

## SEA GRANT PROJECT SUMMARY FORM (90-2)

**TITLE:** Stock structure and contribution of west and east basin walleye to recreational and commercial fisheries in Lake Erie

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**AFFILIATION:** The Ohio State University

**EFFORT:** 1.6 month

**ASSOCIATE INVESTIGATOR:** Wesley A. Larson (co-leader)

**AFFILIATION:** U.S. Geological Survey Wisconsin Cooperative Fishery Research Unit

**EFFORT:** 0 months

**ASSOCIATE INVESTIGATOR:** Kuan-Yu Chen

**AFFILIATION:** The Ohio State University

**EFFORT:** 0 months

**ASSOCIATE INVESTIGATOR:** Jason M. Robinson

**AFFILIATION:** New York State Department of Environmental Conservation

**EFFORT:** 0 months

**ASSOCIATE INVESTIGATOR:** Matthew D. Faust

**AFFILIATION:** Ohio Department of Natural Resources-Division of Wildlife

**EFFORT:** 0.50 months

**ASSOCIATE INVESTIGATOR:** Thomas M. MacDougall

**AFFILIATION:** Ontario Ministry of Natural Resources & Forestry

**EFFORT:** 0 months

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**AFFILIATION:** Ontario Ministry of Natural Resources & Forestry / Trent University

**EFFORT:** 0.75 months

**ASSOCIATE INVESTIGATOR:** Michael G. Sovic

**AFFILIATION:** The Ohio State University

**EFFORT:** 0 months

**ASSOCIATE INVESTIGATOR:** Elizabeth A. Marschall

**AFFILIATION:** The Ohio State University

**EFFORT:** 0.5 months

**SEA GRANT FUNDS:**

**STATE MATCHING FUNDS:**

**PASS-THROUGH FUNDS:**

**PROJECT NUMBER:**

**SEA GRANT STRATEGIC PLAN CLASSIFICATION:**

**KEYWORDS:** Lake Erie, walleye, *Sander vitreus*, stock discrimination, mixed stock analysis, fisheries management

**OBJECTIVES:** (1) *To develop a reliable molecular toolkit to discriminate between west and east basin walleye spawning stocks.* (2) *To use this toolkit to quantify the contributions from both basins to recreational and commercial fisheries in eastern Lake Erie.*

**METHODOLOGY:** To achieve our project objectives, we will use and expand state-of-the-art molecular approaches, and utilize walleye (*Sander vitreus*) collected by partner agencies from Lake Erie spawning groups and fisheries.

**Objective 1.** To obtain a panel of genomic markers (single nucleotide polymorphisms; SNPs) that can reliably discriminate between west and east basin spawning groups, we will build upon prior genomic sequencing work where thousands of SNP loci were screened for their ability to discriminate among western Lake Erie walleye stocks<sup>1</sup> (see below). Specifically, we will bolster sample sizes for previously studied stocks, add new spawning stocks from both basins, and quantify variation in basin-specific genetic signatures. We will improve the efficiency and reduce the expense of our previous genomic methodology by using Restriction-site Associated DNA (RAD) Capture (i.e., Rapture<sup>2</sup>) This modification of the RAD sequencing (RAD-seq) method that we previously used would be novel to the Great Lakes basin, and has potential to benefit ongoing and future stock discrimination efforts in Lake Erie and elsewhere. We will use RAD-seq to develop reference genetic signatures that can discriminate between basins, using fin clips taken from walleye spawning areas in the west basin (Maumee River [MR], Sandusky River [SR], and Ohio reef complex [REEFS], OH; and Detroit River, MI) and east basin (i.e., Van Buren Bay, Cattaraugus Creek, Shorehaven Reef, Lackawanna Shore, NY; and Grand River, ON) in 2017. In-kind sampling contributions by partner agencies (ODNR-DOW, NYSDEC, OMNRF) captured 13-100 fish per spawning area. We will also include samples collected from three west basin stocks (MR, SR, REEFS) during spring 2001<sup>3</sup> and 2012-2013<sup>1</sup> to verify temporal stability of their genetic signatures. DNA libraries will be prepared at OSU and sequenced using an Illumina HiSeq 2500 at OSU's Genomics Shared Resource. Bioinformatic analyses will be performed in AftRAD<sup>4</sup>, and basin-specific genetic signatures will be assessed using *assignPOP*<sup>5</sup>.

**Objective 2.** We will use *assignPOP* to determine the origin(s) (west vs. east basin) of individuals harvested in eastern Lake Erie's recreational fishery (NY waters) and commercial fishery (ON waters). Fin clips were taken from

recreational anglers in NY waters by NYSDEC creel clerks, whereas fin clips were taken from commercial gillnetters at fish processing houses in Ontario by the OMNRF. We budgeted to process a total of 600 fish (spanning both fisheries during both years), which would allow us to conduct Rapture genotyping on ~30 individuals/month/fishery. These analyses will allow us to determine within- and between-year temporal variability in contributions of both basins to eastern Lake Erie's fisheries, which currently remains an important information gap (see **Support Letters**).

**RATIONALE:** Identification of stock structure and use of this information to determine the natal origins of recruits and harvested individuals are central goals of fisheries management. Tools to achieve these goals can help agencies with stock assessment and harvest decision-making, provide a better understanding of population dynamics, and help prioritize management objectives<sup>6,7</sup>.

