

Annual Progress Report to NOAA: October 2010-February 2011

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Effects of Bayshore power plant on ecosystem function in Maumee Bay, western Lake Erie.

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S. Panek (MS); algal ecology

J. Pritt (PhD); larval fish ecology

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Research Technicians:

D. Murphy; Genetics

P. Bichier; Field collection of larval fish and algae

Problem Statement

Our goal is to quantify the possible impact of the Bayshore power plant (Oregon, OH) on ecosystem function of Maumee Bay, in western Lake Erie. Our specific objectives are:

1. Test whether and to what degree fish entrainment affects important species such as walleye and yellow perch.
2. Determine whether heated water from the plant promotes the growth and persistence of nuisance algae such as *Lyngbya wollei*.

During the period from March 2010-February 2011 field sampling and sample processing for both objectives has been successfully completed. Five graduate students have been partially or wholly supported as part of this project. Jeremy Pritt (PhD) and Mark Dufour (MS) worked on Objectives **1a** and **1b**. Both students were recruited specifically to work on this project and are advised by C. Mayer. Amanda Haponski (PhD) and Timothy Sullivan will work on Objective **1c**. Both are advised by C. Stepien. Sarah Panek (MS) will work on Objectives **2a** and **2b**., she is advised by T. Bridgeman.

Progress on Specific Objectives as of September 2010

1. **Test whether and to what degree fish entrainment affects important species such as walleye and yellow perch.**
 - a. **Determine what percent of larval fish exiting the Maumee River during the spring are entrained in the plant.**
 - i. **Quantify numbers of larval fish entrained at the Bayshore power plant from April to June.**
 - ii. **Quantify numbers of larval fish exiting the Maumee River from April to June.**

Sampling was conducted weekly from April through June using two methods, paired bongo nets and hydroacoustics.

Net Collection

Paired cylindrical ichthyoplankton nets with diameters of 0.5m each were fitted with flow meters and two mesh sizes (350 and 500 μm) and towed at 1 m/s. Weekly collections were made in the river and the power plant intake canal. In the river three longitudinal transects of approximately 500m were sampled, whereas 2 transects of similar length were sampled from the power plant intake canal. At all but one transect, two tows were conducted at the surface of the water and two tows were conducted at approximately mid-depth. At the final transect (in the river), only two surface tows were taken because of shallow depths. All samples were preserved in ETOH, which will allow for future genetic testing. Project personnel attended a larval fish identification workshop held at Ohio State's Stone Laboratory on June 26, 2010. All larval fish from samples have been enumerated and identified. Fish have been identified to the lowest possible taxon using morphological characteristics such as: size for developmental stage, placement of the anus, number of muscle segments, and coloration pattern as shown in Figure 1. While walleye (*Sander vitreus*) are easy to distinguish, small yellow perch (*Perca flavescence*) and logperch (*Percina caprodes*) share similar characteristics. We have consulted with John Hageman (instructor for OSU's larval fish identification workshop) and some individuals are being genetically identified (see Objective 1C). Other common taxa included *Morone* spp. (white

perch and white bass) and gizzard shad (*Dorosoma cepedianum*). These groups are easily distinguished by morphological features (Figure 1).

A total of 142,824 larval fish were counted and identified. Samples with large numbers of fish were split using a plankton splitter. The estimated total number of larval fish captured was 605,845. These included twenty species representing ten families (Table 1). Only data from the 350 μ m net are used here because these numbers were consistently higher than from the 500 μ m net. Of the most common taxonomic groups, the rate of entrainment ranged from 5.5 to 22.2% with overall entrainment at 16.2% (Table 2). The density of larval fish was calculated based on the number of fish per sample and the volume of water filtered (calculated from flow meter). Total export numbers were calculated based on the density (number/m³) of larval fish at the three transects sampled across all dates and the discharge taken from the USGS gage at Waterville,

OH. Mean values were calculated from the three transects and two depths for each date. Export for dates between samples were estimated based on linear interpolation between each time point and total export was then determined by summing export across dates. Entrainment was calculated based on density of larval fish in the water intake canal and daily water intake volumes provided by First Energy. Mean values were calculated from the two transects and two depths for each date. Entrainment through time was calculated as for export. There are multiple source of variance that contribute to our overall estimates of export and entrainment. Therefore we will continue to explore additional quantitative methods to better incorporate the variance structure of our data in to the total estimates. The methods we will examine will include a Bayesian hierarchical model that is described in greater detail under objective 1b.

