration for both recreational fisheries and aquaculture. Therefore, strain evaluation and identified best genetically distinct Largemouth Bass populations for fast growth and the optimal source population will result in an immediate impact on the economic return of many small aquaculture operations in the North Central region. The genetic information and markers, and identified LMB strains and the optimal source populations can be used for improvement of LMB broodstock to create fast-growing lines with greater temperature resistance for the NCR,

Recommended Follow-Up Activities

The information from this project strongly suggests the genetic improvement of hatchery LMB broodstock is necessary and feasible. At the same time, eight microsatellite markers have been optimized and tested as a best marker panel for identification of genetically distinct LMB populations. In this project, we have identified the best genetically distinct LMB and the optimal source populations with the potential to exhibit rapid growth to target weight for the NCR. It is recommended that the next step is to breed and cross the best genetically distinct LMB strains and the optimal source populations identified from the above project and create fast-growing lines with greater temperature resistance for the NCR and test their performance. This will specifically address the needs identified by NCRAC to improve LMB production. Research garnered from the SIUC study indicates the role of population genetics and IGF genes to the growth and development of LMB.

Publications, Manuscripts, Workshops, and Conferences

See the Appendix for a cumulative output for all NCRAC-Funded Largemouth Bass activities.