Walleye is an ecologically and economically important species that has been the focus of previous stock discrimination research, especially in Lake Erie<sup>1,3,8-10</sup>. ***Discriminating among stocks and determining their relative contributions to fisheries would support several management information needs.*** Although unquantified, Lake Erie's walleye population is thought to be supported by multiple stocks that spawn in all three lake basins<sup>11-14</sup>. While also unquantified, recent high variation in walleye recruitment to the fishery<sup>15</sup> is thought to be associated with differential production and vulnerabilities of these stocks to fishing, and other human stressors<sup>16,17</sup>. In recent years, fishery harvest dynamics have been shifting, with westerly stocks underperforming relative to easterly ones (S. Ludsins, unpubl. data); these shifts might link to alteration of habitat quality due to climate change but the mechanisms are not well understood.

***Our ability to discriminate among walleye spawning stocks, and to determine their relative stock contributions, has been limited.*** Several approaches, including artificial and natural tags<sup>8,12,14,19</sup> have provided insights into walleye movement patterns, behavior, and stock structure. However, none of these approaches have successfully quantified stock contributions to Lake Erie's fisheries. As a result, the stock-specific management that has been advocated by researchers<sup>19</sup>, and sought by Lake Erie agencies (see **Support Letters**) has been challenging to implement.

These ***information gaps*** underlie the ***central objectives*** of our study: (1) To develop a reliable molecular toolkit to discriminate between west and east basin walleye spawning stocks. (2) To use this toolkit to quantify the contributions from both basins to recreational and commercial fisheries in eastern Lake Erie. By marrying the results from our proposed monthly mixed-stock analyses of fisheries harvest with seasonal movement and population distribution information from ongoing agency assessment activities, as well as related Great Lakes Fishery Commission research studies involving several project PIs (Ludsins, Faust, and Robinson), we will be able to test our ***central hypothesis*** that the east basin fisheries are primarily supported by walleye that originated in the west basin (i.e., they are not produced locally). This understanding would be of great interest to Lake Erie agencies and the Lake Erie Percid Management Advisory Group, which need to review the current Walleye Management Plan during 2020.

Walleye fisheries in Lake Erie are presently divided into five management units and the recommended harvest quotas are estimated only for the west and central basins. Understanding relative contributions of east and west stocks to the eastern fisheries is an identified key management need<sup>18</sup>, the lack of which is currently preventing accurate assessment and thus confident quota setting. Previous studies showed that walleye residing in the east basin are a mixture of east and west basin stocks<sup>20,21</sup>. To quantify the relative contributions of east and west basin stocks to Lake Erie's fisheries, a panel of informative markers is needed to assign individuals of unknown origins to their source basin(s).

Previous studies using a variety of genetic markers, including mtDNA and microsatellites, and our data using SNPs, have demonstrated that significant structure exists between the east basin and west basin stocks, whereas stock structure within the west basin is unclear<sup>1,13,14,22</sup> despite strong natal site fidelity in river spawning stocks<sup>1,10</sup>. Analyses based on microsatellite data, however, have not been reliable, generating inconsistent interpretations between some of the east and west basin stocks<sup>3,14,22</sup>. By contrast, we achieved high assignment accuracy (up to 100%) for the Van Buren Bay stock using a 'machine learning' classification model built from the independent training dataset based on several thousand SNP loci (K. Chen et al., unpubl. data). While informative walleye SNP loci have been identified and the statistical approach to perform mixed stock analyses has been developed, it remains unclear whether the same panel of SNP loci can be used to discern other east basin stocks (Cattaraugus Creek, Shorehaven Reef, Lackawanna Shore, NY; Grand River, ON) from the west basin stocks. Toward this end, we will process and sequence samples collected from both east and west basin stocks and identify a panel of informative SNP loci for discriminating stocks within and between the two basins (**Obj. 1**), and use these to quantify stock contributions to east basin fisheries (**Obj. 2**).

Cuellar-Pinzón et al.<sup>23</sup> suggested that RAD-seq holds more promise for stock discrimination than any other molecular approach. Our preliminary findings suggest this method holds promise for discriminating between the east and west basins, with finer-scale discrimination also a possibility (K. Chen et al., unpubl. data). The value of using RAD-seq is heightened by Rapture methodology<sup>2</sup>. It enables creation of a targeted SNP panel for stock discrimination that is based on RAD-seq markers, reducing the time and money needed to sequence thousands of SNP loci in individuals.

By quantifying the contributions of east and west basin stocks to fisheries, which is a direct charge to the Walleye Task Group<sup>18</sup>, our results will help inform collaborative management policies and harvest allocations among Lake Erie management agencies. Establishing a suite of informative genetic markers will also enable future studies, such as mapping stock contributions to population structure and fisheries across space and time, tracking juvenile movements and habitat use, and reconstructing the population dynamics and demographic structure of the different stocks. We will present our findings in GLFC, LEC, and other scientific meetings, as well as publish one or more manuscripts in peer-reviewed scientific journals. We will also disseminate our findings to the public through meetings such as OSU's Museum of Biological Diversity Open House and Ohio Charter Captains Conference, and train multiple undergraduate students in genetics processing and data analyses.

## References

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