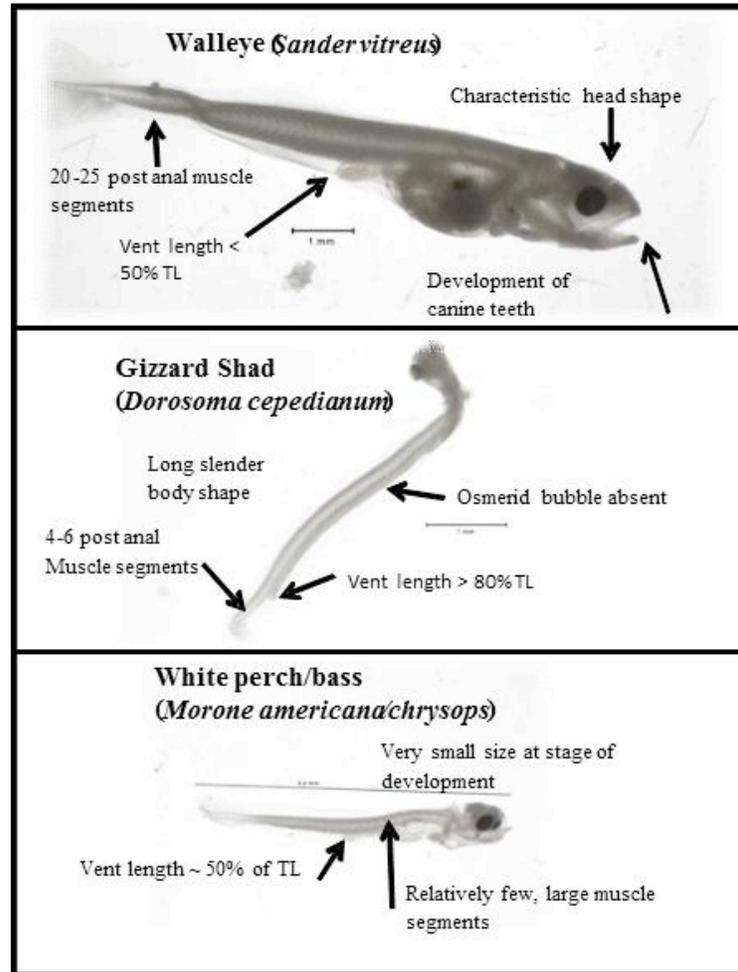


Figure 1: Photographs of three common taxa of larval fish collected from the Maumee River in April 2010 with distinguishing morphological characteristics.

Table 1. All species of larval fish captured in the Maumee River April-May 2011 .
Numbers of individuals that were sampled in the main river channel and in the intake canal of the Bayshore powerplant.

Common name	Genus	Species	Intake	River
Ictiobus spp.	Ictiobus	Ictiobus spp.	124	2757
Quillback	Carpiodes	cyprinus	180	765
White sucker	Catostomus	commersoni	5	6
Lepomis spp.	Lepomis	Lepomis spp.	30	80
Pomoxis spp.	Pomoxis	Pomoxis spp.	24	17
Rock bass	Ambloplites.	rupestris		1
Gizzard shad	Dorosoma	cepedianum	205381	118304
Cyprinidae spp.	Cyprinidae spp.	Cyprinidae spp.	1087	2529
Central stoneroller	Campostoma	anomalum	1	
Common carp	Cyprinus	carpio	18	108
Emerald shiner	Notropis	atherinoides	912	1634
Spottail shiner	Notropis	hudsonius	5	20
Round Goby	Neogobius	melanostomus	5	47
Channel catfish	ictalurus	punctatus	1	44
Morone spp.	Morone	Morone spp.	14083	23447
White bass	Morone	chrysops	28	19
Logperch	Percina	coprodes	146	611
Walleye	Sander	vitreus	133	697
Trout perch	Percopsis	omiscomaycus		1
Freshwater drum	Aplodinotus	grunniens	94693	136924
Unidentified	Unidentified	unidentified	237	741
Total			317093	288752

Table 2: Rates of entrainment for common taxonomic groups of larval fish in the Maumee River in April-June 2011.

Taxonomic Group	Exported from River	Likely Entrained	% entrained
Walleye	48.7 Million	4.1 Million	8.4%
White Bass/Perch	11.8 Billion	647 Million	5.5%
Gizzard Shad	41.9 Billion	9.3 Billion	22.2%
Total	80 Billion	12.6 Billion	16.2%

The density of larval fish did vary greatly across the season and spatially. For example, larval walleye export showed a marked peak on May 10th, with very low (undetectable) density just prior to and after this date. In contrast, gizzard shad do not experience peak export until June (Figure 2). There is also considerable variability in the depths and spatial position at which different species were found. Walleye were most abundant in the deeper portion of the main river shipping channel. They were much less dense in the shallower portion of the river that

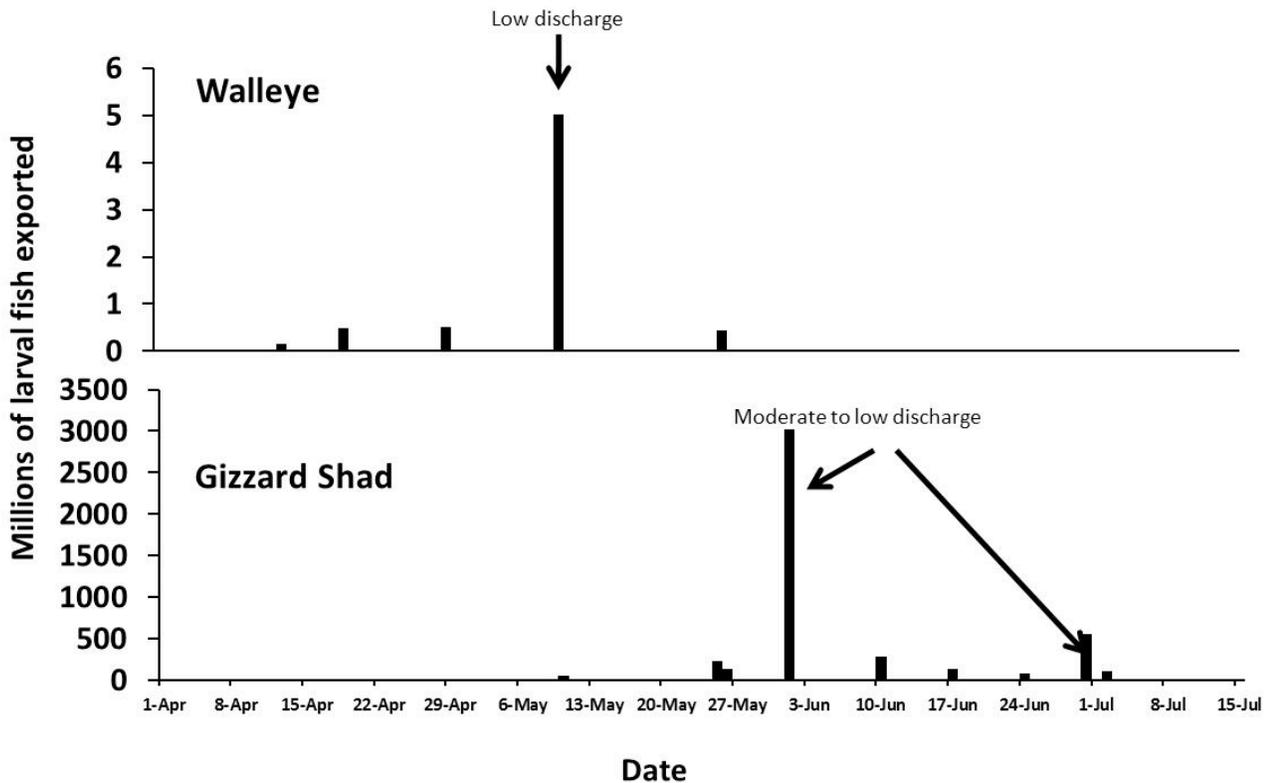


Figure 2: Export of walleye and gizzard shad from the Maumee River in 2011. Differences in peak export, with peaks and lulls shown. River flow conditions, based on USGS gauge at Waterville, OH are indicated for some dates.

passes in front of the entrance to the power plant intake canal (Figure 3). The preference of larval walleye for deeper water may therefore partially result in their being somewhat underrepresented in the larval fish entrained in the plant compared to their overall abundance. In contrast, gizzard shad were most abundant on the shallow bank of the river near the power plant intake canal entrance (Figure 3). Gizzard shad were the most abundant larval fish exported from the Maumee in 2011, comprising ~50% of total larval fish. However, they comprised ~75% of the fish entrained at the Bayshore power plant, suggesting that their spatial distribution and other factors make them highly vulnerable to entrainment. In other years sampled (Ager et al. 2007) gizzard shad were the second most entrained fish suggesting that their relative abundance was lower in those years. Our data suggest that the habitat preferences of larval fish species affects their vulnerability to entrainment other factors such as river flow are also important.

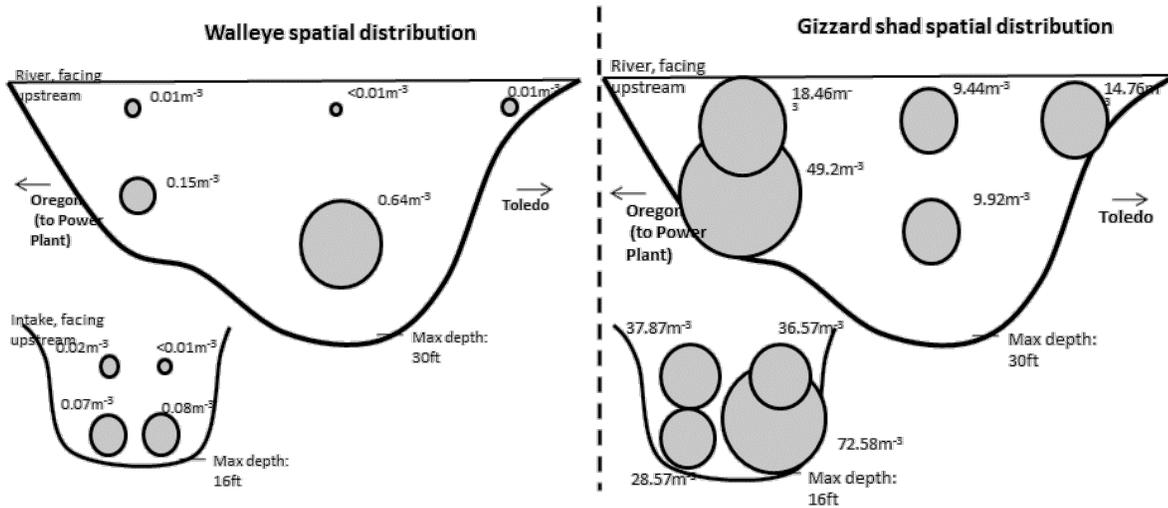


Figure 3: Spatial distribution of larval walleye and gizzard shad in the Maumee River during April-June of 2011. Circle sizes are proportional to fish density.

The proportion of Maumee River flow that was taken into the Bayshore power plant in April-June 2011 varied from 4% to 48%. The power plant took in a relatively constant volume of water during this time period, but river flow as measured at the USGS discharge gauge in Waterville, OH varied considerably as is usual for rivers in spring. The proportion of the total larval fish community that was entrained was therefore negatively, but not linearly, related to Maumee River Discharge (Figure 4). When Maumee River discharge is low, up to 35% of the total larval fish community is entrained in the plant. When discharge is high about 5% are entrained. This pattern may also be partially responsible for why gizzard shade are entrained at such a high rate. This species spawns later in the spring when river flows tend to be lower, at this time a relatively high percentage of total Maumee River flow is entering the power plant.

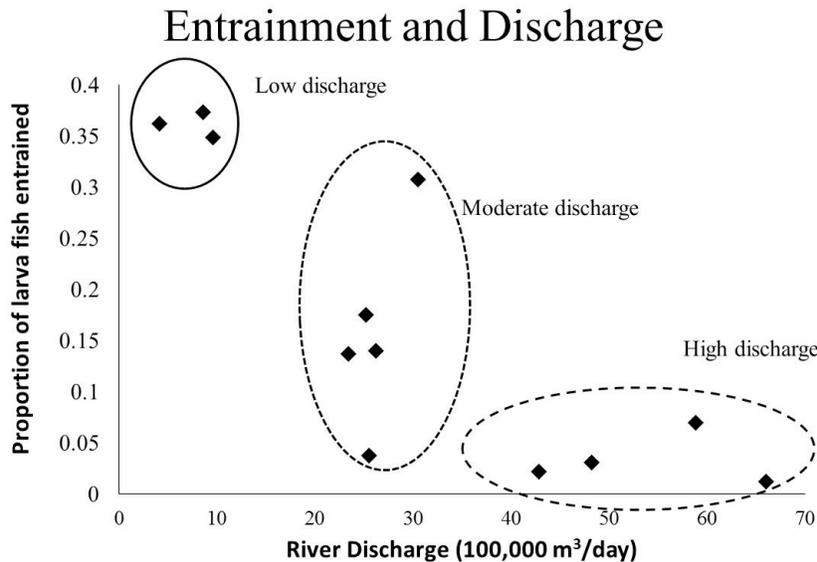


Figure 4: Relationship between Maumee River discharge and the percentage of the larval fish community entrained at the Bayshore power plant.

Existing data on the historical densities of larval fish in the Maumee River have been located and entered into an electronic format (Herdendorf et al. 1977, Paul and Patterson 1977, Snyder 1978, and Mion et al. 1998). There were differences in collection techniques that prevent direct statistical comparison, consequently we are examining peak, rather than average density to minimize the effect of different timing and intensity of sampling. It appears that peak walleye density in 2010 was higher than previous years, though still in the same range (Figure 5).

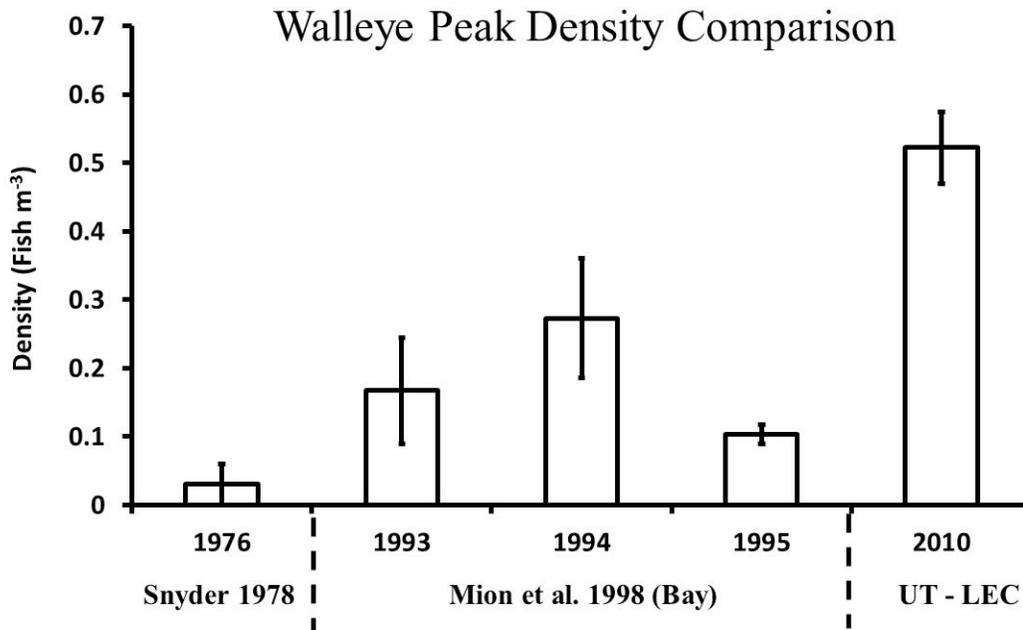


Figure 5: Mean peak density of walleye larvae in April and May in the lower Maumee River. Direct statistical comparisons were not carried out due to differences in collection methods. Error bars are +/- 1 SE.

Further we can compare our estimates of numbers of fish entrained at the plant to collections at the plant screens taken in previous years (Ruetter and Herdendorf 1977; Ager et al. 2007 and Ager et al. 2008).

Hydroacoustics

Hydroacoustic data were collected weekly using a 420kHz and a 200kHz transducer deployed from a stationary boat at two locations in the river channel and in the power plant intake canal. The 420kHz transducer was deployed sideways facing, while the 200kHz transducer was deployed downward facing. At each sampling location, data was collected for 15 to 30 minutes. Extensive field expertise on the deployment of hydroacoustics was provided by Mr. Eric Weimer, of the Ohio Department of Natural Resources, Division of Wildlife. Data files are stored as echograms from which fish density, size, and location can be estimated (Figure 6). Fish that reflect a larger amount of sound energy (seen as green and yellow in Figure 6) are large adults while those that reflect only a small amount of energy (seen as blues and black) are most likely larval and juvenile fish.

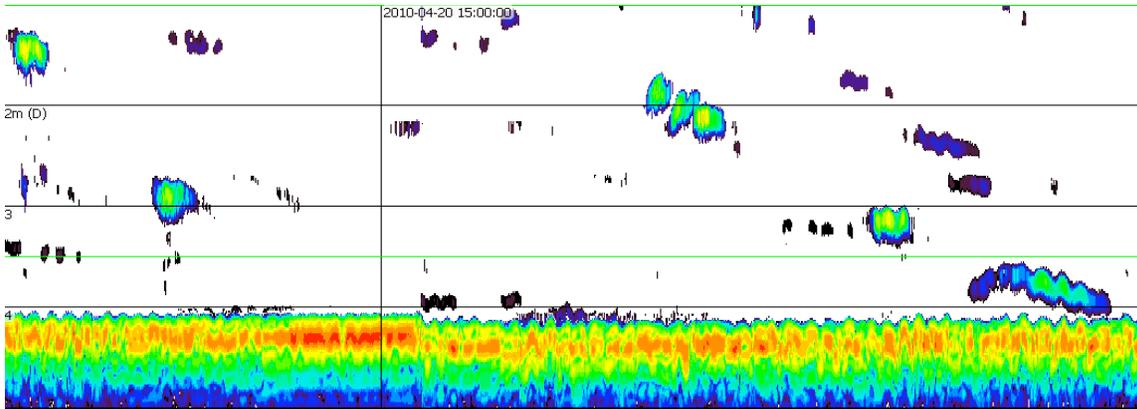


Figure 6: Echogram from the Maumee River taken on 4/20/2010 with a 200kHz downward facing transducer (display from Echoview 4)

In January 2011 J. Pritt, and M. Dufour attended training sponsored by manufacturers of the hardware (Biosonics) and software (EchoView) used for this process. It is likely that larval fish targets are distinguishable from background noise with our data, however all analyses are preliminary at this point. Based on analyses thus far hydroacoustic data suggest that proportional entrainment is similar to values seen from net estimates, however we are still in the process of determining absolute densities of larval fish in the water column.

We plan to continue stationary sampling the spring of 2011 and augment this sampling with mobile transects conducted perpendicular to the river channel. The mobile transects will allow us to capture variability in larval fish densities across the channel while the stationary collections will allow us to examine temporal variability in larval fish drift and quantify larval fish export.

b. Quantify uncertainty in estimates of numbers of larval fish exiting the Maumee River during the spring and determine how this uncertainty affects estimates of impact to the walleye population.

In order to explicitly address uncertainty associated with temporal and spatial variability we will employ a Bayesian multilevel framework (Cha et al. in press). Bayesian models yield probability distributions rather than point estimates, and therefore provide an explicit measure of uncertainty. The Bayesian multilevel approach allows us introduce uncertainty at various levels which will propagate through the model to our final estimates. Additionally, we can disaggregate seasonal data into smaller time units, each of which possesses its own properties while “borrowing” information from the entire time-series. This process, known as “partial pooling”, will increase the precision of estimates generated from records with missing data. This approach will be useful in quantifying larval fish export from the Maumee River and entrainment in the power plant as measurements of fish concentration are point estimates (e.g. weekly) whereas flow data will be continuous (e.g. hourly or daily).

This will be the focus of M. Dufour’s MS thesis. He is currently enrolled in two courses at the University of Toledo that will directly inform this work: Bayesian Methods for Ecology and Statistical Modeling. Mr. Dufour met with his research advisory committee (C. Mayer, C. Stow, E. Roseman, and J. Bossenbroek) in December of 2010 and is making good progress towards his degree.

- c. **Use high-resolution nuclear microsatellite genetic data from 15-20 loci to determine what is the proportion and overall numbers of larval walleye entrained at the Bayshore power plant of the overall stock spawning in the Maumee River, and how this relates to the overall abundance and genetic diversity of walleye in the lake and the fishery. Genetic data thus will be used to calculate the overall number of walleye spawning in the Maumee River in relation to those killed by the power plant; as well as their effective (N of breeding individuals) and overall population size, and their overall numbers in relation to those inhabiting Maumee Bay and Lake Erie overall. These data will be statistically compared with those from the direct counts (1a) and with fishery management estimates.**

Research Plan

Our research objectives are to (1) determine the proportion and overall numbers of larval walleye and yellow perch entrained and impinged at the Bay Shore power plant in relation to their overall spawning stock structure in the western basin of Lake Erie, and (2) evaluate their contribution to overall abundance and genetic diversity across Lake Erie and importance to fishery. Walleye and yellow perch are the largest Great Lakes Fisheries, and the largest numbers are found in western Lake Erie. We are analyzing 15-20 high-resolution nuclear microsatellite loci, in reference to our Lake Erie genetic data bases from 1993-present to determine the overall number of walleye and yellow perch spawning in the Maumee River/western Lake Erie region in relation to those killed by the power plant, as well as their relative effective population sizes (number of breeding individuals that contribute to the next generation), overall population sizes, and temporal and spatial variations. These data are being statistically compared with those from the direct counts and with fishery management estimates, as well as with agency life history data, tagging studies, aging studies, and historic genetic data. During this year 2 of this project, we continued collecting data on the genetic structure of walleye and yellow perch spawning groups in the western basin of Lake Erie, in comparison to other sites, and analyzed the genetic structure of larval walleye and adults from the 2010 spawning run in the Maumee River. Some of the genetic questions being investigated for walleye and yellow perch populations in this project are:

- (a) Is the genetic composition of the larval population in a given area different than that of the spawning adults? If not, does this represent selection?
- (b) Is the population genetic composition of larvae at a given location consistent throughout the spawning run?
- (c) Are genetic estimates of larval effective population size similar to the census size of larval population size estimates based on sampling tows and hydroacoustic measurements?
- (d) Is there a genetic difference in the gene pools of fish that avoid the power plant versus those that are entrained or impinged?
- (e) How do the numbers and genetic compositions of walleye and yellow perch in the western basin compare to those across the entire Lake?

Results will be disseminated through (a) top-tier peer-reviewed scientific journals (our 2009-11 papers on yellow perch and walleye are in the journals *Molecular Ecology*, *Transactions of the American Fisheries Society*, *Journal of Great Lakes Research*, *Great Lakes Fisheries Commission Special Publications*, and *Canadian Journal of Fisheries and Aquatic*

Sciences (b) scientific and management conferences (including *American Fisheries Society*, *International Association for Great Lakes Research*, *American Society of Ichthyologists and Herpetologists*, *Sigma Xi Scientific Honorary Society*, *Great Lakes Fisheries Commission Lake Erie Walleye and Yellow Perch Task Groups*, and *Ohio Fish and Wildlife Management Conference*), (c) workshops for Lake Erie State and Federal Fisheries Managers (Fisheries Genetics workshop occurred December 7, 2010; agenda below), (d) popular articles, and (e) our website (www.utoledo.edu/as/lec/fishery/index.html).

Our 2009-2011 progress includes:

Genetic structure of Lake Erie walleye

Our laboratory studies discerned that many Lake Erie walleye spawning population groups possess unique genetic signatures, distinguishing them from stocks across the other Great Lakes as well as throughout their North American range (Strange and Stepien 2007, Stepien et al. 2009, 2010). Our analyses found that most Lake Erie walleye spawning groups genetically diverge from all others ($F_{ST} = 0.018-0.063$) with the exception of a high gene flow track (less genetic divergence) found along the southern lake shore that included walleye spawning in the Maumee, Sandusky, and Grand Rivers and Van Buren Bay reefs ($F_{ST} = 0.001-0.002$; Strange and Stepien 2007). This region of genetic connectivity characterized spawning groups in 2003, which was the highest walleye recruitment year in the past decade. We thus conducted analyses of additional spawning years to determine whether this pattern is temporally and spatially consistent from year to year, across cohorts, and between the sexes. Ms. Jo Ann Banda (M.S. student) analyzed this area of apparent genetic connectivity among 726 walleye spawning in the Maumee and Sandusky Rivers, and Van Buren Bay reefs using 9 nuclear DNA microsatellite loci from 1995, 1998, 2003, 2007, and 2008. Results revealed overall year-to-year consistency in genetic structure of walleye spawning at the three sites, with some slight annual variation in the Van Buren Bay reef group. Substantial genetic divergence of the Van Buren Bay spawning group from the Maumee and Sandusky River groups reflects its geographic separation. Walleye spawning in the Sandusky and Maumee Rivers were genetically distinguishable from each other when data from all years were combined, suggesting possible sample size effect (i.e., annual sample sizes may not have been large enough to detect their genetic divergence). No significant differences were detected among age cohorts or between the sexes within spawning groups. Results demonstrated the importance of sampling over several years of walleye spawning runs in order to resolve the patterns of overall fine-scale genetic relationships within an open lake system. This study is in manuscript, and is being fine-tuned for submission.

This year, Ph.D. candidate Amanda Haponski tested whether there were genetic differences in walleye returning to spawn early versus late in a spawning run, using 74 individuals from the 2009 Sandusky River run, separated each by ~two weeks (groups of 24-25). No significant differences were discerned, indicating that the genetic diversity and genetic composition of walleye returning during the run were consistent.

Ms. Haponski also tested whether increasing the number of microsatellite loci from 9 to 16 resolved more differences among walleye spawning groups, due to increased resolution power. No significant differences in the overall patterns were discerned.

Maumee River walleye spawning runs from 2005, 2006, 2009, and 2010 were extracted and amplified for 9 loci to expand the temporal sampling realm, and the number of loci is being

increased to 14-16. Ms. Haponski obtained 2010 walleye larvae from the Maumee River to test, using the collections identified by Ph.D. student Mr. Jeremy Pritt. The genetic composition of the larval walleye was compared with that of the adult spawners to address question (a) above. Results showed that walleye larvae sampled on April 19, 2010 significantly differed from adults sampled on April 15. However, larvae sampled on May 10, 2010 genetically matched the April 15 adults, which had spawned ~20 days before. The two larval walleye spawning peaks were statistically similar in genetic composition to one another, addressing question (b).

Genetic structure of western basin Lake Erie yellow perch

Our laboratory has analyzed a large data set of yellow perch spawning sites in Lake Erie, in comparison to variation across the Great Lakes and North America using 15 nuclear microsatellite loci (Sepulveda-Villet and Stepien, in review). We now further are evaluating patterns of genetic consistency versus variation among spawning locations, years, and age cohorts in the western Lake Erie basin. Recently, we compared results from the western Lake Erie spawning group at Monroe MI from 2004 and 2009. Results will serve as a point of comparison for larval yellow perch samples entrained in the Bay Shore Power Plant, and may help to determine possible effect on recruitment into the adult population in western Lake Erie. Preliminary results indicate slight heterozygote deficiency and possibly low levels of inbreeding ($F_{IS}=.113$) for individuals in 2004, whereas those for 2009 suggest slight heterozygote excess ($F_{IS}=-.151$). The genetic composition of yellow perch spawning at Monroe significantly differed between the two years ($F_{ST}=0.026$, $p=0.0001$). However, the overall spatial genetic relationships among spawning groups appeared consistent, i.e., the differences among sites were greater than the annual variation within a given sites (average $F_{ST} = 0.042$). This result was supported by Analysis of Molecular Variance (AMOVA) testing, which indicated that while temporal variation explained 2.17% of the total genetic variation in Lake Erie spawning groups ($p=0.008$), spatial variation explained 3.65% of this variation and was a stronger influence ($p<0.0001$). Results of Barrier analysis for both 2001-2004 and 2009 indicate a consistent barrier to genetic continuity, differentiating yellow perch spawning at the western basin site of Monroe MI from all other Lake Erie spawning groups. These patterns are being further investigated.

Larval Fish Identification

Unknown samples of percid fish larvae were collected by Ph.D. student Jeremy Pritt and identified to the best of his ability and then confirmed by John Hageman of Ohio State University's Stone Laboratory. Eight putative walleye were tested by M.S. student Tim Sullivan for a single nuclear microsatellite locus (*Svi 33*) to confirm that they were walleye. The comparisons were run against a large genetic microsatellite data base developed by the UT LEC GLGL to assess population genetic variation, stock structure, and patterns in walleye, yellow perch, and other percid fishes (see Stepien et al. 2009, 2010, Sepulveda-Villet et al. 2009, Sepulveda-Villet and Stepien, in review, for recent publications). Mr. Sullivan then tested 16 other unknown percid samples to determine their possible species identity. Those did not match yellow perch or walleye, and may have been log perch, which is being further tested using mtDNA sequences.

GLGL Laboratory publications for 2009-2011 providing background data to the current project on walleye and yellow perch population genetics in Lake Erie:

bold=GLGL personnel, *GLGL students

1. “Interplay among phenotypic plasticity, ecological habitat, and population genetics in young yellow perch” by A.D. Parker, **C.A. Stepien, O.J. Sepulveda-Villet**, C.B. Ruehl, and D.J. Uzarski. 2009. *Transactions of the American Fisheries Society*, 138: 899-914. doi: 10.1577/T08-093.1. (We did the genetics for this ecological study led by Grand Valley State University).
2. “Genetic and biogeographic structure of yellow perch (*Perca flavescens*)” by **O.J. Sepulveda-Villet***, **A.M. Ford***, J. Williams, and **C.A. Stepien**. 2009. *Journal of Great Lakes Research*, 35(2): 107-119. doi:10.1016/j.jglr.2008.11.009.
3. “Signatures of vicariance, postglacial dispersal, and spawning philopatry: Population genetics of the walleye *Sander vitreus*” by **C. Stepien, R. Lohner, D. Murphy, O.J. Sepulveda-Villet***, and **A. Haponski***. 2009. *Molecular Ecology*. 18:3411-3428. doi: 10.1111/j.1365-294X.2009.04291.x
4. “Genetic variation of 17 wild yellow perch populations from the Midwest and East coastal United States using microsatellites”. By M. Grzybowski, **O.J. Sepulveda-Villet***, **C.A. Stepien**, D. Rosauer, F. Binkowski, R. Klaper, B. Shepherd, and F. Goetz. 2009. *Transactions of the American Fisheries Society*. 139:270-287. doi: 10.1577/T07-276.1 (Stepien and student Sepulveda-Villet did all genetic analyses, did all figures, and rewrote to supply most narrative about genetic results and discussion).
5. “Status and delineation of walleye genetic stocks across the Great Lakes”. 2010. by **C. A. Stepien, R. Lohner, D. Murphy, A. Haponski, and O.J. Sepulveda-Villet**. In: Status of walleye in the Great Lakes: Proceedings of the 2006 Symposium. (Ed.: E. Roseman, P. Kocovsky, and C. Vandergoot). *Great Lakes Fishery Commission Technical Report* 69: 189-223.
6. “Fine-scale population genetic structure of Lake Erie yellow perch *Perca flavescens*: Any relation to management units?” by **O.J. Sepulveda-Villet*** and **C.A. Stepien**. *In re-review. Canadian Journal of Fisheries and Aquatic Sciences*.

GLGL Laboratory presentations for funding period August 2009- March 2011 related to the current project on walleye and yellow perch population genetics in Lake Erie:

bold=GLGL personnel, *GLGL students

1. *Sigma Xi Scholar’s Celebration Student Research Symposium: Toledo OH*. “Genetic structure of Lake Erie yellow perch: A landscape genetic approach to test management unit congruency” by **O.J. Sepulveda-Villet*** & **C. Stepien**. Oral. 10-24-09.
2. *Ohio Fish and Wildlife Managers Association (OFWMA)*: “Population genetic basis for Lake

Erie yellow perch stock structure and Management Units” by **O. Sepulveda-Villet*** & **C. Stepien**. Poster. 2-8-10.

3. *OFWMA*: “A temporal analysis of genetic connectivity and divergence among Lake Erie walleye spawning groups” by **J. Banda*** & **C. Stepien**. Poster. 2-8-10.

4. *OFWMA*: “Spatial and temporal genetic patterns of Lake Erie yellow perch” by **A. Haponski***, **O. Sepulveda-Villet*** & **C. Stepien**. Poster. 2-8-10.

5. *Great Lakes Fishery Commission Lake Erie Walleye and Yellow Perch Task Groups* “What DNA tells us about walleye and yellow perch in Lake Erie” by **C. Stepien**, **O.J. Sepulveda-Villet***, **A. Haponski***, & **J. Banda***. Oral. 2-23-10.

6. *Lake Erie Millennium Conference*: “Population genetic basis for Lake Erie yellow perch stock structure and Management Units” by **O. Sepulveda-Villet*** & **C. Stepien**. Poster. 4-27-10.

7. *Lake Erie Millennium*: “Temporal and spatial patterns of genetic connectivity and divergence among Lake Erie walleye (*Sander vitreus*) spawning groups” by **J. Banda***, **A. Haponski***, & **C. Stepien**. Poster. 4-27-10.

8. *American Fisheries Society (AFS)*: “Fine-scale population genetic structure of Lake Erie yellow perch *Perca flavescens*: Any relation to management units?” by **O.J. Sepulveda-Villet*** & **C. Stepien**. Poster. 9-10.

9. *AFS*: “Temporal & spatial connectivity & divergence among river & reef spawning groups of walleye: Patterns across 15 years” by **C. Stepien**, **J. Banda***, **D. Murphy**, & **A. Haponski***. Oral. 9-10.

10. *M.S. Thesis defense*, Department of Environmental Sciences. “ Temporal and spatial genetic consistency of walleye (*Sander vitreus*) spawning groups”, by **J. Banda***. Oral. 1-4-11.

11. *Ohio State Research Review* Columbus, OH: “Fine-scale population genetic structure of Lake Erie yellow perch *Perca flavescens*”, **T. Sullivan***, **O.J. Sepulveda-Villet***, & **C. Stepien**. Oral. 1-20-11.

12. *Ohio State Research Review*: “The genetics of walleye Spawning in Lake Erie: Temporal & spatial patterns”, by **A. Haponski***, **J. Banda***, **D. Murphy**, & **C. Stepien**. Oral. 1-20-11.

13. *Ohio Fish and Wildlife Management Association*: “Spatial and temporal variation of Lake Erie yellow perch (*Perca flavescens*) spawning groups”, **T. Sullivan***, **O.J. Sepulveda-Villet***, **A. Haponski***, & **C. Stepien**. Poster. 2-4-11.

14. *OFWMA*: “The genetics of walleye spawning in Lake Erie: Temporal & spatial patterns”. **A. Haponski***, **J. Banda***, **D. Murphy**, & **C. Stepien**. Oral. 2-4-11.

2. Determine whether heated water from the plant promotes the growth and persistence of nuisance algae such as *Lyngbya wollei*.

a. Describe the distribution of *Lyngbya wollei* growth in the vicinity of the thermal plume and a reference location.

Sampling for benthic nuisance algae, primarily *Lyngbya wollei*, was conducted in August 2010. Preliminary data collected in August 2009 as part of an Environmental Protection Agency-funded project (T. Bridgeman, PI) have provided baseline data on the distribution of *Lyngbya*. In 2009 *Lyngbya* biomass immediately in front of the Bayshore power plant was low, however biomass did increase directly to the east of the Bayshore plant and this area is influence by the thermal discharge. In 2010 samples were collected from a larger number of sites and the distribution of sites where *Lyngbya* was present were similar to 2009 (Figure 7). About 70% of the 2010 samples have been dried and are being weighed, the rest will be complete in the spring of 2011. Presence/ absence data indicate that *Lyngbya* is wide spread along the western margin of the basin and is again abundant near the Luna Pier and Monroe power plants. There is no indication that *Lyngbya* presence is related to summer, when water temperatures are uniformly high across the basin (Figure 7).

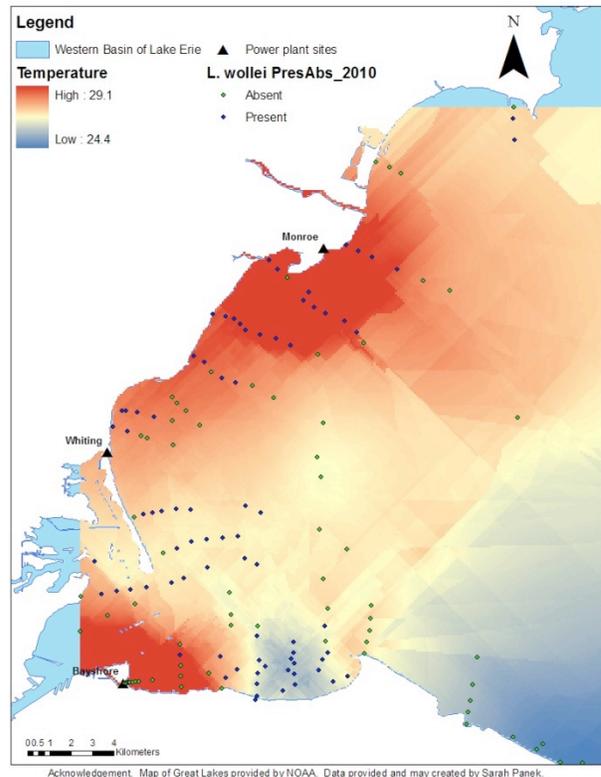


Figure 7: Distribution *Lyngbya* (presence/absence) in the summer of 2010 in western Lake Erie.



Figure 8: *Lyngbya* collected through the ice in winter 2011 in western Lake Erie.

However, it is possible that *Lyngbya* may be affected by temperature

during the winter, when warmer water or lack of shading ice may promote growth. *Lyngbya* samples were collected on February 24, March 1, and March 2 2011 through the ice in locations that, based on the remote-sensing data (ASTER - Advanced Spaceborne Thermal Emission and Reflection Radiometer) are within the thermal influence of the Bayshore and Monroe power plants. *Lyngbya* found at all winter locations appeared to be in a state of partial decay (Figure 8)

with samples near the Michigan shoreline healthier than along the Ohio shoreline. Photosynthesis measurements were made using a PAM fluorometer at each site. Little to no

photosynthetic activity was detected from *Lyngbya* along the Ohio shoreline. Along the Michigan shoreline, photosynthetic activity was detected in *Lyngbya*, but photosynthetic rates were 4 to 5 times lower than during summer months.

- b. Compare environmental variables such as temperature, nutrient availability and substrate type to biomass of *Lyngbya wollei* to determine if algal growth is correlated to these variables.**

A survey of *Lyngbya wollei* in 2008 (Bridgeman and Penamon 2010) suggested that the distribution of *L. wollei* in western Lake Erie may be influenced by water depth and available light and substrate type. Samples and data associated with the summer 2010 surveys including ambient nutrient concentrations, water depth, temperature, benthic light levels, and sediment type are currently under analyses and will be available by the next report. *Lyngbya* photosynthetic activity across a range of temperatures is also being measured in controlled laboratory trials.

Work Plan

We are on schedule with the proposed work plan (see below) as described for each of the specific project objectives.

Task	Fall/Winter 2009/2010	Spring 2010	Summer 2010	Fall/Winter 2010/2011	Spring 2011	Summer 2011	Fall/Winter 2011/2012	Spring 2012
Examine existing data	Ongoing							
Prepare larval fish sampling gear	Complete							
Install acoustic gear & Sample larval fish weekly		Complete			Ongoing			
Process larval fish samples			Complete	Complete		X	X	
Process and analyze hydroacoustic data			Ongoing	Ongoing	X	X	X	X
Analyze genetic data			Ongoing	Ongoing		X	X	
Sample <i>Lyngbya</i>			Complete	Complete		X		
Process <i>Lyngbya</i> samples				Ongoing			X	
Manuscript preparation and submission				Data analysis underway	X	X	X	X
Conference presentations					X	X	X	X

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